

Linkage Map of *Escherichia coli* K-12, Edition 8†

BARBARA J. BACHMANN

Department of Biology, Yale University, New Haven, Connecticut 06511-7444

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INTRODUCTION

This edition of the linkage map is based on the experimental literature from July 1982 through June 1988, on personal communications received during that period or received in response to questions asked during the preparation of the map, and on the literature cited in previous editions of the map. The positions of 1,403 loci are shown in Fig. 1. About 400 new genes have been added in this edition of the map, and a few loci have been removed, either because they were shown to be identical to other loci on the map or because their existence could not be confirmed. The genes included in the map are listed alphabetically in Table 1 with their map positions and functions.

It must be emphasized that these reviews of the linkage data are intended to serve as guides to the literature and not as a substitute for consulting the original research papers. The present map (Fig. 1) is based on data that vary widely in precision, and some map positions are compromises based on contradictory data. Obviously, it is not possible to discuss each of these problems in detail in this review.

All of the literature citations in previous editions of the map (43, 45, 46) can be found in the reprinting of map edition 7 which is included in the comprehensive two-volume review of the cellular and molecular biology of *Escherichia coli* and *Salmonella typhimurium* which was published in 1987 (44).

† A limited supply of the following will be available from ASM: reprints of this article and wall charts (ca. 21 × 24 1/2") of the *E. coli* linkage map. Shipped together in a mailing tube. \$10.50, U.S. and Canada; \$12.50, foreign (surface). Prices are subject to change without notice. All orders must be accompanied by payment in U.S. dollars, drawn on a U.S. bank located within the continental United States, or charged to MasterCard, VISA, or American Express. ASM does not accept wire transfers. Charge card orders may be placed by telephone (202-737-3600) or by fax (202-737-0368). Mail orders should be addressed to: American Society for Microbiology, Publication Sales, 1325 Massachusetts Ave., N.W., Washington, DC 20005-4171.

MAP UNITS

The basic units of the linkage map as drawn in Fig. 1 are still minutes, as determined by time of entry of markers in interrupted conjugation experiments (46). In the 1983 map (43), the entire linkage group was linked by cotransduction data for the first time. Many small regions had been studied in fine detail by restriction mapping and sequencing, and the distances between many loci had been determined in kilobases of DNA.

Since 1983, restriction maps of the *E. coli* chromosome have been produced (584, 1021), and one of these has now been completed to give a physical map of the entire genome (577, 578, 584). Unfortunately, the source of the DNA used in constructing the physical map was strain W3110 (584), which carries an inversion of around 19% of the chromosome. However, the exact endpoints of this inversion have now been determined, and the small gaps in the original restriction map have been closed (577, 578, 587). According to this map, the chromosome comprises 4,750 kilobase pairs (kb) of DNA.

In this edition of the linkage map, I have used the time-of-entry map as a framework, except for the region between the *his* operon and *gyrA*, for which the conjugational and transductional data have been contradictory in the past. Cotransduction data have been converted to map units as described in previous editions of the map, assuming that bacteriophage P1 brings in effectively approximately 2 min of DNA. In converting cotransductional, restriction, and sequencing data into map units, I have assumed that 1 min corresponds to 47.5 kb.

NOMENCLATURE

The system of nomenclature used in this edition of the map is that of Demerec et al. (268), with modifications as discussed in previous editions. The assignment of gene symbols is coordinated by the *E. coli* Genetic Stock Center and the *Salmonella* Genetic Stock Center, in an effort to

avoid the assignment of the same gene symbol to two different genes or the assignment of different gene symbols to genes that are homologous in the two organisms. Allele number assignments are also coordinated by the two stock centers (959). It is important that each mutation be assigned a unique allele number so that it can be recognized in any strain in which it is found. This applies to transposon insertions not in known genes and to deletions as well as to point mutations.

The cumbersome and disparate nomenclatures for the genes affecting flagellar structure and function in *E. coli* and *S. typhimurium* have been revised and brought into agreement by Iino et al. (504), and their proposed uniform nomenclature has been adopted in this edition of the map.

Modifications to the nomenclature for the often duplicated and/or tandemly repeated tRNA genes have been proposed by Fournier and Ozeki (341) and adopted in this edition.

A new convention has been adopted for the loci involved in the termination of replication (267, 343, 460, 463–465, 842) and for a set of repetitive sequences responsible for duplications in the chromosome (652, 944), since these loci do not fit the classical definition of a gene. These loci are being designated *TerA*, *TerB*, etc., and *RhsA*, *RhsB*, etc., respectively. The symbols are italicized but the first letter is capitalized, which should serve to distinguish them from the symbols for genes, gene products, or phenotypes.

The numerous members of the family of dispersed repetitive extragenic palindromic sequences, called P.U.S. or REPS (73, 378), informally, have not been included in this review.

The designations of two genes (*bglC* and *bglS*) in the *bgl* operon at 84 min have been changed to *bglG* and *bglF*, respectively. When it was discovered that the gene coding for β -glucoside transport (*bglC*) is the second gene in the operon and that the positive regulatory gene (*bglS*) is the first gene, rather than the reverse as had been thought previously, the designations for the genes with these two functions were switched, rather than switching the gene order on the map (685, 973). In the hope of preventing confusion about the function affected in mutants isolated before this switch occurred, the designations of these two genes have been changed.

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.

COMMENTS ON THE MAP

0 to 10 min. The locus *arl* has been removed from the map at 2 min because its presence could not be verified (449; J. B. Hayes, personal communication). In the 8-min region, the nucleotide sequence of one end of the hybridization loop of DNA (showing no homology to *S. typhimurium*) which contains the *lac* operon has been determined (159). A sequence similar to sequences shown to be involved in site-specific recombination was identified at or near the junction of the loop with homologous DNA. The 6- to 8-min region is noted for a comparatively high frequency of formation of deletions and inversions.

10 to 20 min. Efforts to confirm the existence of the *minA* gene at 10 min have failed (253). This locus has been removed from the map.

20 to 30 min. The *capS* mutants have apparently been lost (A. Markovitz, personal communication). This locus has been removed from the map at approximately 23 min. The *chlF* mutant has also been lost (J. DeMoss, personal communication), and this locus has been removed from the map at approximately 27 min. Efforts to confirm the existence of the *aroT* locus at 28 min have failed, and there are no mutants, so this marker, too, has been removed from the map.

30 to 40 min. The once mysterious region including the "terminus of replication" is now one of the most intensively studied regions of the map (34, 43, 79). The nature of the terminus region is now quite different from the concept held in 1983 (267, 343, 460, 463–465, 832). The *terC* gene has been removed from the map and replaced by four *Ter* loci.

40 to 50 min. The *aspV* locus was placed at 43 min in error (H. Ozeki, personal communication) and has now been removed. The symbol *aspV* has been reassigned to the asparaginyl tRNA¹ gene at 5.1 min. There is now general agreement on the order of the loci in the *his-gyrA* region, although the precise reasons for the previous contradictory data have not been determined (736). It is still possible that the length and orientation of part of this region are not the same in all of the strains used in earlier mapping studies. In the 1983 map (43) the length of this interval was 4.3 min. Recent cotransduction data confirm this length, which is about 1 min less than that suggested by the physical map (584).

50 to 60 min. The strains described as carrying mutations at the loci *nirE* at 50 min and *nirF* at 53 min have been shown to have normal nitrate reductase activity (680). These loci have been removed from the map. The existence of the *pfkC* locus is very doubtful (D. Fraenkel, personal communication), and it has been removed from the map.

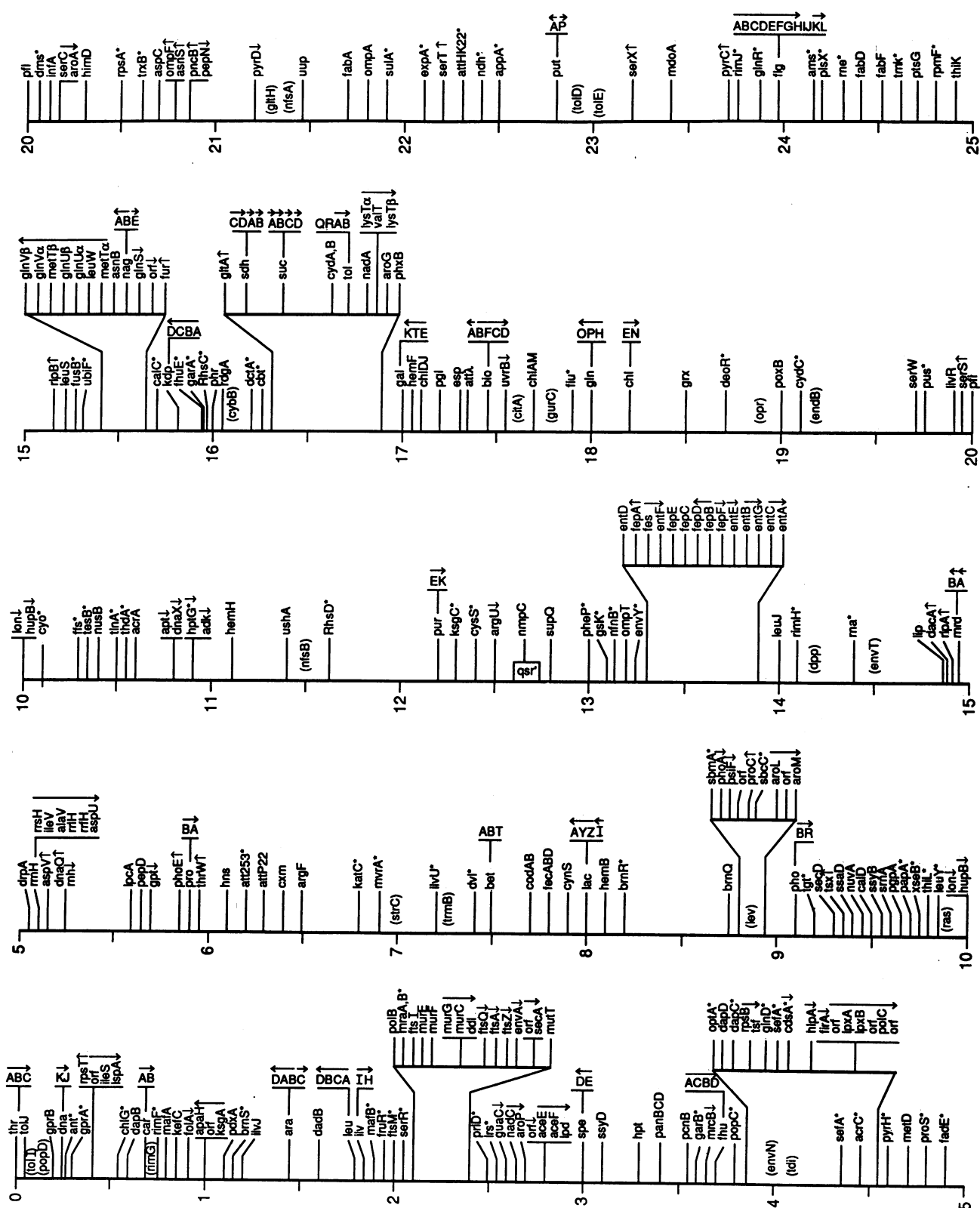
60 to 70 min. The locus *kpsA* should not have been placed on the map, since the *kps* genes do not exist in *E. coli* K-12. This locus has been removed from the map.

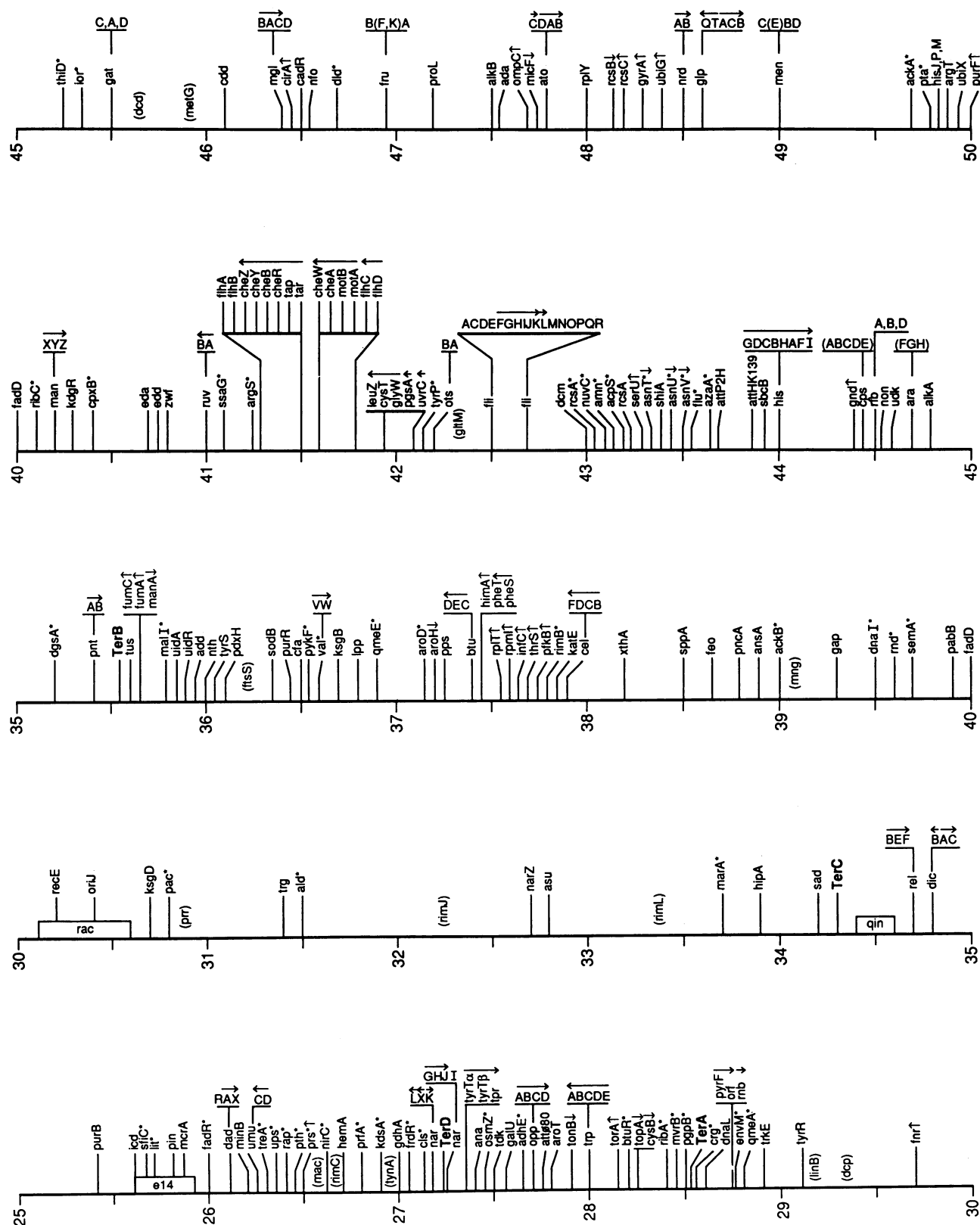
80 to 90 min. In constructing a physical and genetic map of the *ilv-metE* region, Aldea et al. (14) found the length of this region to be about 1.2 min, whereas the physical map of Kohara et al. (584) suggests a distance of about 1.1 min. The length of this region was shown as 0.9 min in the 1983 map (43). These authors devised a new formula for converting cotransduction frequencies to map distance in order to account for these discrepancies. Analysis of all data available gives a length of 1.3 min in my hands, as shown in Fig. 1.

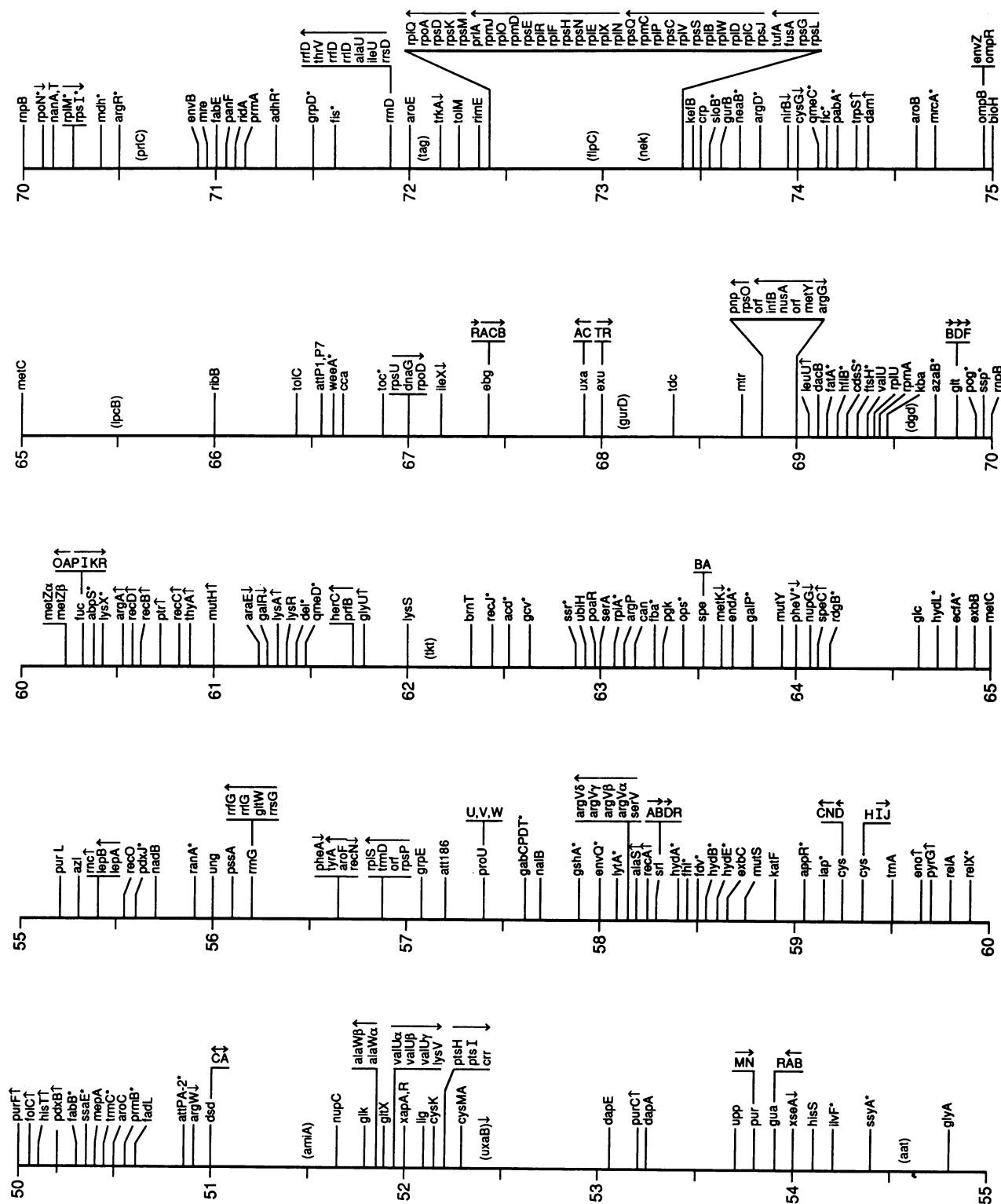
The *dnaP* mutant has been shown to carry a *dnaG* mutation (765), and a second mutation conferring temperature sensitivity could not be found in the strain (T. Yura, personal communication). The *dnaP* locus has been removed from the map at 85 min.

90 to 100 min. There is some uncertainty about the order of genes in the region between the *malB* operon and *uvrA*,

FIG. 1. Linear scale drawings representing the circular linkage 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 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.







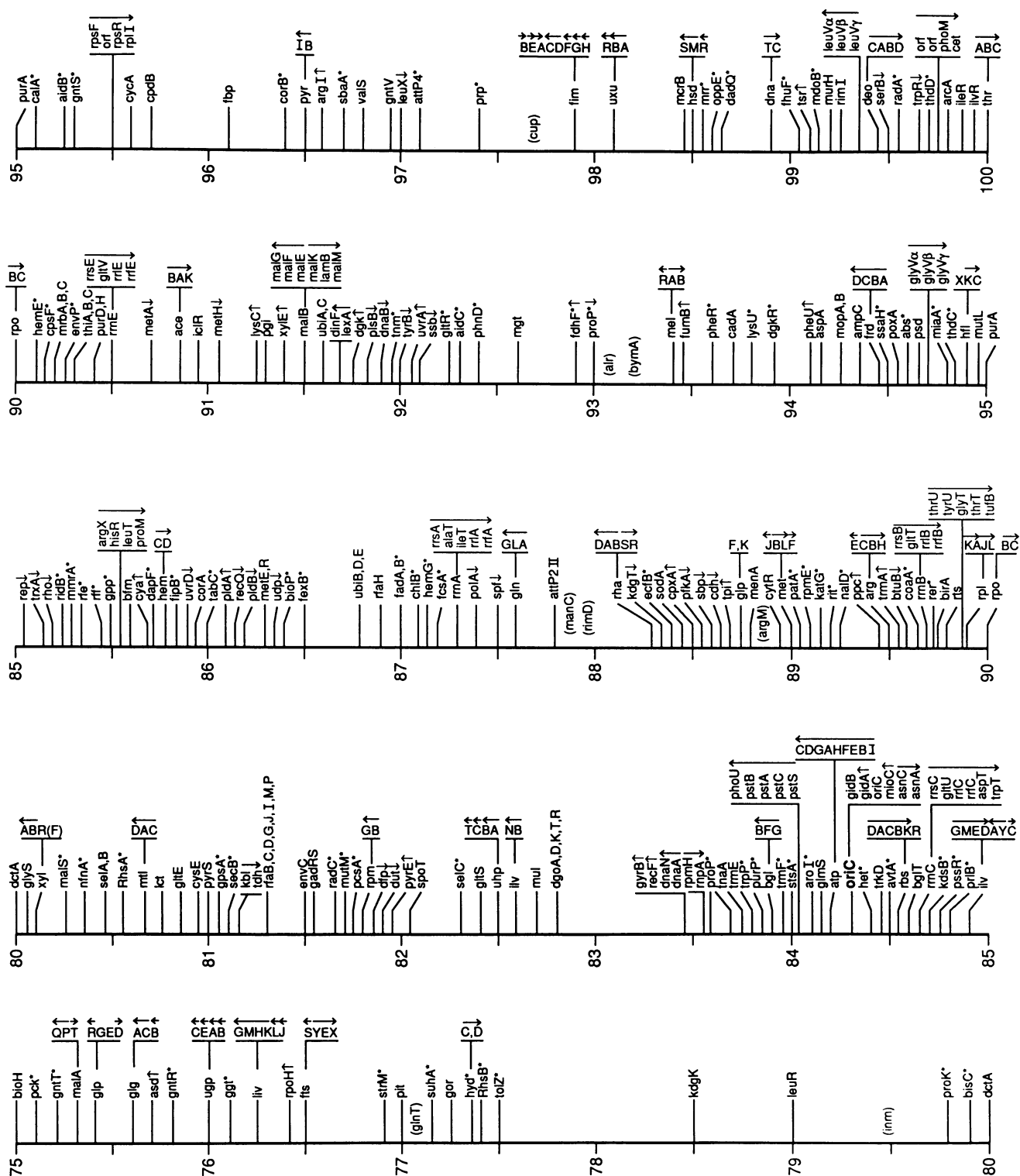


TABLE 1. Genetic markers of *E. coli* K-12

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>aat</i>		(55)	Aminoacyl-tRNA-protein-transferase (EC 2.3.2.6)	B
<i>abpS</i>		60	Low-affinity transport system for arginine and ornithine; periplasmic binding protein	180
<i>abs</i>		95	Sensitivity and permeability to antibiotics and dyes	195
<i>acd</i>		63	Acetaldehyde-CoA dehydrogenase	C
<i>aceA</i>	Acetate	91	<i>icl</i> ; utilization of acetate; isocitrate lyase (EC 4.1.3.1)	A, C, 910
<i>aceB</i>	Acetate	91	<i>mas</i> ; utilization of acetate; malate synthase A (EC 4.1.3.2)	A, C
<i>aceE</i>	Acetate	3	<i>aceE1</i> ; acetate requirement; pyruvate dehydrogenase (decarboxylase component)	A, B, C, 422, 739, 1029
<i>aceF</i>	Acetate	3	<i>aceE2</i> ; acetate requirement; pyruvate dehydrogenase (dihydrolipoyltransacetylase component)	A, B, C, 422, 1029, 1043
<i>aceK</i>		91	Isocitrate dehydrogenase kinase/phosphatase	194, 220, 576, 615, 616
<i>ackA</i>		50	Acetate kinase (EC 2.7.2.1) activity	B, C
<i>ackB</i>		39	Acetate kinase (EC 2.7.2.1) activity	C
<i>acpS</i>		43	CoA:apo-[acyl-carrier protein] pantetheinephosphotransferase (EC 2.7.8.7); holo-[acyl-carrier protein] synthase	C
<i>acrA</i>	Acridine	11	<i>lir</i> , <i>Mb</i> , <i>mbl</i> , <i>mtc</i> ; sensitivity to acriflavine, phenethyl alcohol, and sodium dodecyl sulfate	A, C
<i>acrC</i>	Acridine	4	Sensitivity to acriflavine	C
<i>ada</i>		48	Inducible DNA repair system protecting against methylating and alkylating agents; <i>O</i> ⁶ -methylguanine-DNA methyltransferase	C, 560, 635, 703, 744, 772, 1087, W
<i>add</i>		36	Adenosine deaminase (EC 3.5.4.4)	B
<i>adhE</i>		27	CoA-linked acetaldehyde dehydrogenase and alcohol dehydrogenase	B, C, 232
<i>adhR</i>		71	Regulatory gene for <i>acd</i> and <i>adhE</i>	196, 191, F
<i>adk</i>		11	<i>dnaW</i> ; <i>plsA</i> ; adenylate kinase (EC 2.7.4.3) activity; pleiotropic effects on glycerol-3-phosphate acyltransferase activity	A, B, C, 147
<i>aidB</i>		95	Induced by alkylating agents	1145, T
<i>aidC</i>		92	Induced by alkylating agents	1145
<i>alaS</i>	Alanine	58	<i>ala-act</i> ; alanyl-tRNA synthetase (EC 6.1.1.7)	A, B, C
<i>alaT</i>	Alanine	87	<i>talA</i> ; alanine tRNA 1B; in <i>rrnA</i> operon	B, 587
<i>alaU</i>	Alanine	72	<i>talD</i> ; alanine tRNA 1B; in <i>rrnD</i> operon	B, 587
<i>alaV</i>	Alanine	5	Alanine tRNA 1B in <i>rrnH</i> operon	C, 587
<i>alaW</i>	Alanine	52	Alanine tRNA 2 (tandemly duplicated gene)	587
<i>ald</i>		31	Aldehyde dehydrogenase, NAD-linked	189
<i>alkA</i>	Alkylation	45	<i>aidA</i> ; 3-methyl-adenine DNA glycosylase II, inducible	B, C, 199, 773, 774, 1087, 1145
<i>alkB</i>	Alkylation	47	<i>aidD</i> ; DNA repair system specific for alkylated DNA	560, 561, 1145
<i>alr</i>		(93)	Alanine racemase (EC 5.1.1.1)	A
<i>amiA</i>		(51)	<i>N</i> -Acetylmuramyl-L-alanine amidase activity	1104
<i>amn</i>		43	AMP nucleosidase (EC 3.2.2.4)	636
<i>ampC</i>	Ampicillin	94	β -Lactamase; penicillin resistance	A, B, C, 525
<i>ams</i>		24	Alteration of mRNA stability	C, 183
<i>ana</i>		27	Alcohol dehydrogenase (EC 1.1.1.1) and acetaldehyde dehydrogenase (EC 1.2.1.10) activity	B, C
<i>ansA</i>		39	L-asparaginase I, cytoplasmic	C, 1033
<i>ant</i>		0	Na ⁺ /H antiporter activity	381
<i>apaH</i>		1	Diadenosine tetrakisphosphate	101, 729
<i>appA</i>		22	pH 2.5 acid phosphatase; exopolyphosphatase (EC 3.6.1.11)	117, 250
<i>appR</i>		59	Expression of pH 2.5 acid phosphatase	1110
<i>apt</i>		11	Adenine phosphoribosyltransferase (EC 2.4.2.7)	B, 457, 458
<i>araA</i>	Arabinose	1	L-Arabinose isomerase (EC 5.3.1.4)	A, B, 630
<i>araB</i>	Arabinose	1	Ribulokinase (EC 2.7.1.16)	A, B, C, 293, 630
<i>araC</i>	Arabinose	1	Regulatory gene; activator and repressor protein	A, B, C, 293
<i>araD</i>	Arabinose	1	L-Ribulosephosphate 4-epimerase (EC 5.1.3.4)	A, B, 630
<i>araE</i>	Arabinose	61	Low-affinity L-arabinose transport system; L-arabinose proton symport	A, C, 688, 1052
<i>araF</i>	Arabinose	45	L-Arabinose-binding protein	B, C, 982, 983
<i>araG</i>	Arabinose	45	High-affinity L-arabinose transport system	C, 983
<i>araH</i>	Arabinose	45	High-affinity L-arabinose transport system; membrane protein	983
<i>arcA</i>		100	<i>dye</i> , <i>fexA</i> , <i>msp</i> , <i>seg</i> , <i>sfrA</i> ; negative regulatory gene of genes in aerobic pathways	A, B, C, 160, 161, 286, 519

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>argA</i>	Arginine	61	<i>argB</i> , <i>Arg1</i> , <i>Arg2</i> ; amino acid acetyltransferase; <i>N</i> -acetylglucosamine synthase (EC 2.3.1.1)	A, B, C, 142, 296, 796, 965
<i>argB</i>	Arginine	90	<i>argC</i> ; acetylglutamate kinase (EC 2.7.2.8)	A, B, C
<i>argC</i>	Arginine	90	<i>argH</i> , <i>Arg2</i> ; <i>N</i> -acetyl- γ -glutamyl-phosphate reductase (EC 1.2.1.38)	A, B, C, 88, 854
<i>argD</i>	Arginine	74	<i>argG</i> , <i>Arg1</i> ; acetylornithine δ -aminotransferase (EC 2.6.1.11)	A, 911
<i>argE</i>	Arginine	90	<i>argA</i> , <i>Arg4</i> ; acetylornithine deacetylase (EC 3.5.1.16)	A, B, C, 88, 854
<i>argF</i>	Arginine	7	<i>argD</i> , <i>Arg5</i> ; ornithine carbamoyltransferase (EC 2.1.3.3) (duplicate gene)	A, B, C, 855, 1141
<i>argG</i>	Arginine	69	<i>argE</i> , <i>Arg6</i> ; argininosuccinate synthetase (EC 6.3.4.5)	A
<i>argH</i>	Arginine	90	<i>argF</i> , <i>Arg7</i> ; argininosuccinate lyase (EC 4.3.2.1)	A, B, C
<i>argI</i>	Arginine	97	Ornithine carbamoyltransferase (EC 2.1.3.3) (duplicate gene)	A, B, 86, 855, 921
<i>argM</i>	Arginine	(89)	Acetylornithine transaminase; cryptic gene; may be duplicate of <i>argD</i>	911
<i>argP</i>	Arginine	63	Transport of arginine, ornithine, and lysine	A
<i>argR</i>	Arginine	71	<i>Rarg</i> ; regulatory gene; repressor of <i>arg</i> regulon	A, C, 651
<i>argS</i>	Arginine	(40)	Arginyl-tRNA synthetase (EC 6.1.1.19)	A, 793
<i>argT</i>	Arginine	50	Sequence homologous to <i>argT</i> of <i>S. typhimurium</i> , which codes for lysine-, arginine-, ornithine-binding protein	807
<i>argU</i>	Arginine	13	<i>dnaY</i> , <i>pin</i> ; arginine tRNA 4	B, C, 341, 359, 373, 587
<i>argV</i>	Arginine	58	Arginine tRNA 2 (tandemly quadruplicated gene)	341
<i>argW</i>	Arginine	51	Arginine tRNA 5	587
<i>argX</i>	Arginine	85	Arginine tRNA 3	485, 587
<i>aroA</i>	Aromatic	20	3-enol-pyruvoylshikimate-5-phosphate synthase (EC 2.5.1.19)	A, 291, 292
<i>aroB</i>	Aromatic	75	Dehydroquinate synthase (EC 4.6.1.3)	A, 740
<i>aroC</i>	Aromatic	51	Chorismate synthase (EC 4.6.1.4)	A
<i>aroD</i>	Aromatic	37	3-Dehydroquinate dehydratase (EC 4.2.1.10)	A, C, 118
<i>aroE</i>	Aromatic	72	Dehydroshikimate reductase (EC 1.1.1.25)	A, 24, 730
<i>aroF</i>	Aromatic	57	DAHP synthetase (tyrosine repressible)	A, 488, 1008
<i>aroG</i>	Aromatic	17	DAHP synthetase (phenylalanine repressible)	A, C, 254
<i>aroH</i>	Aromatic	37	DAHP synthetase (tryptophan repressible)	A, C, 118, 290
<i>aroI</i>	Aromatic	84	Function unknown	A
<i>aroL</i>	Aromatic	9	Shikimate kinase II (EC 2.7.1.71)	B, 261, 262
<i>aroM</i>	Aromatic	9	Unknown function; regulated by <i>aroR</i>	261, 262
<i>aroP</i>	Aromatic	3	General aromatic amino acid transport	A, C, 422, 912
<i>aroT</i>	Aromatic	28	<i>aroR</i> , <i>trpR</i> ; transport of aromatic amino acids, alanine, and glycine	A, B
<i>asd</i>		76	<i>dap</i> + <i>hom</i> ; aspartate semialdehyde dehydrogenase (EC 1.2.1.11)	A, C
<i>asnA</i>	Asparagine	84	Asparagine synthetase A (EC 6.3.1.1)	A, B, C, 152
<i>asnB</i>	Asparagine	16	Asparagine synthetase B (EC 6.3.1.1)	B, C, 864
<i>asnC</i>	Asparagine	84	Regulatory gene	277
<i>asnS</i>	Asparagine	21	<i>lcs</i> ; asparaginyl-tRNA synthetase (EC 6.1.1.22)	B, C, 506
<i>asnT</i>	Asparagine	43	Asparagine tRNA	B, C, 341, 587
<i>asnU</i>	Asparagine	43	Asparagine tRNA	587
<i>asnV</i>	Asparagine	43	Asparagine tRNA	587
<i>aspA</i>	Aspartate	94	L-Aspartate ammonia-lyase (aspartase) (EC 4.3.1.1)	A, B, 423
<i>aspC</i>	Aspartate	21	Aspartate aminotransferase (EC 2.6.1.1)	B, 340, 607, 697
<i>aspT</i>	Aspartate	85	<i>tasC</i> ; aspartate tRNA 1, triplicate gene; in <i>rrnC</i> operon	B, C, 587
<i>aspU</i>	Aspartate	5	Aspartate tRNA 1, triplicate gene; in <i>rrnH</i> operon	C, 587
<i>aspV</i>	Aspartate	5	Aspartate tRNA 1, triplicate gene	C, 477, 587
<i>asu</i>		33	Asparagine utilization, as sole nitrogen source	191
<i>atoA</i>	Acetoacetate	48	Acetyl-CoA:acetoacetyl-CoA transferase (EC 2.8.3.-) β -subunit	A, 588
<i>atoB</i>	Acetoacetate	48	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	A, 528
<i>atoC</i>	Acetoacetate	48	Positive regulatory gene	A, 528, 529
<i>atoD</i>	Acetoacetate	48	Acetyl-CoA:acetoacetyl-CoA transferase (EC 2.8.3.-) β -subunit?	528
<i>atpA</i>	ATP	84	<i>papA</i> , <i>uncA</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F_1 sector, α -subunit	A, B, C, 578, 1152
<i>atpB</i>	ATP	84	<i>papD</i> , <i>uncB</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F_0 sector, subunit a	A, B, C, 801, 1146, 1152

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>atpC</i>	ATP	84	<i>papG</i> , <i>uncC</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, ε-subunit	B, C, 1152
<i>atpD</i>	ATP	84	<i>papB</i> , <i>uncD</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, β-subunit	B, C, 1152
<i>atpE</i>	ATP	84	<i>papH</i> , <i>uncE</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₀ sector, subunit c; DCCD-binding protein	B, C, 722, 1152
<i>atpF</i>	ATP	84	<i>uncF</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₀ sector, subunit b	C, 1152
<i>atpG</i>	ATP	84	<i>papC</i> , <i>uncG</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, γ-subunit	B, C, 578, 1152
<i>atpH</i>	ATP	84	<i>papE</i> , <i>uncH</i> ; membrane-bound ATP synthase (EC 3.6.1.3), F ₁ sector, δ-subunit	C, 1152
<i>atpI</i>	ATP	84	<i>uncI</i> ; membrane-bound ATP synthase (EC 3.6.1.3), subunit ?	148, 537, 801, 872, 1146, 1152
<i>attE14</i>	Attachment	26	Attachment site for element e14	C
<i>attHK22</i>	Attachment	22	<i>attHtt</i> ; attachment site for phage HK022	C
<i>attHK139</i>	Attachment	44	Attachment site for phage HK139	C
<i>attλ</i>	Attachment	17	Integration site for prophages λ, 82, and 434	A, B, C
<i>attP1,P7</i>	Attachment	67	<i>loxB</i> ; integration site for phages P1 and P7	C
<i>attP2H</i>	Attachment	44	Phage P2 integration site H	A
<i>attP2II</i>	Attachment	88	Phage P2 integration site II	A
<i>attP4</i>	Attachment	97	Integration site for phage P4	C
<i>attP22</i>	Attachment	6	<i>ata</i> ; integration site for phage P22	A
<i>attPA-2</i>	Attachment	51	Integration site for phage PA-2	B
<i>attφ80</i>	Attachment	28	Integration site for prophage φ80	A, B
<i>att186</i>	Attachment	57	Integration site for prophage 186	A
<i>att253</i>	Attachment	6	Integration site for phage 253	871
<i>avtA</i>		84	Alanine-α-ketoisovalerate transaminase, transaminase C	C, 1155
<i>azaA</i>	Azaserine	44	Resistance or sensitivity to azaserine	C
<i>azaB</i>	Azaserine	70	Resistance or sensitivity to azaserine	C
<i>azl</i>	Azaleucine	55	Regulation of <i>ilv</i> and <i>leu</i> genes; azaleucine resistance	A
<i>betA</i>	Betaine	7	Choline dehydrogenase	21, 1058
<i>betB</i>	Betaine	7	Betaine aldehyde dehydrogenase	21
<i>betT</i>	Betaine	7	High-affinity choline transport	21
<i>bfm</i>		86	Phage BF23 multiplication	A
<i>bglA</i>	β-Glucoside	84	<i>bglD</i> ; phospho-β-glucosidase A	A, B
<i>bglB</i>	β-Glucoside	84	<i>bglA</i> ; phospho-β-glucosidase B	A, B, C, 685, 973
<i>bglF</i>	β-Glucoside	84	<i>bglB</i> , <i>bglC</i> ; β-glucoside transport	A, B, C, 128, 685
<i>bglG</i>	β-Glucoside	84	<i>bglC</i> , <i>bglS</i> ; positive regulatory gene	A, 685, 904, 905, 973
<i>bglT</i>	β-Glucoside	85	<i>bglE</i> ; regulatory gene for phospho-β-glucosidase A synthesis	A
<i>bioA</i>	Biotin	17	7,8-Diaminopelargonic acid synthetase	A, B, C, 1072
<i>bioB</i>	Biotin	17	Biotin synthetase	A, B, C, 1072
<i>bioC</i>	Biotin	17	Block prior to pimeloyl CoA	A, B, 1072
<i>bioD</i>	Biotin	17	Dethiobiotin synthetase	A, B, 1072
<i>bioF</i>	Biotin	17	7-Keto-8-aminopelargonic acid synthetase	A, B, 1072
<i>bioH</i>	Biotin	75	<i>bioB</i> ; block prior to pimeloyl CoA	A, C
<i>bioP</i>	Biotin	86	<i>birB</i> ; biotin transport	A, B, C
<i>birA</i>	Biotin retention	90	<i>bioR</i> , <i>dhbB</i> ; biotin-[acetyl-CoA carboxylase] holoenzyme synthetase; biotin operon repressor	A, B, C, 483
<i>bisC</i>	Biotin sulfoxide	80	Biotin sulfoxide reductase, structural gene	B, C
<i>brnQ</i>	Branched chain	9	Transport system 1 for isoleucine, leucine, and valine	A, B
<i>brnR</i>	Branched chain	8	Component of transport systems 1 and 2 for isoleucine, leucine, and valine	A
<i>brnS</i>	Branched chain	1	Transport system for isoleucine, leucine, and valine	A
<i>brnT</i>	Branched chain	62	Low-affinity transport system for isoleucine	B
<i>btuB</i>	B ₁₂ uptake	90	<i>bfe</i> , <i>btuA</i> , <i>cer</i> ; receptor for vitamin B ₁₂ , E colicins, and phage BF23	A, B, C, 40, 41, 455
<i>btuC</i>	B ₁₂ uptake	37	Vitamin B ₁₂ transport	B, 274, 276, 351
<i>btuD</i>	B ₁₂ uptake	37	Vitamin B ₁₂ transport, membrane-associated protein	274, 276, 351
<i>btuE</i>	B ₁₂ uptake	37	Vitamin B ₁₂ transport, periplasmic protein?	274, 351
<i>btuR</i>	B ₁₂ uptake	28	Regulatory gene affecting <i>btuB</i>	674
<i>bymA</i>		(93)	Bypass of maltose permease at <i>malB</i>	A
<i>cadA</i>	Cadaverine	94	Lysine decarboxylase (EC 4.1.1.18)	C
<i>cadR</i>	Cadaverine	46	<i>lysP?</i> ; regulatory gene for lysine decarboxylase	C, W
<i>calA</i>	Calcium	95	Calcium transport	C

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>calC</i>	Calcium	16	Calcium transport	C
<i>calD</i>	Calcium	10	Calcium transport	C
<i>can</i>	Canavanine	63	Canavanine resistance	A
<i>carA</i>		1	<i>arg + ura, cap, pyrA</i> ; carbamoylphosphate synthase (EC 2.7.2.9), glutamine (light) subunit	A, C, 124, 856
<i>carB</i>		1	<i>arg + ura, cap, pyrA</i> ; carbamoylphosphate synthase (EC 2.7.2.9), ammonia (heavy) subunit	A, C, 811
<i>cbt</i>		16	Dicarboxylate-binding protein production	A, C
<i>cca</i>		67	tRNA nucleotidyl transferase (EC 2.7.7.25)	A, 231
<i>cdd</i>		46	Deoxycytidine deaminase (EC 3.5.4.5)	A, B, C, 541, 736, W
<i>cdh</i>		89	CDP-diglyceride hydrolase	C, 11, 153, 456, 499
<i>cdsA</i>		4	CDP-diglyceride synthetase (CTP:phosphatidate cytidyltransferase) (EC 2.7.7.41)	C, 501
<i>cdsS</i>		69	Stability of CDP-diglyceride synthetase activity	358
<i>celB</i>	Cellobiose	38	Transport of cellobiose, arbutin, and salicin	595, 596, 834, J
<i>celC</i>	Cellobiose	38	Transport of cellobiose, arbutin, and salicin	595, 596, 834, J
<i>celD</i>	Cellobiose	38	Negative regulatory gene	595, 596, 834, J
<i>celF</i>	Cellobiose	38	Phospho- β -glucosidase	595, 596, 834, J
<i>cet</i>	Colicin E2	100	<i>ref, refII</i> ; tolerance to colicin E2	A, C, 287
<i>cfa</i>		36	Cyclopropane fatty acid synthase	413–415
<i>cheA</i>	Chemotaxis	42	Chemotactic response	A, B, C, 1016
<i>cheB</i>	Chemotaxis	41	Chemotactic response; protein methylesterase activity	A, B, C, 768, 1016
<i>cheR</i>	Chemotaxis	41	<i>cheX</i> ; chemotactic response; protein methylesterase activity	B, C, 768, 1016
<i>cheW</i>	Chemotaxis	42	Chemotactic response	B, 768, 1016
<i>cheY</i>	Chemotaxis	41	Chemotactic response	B, C, 201, 714, 768, 1016
<i>cheZ</i>	Chemotaxis	41	Chemotactic response	B, C, 768, 1016
<i>chlA</i>	Chlorate	18	<i>bisA, narA</i> ; biosynthesis of molybdopterin	A, B, C, 534, 901
<i>chlB</i>	Chlorate	87	<i>narB</i> ; nitrate reductase, biosynthesis of molybdopterin	A, B, C, 901
<i>chlD</i>	Chlorate	17	<i>narD</i> ; molybdenum uptake	A, B, C, 531
<i>chlE</i>	Chlorate	18	<i>bisB, narE</i> ; biosynthesis of molybdopterin	A, B, C, 534, 803, 901
<i>chlI</i>	Chlorate	17	Molybdenum transport?	531
<i>chlM</i>	Chlorate	18	Biosynthesis of molybdopterin	534, 1084
<i>chlN</i>	Chlorate	18	Biosynthesis of molybdopterin	534, 803, 1084
<i>cirA</i>	Colicine I resistance	43	<i>feuA</i> ; production of colicin I receptor	A, B, C, 115, 408, 736, W
<i>citA</i>	Citrate	(18)	Cryptic gene of citrate transport system	429
<i>citB</i>	Citrate	(16)	Cryptic gene of citrate transport system	429
<i>cls</i>		27	Cardiolipin synthase activity	B, 817
<i>cmlA</i>	Chloramphenicol	19	Resistance or sensitivity to chloramphenicol	A, 1007
<i>coaA</i>		90	<i>panK</i> ; pantothenate kinase	1134
<i>codA</i>		8	Cytosine deaminase (EC 3.5.4.1)	A
<i>codB</i>		8	Cytosine transport	A
<i>corA</i>	Cobalt resistance	86	Mg ²⁺ transport, system I	B, C, 14
<i>corB</i>	Cobalt resistance	96	Mg ²⁺ transport, system I	B
<i>cpdB</i>		96	2',3'-Cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)	C, 656
<i>cpsA</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsB</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsC</i>		44	Capsular polysaccharide synthesis	1113
		44	Capsular polysaccharide synthesis	1113
<i>cpsD</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsE</i>		44	Capsular polysaccharide synthesis	1113
<i>cpsF</i>		90	Capsular polysaccharide synthesis	1113
<i>cpxA</i>		89	F-pilus formation, surface exclusion, conjugal donor activity	C, 11–13
<i>cpxB</i>		40	F-pilus formation, surface exclusion, conjugal donor activity	C
<i>crg</i>		29	Cold-resistant growth	565
<i>crp</i>		74	<i>cap, csm</i> ; cyclic AMP receptor protein	A, C, 370, 821, 1019
<i>crr</i>		52	<i>gsr, iex, tgs</i> ; glucose phosphotransferase system enzyme III ^{Glc}	B, C, 134, 136, 270, 794, 835, 945
<i>cup</i>		98	Uptake of carbohydrates	686
<i>cxm</i>		6	<i>cxr</i> ; methylglyoxal synthesis	A, B
<i>cyaA</i>		86	Adenylate cyclase (EC 4.6.1.1)	A, B, C, 6–8, 14, 59, 70, 578, 588, 930, 931

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>cybB</i>		(16.5)	Cytochrome <i>b</i> ₅₆₁	762
<i>cycA</i>	Cycloserine	96	<i>dagA</i> ; resistance to D-cycloserine and D-serine; transport of D-alanine, D-serine, and glycine	A, B
<i>cydA</i>		17	Cytochrome <i>d</i> terminal oxidase, polypeptide subunit I	C, 400, 401
<i>cydB</i>		17	Cytochrome <i>d</i> terminal oxidase, polypeptide subunit II	A, B, 400–402
<i>cydC</i>		19	Cytochrome <i>d</i> terminal oxidase, possibly heme <i>d</i> component	371
<i>cyn</i>		8	<i>cnt</i> ; cyanate aminohydrolase (EC 3.5.5.3), cyanase	424, 1063, 1064
<i>cyo</i>		10	Cytochrome <i>o</i> terminal oxidase complex	38, 39
<i>cysA</i>	Cysteine	52	Sulfate permease; chromate resistance	A, B, 945, 1012
<i>cysB</i>	Cysteine	28	Positive regulator for <i>cys</i> regulon	A, B, 825
<i>cysC</i>	Cysteine	59	Adenosine 5'-phosphosulfate kinase (EC 2.7.1.25)	A, 640
<i>cysD</i>	Cysteine	59	ATP sulfurylase (ATP:sulfate adenylyltransferase) (EC 2.7.7.4)	A, 493, 640
<i>cysE</i>	Cysteine	81	Serine acetyltransferase (EC 2.3.1.30)	A, B, 269
<i>cysG</i>	Cysteine	74	Siroheme synthesis	A, C, 522, 679, 680
<i>cysH</i>	Cysteine	59	Adenylylsulfate reductase (EC 1.8.99.2)	A, 493, 641
<i>cysI</i>	Cysteine	59	<i>cysQ</i> ; sulfite reductase (EC 1.8.1.2), α subunit	A, 493, 641
<i>cysJ</i>	Cysteine	59	<i>cysP</i> ; sulfite reductase (EC 1.8.1.2), β subunit	A, 493, 641
<i>cysK</i>	Cysteine	52	<i>cysZ</i> ; O-Acetylserine sulfhydrylase A (EC 4.2.99.8)	B, C, 120, 134, 945, 1012
<i>cysM</i>	Cysteine	52	O-Acetylserine sulfhydrylase B (EC 4.2.99.8)	945, 1012
<i>cysN</i>	Cysteine	59	ATP-sulfurylase (ATP:sulfate adenylyltransferase) (EC 2.7.7.4), subunit	640
<i>cysS</i>	Cysteine	12	CysteinyI-tRNA synthetase (EC 6.1.1.16)	C
<i>cysT</i>	Cysteine	42	Cysteine tRNA	341, 587
<i>cytR</i>		89	Regulatory gene for <i>deo</i> operon, <i>udp</i> and <i>cdd</i>	A, B, 63, 1130
<i>dacA</i>		15	D-Alanine carboxypeptidase, fraction A; penicillin-binding protein 5	A, B, C, 141, 832, 1048
<i>dacB</i>		69	D-Alanine carboxypeptidase, fraction B; penicillin-binding protein 4	B, C
<i>dadA</i>		26	<i>dadR</i> ; D-amino acid dehydrogenase subunit	A, B, C, 1173
<i>dadB</i>		2	<i>alnA</i> ; D-amino acid dehydrogenase subunit	A, B, C
<i>dadQ</i>		99	<i>alnR</i> ; regulatory gene for <i>dad</i> regulon	A, C
<i>dadR</i>		26	Regulatory gene	1173
<i>dadX</i>		26	<i>msuA</i> ?; alanine racemase (EC 5.1.1.1)	1173
<i>dam</i>		74	DNA adenine methylase	A, B, C, 32, 139
<i>dapA</i>	Diaminopimelate	53	Dihydrodipicolinate synthase (EC 4.2.1.52)	A, 833, 909
<i>dapB</i>	Diaminopimelate	1	Dihydrodipicolinate reductase (EC 1.3.1.26)	A, C, 125
<i>dapC</i>	Diaminopimelate	4	Tetrahydrodipicolinate succinylase	A, C
<i>dapD</i>	Diaminopimelate	4	Tetrahydrodipicolinate N-succinyltransferase	A, C, 908
<i>dapE</i>	Diaminopimelate	53	<i>dapB</i> ; N-succinyl-diaminopimelate deacylase	A, 833, 909
<i>dapF</i>	Diaminopimelate	86	Diaminopimelate epimerase	907
<i>dcd</i>		(46)	<i>paxA</i> ; 2'-deoxycytidine 5'-triphosphate deaminase (EC 3.5.4.-) activity	B
<i>dcm</i>		43	<i>mec</i> ; DNA cytosine methylase	A, B, 90
<i>dcp</i>		(29)	Dipeptidyl carboxypeptidase	B
<i>dctA</i>		80	Uptake of C4-dicarboxylic acids	A
<i>dctB</i>		16	Uptake of C4-dicarboxylic acids	A
<i>ddl</i>		2	D-Alanine:D-alanine ligase	A, B, C, 914
<i>del</i>	Deletion	61	Frequency of IS1-mediated deletion	B
<i>deoA</i>	Deoxyribose	100	<i>tpg</i> , <i>TP</i> ; thymidine phosphorylase (EC 2.4.2.4)	A, B, C, 1127, 1128
<i>deoB</i>	Deoxyribose	100	<i>drm</i> , <i>thyR</i> ; phosphopentomutase (EC 2.7.5.6)	A, B, C, 1127
<i>deoC</i>	Deoxyribose	100	<i>dra</i> , <i>thyR</i> ; deoxyribose-phosphate aldolase (EC 4.1.2.4)	A, B, C, 243, 1126
<i>deoD</i>	Deoxyribose	100	<i>pup</i> ; purine-nucleoside phosphorylase (EC 2.4.2.1)	A, B, C, 617
<i>deoR</i>	Deoxyribose	19	<i>nucR</i> ; regulatory gene for <i>deo</i> operon	A, B, 1007, 1129
<i>dfp</i>		82	<i>dnaS</i> , <i>dut</i> ; flavoprotein affecting synthesis of DNA and pantothenate metabolism	1030, 1031
<i>dgd</i>		(70)	D-Galactose dehydrogenase production	B
<i>dgkA</i>	Diglyceride	92	Diglyceride kinase	B, C, 646
<i>dgkR</i>	Diglyceride	94	Level of diglyceride kinase	C
<i>dgoA</i>	D-Galactonate	82	2-Oxo-3-deoxygalactonate 6-phosphate aldolase (EC 4.1.2.21)	B
<i>dgoD</i>	D-Galactonate	82	Galactonate dehydratase (EC 4.2.1.6)	B
<i>dgoK</i>	D-Galactonate	82	2-Oxo-3-deoxygalactonate kinase (EC 2.7.1.58)	B
<i>dgoR</i>	D-Galactonate	82	Regulatory gene	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
<i>dgoT</i>	D-Galactonate	82	Galactonate transport	B
<i>dgsA</i>		35	Function of enzyme IIA/IIB of phosphotransferase system	C, 757
<i>dicA</i>		35	Regulatory gene	80, 81
<i>dicB</i>		35	Control of cell division	80, 81
<i>dicC</i>		35	Regulatory gene	80, 81
<i>dinF</i>		92	Locus induced by UV and mitomycin C; subject to <i>recA</i> and <i>lexA</i> regulation	C, 598
<i>dld</i>		(47)	D-Lactate dehydrogenase (EC 1.1.1.28)	C, 170, 932
<i>dms</i>		20	Dimethyl sulfoxide reductase	95
<i>dnaA</i>	DNA	83	DNA biosynthesis; initiation	A, B, C, 434, 578, 815
<i>dnaB</i>	DNA	92	<i>groP</i> , <i>grpA</i> ; DNA biosynthesis; chain elongation	A, B, C, 783
<i>dnaC</i>	DNA	99	<i>dnaD</i> ; DNA biosynthesis; initiation and chain elongation	A, B, 784, 927
<i>dnaE</i>	DNA	4	See <i>polC</i>	
<i>dnaG</i>	DNA	67	<i>dnaP</i> , <i>parB</i> ; DNA biosynthesis; primase	A, B, C, 157, 677, 765, 784, 808, 927, 1018, 1086, 1182
<i>dnaI</i>	DNA	40	DNA biosynthesis	A
<i>dnaJ</i>	DNA	0	<i>groPAB</i> , <i>groPC</i> ; DNA biosynthesis	B, 66, 814, 1196
<i>dnaK</i>	DNA	0	<i>groPAB</i> , <i>groPC</i> , <i>groPF</i> , <i>grpF</i> ; DNA biosynthesis	B, 64, 951
<i>dnaL</i>	DNA	29	<i>dnaK</i> ; DNA biosynthesis	B
<i>dnaN</i>	DNA	83	DNA biosynthesis; DNA polymerase III holoenzyme, β -subunit	C, 27, 434, 815, 894
<i>dnaQ</i>	DNA	5	<i>mutD</i> , DNA polymerase III holoenzyme, ϵ subunit, mutator activity	B, C, 225, 278, 298, 690, 707, 806, 971
<i>dnaT</i>	DNA	99	DNA biosynthesis; primasomal protein i	B, 709, 784
<i>dnaX</i>	DNA	11	<i>dnaZ</i> ; DNA biosynthesis; DNA polymerase III holoenzyme, τ and γ subunits; DNA elongation factor III	B, C, 335, 583, 631, 761, 927, 1207
<i>dpp</i>	Dipeptide	(14)	Transport of dipeptides	A, B
<i>drpA</i>		5	DNA and RNA biosynthesis	626
<i>dsdA</i>	D-Serine	51	D-Serine deaminase	A, B, C, 119, 724
<i>dsdC</i>	D-Serine	51	Regulatory gene for <i>dsdA</i>	A, C, 119, 723, 830
<i>dut</i>	dUTPase	82	<i>dnaS</i> , <i>sof</i> ; deoxyuridinetriphosphatase (EC 3.6.1.23)	A, B, C, 672, 673, 1031
<i>dvl</i>		7	Sensitivity to sodium dodecyl sulfate and toluidine blue plus light	1151
<i>ebgA</i>		67	Phospho- β -D-galactosidase, α subunit; cryptic gene	A, B, 430, 1050, 1051, J
<i>ebgB</i>		67	Possible homolog of <i>lacY</i> ; in <i>ebg</i> operon	430, 1051, J
<i>ebgC</i>		67	Phospho- β -D-galactosidase, β subunit; cryptic gene	430, J
<i>ebgR</i>		67	Regulatory gene	B, 430, 1051, J
<i>ecfA</i>	Energy-coupling factor	65	Pleiotropic effects on active transport coupling to metabolic energy; may be <i>metC</i>	B
<i>ecfB</i>	Energy-coupling factor	88	<i>eup</i> , <i>ssd</i> ; generalized resistance to aminoglycoside antibiotics; coupling of metabolic energy to active transport	B, C, 863
<i>eda</i>		41	<i>kdgA</i> , <i>kga</i> ; 2-keto-3-deoxygluconate 6-phosphate aldolase (EC 4.1.2.14)	A
<i>edd</i>		41	Phosphogluconate dehydratase (EC 4.2.1.12)	A
<i>endA</i>		64	DNA-specific endonuclease I	B
<i>eno</i>		60	Enolase (EC 4.2.1.11)	A, B, C, 1169
<i>entA</i>	Enterochelin	14	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase	A, B, C, 333, 770, 850
<i>entB</i>	Enterochelin	14	2,3-Dihydro-2,3-dihydroxybenzoate synthetase	A, B, C, 333, 770, 850
<i>entC</i>	Enterochelin	14	Isochorismate synthetase	A, B, C, 333, 770, 850
<i>entD</i>	Enterochelin	13	Enterochelin synthetase, component D	A, B, C, 205, 334
<i>entE</i>	Enterochelin	14	Enterochelin synthetase, component E	A, B, C, 333, 770, 850
<i>entF</i>	Enterochelin	14	Enterochelin synthetase, component F	A, B, C, 205, 333, 845
<i>entG</i>	Enterochelin	14	Enterochelin synthetase, component G	A, B, C, 333, 770, 850
<i>envA</i>	Envelope	2	Cell envelope and cell separation	A, B, C, 71, 535, 1060
<i>envB</i>	Envelope	71	<i>mon</i> , <i>rodY</i> ; cell shape and sensitivity to antibiotics	A, B, 1147
<i>envC</i>	Envelope	81	Anomalous cell division; chain formation	A, 556
<i>envM</i>	Envelope	28	Osmotically remedial envelope defect	A
<i>envN</i>	Envelope	(4)	Osmotically remedial envelope defect	A
<i>envP</i>	Envelope	90	Osmotically remedial envelope defect	A
<i>envQ</i>	Envelope	58	Osmotically remedial envelope defect	A
<i>envT</i>	Envelope	(15)	Osmotically remedial envelope defect	A
<i>envY</i>	Envelope	13	Envelope protein; thermoregulation of porin synthesis	675

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>envZ</i>	Envelope	75	<i>ompB</i> , <i>perA</i> , <i>tpo</i> ; production of outer membrane proteins; regulatory gene	C, 179, 213, 363, 364, 748, 749, 933, 1191
<i>esp</i>		17	Site for efficient packaging of phage T1	B
<i>exbB</i>		65	Uptake of enterochelin; resistance or sensitivity to colicins	A, B, 302
<i>exbC</i>		59	Uptake of enterochelin; resistance or sensitivity to colicins	B
<i>expA</i>		22	Expression of a group of exported proteins	C
<i>exuR</i>		68	Negative regulatory gene for <i>exu</i> regulon, <i>exuT</i> , <i>uxaCA</i> , and <i>uxaB</i>	B, C, 489, 710
<i>exuT</i>		68	Transport of hexuronates	B, C, 102, 489, 710, 711
<i>e14</i>		26	Cryptic chromosomal element able to be excised; see <i>lit</i> , <i>mcrA</i> , <i>pin</i> and <i>sfiC</i>	137, 138, 553, 684, 861, 862, 887, 1139
<i>fabA</i>	Fatty acid biosynthesis	22	β -Hydroxydecanoyl thioester dehydrase (EC 4.2.1.60)	A, 228
<i>fabB</i>	Fatty acid biosynthesis	50	<i>fabC</i> ; β -ketoacyl-[acyl-carrier protein] synthase I (EC 2.3.1.41)	A, B, C
<i>fabD</i>	Fatty acid biosynthesis	24	Malonyl-CoA-[acyl carrier protein] transacylase (EC 2.3.1.39)	A, C
<i>fabE</i>	Fatty acid biosynthesis	71	Acetyl-CoA carboxylase (EC 6.4.1.2)	B, 1147
<i>fabF</i>	Fatty acid biosynthesis	24	<i>cvc</i> , <i>vtrB</i> , β -ketoacyl-[acyl carrier protein] synthase II (EC 2.3.1.41)	B, C, 1123
<i>fadA</i>	Fatty acid degradation	87	<i>oldA</i> ; thiolase I (EC 2.3.1.16)	A, C, 1032, 1202
<i>fadB</i>	Fatty acid degradation	87	<i>oldB</i> ; 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35), 3-hydroxyacyl-CoA epimerase (EC 5.1.2.3), Δ^3 -C15- Δ^2 -trans-enoyl-CoA (EC 5.3.3.8) and enoyl-CoA-hydratase (crotonase) (EC 4.2.1.17)	A, 1032, 1201, 1202
<i>fadD</i>	Fatty acid degradation	40	<i>oldD</i> ; acyl-CoA synthetase (EC 6.2.1.3)	A, B
<i>fadE</i>	Fatty acid degradation	5	Electron transport flavoprotein of β -oxidation	A, C
<i>fadL</i>	Fatty acid degradation	51	<i>ttr</i> ; transport of long-chain fatty acids and sensitivity to phage T2	B, 98, 99, 755
<i>fadR</i>	Fatty acid degradation	26	<i>dec</i> , <i>oleR</i> , <i>thdB</i> ; negative regulatory gene for <i>fad</i> regulon	B, C, 2, 279, F 275
<i>fatA</i>		69	Utilization of <i>trans</i> -unsaturated fatty acids	A
<i>fba</i>		63	<i>alc</i> , <i>fda</i> ; fructose-bisphosphate aldolase (EC 4.1.2.13)	A, 578, 985
<i>fbp</i>		96	<i>fdp</i> ; fructose-bisphosphatase (EC 3.1.3.11)	B
<i>fcsA</i>		86	Cell division; septation	97, 840, 1188, 1189, 1220, 1221
<i>fdhF</i>		93	Formate dehydrogenase (formate hydrogen-lyase linked), selenopolypeptide	962, 1204
<i>fdv</i>		59	<i>ant</i> ?; formate dehydrogenase-2-activity	B, C, 882, 1218
<i>fecA</i>	Iron	93	Citrate-dependent iron transport, outer membrane receptor	B, C, 882, 1218
<i>fecB</i>	Iron	8	Citrate-dependent iron transport, periplasmic protein	882
<i>fecD</i>	Iron	8	Citrate-dependent iron transport, membrane-bound protein	438
<i>feo</i>	Iron	39	Ferrous iron transport system	A, B, C, 205, 334, 676, 829, 853, 1185
<i>fepA</i>	Iron	13	<i>cbr</i> , <i>cbt</i> , <i>feuB</i> ; receptor for ferric enterobactin (enterochelin) and colicins B and D	129, 829, 852, 853, 1185
<i>fepB</i>	Iron	13	Ferric enterobactin (enterochelin) uptake; periplasmic component	829, 852
<i>fepC</i>	Iron	13	Ferric enterobactin (enterochelin) uptake; cytoplasmic membrane component	829
<i>fepD</i>	Iron	13	Ferric enterobactin (enterochelin) uptake	829
<i>fepE</i>	Iron	13	Ferric enterobactin (enterochelin) uptake	829
<i>fepF</i>	Iron	13	Ferric enterobactin (enterochelin) uptake	A, B, C, 205, 334, 845
<i>fes</i>	Iron	13	Enterochelin esterase	C
<i>fexB</i>		86	FexA phenotype affected	144, 486
<i>ffs</i>		10	4.5S RNA	962
<i>fhl</i>		58	Formate hydrogen-lyase activity, possibly electron transport system	129, 222, 223, 321
<i>fhuA</i>	Ferric hydroxamate uptake	4	<i>tonA</i> , <i>T1</i> , <i>T5rec</i> ; outer membrane receptor for ferrichrome, colicin M, and phages T1, T5, and ϕ 80	C, 129, 321, 591, 883
<i>fhuB</i>	Ferric hydroxamate uptake	4	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	129, 154, 221, 321
<i>fhuC</i>	Ferric hydroxamate uptake	4	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	129, 154, 221, 321
<i>fhuD</i>	Ferric hydroxamate uptake	4	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	129, 154, 221, 321

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>fhuE</i>	Ferric hydroxamate up-take	16	Outer membrane receptor for ferric-rhodotorulic acid	436, 968
<i>fhuF</i>	Ferric hydroxamate up-take	99	Ferric hydroxamate transport	439
<i>fic</i>		74	Filamentation in presence of cyclic AMP in mutant	1125
<i>fimA</i>	Fimbriae	98	<i>fimD</i> , <i>pilA</i> ; type 1 fimbriae (pilin), structural gene	A, B, C, 3, 304, 346, 347, 572, 575
<i>fimB</i>	Fimbriae	98	<i>pil</i> ; regulatory gene for expression of <i>himA</i>	A, B, C, 304, 573, 575
<i>fimC</i>	Fimbriae	98	<i>pil</i> ; biosynthesis of type 1 fimbriae	A, B, C, 575
<i>fimD</i>	Fimbriae	98	<i>pil</i> ; biosynthesis of type 1 fimbriae	A, B, C, 575
<i>fimE</i>	Fimbriae	98	Regulatory gene for expression of <i>fimA</i>	304, 573
<i>fimF</i>	Fimbriae	98	Fimbrial morphology	574
<i>fimG</i>	Fimbriae	98	Fimbrial morphology	574
<i>fimH</i>	Fimbriae	98	Minor fimbrial subunit, adhesin	574
<i>fipB</i>		86	Morphogenesis of phage F1	665
<i>fipC</i>		(73)	Morphogenesis of phage F1	665
<i>firA</i>		4	Affects transcription	B, 1, 210, G
<i>fis</i>		72	Site-specific DNA inversion	581
<i>fiu</i>		18	Ferric iron uptake, outer membrane protein	436
<i>flgA</i>	Flagella	24	<i>flaU</i> ; flagellar synthesis	B, C, 586
<i>flgB</i>	Flagella	24	<i>flbA</i> ; flagellar synthesis	B, C
<i>flgC</i>	Flagella	24	<i>flaW</i> ; flagellar synthesis, basal-body protein	B, C
<i>flgD</i>	Flagella	24	<i>flaV</i> ; flagellar synthesis, basal-body rod modification	B
<i>flgE</i>	Flagella	24	<i>flaK</i> ; flagellar synthesis, hook protein	B
<i>flgF</i>	Flagella	24	<i>flaX</i> ; flagellar synthesis, basal-body rod protein	B, C
<i>flgG</i>	Flagella	24	<i>flaL</i> ; flagellar synthesis, basal-body rod protein	B
<i>flgH</i>	Flagella	24	<i>flaY</i> ; flagellar synthesis, basal-body L-ring protein	B, C, 536
<i>flgI</i>	Flagella	24	<i>flaM</i> ; flagellar synthesis, basal-body P-ring protein	B, 536
<i>flgJ</i>	Flagella	24	<i>flaZ</i> ; flagellar synthesis	B, C
<i>flgK</i>	Flagella	24	<i>flaS</i> ; flagellar synthesis, hook-associated protein	B, C
<i>flgL</i>	Flagella	24	<i>flaT</i> ; flagellar synthesis, hook-associated protein	B
<i>flhA</i>	Flagella	41	<i>flaH</i> ; flagellar synthesis	A
<i>flhB</i>	Flagella	41	<i>flaG</i> ; flagellar synthesis	A, C
<i>flhC</i>	Flagella	42	<i>flaI</i> ; flagellar synthesis; regulatory gene	A, 68
<i>flhD</i>	Flagella	42	<i>flbB</i> ; flagellar synthesis; regulatory gene; flagellum-specific σ factor	B, C, 68
<i>fliA</i>	Flagella	43	<i>flaD</i> ; flagellar synthesis; regulation of late gene expression	A, B, C, 544, 586
<i>fliC</i>	Flagella	43	<i>flaF</i> , <i>hag</i> ; flagellin; flagellar synthesis, filament structural protein	A, B, C, 612
<i>fliD</i>	Flagella	43	<i>flbC</i> ; flagellar synthesis, hook-associated protein 2	C
<i>fliE</i>	Flagella	43	<i>flaN</i> ; flagellar synthesis	A, B, C
<i>fliF</i>	Flagella	43	<i>flaBI</i> ; flagellar synthesis, basal-body M-ring protein	A, B, C, 69
<i>fliG</i>	Flagella	43	<i>flaBII</i> ; flagellar synthesis, motor switching and energizing	A, B, C, 69
<i>fliH</i>	Flagella	43	<i>flaBIII</i> ; flagellar synthesis	A, B, C, 69
<i>fliI</i>	Flagella	43	<i>flaC</i> ; flagellar synthesis	A, B, C, 69
<i>fliJ</i>	Flagella	43	<i>flaO</i> ; flagellar synthesis	A, B, 69
<i>fliK</i>	Flagella	43	<i>flaE</i> ; flagellar synthesis, hook length control	A, B, 69
<i>fliL</i>	Flagella	43	<i>flaAI</i> ; flagellar synthesis	A, B, C, 69, 604, 696
<i>fliM</i>	Flagella	43	<i>flaAII</i> ; flagellar synthesis, motor switching and energizing	A, B, C, 202, 604
<i>fliN</i>	Flagella	43	<i>motD</i> ; flagellar synthesis, motor switching and energizing	696
<i>fliO</i>	Flagella	43	<i>flbD</i> ; flagellar synthesis	696
<i>fliP</i>	Flagella	43	<i>flaR</i> ; flagellar synthesis	A, B, C, 696
<i>fliQ</i>	Flagella	43	<i>flaQ</i> ; flagellar synthesis	A, B, 696
<i>fliR</i>	Flagella	43	<i>flaP</i> ; flagellar synthesis	A, B, 696
<i>flu</i>	Fluffing	44	Metastable gene affecting surface properties, piliation, and colonial morphology	B
<i>fnr</i>		30	<i>nirA</i> , <i>nirR</i> ; regulatory gene for nitrite and nitrate reductases, hydrogenase, and fumarate reductase	A, B, C, 994, 995
<i>folA</i>	Folate	1	<i>tmrA</i> ; dihydrofolate reductase (EC 1.5.1.3); trimethoprim resistance	A, B, C, 101
<i>folC</i>	Folate	50	Dihydrofolate:folylpolyglutamate synthetase	111, 323, 807
<i>frdA</i>		94	Fumarate reductase (EC 1.3.99.1), flavoprotein subunit	A, B, C, 538
<i>frdB</i>		94	Fumarate reductase (EC 1.3.99.1), iron-sulfur protein subunit	C, 538

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>frdC</i>		94	Fumarate reductase (EC 1.3.99.1), membrane anchor polypeptide	C, 538
<i>frdD</i>		94	Fumarate reductase (EC 1.3.99.1), membrane anchor polypeptide	C, 538
<i>frdR</i>		27	Regulation of electron transport and fermentation-associated genes; may be <i>ana</i>	546
<i>fruA</i>	Fructose	47	<i>ptsF</i> ; fructose phosphotransferase enzyme II	A, B, C, 367, W
<i>fruB</i>	Fructose	47	Fructose phosphotransferase enzyme III	367, W
<i>fruF</i>	Fructose	47	<i>fpr</i> ; phosphohistidinoprotein-hexose phosphotransferase, fructose-specific	A, B, C, 281, 367, 589, W
<i>fruK</i>	Fructose	47	<i>fpk</i> ; fructose-1-phosphate kinase (EC 2.7.1.3)	A, B, C, 115, 367, 736, W
<i>fruR</i>	Fructose	2	<i>fruC</i> ; regulatory gene; possibly repressor of <i>fru</i> operon	367, 590
<i>ftsA</i>		2	<i>divA</i> ; cell division	A, B, C, 78, 535, 913, 1059, 1206
<i>ftsE</i>		76	Cell division	B, 377, 954
<i>ftsH</i>		69	Cell division	B
<i>ftsI</i>		2	<i>pbp</i> , <i>sep</i> ; peptidoglycan synthetase; septum formation; penicillin-binding protein 3	B, C, 78, 775
<i>ftsM</i>		2	Cell division	284
<i>ftsQ</i>		76	Cell division	C, 78, 913, 914, 1206
<i>ftsS</i>		76	Cell division	377, 954
<i>ftsX</i>		76	Cell division	377
<i>ftsY</i>		76	Cell division	377
<i>ftsZ</i>		2	<i>sfiB</i> , <i>sulB</i> ; cell division	B, C, 78, 535, 1059, 1205, 1206
<i>fucA</i>	Fructose	60	<i>fucC</i> ; L-fucose-1-phosphate aldolase	A, B, 182, 190, 1013, 1217
<i>fucI</i>	Fructose	60	L-Fucose isomerase	A, B, 190, 1217
<i>fucK</i>	Fructose	60	L-Fucose kinase (EC 2.7.1.51)	A, B, 190, 1217
<i>fucO</i>	Fructose	60	L-1,2-Propanediol oxidoreductase	A, B, 190, 1013, 1217
<i>fucP</i>	Fructose	60	Fucose permease	182, 190, 1013, 1217
<i>fucR</i>	Fructose	60	Positive regulatory protein	190, 1014, 1217
<i>fumA</i>	Fumarate	36	Regulatory gene?	421, 737, 738
<i>fumB</i>	Fumarate	93	Regulatory gene?	420, 421
<i>fumC</i>	Fumarate	36	Fumarase	420
<i>fur</i>		16	Ferric iron uptake; negative regulatory gene, repressor protein	51, 52, 266, 437, 969, K
<i>fusA</i>	Fusidic acid	73	<i>far</i> ; protein chain elongation factor EF-G	A, B, C, 1215
<i>fusB</i>	Fusidic acid	15	Pleiotropic effects on RNA synthesis, ribosomes, and ribosomal protein S6	B
<i>gabC</i>	γ -Aminobutyrate	58	Regulatory gene for <i>gabPDT</i>	A, B, C
<i>gabD</i>	γ -Aminobutyrate	58	Succinate-semialdehyde dehydrogenase (EC 1.2.1.16), NADP-dependent, activity	B, C
<i>gabP</i>	γ -Aminobutyrate	58	Transport of γ -aminobutyrate	B, C
<i>gabT</i>	γ -Aminobutyrate	58	Aminobutyrate aminotransferase (EC 2.6.1.19) activity	A, B, C
<i>gadR</i>		82	Regulatory gene for <i>gadS</i>	A
<i>gadS</i>		82	Glutamate decarboxylase (EC 4.1.1.15)	A
<i>galE</i>	Galactose	17	<i>galD</i> ; UDP-galactose 4-epimerase	A, B, C, 634
<i>galK</i>	Galactose	17	<i>galA</i> ; galactokinase (EC 2.7.1.6)	A, 260
<i>galP</i>	Galactose	64	<i>Pgal</i> ; galactose permease	B
<i>galR</i>	Galactose	61	<i>Rgal</i> ; regulatory gene; repressor of <i>galETK</i> operon	A, C
<i>galT</i>	Galactose	17	<i>galB</i> ; galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)	A, 219, 634
<i>galU</i>	Galactose	28	Glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	A, B
<i>gap</i>		39	<i>gad</i> ; glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)	A, B
<i>garA</i>	Glucarate	16	Glucarate utilization	C
<i>garB</i>	Glucarate	4	Glucarate utilization	C
<i>gatA</i>	Galactitol	45	Galactitol-specific enzyme II of phosphotransferase system	B, C, 655, 736
<i>gatC</i>	Galactitol	45	Regulatory gene	B, C, 655, 736
<i>gatD</i>	Galactitol	45	Galactitol-1-phosphate dehydrogenase	B, C, 655, 736
<i>gcv</i>		63	Glycine cleavage pathway	858, 1040
<i>gdhA</i>		27	Glutamate dehydrogenase	B, C, 73, 726, 1135, 1136

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>ggt</i>		76	γ -Glutamyltranspeptidase (EC 2.3.2.2)	1068, 1069
<i>gidA</i>		84	Glucose-inhibited division; chromosome replication?	152, 578, 1152
<i>gidB</i>		84	Glucose-inhibited division; chromosome replication?	578, 801, 1152
<i>glc</i>	Glycolate	65	Utilization of glycolate, malate synthase G (EC 4.1.3.2)	A
<i>glgA</i>	Glycogen	76	Glycogen synthase (EC 2.4.1.21)	A, B, C, 602
<i>glgB</i>	Glycogen	76	1,4- α -Glucan branching enzyme (EC 2.4.1.18)	A, B, C, 50
<i>glgC</i>	Glycogen	76	Glucose-1-phosphate adenylyltransferase (EC 1.7.7.27)	A, B, C, 49
<i>glk</i>		52	Glucokinase (EC 2.7.1.2)	A
<i>glmS</i>	Glucosamine	84	L-glutamine:D-fructose-6-phosphate aminotransferase (EC 2.6.1.16)	A, B, C, 1152
<i>glnA</i>	Glutamine	88	Glutamine synthetase (EC 6.3.1.2)	A, B, C, 212, 224, 742, 902, 915
<i>glnD</i>	Glutamine	4	Uridyltransferase	B, C
<i>glnF</i>	Glutamine	70	See <i>rpoN</i>	B, C
<i>glnG</i>	Glutamine	88	<i>glnT</i> , <i>ntrC</i> ; negative regulatory gene for <i>glnA</i>	C, 682, 742
<i>glnH</i>	Glutamine	18	Periplasmic glutamine-binding protein	804, 805
<i>glnL</i>	Glutamine	88	<i>glnR</i> , <i>ntrB</i> ; negative regulatory gene for <i>glnA</i>	C, 682, 742, 805, 902, 915, 1122
<i>glnP</i>	Glutamine	18	Glutamine high-affinity transport system; membrane component	C, 805
<i>glnQ</i>		18	Glutamine high-affinity transport system	805
<i>glnR</i>	Glutamine	24	Level of glutaminyl-tRNA synthetase	C
<i>glnS</i>	Glutamine	16	Glutaminyl-tRNA synthetase (EC 6.1.1.18)	A, 864, 916, 1199
<i>glnT</i>	Glutamine	(75)	Levels of glutamine tRNA 1 and glutamine synthetase	B
<i>glnU</i>	Glutamine	15	<i>supB</i> ; glutamine tRNA 1 (tandemly duplicated gene)	B, C, 341, 587, 864
<i>glnV</i>	Glutamine	15	<i>supE</i> , <i>Su2</i> , <i>sull</i> ; glutamine tRNA 2 (tandemly duplicated gene)	B, C, 341, 587, 864
<i>glpA</i>	Glycerol phosphate	49	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), large subunit	A, B, C, 208, 301
<i>glpB</i>	Glycerol phosphate	49	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit	208, 301
<i>glpC</i>	Glycerol phosphate	49	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), small subunit	208, 301
<i>glpD</i>	Glycerol phosphate	75	<i>glyD</i> ; <i>sn</i> -glycerol-3-phosphate dehydrogenase (aerobic)	A, 980, 981
<i>glpE</i>	Glycerol phosphate	75	Gene of <i>glp</i> regulon	981
<i>glpF</i>	Glycerol phosphate	89	Facilitated diffusion of glycerol	A
<i>glpG</i>	Glycerol phosphate	75	Gene of <i>glp</i> regulon	981
<i>glpK</i>	Glycerol phosphate	89	Glycerol kinase (EC 2.7.1.30)	A, 215, 844
<i>glpQ</i>	Glycerol phosphate	49	Glycerol-3-phosphate diesterase	C, 619
<i>glpR</i>	Glycerol phosphate	75	Regulatory gene	A, 979, 981
<i>glpT</i>	Glycerol phosphate	49	<i>sn</i> -Glycerol-3-phosphate permease	A, B, C, 301, 303
<i>gltA</i>	Glutamate	16	<i>glut</i> ; citrate synthase (EC 4.1.3.7)	A, C, 110, 492, 795, 1174, 1184
<i>gltB</i>	Glutamate	70	<i>aspB</i> ; glutamate synthase, large subunit	A, B, C, 178, 360, 824
<i>gltD</i>	Glutamate	70	<i>aspB</i> ; glutamate synthase, small subunit	178, 360, 824
<i>gltE</i>	Glutamate	81	Glutamyl-tRNA synthetase; possible regulatory subunit	A
<i>gltF</i>	Glutamate	70	Regulatory gene?	178
<i>gltH</i>	Glutamate	(21)	Requirement	A
<i>gltM</i>	Glutamate	(43)	Level of glutamyl-tRNA synthetase activity	A
<i>gltR</i>	Glutamate	92	Regulatory gene for glutamate permease	A
<i>gltS</i>	Glutamate	82	<i>gltC</i> ; glutamate permease	A
<i>gltT</i>	Glutamate	90	<i>tgtB</i> ; glutamate tRNA 2; in <i>rrnB</i> operon	B, C, 587, 858, 885
<i>gltU</i>	Glutamate	85	<i>tgtC</i> ; glutamate tRNA 2; in <i>rrnC</i> operon	B, 587
<i>gltV</i>	Glutamate	90	<i>tgtE</i> ; glutamate tRNA 2; in <i>rrnE</i> operon	B, 587
<i>gltW</i>	Glutamate	56	Glutamate tRNA 2; in <i>rrnG</i> operon	C, 587
<i>gltX</i>	Glutamate	52	Catalytic subunit for glutamyl-tRNA synthetase (EC 6.1.1.17)	A, 131, 961, D
<i>glyA</i>	Glycine	55	Serine hydroxymethyltransferase (EC 2.1.2.1)	A, C, 859, 860, 1039
<i>glyS</i>	Glycine	80	<i>gly-act</i> ; glycine-tRNA synthetase (EC 6.1.1.14)	A, 132, 566
<i>glyT</i>	Glycine	90	<i>supA36</i> , <i>sumA</i> , <i>sup15B</i> ; glycine tRNA 2	A, B, C, 587
<i>glyU</i>	Glycine	62	<i>suA36</i> , <i>sufD</i> , <i>sumB</i> , <i>supT</i> ; glycine tRNA 1	A, 587
<i>glyV</i>	Glycine	95	<i>suA58</i> , <i>suA78</i> ; glycine tRNA 3 (duplicate gene, tandemly triplicated)	A, B, 341, 587
<i>glyW</i>	Glycine	42	<i>suA58</i> , <i>suA78</i> ; glycine tRNA 3 (duplicate gene)	A, C, 587, 1117
<i>gnd</i>		44	Gluconate-6-phosphate dehydrogenase, (EC 1.1.1.44) decarboxylating	A, C, 788

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>gntR</i>	Gluconate	76	Regulatory gene for <i>edd</i> ; transport and phosphorylation of gluconate	A, B
<i>gntS</i>	Gluconate	95	<i>gntM</i> , <i>usgA</i> ; second system for transport and possibly phosphorylation of gluconate	B
<i>gntT</i>	Gluconate	75	<i>gntM</i> , <i>usgA</i> ; high-affinity transport of gluconate	A, B, 515
<i>gntV</i>	Gluconate	97	Glukokinase, thermosensitive	515
<i>gor</i>		77	Glutathione oxidoreductase (EC 1.6.4.2)	C, 308, 407
<i>gpp</i>		85	Guanosine pentaphosphatase activity	B, 14, 84
<i>gprA</i>		0	Replication of certain lambdoid phage	812
<i>gprB</i>		0	Replication of certain lambdoid phage	812
<i>gpsA</i>		81	<i>sn</i> -Glycerol-3-phosphate dehydrogenase [NAD(P) ⁺] (EC 1.1.1.94)	A, B
<i>gpt</i>		6	<i>gpp</i> , <i>gxu</i> ; guanine-hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	A, B, 523, 810, 881, 906
<i>grpD</i>		71	Initiation of phage lambda DNA replication; host DNA synthesis	B
<i>grpE</i>		57	Phage lambda replication; host DNA synthesis	B
<i>grx</i>		19	Glutaredoxin	473, 594, 934
<i>gshA</i>		58	Glutathione synthetase (EC 6.3.2.2)	B, 404, 431
<i>gsk</i>		13	Guanosine kinase	B
<i>guaA</i>	Guanine	54	<i>gua_b</i> ; GMP synthetase (EC 6.3.4.1)	A, B, 1097
<i>guaB</i>	Guanine	54	<i>gua_a</i> ; IMP dehydrogenase (EC 1.2.1.14)	A, B, 1089, 1090, 1094
<i>guaC</i>	Guanine	3	GMP reductase (EC 1.6.6.8)	A, F, 751, 912
<i>guaR</i>	Guanine	54	Regulatory gene	1096
<i>gurB</i>		74	Utilization of methyl-β-D-glucuronide; possibly <i>crp</i>	A
<i>gurC</i>		(18)	Utilization of methyl-β-D-glucuronide	A
<i>gurD</i>		(68)	Utilization of methyl-β-D-glucuronide	A
<i>gyrA</i>	Gyrase	48	<i>nalA</i> ; DNA gyrase (EC 5.99.1.3), subunit A; resistance or sensitivity to nalidixic acid	A, B, C, 497, 732, 733, 1208
<i>gyrB</i>	Gyrase	83	<i>acrB</i> , <i>cou</i> , <i>himB</i> , <i>nalC</i> , <i>pcbA</i> ; DNA gyrase (EC 5.99.1.3), subunit B; resistance or sensitivity to coumermycin	B, C, 4, 5, 732, 733, 1197
<i>hemA</i>	Hemin	27	Glutamyl-tRNA dehydrogenase	A, 42
<i>hemB</i>	Hemin	8	<i>ncf</i> ; 5-aminolevulinatase dehydratase (EC 4.2.1.24) activity	A, B, 642
<i>hemC</i>	Hemin	86	<i>popE</i> ; porphobilinogen deaminase (EC 4.3.1.18)	B, 539, 965, 966, 1091
<i>hemD</i>	Hemin	86	Uroporphyrinogen III synthase (EC 4.2.1.75)	B, 539, 540, 965, 966
<i>hemE</i>	Hemin	90	<i>hemC</i> ; uroporphyrinogen decarboxylase (EC 4.1.1.37)	A
<i>hemF</i>	Hemin	17	<i>popB</i> , <i>sec</i> ; coproporphyrinogen III oxidase (EC 1.3.3.3)	A
<i>hemG</i>	Hemin	87	Protoporphyrinogen oxidase activity	C
<i>hemH</i>	Hemin	11	<i>hemG</i> , <i>popA</i> ; ferrochelatase (EC 4.99.1.1)	A
<i>het</i>		84	<i>cop</i> ; binding of DNA sequences in <i>oriC</i> region to outer membrane; possibly structural gene for DNA-binding protein	A, C
<i>herC</i>		62	Suppressor of ColE1 mutation in primer RNA	564
<i>hflB</i>		69	Lysogeny and level of phage lambda <i>cII</i> protein	62
<i>hflC</i>		95	<i>hflA</i> ; high frequency of lysogenization by phage lambda	61
<i>hflK</i>		95	<i>hflA</i> ; high frequency of lysogenization by phage lambda	61
<i>himA</i>		37	<i>hid</i> ; integration host factor (IHF), α subunit; site-specific recombination	C, 727, 728
<i>himD</i>		20	<i>hip</i> ; integration host factor (IHF), β subunit; site-specific recombination	C, 332, 567
<i>hipA</i>		34	Frequency of persistence following inhibition of murein synthesis	759, 760
<i>hisA</i>	Histidine	44	<i>N</i> -(5'-phospho-L-ribosylformimino)-5-amino-1-(5'-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	A
<i>hisB</i>	Histidine	44	Imidazoleglycerolphosphate dehydratase (EC 4.2.1.19) and histidinol phosphate phosphatase (EC 3.1.3.15)	A, 193, 410
<i>hisC</i>	Histidine	44	Histidinol phosphate aminotransferase (EC 2.6.1.9)	A, 409, 410
<i>hisD</i>	Histidine	44	L-Histidinol:NAD ⁺ oxidoreductase (EC 1.1.1.23)	A, C, 192
<i>hisE</i>	Histidine	44	See <i>hisI</i>	A
<i>hisF</i>	Histidine	44	Cyclase	A
<i>hisG</i>	Histidine	44	ATP phosphoribosyltransferase (EC 2.4.2.17)	A, B, C
<i>hisH</i>	Histidine	44	Amido transferase	A
<i>hisI</i>	Histidine	44	<i>hisE</i> ; phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19), phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	A, 192

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>hisJ</i>	Histidine	50	Histidine-binding protein of high-affinity histidine transport system	C
<i>hisM</i>	Histidine	50	Histidine transport	592
<i>hisP</i>	Histidine	50	Histidine permease	C, 592
<i>hisR</i>	Histidine	(86)	<i>hisT</i> ; histidine tRNA	B, 485, 587
<i>hisS</i>	Histidine	54	Histidinyl-tRNA synthetase (EC 6.1.1.21)	B, C, 345
<i>hisT</i>	Histidine	50	<i>asuC</i> , <i>leuK</i> ; pseudouridylate synthase I	B, C, 29–31, 708, 807, 984
<i>hlpA</i>		4	<i>skp</i> ; histonelike protein HLP-I (BH1); DNA-binding nucleoid-associated protein	1, 210, 469, 621, G
<i>hns</i>		6	Histonelike protein HLP-II (HU, BH2, HD, NS); DNA-binding protein	870
<i>hpt</i>		3	Hypoxanthine phosphoribosyltransferase	A
<i>hsdM</i>	Host specificity	99	<i>hs</i> , <i>hsm</i> , <i>hsp</i> , <i>rm</i> ; host modification; DNA methylase M	A, C, 660
<i>hsdR</i>	Host specificity	99	<i>hs</i> , <i>hsp</i> , <i>hsr</i> , <i>rm</i> ; host restriction; endonuclease R	A, C, 660
<i>hsdS</i>	Host specificity	99	<i>hss</i> ; specificity determinant for <i>hsdM</i> and <i>hsdR</i>	A, C, 391, 660, 767
<i>htpG</i>		11	Heat shock protein C 62.5	65
<i>htpR</i>			See <i>rpoH</i>	
<i>hupB</i>		10	Histonelike protein HU-1 (HU-β, NS1)	551, 552, 1053
<i>hydA</i>		58	Hydrogenase 1 activity	557, 629, 962
<i>hydB</i>		59	Hydrogenase activity	629, 962, 1161
<i>hydC</i>		77	Formate hydrogenlyase activity and fumarate-dependent H ₂ uptake; possibly nickel metabolism	1187
<i>hydD</i>		77	Formate hydrogen-lyase activity and fumarate-dependent H ₂ uptake	1187
<i>hydE</i>		59	Hydrogenase activity	188
<i>hydL</i>		65	<i>hup?</i> ; hydrogenase L, possibly same as hydrogenase 3; hydrogen uptake	629, 1047
<i>iap</i>		59	Alkaline phosphatase isozyme conversion	B, 512, 780
<i>icd</i>		26	Isocitrate dehydrogenase, NADP ⁺ specific (EC 1.1.1.42)	B, C
<i>iclR</i>		91	Regulatory gene for <i>aceBA</i> operon	A, C
<i>ileR</i>		100	<i>avr</i> , <i>ftrA?</i> ; negative regulatory gene of <i>thr</i> and <i>ilv</i> operons	532, 533, 1164
<i>ileS</i>	Isoleucine	0	Isoleucyl-tRNA synthetase (EC 1.1.1.5)	A, B, 549, 741, 899, 1102, 1192, 1196
<i>ileT</i>	Isoleucine	87	<i>tilA</i> ; isoleucine tRNA 1; in <i>rrnA</i> operon	B, 587
<i>ileU</i>	Isoleucine	72	<i>tilD</i> ; isoleucine tRNA 1; in <i>rrnD</i> operon	B, 587
<i>ileV</i>	Isoleucine	5	Isoleucine tRNA 1; in <i>rrnH</i> operon	C, 587
<i>ileX</i>	Isoleucine	67	Isoleucine tRNA 2	766
<i>ilvA</i>	Isoleucine-valine	85	<i>ile</i> ; threonine deaminase (EC 4.2.1.16)	A, B, C, 14, 285, 623
<i>ilvB</i>	Isoleucine-valine	83	Acetohydroxy acid synthase I (EC 4.1.3.18), valine-sensitive, large subunit	A, B, C, 349, 350, 448, 543, 993, 1167
<i>ilvC</i>	Isoleucine-valine	85	<i>ilvA</i> ; ketol-acid reductoisomerase (EC 1.1.1.86)	A, B, C, 14, 70, 1165
<i>ilvD</i>	Isoleucine-valine	85	<i>ilvB</i> ; dihydroxyacid dehydratase (EC 4.2.1.9)	A, B, C, 14, 285, 623
<i>ilvE</i>	Isoleucine-valine	85	<i>ilvC</i> , <i>ilvJ</i> ; branched-chain amino-acid aminotransferase (EC 2.6.1.42)	A, B, C, 14, 168, 285, 606, 623, 664, 1166
<i>ilvF</i>	Isoleucine-valine	54	Acetohydroxy acid synthase (valine insensitive) activity	A
<i>ilvG</i>	Isoleucine-valine	85	Acetohydroxy acid synthase II (EC 4.1.3.18), valine-insensitive, large subunit	A, B, C, 14, 285, 623, 670
<i>ilvH</i>	Isoleucine-valine	2	Acetohydroxy acid synthase III (EC 4.1.3.18), valine-sensitive, small subunit	A, B, C, 1037
<i>ilvI</i>	Isoleucine-valine	2	Acetohydroxy acid synthase III (EC 4.1.3.18), valine-sensitive, large subunit	A, B, C, 447, 1037
<i>ilvJ</i>	Isoleucine-valine	2	Acetohydroxy acid synthase IV (EC 4.1.3.18), valine-insensitive	C
<i>ilvM</i>	Isoleucine-valine	85	Acetohydroxy acid synthase II (EC 4.1.3.18), valine-insensitive, small subunit	623, 664, 670, 1166
<i>ilvN</i>	Isoleucine-valine	83	Acetohydroxy acid synthase II (EC 4.1.3.18), valine-sensitive, small subunit	349, 1167
<i>ilvR</i>	Isoleucine-valine	100	Positive regulatory gene of <i>thr</i> and <i>ilv</i> operons	533
<i>ilvU</i>	Isoleucine-valine	7	Regulation of <i>ileS</i> and modification of isoleucine tRNA 2 and valine tRNA 2	C
<i>ilvY</i>	Isoleucine-valine	85	Positive regulatory locus for <i>ilvC</i>	B, C, 14, 1165
<i>infA</i>		20	Protein chain initiation factor 1	960
<i>infB</i>		69	<i>ssyG</i> ; protein chain initiation factor 2	C, 510, 776, 865, 866, 868, 999–1001

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>infC</i>		38	<i>fit?</i> ; protein chain initiation factor 3	B, C, 158, 249, 306, 717, 878, 1170, 1190
<i>inm</i>		(79)	Susceptibility to mutagenesis by nitrosoguanidine	C
<i>ior</i>		45	Radiation sensitivity, particularly γ rays; recombination ability decreased	317
<i>katC</i>	Catalase	7	Catalase activity	B
<i>katE</i>	Catalase	38	Biosynthesis of catalase hydroperoxidase HPII (III)	661, 662
<i>katF</i>	Catalase	59	<i>nur</i> ; biosynthesis of catalase hydroperoxidase HPII (III) and exonuclease III; regulatory gene	662, 950, 955
<i>katG</i>	Catalase	89	Catalase-peroxidase hydroperoxidase HPI (I), structural gene	663, 1112
<i>kba</i>		69	Ketose-bis-phosphate aldolase, temperature-sensitive enzyme, active on D-tagatose-1,6-diphosphate	B
<i>kbl</i>		81	2-Amino-3-ketobutyrate CoA ligase (EC 2.3.1.29) (glycine acetyltransferase)	28, 892
<i>kdgK</i>	Ketodeoxygluconate	78	Ketodeoxygluconokinase (EC 2.7.1.45)	A
<i>kdgR</i>	Ketodeoxygluconate	40	Regulatory gene for <i>kdgK</i> , <i>kdgT</i> , and <i>eda</i>	A
<i>kdgT</i>	Ketodeoxygluconate	88	2-Keto-3-deoxy-D-gluconate transport system	A, B, 698
<i>kdpA</i>	Potassium dependence	16	<i>kac</i> ; high-affinity potassium transport system; probably K^+ -stimulated ATPase	A, B
<i>kdpB</i>	Potassium dependence	16	<i>kac</i> ; high-affinity potassium transport system	A, B
<i>kdpC</i>	Potassium dependence	16	<i>kac</i> ; high-affinity potassium transport system	A, B
<i>kdpD</i>	Potassium dependence	16	<i>kac</i> ; high-affinity potassium transport system; regulatory gene	A, B
<i>kdsA</i>		27	3-Deoxy-D-manno-octulosonic acid 8-phosphate synthase	1180, 1181
<i>kdsB</i>		85	CTP: CMP-3-deoxy-D-manno-octulosonate cytidyltransferase	382, 383, 848
<i>kefB</i>	K^+ efflux	73	<i>trkB</i> ; NEM-activable K^+/H^+ antiporter	A, 54
<i>kefC</i>	K^+ efflux	1	<i>trkC</i> ; NEM-activable K^+/H^+ antiporter	54
<i>ksgA</i>	Kasugamycin	1	S-Adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase	A, C, 101, 1138
<i>ksgB</i>	Kasugamycin	37	Second step (high-level) resistance to kasugamycin	A, B, C, 415
<i>ksgC</i>	Kasugamycin	12	Kasugamycin resistance; affects ribosomal protein S2	B
<i>ksgD</i>	Kasugamycin	31	Kasugamycin resistance	C
<i>lacA</i>	Lactose	8	<i>a</i> , <i>lacAc</i> ; galactoside acetyltransferase (EC 2.3.1.18)	A, B, 453
<i>lacI</i>	Lactose	8	<i>i</i> ; regulatory gene; repressor protein of <i>lac</i> operon	A, B, C, 478
<i>lacY</i>	Lactose	8	<i>y</i> ; galactoside permease (M protein)	A, B, C
<i>lacZ</i>	Lactose	8	<i>z</i> ; β -D-galactosidase (EC 3.2.1.23)	A, B, C, 547
<i>lamB</i>	Lambda	92	<i>malB</i> ; phage lambda receptor protein; maltose high-affinity uptake system	A, B, C
<i>lct</i>	Lactate	81	D-Lactate dehydrogenase (EC 1.1.1.27)	A, 653
<i>lepA</i>		55	GTP-binding membrane protein; function unknown	700, 701
<i>lepB</i>		55	Leader peptidase (signal peptidase I)	C, 700, 1183
<i>leuA</i>	Leucine	2	α -Isopropylmalate synthase (EC 4.1.3.12)	A, C, 368
<i>leuB</i>	Leucine	2	β -Isopropylmalate dehydrogenase (EC 1.1.1.85)	A, C
<i>leuC</i>	Leucine	2	α -Isopropylmalate isomerase subunit	A, C
<i>leuD</i>	Leucine	2	α -Isopropylmalate isomerase subunit	A, C
<i>leuJ</i>	Leucine	14	<i>flr</i> ; regulation of <i>leu</i> and <i>ilv</i> operons	532
<i>leuK</i>	Leucine	19	See <i>hisT</i>	
<i>leuR</i>	Leucine	79	Level of leucyl-tRNA synthetase	B
<i>leuS</i>	Leucine	15	Leucyl-tRNA synthetase (EC 6.1.1.4)	A, B, C, 444
<i>leuT</i>	Leucine	(86)	Leucine tRNA 1 (duplicate gene)	B, 485, 587
<i>leuU</i>	Leucine	(69)	Leucine tRNA 2	B, 587, 1150
<i>leuV</i>	Leucine	(99)	Leucine tRNA 1 (duplicate gene, tandemly triplicated)	B, 289, 341, 587
<i>leuW</i>	Leucine	15	Leucine tRNA 3	B, C, 587, 864
<i>leuX</i>	Leucine	97	<i>Su-6</i> , <i>supP</i> ; leucine tRNA 5	B, C, 587, 1092, 1210
<i>leuY</i>	Leucine	10	Level of leucyl-tRNA synthetase	B
<i>leuZ</i>	Leucine	42	Leucine tRNA 4	587
<i>lev</i>	Levallorphan	(9)	Resistance to levallorphan	B
<i>lexA</i>		92	<i>exrA</i> , <i>spr</i> , <i>tsl</i> , <i>umuA</i> ; regulatory gene for SOS operon	A, B, C
<i>lig</i>	Ligase	52	<i>dnaL</i> , <i>pdeC</i> ; DNA ligase	A, B, 513
<i>linB</i>	Lincomycin	(29)	High-level resistance to lincomycin	A
<i>lip</i>	Lipoate	15	Requirement	A, C
<i>lit</i>		25	Phage T4 late-gene expression; locus of element e14	B, 553, 554, L
<i>livG</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system; membrane component	C, 791

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>livH</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system; membrane component	B, C, 790
<i>livJ</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system; periplasmic binding protein for leucine, isoleucine, and valine	B, C, 613, 1098
<i>livK</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system; leucine-specific periplasmic binding protein	B, C, 613, 790, 791, 1098
<i>livL</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport	P
<i>livM</i>	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport	790, 791
<i>livR</i>	Leucine, isoleucine, and valine	20	<i>lss</i> , <i>lstR</i> ; high-affinity branched-chain amino acid transport system; regulatory gene; repressor protein	B, 25, P
<i>lon</i>	Long form	10	<i>capR</i> , <i>deg</i> , <i>dir</i> , <i>muc</i> ; DBA-binding, ATP-dependent protease La	A, B, C, 366
<i>lpcA</i>	Lipopolysaccharide core	6	<i>tfrA</i> ; lipopolysaccharide core synthesis; resistance to phages T4, T7, and P1; deficiency in conjugation	A, B, Q
<i>lpcB</i>	Lipopolysaccharide core	(65)	<i>pon</i> ; lipopolysaccharide core synthesis	A
<i>lpd</i>		3	<i>dhl</i> ; lipamide dehydrogenase (NADH) (EC 1.6.4.3)	A, B, C, 422, 1029, 1044
<i>lpp</i>	Lipoprotein	36	<i>mlpA</i> ; murein lipoprotein structural gene	B, C, 415
<i>lpxA</i>		4	UDP-N-acetylglucosamine acetyltransferase	210, 229, 230
<i>lpxB</i>		4	<i>pgsB</i> ; lipid A disaccharide synthase	210, 229, 230, 1103
<i>lrs</i>		3	Level of leucine tRNA	C
<i>lspA</i>		1	Prolipoprotein signal peptidase (SPaseII)	B, 505, 549, 741, 899, 1102, 1192, 1195, 1196, 1212
<i>lysA</i>	Lysine	61	Diaminopimelate decarboxylase (EC 4.1.1.20)	A, C, 1054, 1056
<i>lysC</i>	Lysine	91	<i>apk</i> ; aspartokinase III	A, B, C, 175, 176
<i>lysR</i>	Lysine	61	Positive regulatory gene	1055, 1056
<i>lysS</i>	Lysine	62	Lysyl tRNA synthetase, constitutive	186, 310
<i>lysT</i>	Lysine	17	<i>suß</i> , <i>supG</i> , <i>supL</i> ; lysine tRNA (duplicated gene)	B, 341, 587, 880, 1211
<i>lysU</i>	Lysine	94	Lysyl tRNA synthetase, inducible	186, 1137
<i>lysV</i>	Lysine	52	<i>supN</i> ; lysine tRNA (duplicated gene)	A, 587, 1121, D
<i>lysX</i>	Lysine	60	Lysine excretion	A
<i>lytA</i>		58	Tolerance to β -lactams; autolysis defective?	442, 1004
<i>mac</i>	Macrolide	(27)	Erythromycin growth dependence	A
<i>mafA</i>		1	Maintenance of F-like plasmids	A, B
<i>mafB</i>		2	Maintenance of F-like plasmids	B
<i>malE</i>	Maltose	92	<i>malB</i> ; periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis	A, B, C, 75, 76, 294, 816
<i>malF</i>	Maltose	92	<i>malB</i> ; maltose transport; cytoplasmic membrane protein	A, B, 353
<i>malG</i>	Maltose	92	<i>malB</i> ; active transport of maltose and maltodextrins	B, 251, 344
<i>malI</i>	Maltose	36	Production of oligosaccharide, probably glucose polymer	300
<i>malK</i>	Maltose	92	<i>malB</i> ; maltose permeation	A, B, C, 75, 76, 379, 816
<i>malM</i>	Maltose	92	<i>molA</i> ; periplasmic protein; function not known	380
<i>malP</i>	Maltose	75	<i>malA</i> ; maltodextrin phosphorylase (EC 2.4.1.1)	A, B, C
<i>malQ</i>	Maltose	75	<i>malA</i> ; amyloamylase (EC 2.4.1.25)	A
<i>malS</i>	Maltose	80	α -Amylase	348
<i>malT</i>	Maltose	75	<i>malA</i> ; positive regulatory gene for <i>mal</i> regulon	A, B, C, 209
<i>manA</i>	Mannose	36	<i>pni</i> ; mannose-6-phosphate isomerase (EC 5.3.1.8)	A, C, 737, 738
<i>manC</i>	Mannose	(88)	<i>mni</i> ; D-mannose isomerase regulation; utilization of D-lyxose	B
<i>manX</i>	Mannose	40	<i>gptB</i> , <i>mpt</i> , <i>ptsL</i> , <i>ptsM</i> , <i>ptsX</i> ; mannose phosphotransferase system, protein II-A (III)	313, 315, 831, 1175
<i>manY</i>	Mannose	40	<i>pel</i> , <i>ptsP</i> , <i>ptsM</i> ; mannose phosphotransferase system; Pel protein II-P; penetration of phage lambda	313, 315, 831, 1175
<i>manZ</i>	Mannose	40	<i>gptB</i> , <i>mpt</i> , <i>ptsM</i> , <i>ptsX</i> ; mannose phosphotransferase system, enzyme IIB (II M)	831, 1175
<i>marA</i>		34	Multiple antibiotic resistance; tetracycline efflux system	369
<i>mcrA</i>		25	<i>rglA</i> ; restriction of DNA at 5-methyl cytosine residues; locus of <i>e14</i>	887, 888, 890, L
<i>mcrB</i>		98	<i>rglB</i> ; restriction of DNA at 5-methylcytosine residues	887, 888, 890, 924, 925
<i>mdh</i>		70	Malate dehydrogenase (EC 1.1.1.37)	A, 718, 1067, 1144
<i>mdoA</i>	Membrane-derived oligosaccharides	23	Membrane-localized component of glucosyl transferase system	112

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>mdoB</i>	Membrane-derived oligosaccharides	99	Phosphoglycerol transferase I activity	325, 521
<i>melA</i>	Melibiose	93	<i>mel-7</i> ; α -galactosidase (EC 3.2.1.22)	A, 433, 648, 1003, 1162
<i>melB</i>	Melibiose	93	<i>mel-4</i> ; thiomethylgalactoside permease II	A, 433, 1203
<i>melR</i>	Melibiose	93	Regulatory gene	1162
<i>menA</i>	Menaquinone	89	Conversion of 1,4-dihydroxy-2-naphthoate to demethylmenaquinone	A, B
<i>menB</i>	Menaquinone	49	1,4-Dihydroxy-2-naphthoate synthase	B, C, 996, 997
<i>menC</i>	Menaquinone	49	Conversion of chorismate to <i>o</i> -succinylbenzoate	B, C, 996, 997
<i>menD</i>	Menaquinone	49	Menaquinone biosynthesis	C, 996, 997
<i>menE</i>	Menaquinone	49	<i>o</i> -Succinylbenzoate-CoA synthase	996
<i>mepA</i>		50	Murein DD-endopeptidase	503
<i>metA</i>	Methionine	91	<i>met</i> ₃ ; homoserine transsuccinylase (EC 2.3.1.46)	A, C, 734, N
<i>metB</i>	Methionine	89	<i>met-1</i> , <i>met</i> ₁ ; cystathionine γ -synthase (EC 4.2.99.9)	A, C, 288, 405, 406, 569, 647, 946
<i>metC</i>	Methionine	65	Cystathionine γ -lyase (EC 4.4.1.1)	A, 82, 735
<i>metD</i>	Methionine	5	High-affinity uptake of D- and L-methionine	A, B
<i>metE</i>	Methionine	86	<i>metB</i> ₁₂ ; tetrahydropteroyltryglutamate methyltransferase (EC 2.1.1.14)	A, 14, 15, 822
<i>metF</i>	Methionine	89	<i>met-2</i> , <i>met</i> ₂ ; 5,10-methylenetetrahydrofolate reductase (EC 1.1.1.68)	A, C, 405, 569, 946, 947, 1111
<i>metG</i>	Methionine	(46)	Methionyl-tRNA synthetase	A, B, 245
<i>metH</i>	Methionine	91	B ₁₂ -dependent homocysteine-N ⁵ -methyltetrahydrofolate transmethylase	A, B, 822, N
<i>metJ</i>	Methionine	89	Regulatory gene; repressor of <i>metF</i>	A, B, C, 405, 569, 647, 946, 1020
<i>metK</i>	Methionine	64	Methionine adenosyltransferase (EC 2.5.1.6)	A, B, 127, 705
<i>metL</i>	Methionine	89	<i>metM</i> ; aspartokinase II (EC 2.7.2.4), homoserine dehydrogenase II (EC 1.1.1.3)	A, C, 288, 405, 406, 569, 946, 1214
<i>metR</i>	Methionine	86	Regulatory gene for <i>metE</i> and <i>metH</i>	1124
<i>metT</i>	Methionine	15	Methionine tRNA _m (duplicated gene)	B, C, 341, 587, 864
<i>metY</i>	Methionine	(69)	Methionine tRNA ₂ (tandemly duplicated gene)	B, 510, 511, 587
<i>metZ</i>	Methionine	(60)	Methionine tRNA ₁ (tandemly duplicated gene)	B, 587, 769
<i>mgIA</i>	Methyl-galactoside	46	<i>mgIP</i> ; methyl-galactoside transport and galactose taxis, cytoplasmic membrane protein	A, B, C, 115, 440, 736, 975, W
<i>mgIB</i>	Methyl-galactoside	46	<i>mgIP</i> ; galactose-binding protein; receptor for galactose taxis	A, B, C, 440, 736, 975, 982, W
<i>mgIC</i>	Methyl-galactoside	46	<i>mgIP</i> ; methyl-galactoside transport and galactose taxis	A, B, C, 440, 736, W
<i>mgID</i>	Methyl-galactoside	45	Regulatory locus for methyl-galactoside transport	B, C
<i>mgIR</i>	Methyl-galactoside	(16)	R-MG; regulatory gene	A
<i>mgI</i>	Magnesium transport	93	Mg ²⁺ transport, system II	B
<i>miaA</i>		95	<i>trpX</i> ; 2-methylthio-N ⁶ -isopentyladenosine hypermodification	357
<i>micF</i>		48	<i>stc</i> ; regulatory antisense RNA affecting <i>ompF</i> expression	20, 743, 747, 756
<i>minB</i>	Minicell	26	Formation of minute cells containing no DNA; complex locus; position of division septum	A, C, 259
<i>mioC</i>		84	Initiation of chromosome replication	659
<i>mmrA</i>		85	Recovery in rich medium following UV irradiation	990
<i>mng</i>	Manganese	(39)	Resistance or sensitivity to manganese	A
<i>mopA</i>	Morphogenesis of phages	94	<i>groE</i> , <i>groEL</i> , <i>hdh</i> , <i>tabB</i> ; head assembly of phages T4 and lambda	A, B, C
<i>mopB</i>	Morphogenesis of phages	94	<i>groE</i> , <i>groES</i> , <i>hdh</i> , <i>tabB</i> ; head assembly of phages T4 and lambda	A, B, C
<i>motA</i>	Motility	42	<i>flaJ</i> ; flagellar paralysis	A, B, 258, 1016
<i>motB</i>	Motility	42	<i>flaJ</i> ; flagellar paralysis	A, B, 1016, 1038
<i>mraA</i>	Murein	2	D-Alanine carboxypeptidase	A
<i>mraB</i>	Murein	2	D-Alanine requirement; cell wall peptidoglycan biosynthesis	A
<i>mrba</i>	Murein	90	UDP-N-acetylglucosaminyl-3-enolpyruvate reductase activity	A
<i>mrbb</i>	Murein	90	D-Alanine requirement; cell wall peptidylglycan biosynthesis	A
<i>mrbc</i>	Murein	90	Cell wall peptidylglycan biosynthesis	A
<i>mrca</i>	Murein	75	<i>ponA</i> ; peptidoglycan synthetase; cell wall synthesis; penicillin-binding protein 1A	B, C, 140

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>mrcB</i>	Murein	75	<i>ponB</i> ; peptidoglycan synthetase; cell wall synthesis; penicillin-binding protein 1Bs	B, C, 140, 562, 917
<i>mrda</i>		15	<i>pbpA</i> ; cell shape; penicillin-binding protein 2	B, C, 35, 36, 78, 1048, 1049
<i>mrdb</i>		15	<i>rodA</i> ; cell shape; sensitivity to radiation and drugs	A, B, C, 35, 36, 78, 1048, 1049
<i>mre</i>		71	Cell shape; sensitivity to antibiotics	1147
<i>mrr</i>		99	Restriction of methylated adenine	454
<i>mtlA</i>	Mannitol	81	Mannitol-specific enzyme II of phosphotransferase system	A, B, C, 628
<i>mtlC</i>	Mannitol	81	Regulatory locus	A, B
<i>mtlD</i>	Mannitol	81	Mannitol-1-phosphate dehydrogenase (EC 1.1.1.17)	A, B, C
<i>mtl</i>	Methyltryptophan	69	Resistance to 5-methyltryptophan	A, B
<i>mul</i>		83	Mutability of UV-irradiated phage λ	A
<i>murC</i>	Murein	2	L-Alanine-adding enzyme	A, B, C
<i>murE</i>	Murein	2	<i>meso</i> -Diaminopimelate-adding enzyme	A, B
<i>murF</i>	Murein	2	<i>mra</i> ; D-alanyl:D-alanine-adding enzyme	A, B
<i>murG</i>	Murein	2	Murein or envelope biosynthesis	C
<i>murH</i>	Murein	99	Peptidoglycan synthesis, late stage	238
<i>mutD</i>	Mutator	5	See <i>dnaQ</i>	
<i>mutH</i>	Mutator	61	<i>mutR</i> , <i>prv</i> ; methyl-directed mismatch repair	A, B, 398, 399
<i>mutL</i>	Mutator	95	<i>mut-25</i> ; methyl-directed mismatch repair	A
<i>mutM</i>	Mutator	82	G · C → T · A transversions	165
<i>mutS</i>	Mutator	59	Methyl-directed mismatch repair	A, B
<i>mutT</i>	Mutator	2	A · T → C · G transversions; a nucleoside triphosphate	A, B, 9, 91
<i>mutY</i>	Mutator	64	G · C → T · A transversions	800
<i>mvrA</i>		7	Resistance or sensitivity to methyl viologen	753
<i>nadA</i>	NAD	17	<i>nicA</i> ; quinolinate synthetase, A protein	A
<i>nadB</i>	NAD	56	<i>nicB</i> ; quinolinate synthetase, B protein	A
<i>nadC</i>	NAD	3	Quinolinate phosphoribosyl transferase	A, C, 422, 912
<i>nagA</i>	N-Acetylglucosamine	16	N-Acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	A, 864
<i>nagB</i>	N-Acetylglucosamine	16	<i>glmD</i> ; glucosamine-6-phosphate deaminase	A, 864, 916
<i>nagE</i>	N-Acetylglucosamine	16	<i>ptsN</i> ; N-acetylglucosamine-specific enzyme II of phosphotransferase system	C, 864, 916
<i>nalA</i>	Nalidixic acid	48	See <i>gyrA</i>	
<i>nalB</i>	Nalidixic acid	58	Resistance or sensitivity to nalidixic acid	A
<i>nalD</i>	Nalidixic acid	89	Penetration of nalidixic acid through outer membrane	484
<i>nanA</i>		70	N-Acetylneuraminatase lyase (aldolase) (EC 4.1.3.3)	1143
<i>nanT</i>		70	Sialic acid transport	1143
<i>narG</i>	Nitrate reductase	27	<i>chlC</i> , <i>narC</i> ; nitrate reductase (EC 1.7.99.4), α subunit	A, B, C, 299, 427, 643, 644, 725, 920, 1024
<i>narH</i>	Nitrate reductase	27	<i>chlC</i> ; nitrate reductase (EC 1.7.99.4), β subunit	A, B, C, 299, 1024
<i>narI</i>	Nitrate reductase	27	<i>chlI</i> ; cytochrome b_{NR} , nitrate reductase (EC 1.7.99.4), γ subunit	A, B, C, 427, 920, 1024
<i>narJ</i>	Nitrate reductase	27	Nitrate reductase (EC 1.7.99.4), δ subunit	1024
<i>narK</i>	Nitrate reductase	27	Regulatory gene	1046
<i>narL</i>	Nitrate reductase	27	<i>narR</i> ; regulatory gene	518, 1046
<i>narX</i>	Nitrate reductase	27	<i>narR</i> ; regulatory gene	1046
<i>narZ</i>	Nitrate reductase	33	Cryptic gene(s) encoding a second nitrate reductase	114
<i>ndh</i>		22	Respiratory NADH dehydrogenase	B, C
<i>neaB</i>	Neamine	74	Resistance to neamine	A, B
<i>nek</i>		73	<i>amk</i> ; resistance to neomycin, kanamycin, and other aminoglycoside antibiotics	A, B
<i>nfnA</i>		80	Sensitivity to nitrofurantoin	967
<i>nfnB</i>		13	Sensitivity to nitrofurantoin	967
<i>nfo</i>		47	Endonuclease IV	233, W
<i>nfsA</i>	Nitrofurazone sensitivity	(21)	Nitrofurantoin reductase I activity	B
<i>nfsB</i>	Nitrofurazone sensitivity	(11)	Nitrofurantoin reductase I activity	B
<i>nirB</i>	Nitrate reductase	74	<i>nirD</i> ; NADH-nitrate oxidoreductase (EC 1.6.6.4)	522, 526, 679, 680
			aproprotein, structural gene	
<i>nirC</i>	Nitrate reductase	26	NADH-nitrate reductase (EC 1.6.6.4) activity	B
<i>nmpC</i>	New membrane protein	13	Outer membrane porin protein; locus of <i>qsr</i> prophage	B, 462
<i>non</i>	Nonmucoid	45	Capsule formation	A
<i>nrdA</i>		49	<i>dnaF</i> ; ribonucleoside diphosphate reductase (EC 1.17.4.1) subunit B1	A, B, C, 173, 802, 1118

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>nrdB</i>		49	<i>ftsB</i> ; ribonucleoside diphosphate reductase (EC 1.17.4.1) subunit B1	A, B, C, 173, 593, 1082
<i>nth</i>		36	“Endonuclease III”; a DNA glycosylase and phosphoric monoester lyase	53, 234, 1163
<i>nupC</i>		52	Transport of nucleosides, except guanosine	B, C
<i>nupG</i>		64	Transport of nucleosides	B, 800, 1171
<i>nusA</i>		69	Transcription termination; L factor	B, C, 407, 510, 511, 608, 776, 868, 949
<i>nusB</i>		10	<i>groNB</i> ; transcription termination; L factor	B, C, 509, 1071
<i>nuvA</i>		9	Uridine thiolation factor A activity	B
<i>nuvC</i>		43	Thiazole biosynthesis; 4-thiouridine modification of tRNA; near-UV sensitivity and resistance	940
<i>ompA</i>	Outer membrane protein	22	<i>con</i> , <i>tolG</i> , <i>tut</i> ; outer membrane protein 3a (II*;G;d), structural gene	A, B, C, 207, 403
<i>ompC</i>	Outer membrane protein	48	<i>meoA</i> , <i>par</i> ; outer membrane protein 1b (Ib;c), structural gene	B, C, 745, 746
<i>ompF</i>	Outer membrane protein	21	<i>cmlB</i> , <i>coa</i> , <i>cry</i> , <i>tolF</i> ; outer membrane protein 1a (Ia;b;F), structural gene	B, C, 239, 506, 507, 697, 1085
<i>ompR</i>	Outer membrane protein	75	<i>ompB</i> ; positive regulatory gene for <i>ompC</i> and <i>ompF</i>	B, C, 213, 364, 748, 749, 785, 1191
<i>ompT</i>		13	Outer membrane protein 3b (a), a protease	387, 411, 412, 933
<i>oppA</i>		28	Oligopeptide transport; periplasmic binding protein	A, B, C, 22, 468
<i>oppB</i>		28	Oligopeptide transport	22, 468
<i>oppC</i>		28	Oligopeptide transport	22, 468
<i>oppD</i>		28	Oligopeptide transport	22, 468
<i>oppE</i>		28	Oligopeptide transport	22
<i>opr</i>		(19)	Rate of degradation of aberrant subunit proteins of RNA polymerase	988
<i>ops</i>		63	Level of exopolysaccharide production	1219
<i>optA</i>		4	Deoxyguanosine 5'-triphosphate triphosphohydrolase activity; phage T7 DNA metabolism	C, 72
<i>oriC</i>	Origin of replication	84	<i>poh?</i> ; origin of replication of chromosome	B, C, 152, 542, 578, 712, 819, 820, 987, 1057, 1073, 1152
<i>oriJ</i>	Origin of replication	30	Origin function of <i>rac</i> prophage	C
<i>osmZ</i>		27	<i>bglY</i> , <i>cur</i> , <i>fimG</i> , <i>topX</i> ; DNA supercoiling; expression of genes subject to osmotic regulation	232, 461, 1027
<i>otsA</i>		42	Trehalose phosphate synthase (EC 2.4.1.15) production	374
<i>otsB</i>		42	Trehalose phosphate synthase (EC 2.4.1.15) production	374
<i>pabA</i>	<i>p</i> -Aminobenzoate	74	<i>p</i> -Aminobenzoate synthetase, CoII	A, 555
<i>pabB</i>	<i>p</i> -Aminobenzoate	40	<i>p</i> -Aminobenzoate synthetase, CoII	A, B, 384
<i>pac</i>		31	Phenylacetate degradation	216
<i>panB</i>	Pantothenate	3	Ketopantoate hydroxymethyltransferase (EC 4.1.2.12)	A, B, C
<i>panC</i>	Pantothenate	3	Pantothenate synthetase (EC 6.3.2.1)	A, B, C
<i>panD</i>	Pantothenate	3	Aspartate 1-decarboxylase (EC 4.1.1.11)	A, B, C
<i>panF</i>	Pantothenate	71	Pantothenate permease	1133
<i>pat</i>		89	Putrescine aminotransferase activity	989
<i>pbpA</i>			See <i>mrda</i>	B, C, 149
<i>pbpB</i>			See <i>ftsI</i>	
<i>pck</i>		75	Phosphoenolpyruvate carboxykinase (EC 4.1.1.49)	C
<i>pcnB</i>		4	Plasmid copy number	666
<i>pcsA</i>		82	Cell division; chromosome segregation	B
<i>pdxA</i>	Pyridoxine	1	Requirement	A, B, C
<i>pdxB</i>	Pyridoxine	50	Placement of 5, 5', and 6' carbons into pyridine ring of pyridoxine	A, B, 30, 31
<i>pdxC</i>			See <i>serC</i>	
<i>pdxH</i>	Pyridoxine	36	Pyridoxinephosphate oxidase	A, B, 415
<i>pdxJ</i>	Pyridoxine	56	Requirement	A, B
<i>pepD</i>	Peptides	6	<i>pepH</i> ; peptidase D, a dipeptidase	A, B, 145, 571
<i>pepN</i>	Peptides	21	Aminopeptidase N	B, C, 55–57, 145, 336, 719–721
<i>pfkA</i>		89	6-Phosphofructokinase I (EC 2.7.1.11)	A, B, 240, 456
<i>pfkB</i>		38	Level of 6-phosphofructokinase II; suppressor of <i>pfkA</i>	A, B, C, 241
<i>pfl</i>		20	Pyruvate formate-lyase	B, 839
<i>pgi</i>		91	Glucosephosphate isomerase (EC 5.3.1.9)	A, N
<i>pgk</i>		63	Phosphoglycerate kinase (EC 2.7.2.3)	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
<i>pgl</i>		17	<i>blu</i> ; 6'-phosphogluconolactonase (EC 3.1.1.31)	A
<i>pgm</i>		(15)	Phosphoglucomutase (EC 2.7.5.1)	A
<i>pgpA</i>		10	Phosphatidylglycerophosphate phosphatase, membrane bound	500
<i>pgpB</i>		28	Phosphatidylglycerophosphate phosphatase, membrane bound	500
<i>pgsA</i>		42	Phosphatidylglycerophosphate synthetase (EC 2.7.8.5)	A, B, C, 386
<i>pgsB</i>			See <i>lpxB</i>	
<i>pheA</i>	Phenylalanine	57	Chorismate mutase-P-prephenate dehydrogenase	A, B, C, 488
<i>pheP</i>	Phenylalanine	13	Phenylalanine-specific transport system	C
<i>pheR</i>	Phenylalanine	94	Regulatory gene for <i>pheA</i>	C, 395
<i>pheS</i>	Phenylalanine	37	<i>phe-act</i> ; phenylalanyl-tRNA synthetase (EC 6.1.1.20), α subunit	A, B, C, 306, 320, 727, 728, 867, 1035, 1036, 1190
<i>pheT</i>	Phenylalanine	37	<i>pheS</i> ; phenylalanyl-tRNA synthetase (EC 6.1.1.20), β subunit	A, B, C, 306, 320, 727, 728, 867, 1035, 1190
<i>pheU</i>	Phenylalanine	94	Phenylalanyl-tRNA (duplicate gene)	357, 587, 976
<i>pheV</i>	Phenylalanine	64	Phenylalanyl-tRNA (duplicate gene)	166, 587, 1179
<i>phnD</i>		92	<i>psiD</i> ; carbon-phosphorus lyase	1148, U
<i>phoA</i>	Phosphate	9	Alkaline phosphatase (EC 3.1.3.1)	A, B, C, 184, 1011
<i>phoB</i>	Phosphate	9	<i>phoRc</i> , <i>phoT</i> ; positive regulatory gene for <i>pho</i> regulon	A, B, C, 691, 693, 695, 1006, 1157
<i>phoE</i>	Phosphate	6	<i>ompE</i> ; outer membrane pore protein e (E,Ic,NmpAB), structural gene	C, 450, 810, 827, 1106
<i>phoM</i>	Phosphate	100	Positive regulatory gene for <i>pho</i> regulon	C, 17, 671, 694, 695, 1105, 1156, 1159
<i>phoR</i>	Phosphate	9	<i>nmpB</i> , <i>phoR1</i> , <i>R1pho</i> ; positive and negative regulatory gene for <i>pho</i> regulon	A, B, C, 692, 695, 1006, 1157
<i>phoS</i>	Phosphate	84	See <i>pstS</i>	
<i>phoT</i>	Phosphate	84	See <i>pstA</i> , <i>pstB</i> , and <i>phoU</i>	
<i>phoU</i>	Phosphate	84	<i>phoT</i> ; high-affinity phosphate-specific transport system, regulatory gene	C, 16, 18, 779, 1065
<i>phr</i>	Photoreactivation	16	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	A, B, 495, 957, 958
<i>phxB</i>	Phi-X	17	Adsorption of ϕ X174	B
<i>pil</i>	Pili	98	See <i>fim</i>	
<i>pin</i>		26	Inversion of adjacent DNA; locus of element e14	312, 563, 861, 862, 1139, L
<i>pit</i>	P _i transport	77	Low-affinity P _i transport	A, 308, 309
<i>pldA</i>		86	Detergent-resistant phospholipase A	A, 14, 263, 264, 471, 472, 579
<i>pldB</i>		86	Lysophospholipase L ₂	14, 472, 579, 580
<i>plsA</i>	Phospholipid synthesis	11	See <i>adk</i>	
<i>plsB</i>	Phospholipid synthesis	92	Glycerolphosphate acyltransferase activity	A, B, C, 646
<i>plsX</i>	Phospholipid synthesis	24	Glycerolphosphate auxotrophy in <i>plsB</i> background	620
<i>pncA</i>	Pyridine nucleotide cycle	39	<i>nam</i> ; nicotinamide deamidase (EC 3.5.1.19)	A, B
<i>pncB</i>	Pyridine nucleotide cycle	(21)	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	C
<i>pnp</i>		69	Polynucleotide phosphorylase (EC 2.7.7.8)	A, C, 227, 318, 470, 873, 897, 898, 1078
<i>pntA</i>		35	Pyridine nucleotide transhydrogenase (EC 1.6.1.1), α subunit	B, 197, 198
<i>pntB</i>		35	Pyridine nucleotide transhydrogenase (EC 1.6.1.1), β subunit	197, 198
<i>poaR</i>		63	Regulation of proline oxidase production	A
<i>pog</i>		70	Growth of phage P1	C
<i>polA</i>	Polymerase	87	<i>resA</i> ; DNA polymerase I (EC 2.7.7.7)	A, B, C
<i>polB</i>	Polymerase	2	DNA polymerase II (EC 2.7.7.7)	A
<i>polC</i>	Polymerase	4	<i>dnaE</i> ; DNA biosynthesis; DNA polymerase III α subunit	A, B, C, 998, 1103, 1168
<i>popC</i>	Porphyrin	4	Synthesis of δ -aminolevulinate	A
<i>popD</i>	Porphyrin	(1)	Level of 5-aminolevulinate dehydratase (EC 4.2.1.24) activity	A, B
<i>poxA</i>		95	Regulatory gene for <i>poxB</i>	C
<i>poxB</i>		19	Pyruvate oxidase (EC 1.2.2.2), structural gene	C, 185, 396, 397
<i>ppc</i>	Phosphoenolpyruvate	89	<i>glu</i> , <i>asp</i> ; phosphoenolpyruvate carboxylase (EC 4.1.1.31)	A, B, C, 354, 943
<i>pps</i>	Phosphoenolpyruvate	37	Phosphoenolpyruvate synthase	A
<i>prfA</i>		27	<i>asuA</i> ?, <i>sueB</i> , <i>uar</i> , <i>ups</i> ?; protein release factor 1	174, 941, 942
<i>prfB</i>		62	<i>supK</i> ; protein release factor 2	564

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>prlA</i>		73	<i>secY</i> ; protein export; membrane protein	10, 181, 311, 516, 517, 1002, 1009
<i>prlB</i>		85	Protein export	311
<i>prlC</i>		71	Protein export	311
<i>prlD</i>		2	Protein export	60
<i>prmA</i>		71	<i>prm-1</i> ; methylation of 50S ribosomal subunit protein L11	B
<i>prmB</i>		51	<i>prm-2</i> ; methylation of 50S ribosomal subunit protein L3	B
<i>proA</i>	Proline	6	<i>proI</i> ; γ -glutamyl phosphate reductase (EC 1.2.1.41)	A, C, 272, 450, 687, 797
<i>proB</i>	Proline	6	<i>pro2</i> ; γ -glutamyl kinase (EC 2.7.2.11)	A, C, 272, 450, 687, 797
<i>proC</i>	Proline	9	<i>pro3</i> , <i>pro2</i> ; pyrroline-5-carboxylate reductase (EC 1.5.1.2)	A, C, 262, 273
<i>proK</i>	Proline	80	<i>proV</i> ; proline tRNA 1	341, 587, 599
<i>proL</i>	Proline	47	<i>proW</i> ; proline tRNA 2	587
<i>proM</i>	Proline	86	<i>proU</i> ; proline tRNA 3	587
<i>proP</i>	Proline	93	Low-affinity transport system for glycine betaine and proline; proline permease II	C, 392, 393, 716
<i>proS</i>	Proline	5	Prolyl-tRNA synthetase (EC 1.1.1.15)	C
<i>proT</i>	Proline	83	Proline transport	B, C
<i>proU</i>	Proline	57	<i>osrA</i> ; high-affinity transport system for glycine betaine and proline	319, 392, 394, 418, 716, I
<i>proV</i>	Proline	57	High-affinity transport system for glycine betaine and proline; glycine betaine-binding protein	319, 341, 394, I
<i>proW</i>	Proline	57	High-affinity transport system for glycine betaine and proline	I
<i>prp</i>	Propionate	97	Propionate metabolism	C
<i>prr</i>		31	γ -Aminobutyraldehyde (pyrroline) dehydrogenase activity	989
<i>prs</i>		26	Phosphoribosylpyrophosphate synthetase (EC 2.7.6.1)	C, 480–482
<i>psd</i>		95	Phosphatidylserine decarboxylase	A, B
<i>psiF</i>		9	Induced by phosphate starvation	184, 1158, U
<i>pssA</i>		56	Phosphatidylserine synthetase (EC 2.7.8.8)	B, C
<i>pssR</i>		85	Regulatory gene	1026
<i>pstA</i>		84	<i>phoR2b</i> , <i>phoT</i> , <i>R2pho</i> ; high-affinity phosphate-specific transport system	A, B, C, 16, 18, 922, 1066
<i>pstB</i>		84	<i>phoT</i> ; high-affinity phosphate-specific transport system, cytoplasmic membrane protein?	A, B, C, 16, 18, 638, 922, 1066
<i>pstC</i>		84	<i>phoW</i> ; high-affinity phosphate-specific transport system, cytoplasmic membrane component	A, B, C, 16, 18, 922, 1066
<i>pstS</i>		84	<i>nmpA</i> , <i>phoR2a</i> , <i>phoS</i> , <i>R2pho</i> ; high-affinity phosphate-specific transport system; periplasmic phosphate-binding protein	A, B, C, 16, 18, 146, 520, 639, 683, 754, 922, 1065, 1066
<i>pta</i>		50	Phosphotransacetylase (EC 2.3.1.8) activity	B, C
<i>pth</i>		26	Peptidyl-tRNA hydrolase	A
<i>ptr</i>		61	Protease III	C, 61, 200, 295, 296, 330
<i>ptsG</i>	Phosphotransferase system	25	<i>car</i> , <i>CR</i> , <i>gpt</i> , <i>gptA</i> , <i>tgl</i> , <i>umg</i> ; glucosylphosphotransferase enzyme II	A, B, 123, 314
<i>ptsH</i>	Phosphotransferase system	52	<i>ctr</i> , <i>Hpr</i> ; phosphohistidinoprotein-hexose phosphotransferase (EC 2.7.1.69)	A, B, 134–136, 270, 271, 835, 945
<i>ptsI</i>	Phosphotransferase system	52	<i>ctr</i> ; phosphotransferase system enzyme I	A, B, 134–136, 270, 271, 835, 945
<i>purA</i>	Purine	95	<i>ade_k</i> , <i>Ad₄</i> ; adenylosuccinate synthetase (EC 6.3.4.4)	A
<i>purB</i>	Purine	25	<i>ade_h</i> ; adenylosuccinate lyase (EC 4.3.2.2)	A, L
<i>purC</i>	Purine	53	<i>ade_g</i> ; phosphoribosylaminoimidazole-succinocarboxamide synthetase (EC 6.3.2.6)	A, 833
<i>purD</i>	Purine	90	<i>adh_a</i> ; phosphoribosylglycineamide synthetase (EC 6.3.4.13)	A
<i>purE</i>	Purine	12	<i>ade₃</i> , <i>ade_f</i> , <i>Pur₂</i> ; phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21), catalytic subunit	A, C, 548, 1095
<i>purF</i>	Purine	50	<i>ade_{u,b}</i> , <i>purC</i> ; amidophosphoribosyl transferase (EC 2.4.2.14)	A, C, 689, 807
<i>purG</i>	Purine		See <i>purM</i>	
<i>purH</i>	Purine	90	<i>ade_i</i> , <i>purJ</i> ; phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	A
<i>purI</i>	Purine		See <i>purL</i>	
<i>purK</i>	Purine	12	<i>purE₂</i> ; phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21), CO ₂ -fixing subunit	548, 1095

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>purL</i>	Purine	55	<i>purL</i> ; phosphoribosylformylglycineamide synthetase (EC 6.3.5.3); homologous to <i>purG</i> of <i>S. typhimurium</i>	A, C, 479
<i>purM</i>	Purine		<i>purG</i> ; phosphoribosylaminoimidazole synthetase (EC 6.3.3.1) homologous to <i>purL</i> of <i>S. typhimurium</i>	A, B, C, 479, 1022, 1023
<i>purN</i>	Purine	54	<i>ade_c</i> ; 5'-phosphoribosylglycinamide transformylase (EC 2.1.2.2)	1023
<i>purP</i>	Purine	84	High-affinity adenine transport	156, E
<i>purR</i>	Purine	36	Regulatory gene for <i>pur</i> regulon	568, 919, S
<i>pus</i>		20	Effect of suppressors on <i>relB</i> mutations	C
<i>putA</i>	Proline utilization	23	<i>poaA</i> ; proline dehydrogenase (EC 1.5.99.8)	A, C, 752, 778
<i>putP</i>	Proline utilization	23	Proline utilization; major proline permease	C, 752, 777, 778
<i>pykF</i>		37	Pyruvate kinase F	365
<i>pyrA</i>	Pyrimidine	1	See <i>car</i>	
<i>pyrB</i>	Pyrimidine	97	Aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit	A, B, C, 474, 578, 637, 789, 838, 921, 1119
<i>pyrC</i>	Pyrimidine	24	Dihydroorotase (EC 3.5.2.3)	A, 48, 530, 1178
<i>pyrD</i>	Pyrimidine	21	Dihydroorotate oxidase (EC 1.3.3.1)	A, 530, 618
<i>pyrE</i>	Pyrimidine	82	Orotate phosphoribosyltransferase (EC 2.4.2.10)	A, C, 876, 877
<i>pyrF</i>	Pyrimidine	28	Orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	A, 282, 530, 1120
<i>pyrG</i>	Pyrimidine	60	CTP synthetase (EC 6.3.4.2)	B, C, 1169
<i>pyrH</i>	Pyrimidine	5	UMP kinase	A
<i>pyrI</i>	Pyrimidine	97	Aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit	C, 474, 838, 921
<i>pyrS</i>	Pyrimidine	81	Regulatory gene	809
<i>qin</i>		35	kim; cryptic lambdoid phage	122, 316
<i>qmeA</i>		29	<i>gts</i> ; unspecified membrane defect	A
<i>qmeC</i>		74	Unspecified membrane defect; tolerance to glycine, penicillin sensitivity	A
<i>qmeD</i>		61	Unspecified membrane defect; tolerance to glycine, penicillin sensitivity	A
<i>qmeE</i>		37	Unspecified membrane defect	A
<i>qsr'</i>		13	Cryptic lambdoid phage	23, 109, 462, 545
<i>rac</i>		30	Defective prophage <i>rac</i> ; see <i>recE</i> and <i>oriI</i>	A, C, 1176, 1177
<i>radA</i>		100	Sensitivity to γ and UV radiation and methyl methanesulfonate	280
<i>radC</i>		82	Sensitivity to radiation	A, 322
<i>ranA</i>		56	RNA metabolism	A
<i>rap</i>		26	Growth of phage lambda	419
<i>ras</i>	Radiation sensitivity	(10)	Sensitivity to UV and X-rays	A
<i>rbsA</i>	Ribose	84	<i>rbsP</i> , <i>rbsT</i> ; D-ribose high-affinity transport system; membrane-associated protein	85, 502, 667
<i>rbsB</i>	Ribose	84	<i>rbsP</i> ; D-ribose periplasmic binding protein	502, 667
<i>rbsC</i>	Ribose	84	<i>rbsP</i> , <i>rbsT</i> ; D-ribose high-affinity transport system; membrane-associated protein	85, 502, 667
<i>rbsD</i>	Ribose	84	<i>rbsP</i> ; D-ribose high-affinity transport system; membrane-associated protein	85
<i>rbsK</i>	Ribose	84	Ribokinase (EC 2.7.1.15)	A, B, C, 475, 502, 667
<i>rbsR</i>	Ribose	84	Regulatory gene	667
<i>rcsA</i>		43	Positive regulatory gene for capsule synthesis	390, 1107
<i>rcsB</i>		48	Positive regulatory gene for capsule synthesis	133, 390
<i>rcsC</i>		48	Negative regulatory gene for capsule synthesis	133, 390
<i>rdgA</i>		16	Dependence of growth upon <i>recA</i> gene product	C
<i>rdgB</i>		64	Dependence of growth and viability upon <i>recA</i> function	204
<i>recA</i>	Recombination	58	<i>lexB</i> , <i>recH</i> , <i>rnmB</i> , <i>tif</i> , <i>umuB</i> , <i>zab</i> ; general recombination, DNA repair and induction of phage lambda	A, B, C
<i>recB</i>	Recombination	61	<i>rroA</i> ; recombination and DNA repair; exonuclease V (EC 3.1.11.5)	A, B, C, 296, 329, 965
<i>recC</i>	Recombination	61	Recombination and DNA repair; exonuclease V (EC 3.1.11.5)	A, B, C, 296, 331, 333, 965
<i>recD</i>	Recombination	61	Recombination and DNA repair; exonuclease V (EC 3.1.11.5), α subunit	19, 94, 328
<i>recE</i>	Recombination	30	<i>rac</i> ; locus of <i>rac</i> prophage; recombination and DNA repair; exonuclease VIII	A, B, C, 342, 1177
<i>recF</i>	Recombination	83	<i>uvrF</i> ; recombination and DNA repair	A, B, C, 4, 27, 100, 894
<i>recJ</i>	Recombination	62	Recombination and DNA repair	668, 669
<i>recN</i>	Recombination	57	<i>radB</i> ; recombination and DNA repair	658, 851, 926, 963, 964

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>recO</i>	Recombination	56	Conjugational recombination and DNA repair	585
<i>recQ</i>	Recombination	86	Conjugational recombination and DNA repair	14, 508, 781, 782
<i>relA</i>	Relaxed	60	RC; regulation of RNA synthesis; stringent factor; ATP:GTP 3'-pyrophosphotransferase	A, B
<i>relB</i>	Relaxed	35	Regulation of RNA synthesis	B, C, 74
<i>relE</i>	Relaxed	35	Locus in <i>relB</i> operon; function unknown	74, 372
<i>relF</i>	Relaxed	35	Locus in <i>relB</i> operon; function unknown	74, 372
<i>relX</i>	Relaxed	60	Control of synthesis of guanosine-5'-diphosphate-3'-diphosphate	B
<i>rep</i>		85	<i>dasC?</i> , <i>mmrA?</i> ; Rep helicase, a single-stranded DNA dependent ATPase	A, B, C, 14, 70, 92, 93, 285, 376
<i>rer</i>		90	Resistance to UV and γ -radiation	B
<i>rfa</i>	Rough	81	<i>con</i> , <i>lpsA</i> , <i>phx</i> ; cluster of genes coding for enzymes involved in lipopolysaccharide core biosynthesis	A, B
<i>rfaB</i>	Rough	81	UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase	226
<i>rfaC</i>	Rough	81	Lipopolysaccharide core biosynthesis; proximal hexose	C
<i>rfaD</i>	Rough	81	ADP-L-Glycero-D-mannoheptose-6-epimerase	C, 211
<i>rfaG</i>	Rough	81	Lipopolysaccharide core biosynthesis; glucosyltransferase I	226
<i>rfaH</i>	Rough	87	<i>sfrB</i> ; lipopolysaccharide core biosynthesis; positive regulation of production of glucosyltransferase; expression of <i>tra</i> operon of F factor; antiterminator	226, 900
<i>rfaI</i>	Rough	81	UDP-D-galactose:(glucosyl)lipopolysaccharide- α -1,3-D-galactosyltransferase	226
<i>rfaJ</i>	Rough	81	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase	226
<i>rfaM</i>	Rough	81	Lipopolysaccharide core biosynthesis; glucosyltransferase II	226
<i>rfaP</i>	Rough	81	Lipopolysaccharide core biosynthesis; phosphorylation of core heptose	C
<i>rfbA</i>	Rough	45	TDP-glucose pyrophosphorylase	A
<i>rfbB</i>	Rough	45	TDP-glucose oxidoreductase	A
<i>rfbD</i>	Rough	45	TDP-rhamnose synthetase	A
<i>rfe</i>	Rough	(85)	Synthesis of enterobacterial common antigen and O antigen	B, 731
<i>rff</i>	Rough	(85)	Synthesis of enterobacterial common antigen	B, 731
<i>rhaA</i>	Rhamnose	88	L-Rhamnose isomerase (EC 5.3.1.14)	A, 1101
<i>rhaB</i>	Rhamnose	88	Rhamnulokinase (EC 2.7.1.5)	A, 1101
<i>rhaD</i>	Rhamnose	88	Rhamnulose-1-phosphate aldolase (EC 4.1.2.19)	A, 1101
<i>rhaR</i>	Rhamnose	88	<i>rhaC</i> ; positive regulatory gene	1101
<i>rhaS</i>	Rhamnose	88	<i>rhaC</i> ; positive regulatory gene	1101
<i>rho</i>		85	<i>nitA</i> , <i>psu</i> , <i>rnsC</i> , <i>SuA</i> , <i>sun</i> , <i>tsu</i> ; transcription termination factor rho; polarity suppressor	A, B, C, 14, 70, 143, 167, 650, 713, 857
<i>RhsA</i>		81	Repetitive sequence responsible for duplications within chromosome	652, 944
<i>RhsB</i>		77	Repetitive sequence responsible for duplications within chromosome	652, 944
<i>RhsC</i>		16	Repetitive sequence responsible for duplications within chromosome	944
<i>RhsD</i>		12	Repetitive sequence responsible for duplications within chromosome	944
<i>ribA</i>	Riboflavin	28	GTP cyclohydrolase II	C, 58, 1088
<i>ribB</i>	Riboflavin	66	Block before 6,7-dimethyl-8-ribityllumazine	C, 58, 1088
<i>ribC</i>	Riboflavin	40	Riboflavin synthase	58, 1088, R
<i>ridA</i>		71	Transcription and translation; rifampin and kasugamycin dependence	C
<i>ridB</i>		85	Transcription and translation; rifampin dependence	236
<i>rimB</i>	Ribosomal modification	38	Maturation of 50S ribosomal subunit	A, 415
<i>rimC</i>	Ribosomal modification	(26)	Maturation of 50S ribosomal subunit	A
<i>rimD</i>	Ribosomal modification	(88)	Maturation of 50S ribosomal subunit	A
<i>rimE</i>	Ribosomal modification	72	Modification of ribosomal proteins	B, 730
<i>rimF</i>	Ribosomal modification	1	<i>res</i> ; ribosomal modification	A
<i>rimG</i>	Ribosomal modification	(1)	<i>ramB</i> ; modification of 30S ribosomal subunit protein S4	A
<i>rimH</i>	Ribosomal modification	14	<i>stsB</i> ; ribosomal modification	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
<i>rimI</i>	Ribosomal modification	99	Modification of 30S ribosomal subunit protein S18; acetylation of N-terminal alanine	B, C, 1209
<i>rimJ</i>	Ribosomal modification	(32)	Modification of 30S ribosomal subunit protein S5; acetylation of N-terminal alanine	B, 524, 1209
<i>rimL</i>	Ribosomal modification	(33)	Modification of 30S ribosomal subunit protein L7; acetylation of N-terminal serine	C
<i>rit</i>		89	Affects thermostability of 50S ribosomal subunit	B
<i>rlpA</i>		15	A minor lipoprotein	1076
<i>rlpB</i>		15	A minor lipoprotein	1076
<i>rna</i>	RNase	14	<i>rns</i> , <i>rnsA</i> ; RNase I	A
<i>rnb</i>	RNase	29	RNase II	B, C
<i>rnc</i>	RNase	55	RNase III	A, B, 699, 787, 1160
<i>rnd</i>	RNase	40	RNase D	C, 1216
<i>rne</i>	RNase	24	RNase E activity	B, C, 893
<i>rnh</i>	RNase	5	<i>dasF</i> , <i>herA</i> , <i>sdrA</i> , <i>sin</i> ; RNase H (EC 3.1.26.4)	C, 225, 550, 690, 771, 806, 813, 1108
<i>rnpA</i>	RNase	83	RNase P, protein component	435
<i>rnpB</i>	RNase	70	RNase P, RNA subunit, M1 RNA	B, C, 758, 895, 896, 952
<i>rodA</i>		15	See <i>mrdb</i>	
<i>rplA</i>		63	Ribose phosphate isomerase (EC 5.3.1.6), constitutive	A
<i>rplA</i>	Ribosomal protein, large	90	50S ribosomal subunit protein L1	A, B, C, 283, 491, 889
<i>rplB</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L2	A, B, 1222
<i>rplC</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L3	A, B, 1222
<i>rplD</i>	Ribosomal protein, large	73	<i>eryA</i> ; 50S ribosomal subunit protein L4	A, B, C, 1222
<i>rplE</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L5	A, B, 181
<i>rplF</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L6	A, B, 181
<i>rplI</i>	Ribosomal protein, large	96	50S ribosomal subunit protein L9	B, 974
<i>rplJ</i>	Ribosomal protein, large	90	50S ribosomal subunit protein L10	A, B, C, 203, 283, 491, 889
<i>rplK</i>	Ribosomal protein, large	90	<i>relC</i> ; 50S ribosomal subunit protein L11	A, B, C, 283, 491, 889
<i>rplL</i>	Ribosomal protein, large	90	50S ribosomal subunit protein L7/L12	A, B, C, 283, 491, 889
<i>rplM</i>	Ribosomal protein, large	70	50S ribosomal subunit protein L13	C, 514
<i>rplN</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L14	A, B, 181
<i>rplO</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L15	A, B, 181, 516
<i>rplP</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L16	A, B, 1222
<i>rplQ</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L17	A, B, C, 77, 181, 730
<i>rplR</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L18	A, B, 181
<i>rplS</i>	Ribosomal protein, large	57	50S ribosomal subunit protein L19	B, 164
<i>rplT</i>	Ribosomal protein, large	38	<i>pdzA</i> ; 50S ribosomal subunit protein L20	320
<i>rplU</i>	Ribosomal protein, large	69	50S ribosomal subunit protein L21	B
<i>rplV</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L22	A, B, 1222
<i>rplW</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L23	B, 1222
<i>rplX</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L24	A, B, 181, 235
<i>rplY</i>	Ribosomal protein, large	48	50S ribosomal subunit protein L25	B
<i>rpmA</i>	Ribosomal protein, large	69	50S ribosomal subunit protein L27	B
<i>rpmB</i>	Ribosomal protein, large	82	50S ribosomal subunit protein L28	B, C, 1031
<i>rpmC</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L29	A, B, 1222
<i>rpmD</i>	Ribosomal protein, large	73	50S ribosomal subunit protein L30	A, B, 181
<i>rpmE</i>	Ribosomal protein, large	89	50S ribosomal subunit protein L31	C
<i>rpmF</i>	Ribosomal protein, large	24	50S ribosomal subunit protein L32	524
<i>rpmG</i>	Ribosomal protein, large	82	50S ribosomal subunit protein L33	B, C, 1031
<i>rpmH</i>	Ribosomal protein, large	83	<i>rimA</i> , <i>ssaF</i> ; 50S ribosomal subunit protein L34	C, 823, O
<i>rpmI</i>	Ribosomal protein, large	38	50S ribosomal subunit protein A	1149
<i>rpmJ</i>	Ribosomal protein, large	73	50S ribosomal subunit protein X	181, 1149
<i>rpoA</i>	RNA polymerase	73	RNA polymerase (EC 2.7.7.6), α subunit	A, B, C, 77, 181, 730, 928, 929
<i>rpoB</i>	RNA polymerase	90	<i>groN</i> , <i>nitB</i> , <i>rif</i> , <i>ron</i> , <i>stl</i> , <i>stv</i> , <i>tabD</i> ; RNA polymerase (EC 2.7.7.6), β subunit	A, B, C, 283, 491, 889
<i>rpoC</i>	RNA polymerase	90	<i>tabD</i> ; RNA polymerase (EC 2.7.7.6), β subunit	A, B, C, 283, 889
<i>rpoD</i>	RNA polymerase	67	<i>alt</i> ; RNA polymerase (EC 2.7.7.6), σ^{70} subunit	B, C, 157, 677, 1086
<i>rpoH</i>	RNA polymerase	76	<i>fam</i> , <i>hin</i> , <i>htpR</i> ; RNA polymerase (EC 2.7.7.6), σ^{32} subunit; regulatory gene for proteins induced at high temperatures	C, 416, 417, 614, 792, 1098, 1116, 1213
<i>rpoN</i>	RNA polymerase	70	<i>glnF</i> , <i>ntaA</i> ; RNA polymerase (EC 2.7.7.6), σ^{60} subunit	B, C, 70, 177, 467, 494
<i>rpsA</i>	Ribosomal protein, small	21	<i>ssyF</i> ; 30S ribosomal subunit protein S1	B, C, 291, 841, 1001
<i>rpsB</i>	Ribosomal protein, small	4	30S ribosomal subunit protein S2	A, B, C

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>rpsC</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S3	A, B, 1222
<i>rpsD</i>	Ribosomal protein, small	73	<i>ramA</i> , <i>sud2</i> ; 30S ribosomal subunit protein S4	A, B, C, 77, 181
<i>rpsE</i>	Ribosomal protein, small	73	<i>eps</i> , <i>spcA</i> , <i>spc</i> ; 30S ribosomal subunit protein S5	A, B, 181
<i>rpsF</i>	Ribosomal protein, small	95	30S ribosomal subunit protein S6	A, B, 974
<i>rpsG</i>	Ribosomal protein, small	73	<i>K12</i> ; 30S ribosomal subunit protein S7	A, B, C
<i>rpsH</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S8	A, B, 181
<i>rpsI</i>	Ribosomal protein, small	70	30S ribosomal subunit protein S9	237, 514
<i>rpsJ</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S10	A, B, C
<i>rpsK</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S11	A, B, C, 77, 181
<i>rpsL</i>	Ribosomal protein, small	73	<i>strA</i> ; 30S ribosomal subunit protein S12	A, B, C
<i>rpsM</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S13	A, B, C, 77, 181
<i>rpsN</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S14	A, B, 181
<i>rpsO</i>	Ribosomal protein, small	69	<i>secC</i> ; 30S ribosomal subunit protein S15	B, C, 318, 324, 873, 898, 903, 1077, 1078, H
<i>rpsP</i>	Ribosomal protein, small	57	30S ribosomal subunit protein S16	B, 164
<i>rpsQ</i>	Ribosomal protein, small	73	<i>neaA</i> ; 30S ribosomal subunit protein S17	A, B, 1222
<i>rpsR</i>	Ribosomal protein, small	96	30S ribosomal subunit protein S18	A, B, 974
<i>rpsS</i>	Ribosomal protein, small	73	30S ribosomal subunit protein S19	A, B, 1222
<i>rpsT</i>	Ribosomal protein, small	0	<i>supS20</i> ; 30S ribosomal subunit protein S20	A, B, 681, 1196
<i>rpsU</i>	Ribosomal protein, small	67	30S ribosomal subunit protein S21	B, C, 157, 677
<i>rrfA</i>	rRNA 5S	87	5S rRNA gene of <i>rrnA</i> operon	B, C
<i>rrfB</i>	rRNA 5S	90	5S rRNA gene of <i>rrnB</i> operon	B, C
<i>rrfC</i>	rRNA 5S	85	5S rRNA gene of <i>rrnC</i> operon	B, C
<i>rrfD</i>	rRNA 5S	72	5S rRNA gene of <i>rrnD</i> operon	C
<i>rrfE</i>	rRNA 5S	90	5S rRNA gene of <i>rrnE</i> operon	B, C
<i>rrfG</i>	rRNA 5S	56	5S rRNA gene of <i>rrnG</i> operon	C
<i>rrfH</i>	rRNA 5S	5	5S rRNA gene of <i>rrnH</i> operon	C
<i>rrlA</i>	rRNA, 23S	87	23S rRNA gene of <i>rrnA</i> operon	A, B, C
<i>rrlB</i>	rRNA, 23S	90	23S rRNA gene of <i>rrnB</i> operon	B, C
<i>rrlC</i>	rRNA, 23S	85	23S rRNA gene of <i>rrnC</i> operon	B
<i>rrlD</i>	rRNA, 23S	72	23S rRNA gene of <i>rrnD</i> operon	B, C
<i>rrlE</i>	rRNA, 23S	90	23S rRNA gene of <i>rrnE</i> operon	B, C
<i>rrlG</i>	rRNA, 23S	56	23S rRNA gene of <i>rrnG</i> operon	B, C
<i>rrlH</i>	rRNA, 23S	5	23S rRNA gene of <i>rrnH</i> operon	C
<i>rrnA</i>	rRNA	87	<i>cqsA</i> ; rRNA operon	A, B, C, 578
<i>rrnB</i>	rRNA	90	<i>cqsE</i> , <i>rrnB1</i> ; rRNA operon	A, B, C, 89, 446
<i>rrnC</i>	rRNA	85	<i>cqsb</i> , <i>rrnB</i> , <i>rrnB2</i> ; rRNA operon	A, B, C, 446, 578
<i>rrnD</i>	rRNA	72	<i>cqsD</i> ; rRNA operon	B, C
<i>rrnE</i>	rRNA	90	<i>rrnD1</i> ; rRNA operon	B, C, 645
<i>rrnG</i>	rRNA	56	rRNA operon	B, C, 446
<i>rrnH</i>	rRNA	5	rRNA operon	C
<i>rrsA</i>	rRNA, 16S	87	16S rRNA gene of <i>rrnA</i> operon	B
<i>rrsB</i>	rRNA, 16S	90	16S rRNA gene of <i>rrnB</i> operon	B, C, 89, 121
<i>rrsC</i>	rRNA, 16S	85	16S rRNA gene of <i>rrnC</i> operon	B
<i>rrsD</i>	rRNA, 16S	72	16S rRNA gene of <i>rrnD</i> operon	B
<i>rrsE</i>	rRNA, 16S	90	16S rRNA gene of <i>rrnE</i> operon	B
<i>rrsG</i>	rRNA, 16S	56	16S rRNA gene of <i>rrnG</i> operon	B, C
<i>rrsH</i>	rRNA, 16S	5	16S rRNA gene of <i>rrnH</i> operon	C
<i>rts</i>		90	<i>ts-9</i> ; uncharacterized growth defect	A, B, C, 1079
<i>ruvA</i>		41	Filament formation and sensitivity to UV radiation	A, 37, 87, 1010
<i>ruvB</i>		41	Filament formation and sensitivity to UV radiation	87
<i>sad</i>		34	Succinate-semialdehyde dehydrogenase (EC 1.2.1.16), NAD dependent	C, 702
<i>sbaA</i>		97	Regulation of serine and branched-chain amino acid metabolism	C
<i>sbcB</i>		44	<i>xonA</i> ; exonuclease I; suppression of <i>recB recC</i> mutations	A, 846, 847, 879
<i>sbcC</i>		9	Suppression of <i>recB recC</i> mutations	657
<i>sbp</i>		89	Periplasmic sulfate-binding protein	456
<i>sbmA</i>		9	Sensitivity to microcin B17	622
<i>sdhA</i>		16	Succinate dehydrogenase (EC 1.3.99.1), flavoprotein subunit	A, C, 247, 1174, 1184
<i>sdhB</i>		16	Succinate dehydrogenase (EC 1.3.99.1), iron sulfur protein	A, C, 247, 1174, 1184
<i>sdhC</i>		16	<i>cybA</i> ; succinate dehydrogenase (EC 1.3.99.1), cytochrome <i>b</i> ₅₅₆	A, C, 763, 764

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>sdhD</i>		16	Succinate dehydrogenase (EC 1.3.99.1), hydrophobic subunit	A, C, 1174, 1184
<i>secA</i>		2	<i>azi</i> , <i>pea</i> ; secretion of envelope proteins	C, 71, 972, O
<i>secB</i>		81	Protein export	600, 601
<i>secD</i>		9	Protein export	361
<i>sefA</i>		4	Septum formation	B
<i>selA</i>	Selenium	81	<i>fdhA</i> ; selenium metabolism; biosynthesis or incorporation of selenocystein	632
<i>selB</i>	Selenium	81	<i>fdhA</i> ; selenium metabolism; biosynthesis or incorporation of selenocystein	632
<i>selC</i>	Selenium	82	<i>fdhC</i> ; selenium metabolism; selenocysteine tRNA	587, 632, 633
<i>semA</i>		40	Sensitivity to microcin E492	884
<i>serA</i>	Serine	63	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	A, 1100
<i>serB</i>	Serine	100	Phosphoserine phosphatase (EC 3.1.3.3)	A, C, 362, 799
<i>serC</i>	Serine	20	<i>pdxC</i> ; 3-phosphoserine aminotransferase (EC 2.6.1.52)	A, B, 291
<i>serR</i>	Serine	2	Level of seryl-tRNA synthetase	B
<i>serS</i>	Serine	20	Seryl-tRNA synthetase (EC 6.1.1.11)	A, 445
<i>serT</i>	Serine	(22)	<i>divE</i> ; serine tRNA 1	B, 587, 1081
<i>serU</i>	Serine	43	<i>supD</i> , <i>supH</i> , <i>Su-1</i> , <i>sul</i> ; serine tRNA 2	A, C, 587, 1041, 1093
<i>serV</i>	Serine	(58)	Serine tRNA 3	B, 587
<i>serW</i>	Serine	20	Serine tRNA 5 (duplicate gene)	587, 960
<i>serX</i>	Serine	23	Serine tRNA 5 (duplicate gene)	587
<i>sfic</i>		26	Cell division inhibition; locus of element e14	246, 684, L
<i>shiA</i>	Shikimate	43	Shikimate and dehydroshikimate permease	A
<i>sloB</i>	Slow growth	74	Low growth rate; tolerance to amdinopenicillin and nalidixic acid	B
<i>sodA</i>		88	Superoxide dismutase, manganese	172, 1080, 1109
<i>sodB</i>		36	Superoxide dismutase, iron	171, 172, 415, 798
<i>speA</i>	Spermidine	64	Arginine decarboxylase (EC 4.1.1.19)	A, 127
<i>speB</i>	Spermidine	64	Agmatinase (EC 3.5.3.11)	A, 127
<i>speC</i>	Spermidine	64	Ornithine decarboxylase (EC 4.1.1.17)	A, B, 127
<i>speD</i>	Spermidine	3	S-Adenosylmethionine decarboxylase (EC 4.1.1.50)	B, 1074, 1075
<i>speE</i>	Spermidine	3	Spermidine synthase (putrescine aminopropyltransferase) (EC 2.5.1.16)	1074, 1075
<i>spf</i>		87	"Spot 42" RNA	C, 869
<i>spoT</i>		82	Guanosine 3',5'-bis(diphosphate) 3'-pyrophosphatase	A, B
<i>sppA</i>		39	Protease IV, a signal peptide peptidase	498, 1070
<i>srlA</i>	Sorbitol	58	<i>gutA</i> , <i>sbl</i> ; D-glucitol-specific enzyme II of phosphotransferase system	A, B, C, 1193, 1194
<i>srlB</i>	Sorbitol	58	<i>gutB</i> ; D-glucitol (sorbitol)-specific enzyme III of phosphotransferase system	1193, 1194
<i>srlD</i>	Sorbitol	58	<i>gutD</i> , <i>sbl</i> ; glucitol (sorbitol)-6-phosphate dehydrogenase (EC 1.1.1.140)	A, B, C, 1193, 1194
<i>srlR</i>	Sorbitol	58	Regulatory gene	B, C
<i>srnA</i>		10	Degradation of stable RNA	A
<i>ssaD</i>		9	Suppression of <i>secA</i> mutation	361, 823
<i>ssaE</i>		50	Suppression of <i>secA</i> mutation	361
<i>ssaG</i>		41	Suppression of <i>secA</i> mutation	361
<i>ssaH</i>		94	Suppression of <i>secA</i> mutation	361
<i>ssb</i>	Single-strand binding	92	<i>exrB</i> , <i>lexC</i> ; single-strand DNA-binding protein	B, C
<i>ssp</i>		70	Stringent starvation protein	355, 356, 986
<i>ssr</i>		63	Stable 6S RNA	487, 627
<i>ssyA</i>		54	Suppressor of <i>secY</i> mutation	1000
<i>ssyB</i>		10	Suppressor of <i>secY</i> mutation	1001
<i>ssyD</i>		3	Suppressor of <i>secY</i> mutation	1001
<i>strC</i>	Streptomycin	7	<i>strB</i> ; low-level streptomycin resistance	A
<i>strM</i>	Streptomycin	77	Control of ribosomal ambiguity	A
<i>stsA</i>		84	Altered RNase activity	A
<i>sucA</i>	Succinate	16	<i>lys</i> + <i>met</i> ; succinate requirement; α -ketoglutarate dehydrogenase (decarboxylase component)	A, C, 151, 247, 248, 1174, 1184
<i>sucB</i>	Succinate	16	<i>lys</i> + <i>met</i> ; succinate requirement; α -ketoglutarate dehydrogenase (dihydrolipoyltranssuccinase component)	A, C, 151, 1028, 1029
<i>sucC</i>	Succinate	16	Succinyl-CoA synthetase (EC 6.2.1.5), β subunit	150, 151, 1028, 1029
<i>sucD</i>	Succinate	16	Succinyl-CoA synthetase (EC 6.2.1.5), α subunit	150, 151
<i>suhA</i>		77	Induction of heat shock genes	1099

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>sulA</i>		22	<i>sfiA</i> , <i>suf</i> ; suppressor of <i>lon</i>	A, B, 206, 750
<i>sulB</i>		2	See <i>ftsZ</i>	
<i>supB</i>	Suppressor	16	<i>su_B</i> ; suppressor of ochre (UAA) and amber (UAG) mutations; see <i>glnU</i>	
<i>supC</i>	Suppressor	27	<i>su_C</i> , <i>Su-4</i> ; suppressor of ochre (UAA) and amber (UAG) mutations; see <i>tyrT</i>	
<i>supD</i>	Suppressor	43	<i>su_I</i> , <i>Su-1</i> ; suppressor of ochre (UAG) mutations; see <i>serU</i>	
<i>supE</i>	Suppressor	15	<i>su_{II}</i> , <i>Su-2</i> ; suppressor of ochre (UAG) mutations; see <i>glnV</i>	
<i>supF</i>	Suppressor	27	<i>su_{III}</i> , <i>Su-3</i> ; suppressor of amber (UAG) mutations; see <i>tyrT</i>	
<i>supG</i>	Suppressor	17	<i>su-5</i> ; suppressor of ochre (UAA) and amber (UAG) mutations; see <i>lysT</i>	
<i>supH</i>	Suppressor	43	Suppressor; see <i>serU</i>	
<i>supK</i>	Suppressor	62	Suppressor of opal (UGA) mutations; see <i>prfB</i>	
<i>supL</i>	Suppressor	17	<i>su_g</i> ; suppressor of ochre (UAA) and amber (UAG) mutations; see <i>lysT</i>	
<i>supM</i>	Suppressor	90	Suppressor of ochre (UAA) and amber (UAG) mutations, see <i>tyrU</i>	
<i>supN</i>	Suppressor	52	Suppressor of ochre (UAA) and amber (UAG) mutations; see <i>lysV</i>	
<i>supO</i>	Suppressor	27	Suppressor of ochre (UAA) and amber (UAG) mutations; see <i>tyrT</i>	
<i>supP</i>	Suppressor	97	<i>Su-6</i> ; suppressor of amber (UAG) mutations; see <i>leuX</i>	
<i>supQ</i>	Suppressor	13	Suppressor	A
<i>tabC</i>		86	Development of phage T4	B
<i>tag</i>		(72)	3-Methyladenine DNA glycosylase I, constitutive	B, C, 199, 953, 1042
<i>tap</i>		42	Methyl-accepting chemotaxis protein IV	C, 597, 1016, 1017
<i>tar</i>		42	<i>cheM</i> ; methyl-accepting chemotaxis protein II	B, C, 597, 1016, 1017
<i>tdc</i>		68	Threonine dehydratase (EC 4.2.1.16)	252, 388, 389
<i>tdh</i>		81	Threonine dehydrogenase (EC 1.1.1.103)	891, 892
<i>tdi</i>		(4)	Transduction, transformation and rates of mutation	B
<i>tdk</i>		27	Thymidine kinase (EC 2.7.1.75)	A, B
<i>TerA</i>	Terminus	28	DNA replication fork inhibition	267, 343, 460, 463–465, 842, M
<i>TerB</i>	Terminus	36	DNA replication fork inhibition	267, 343, 460, 463–465, 842, M
<i>TerC</i>	Terminus	34	DNA replication fork inhibition	343, 460, M
<i>TerD</i>	Terminus	27	DNA replication fork inhibition	343, 460, M
<i>tesB</i>		10	Thioesterase II	786
<i>tgt</i>		9	tRNA-guanine transglycosylase	C
<i>thdA</i>	Thiophene degradation	11	Utilization of furans and thiophenes; may be <i>tln</i>	2, F
<i>thdC</i>	Thiophene degradation	95	Utilization of furans and thiophenes	2, F
<i>thdD</i>	Thiophene degradation	100	Utilization of furans and thiophenes	2, F
<i>thiA</i>	Thiamin	90	Thiamin thiazole requirement	A
<i>thiB</i>	Thiamin	90	Thiaminphosphate pyrophosphorylase (EC 2.5.1.3)	A
<i>thiC</i>	Thiamin	90	Thiamin pyrimidine requirement	A
<i>thiD</i>	Thiamin	45	Phosphomethylpyrimidine kinase activity	C
<i>thiK</i>	Thiamin	25	Thiamin kinase	C
<i>thiL</i>	Thiamin	10	Thiamin monophosphate kinase	C
<i>thrA</i>	Threonine	0	<i>HS</i> , <i>thrD</i> ; aspartokinase I-homoserine dehydrogenase I (EC 2.3.2.4–EC 1.1.1.3)	A, B, C, 244, 678
<i>thrB</i>	Threonine	0	Homoserine kinase (EC 2.7.1.39)	A, C, 948
<i>thrC</i>	Threonine	0	Threonine synthase (EC 4.2.99.2)	A, C, 836
<i>thrS</i>	Threonine	38	Threonyl-tRNA synthetase (EC 6.1.1.3)	B, C, 717, 867, 878, 1034, 1170, 1190
<i>thrT</i>	Threonine	90	Threonine tRNA 3	A, B, C, 587
<i>thrU</i>	Threonine	90	Threonine tRNA 4	B, C, 587
<i>thrV</i>	Threonine	72	Threonine tRNA 1; at distal end of <i>rrnD</i> operon	C, 214, 587
<i>thrW</i>	Threonine	6	Threonine tRNA 2	214, 242, 587
<i>thyA</i>	Thymine	61	Thymidylate synthetase (EC 2.1.1.45)	A, C, 83, 296, 965
<i>tkt</i>		(62)	Transketolase (EC 2.2.1.1)	A
<i>tlnA</i>		11	<i>tlnI</i> ; resistance or sensitivity to thiolutin	C
<i>tmk</i>		25	Deoxythymidine kinase	96, 257
<i>tnaA</i>		84	<i>ind</i> , <i>tnaR</i> ; tryptophanase (EC 4.1.99.1)	A, B, C, 1045

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TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>tnm</i>		92	Transposition of Tn9 and other transposons; development of phage Mu	C
<i>toc</i>		67	Compensation for loss of DNA topoisomerase I	886
<i>tolA</i>	Tolerance	17	<i>cim</i> , <i>excC</i> , <i>lky</i> , <i>tol-2</i> ; tolerance to group A colicins and single-stranded filamentous DNA phage	A, 337, 1061, 1062, V
<i>tolB</i>	Tolerance	17	<i>tol-3</i> ; tolerance to colicins E2, E3, A, and K	A, 337, 624, 625, 1061, 1062, V
<i>tolC</i>	Tolerance	66	<i>colE1-i</i> , <i>mtcB</i> , <i>refl</i> , <i>tol-8</i> ; specific tolerance to colicin E1, expression of outer membrane proteins	A, C, 425, 426, 826
<i>tolD</i>	Tolerance	(23)	Tolerance to colicins E2 and E3; ampicillin resistance	A
<i>tolE</i>	Tolerance	(23)	Tolerance to colicins E2 and E3; ampicillin resistance	A
<i>tolI</i>	Tolerance	(0)	Tolerance to colicins Ia and Ib	A
<i>tolJ</i>	Tolerance	0	Resistance to colicins L, A, and S4; partial resistance to colicins E and K	B
<i>tolM</i>	Tolerance	72	<i>cmt</i> ; high-level tolerance to colicin M	C, 432, 730
<i>tolQ</i>	Tolerance	17	<i>fii</i> , <i>tolP?</i> ; tolerance to group A colicins and single-stranded filamentous DNA phage	1061, 1062, V
<i>tolR</i>	Tolerance	17	Tolerance to group A colicins and single-stranded filamentous DNA phage	1062, V
<i>tolZ</i>	Tolerance	77	Tolerance to colicins E2, E3, D, Ia, and Ib; generation of chemical proton gradient	715
<i>tonA</i>	T-one	4	See <i>fhuA</i>	
<i>tonB</i>	T-one	28	<i>exbA</i> , <i>Tlrec</i> ; uptake of chelated iron and cyanobalimin; sensitivity to phages T1 and ϕ 80 and colicins	A, B, C, 874, 875
<i>topA</i>	Topoisomerase	28	<i>supX</i> ; DNA topoisomerase I, ω protein	C, 704, 825, 1115, 1154
<i>torA</i>		28	Trimethylamine N-oxide reductase	837
<i>tpiA</i>		89	Triosephosphate isomerase (EC 5.3.1.1)	A, B, 456, 849
<i>tpr</i>		27	A protaminelike protein	C
<i>treA</i>	Trehalose	26	Trehalase, periplasmic	B, 116, 730
<i>trg</i>		31	Methyl-accepting chemotaxis protein III	B, C, 113, 441
<i>trkA</i>		72	Transport of potassium	A, 432, 730
<i>trkB</i>		73	See <i>kefB</i>	
<i>trkC</i>		1	See <i>kefB</i>	
<i>trkD</i>		84	Transport of potassium	A, B, C
<i>trkE</i>		29	Transport of potassium	A
<i>trmA</i>	tRNA methyltransferase	90	tRNA (uracil-5)-methyltransferase (EC 2.1.1.35)	A, B, C, 654
<i>trmB</i>	tRNA methyltransferase	(7)	tRNA (guanine-7)-methyltransferase (EC 2.1.1.33)	A
<i>trmC</i>	tRNA methyltransferase	(56)	5-Methylaminoethyl-2-thiouridine in tRNA	A, B, 428
<i>trmD</i>	tRNA methyltransferase	(57)	tRNA (guanine-7)-methyltransferase (EC 2.1.1.31)	B, 162–164
<i>trmE</i>	tRNA methyltransferase	84	<i>asuE?</i> ; 5-methylaminoethyl-2-thiouridine biosynthesis	307
<i>trmF</i>	tRNA methyltransferase	84	5-methylaminoethyl-2-thiouridine biosynthesis	307
<i>trnA</i>		59	<i>glnU</i> ; level of several tRNAs	C
<i>trpA</i>	Tryptophan	28	<i>tryp-2</i> ; tryptophan synthase (EC 4.2.1.20), A protein	A, B, C
<i>trpB</i>	Tryptophan	28	<i>tryp-1</i> ; tryptophan synthase (EC 4.2.1.20), B protein	A, C
<i>trpC</i>	Tryptophan	28	<i>tryp-3</i> ; N-(5-phosphoribosyl)anthranilate isomerase	A, B, C
<i>trpD</i>	Tryptophan	28	<i>tryE</i> ; glutamine amidotransferase-phosphoribosyl anthranilate transferase	A, C
<i>trpE</i>	Tryptophan	28	<i>anth</i> , <i>tryp-4</i> , <i>tryD</i> ; anthranilate synthase (EC 4.1.3.27)	A, B, C
<i>trpP</i>	Tryptophan	84	Low-affinity tryptophan-specific permease	C
<i>trpR</i>	Tryptophan	100	<i>Rtry</i> ; regulation of <i>trp</i> operon and <i>aroH</i> ; <i>trp</i> aporepressor	A, B, C
<i>trpS</i>	Tryptophan	74	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	A, B, C
<i>trpT</i>	Tryptophan	85	<i>su7</i> , <i>su8</i> , <i>su9</i> , <i>supU</i> , <i>supV</i> ; tryptophan tRNA gene at distal end of <i>rrnC</i> operon	A, B, C, 587
<i>trxA</i>	Thioredoxin	86	<i>fip</i> , <i>tsnC</i> ; thioredoxin	B, 14, 649, 650, 713, 935, 936, 938, 1153
<i>trxB</i>	Thioredoxin	21	Thioredoxin reductase	431, 937, 939
<i>tsf</i>		4	Protein chain elongation factor, EF-Ts	B, C
<i>tsr</i>		99	<i>cheD</i> ; methyl-accepting chemotaxis protein I	B, C, 126, 169
<i>tsx</i>	T-six	9	<i>nupA</i> , <i>T6rec</i> ; nucleoside uptake; receptor for phage T6 and colicin K	A, B, 130
<i>tufA</i>		74	Protein chain elongation factor; EF-Tu (duplicate gene)	A, B, C
<i>tufB</i>		90	Protein chain elongation factor; EF-Tu (duplicate gene)	A, B, C, 1079
<i>tus</i>		36	DNA-binding protein; inhibition of replication at <i>Ter</i> sites	C, 464, 466, 842, M
<i>tynA</i>		(27)	Tyramine oxidase (EC 1.4.3.4)	B

Continued on following page

TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>tyrA</i>	Tyrosine	57	Chorismate mutase T (EC 5.4.99.5)–prephenate dehydrogenase (EC 1.3.1.12)	A, 488
<i>tyrB</i>	Tyrosine	92	Tyrosine aminotransferase (EC 2.6.1.5), tyrosine repressible	B, 340, 605, 1200
<i>tyrP</i>	Tyrosine	42	Tyrosine-specific transport system	C, 558, 559, 1186
<i>tyrR</i>	Tyrosine	29	Regulation of <i>aroF</i> , <i>aroG</i> , and <i>tyrA</i> and aromatic amino acid transport systems	A, B, C, 217, 218
<i>tyrS</i>	Tyrosine	36	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	A, B, C, 67
<i>tyrT</i>	Tyrosine	27	<i>suI_{III}</i> , <i>Su-3</i> , <i>su_c</i> , <i>Su-4</i> , <i>supF</i> , <i>supE</i> , <i>tyrV</i> ; tyrosine tRNA 1 (tandemly duplicated gene)	A, B, C, 587
<i>tyrU</i>	Tyrosine	90	<i>supM</i> ; tyrosine tRNA 2	A, B, C, 587
<i>ubiA</i>	Ubiquinone	92	4-Hydroxybenzoate → 3-octaprenyl 4-hydroxybenzoate	A, C
<i>ubiB</i>	Ubiquinone	87	2-Octaprenylphenol → 2-octaprenyl-6-methoxyphenol	A
<i>ubiC</i>	Ubiquinone	92	Chorismate lyase	A
<i>ubiD</i>	Ubiquinone	87	3-Octaprenyl-4-hydroxybenzoate → 2-octaprenylphenol	A
<i>ubiE</i>	Ubiquinone	87	2-Octaprenyl-6-methoxy-1,4-benzoquinone → 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	A
<i>ubiF</i>	Ubiquinone	15	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone → 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone	A
<i>ubiG</i>	Ubiquinone	48	2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone → ubiquinone 8	A, B, C, 375
<i>ubiH</i>	Ubiquinone	63	2-Octaprenyl-6-methoxyphenol → 2-octaprenyl-6-methoxy-1,4-benzoquinone	A
<i>ubiX</i>	Ubiquinone	50	Sequence homologous to <i>ubiX</i> of <i>S. typhimurium</i> , which codes for polyprenyl <i>p</i> -hydroxybenzoate carboxylase	807
<i>udk</i>		45	Uridine kinase (EC 2.7.1.48)	A, C
<i>udp</i>		86	Uridine phosphorylase (EC 2.4.2.3)	A, 14, 15
<i>ugpA</i>		76	<i>sn</i> -Glycerol-3-phosphate transport system	A, 828, 977, 978
<i>ugpB</i>		76	<i>sn</i> -Glycerol-3-phosphate transport system; periplasmic binding protein	C, 828, 977, 978
<i>ugpC</i>		76	<i>sn</i> -Glycerol-3-phosphate transport system	828, 977, 978
<i>ugpE</i>		76	<i>sn</i> -Glycerol-3-phosphate transport system, membrane protein	828, 977, 978
<i>uhpA</i>		82	Positive activator of <i>uhpT</i> transcription	352, 543, 993, 1172
<i>uhpB</i>		82	Regulatory gene	352, 1172
<i>uhpC</i>		82	Regulatory gene	A, B, C, 352, 543, 993, 1172
<i>uhpR</i>		82	Regulation of hexose phosphate transport; possibly outer membrane receptor for glucose 6-phosphate	A, B, C
<i>uhpT</i>		82	Transport of hexose phosphates, transport protein	A, B, C, 352, 543, 993, 1172
<i>uidA</i>		36	<i>gurA</i> ; β-D-glucuronidase (EC 3.2.1.31)	A, B, C, 107, 527
<i>uidR</i>		36	Regulatory gene	A, B, C, 105, 107, 108
<i>umuC</i>		26	<i>uvr</i> , induction of mutations by UV; error-prone repair	B, 137, 259, 305, 570, 706, 843, 1005
<i>umuD</i>		26	<i>uvr</i> ; inducible mutagenesis; error-prone repair	C, 259, 305, 570, 706, 843, 1005
<i>unc</i>			See <i>atp</i>	
<i>ung</i>		56	Uracil-DNA-glycosylase	B, 1142
<i>upp</i>		54	<i>uraP</i> ; uracil phosphoribosyltransferase (EC 2.4.2.9)	A, B, 476
<i>ups</i>		26	Efficiency of nonsense suppressors	B, 941
<i>ushA</i>		11	UDP-glucose hydrolase (F'-nucleotidase)	A, B, C, 155
<i>uup</i>		21	Precise excision of insertion elements	476
<i>uvrA</i>	Ultraviolet	92	<i>dar</i> ; repair of UV damage to DNA; excision nuclease	A, B, C, 496
<i>uvrB</i>	Ultraviolet	18	<i>dar-1,6</i> ; DNA repair; excision nuclease	A, B, C, 26, 47, 1072
<i>uvrC</i>	Ultraviolet	42	<i>dar-4,5</i> ; repair of UV damage to DNA; excision nuclease	A, C, 338, 339, 956, 991, 992, 1140
<i>uvrD</i>	Ultraviolet	86	<i>dar-2</i> , <i>dda</i> , <i>mutU</i> , <i>pdeB</i> , <i>recL</i> , <i>uvrE</i> , <i>uvr502</i> ; DNA-dependent ATPase I and DNA helicase II	A, B, C, 14, 33, 297, 326, 327, 459, 603, 1083, 1198
<i>uxaA</i>		68	Altronate hydrolase (EC 4.2.1.7)	A, B, C
<i>uxaB</i>		(52)	Altronate oxidoreductase (EC 1.1.1.58)	A, B, 103, 104, 490, 711
<i>uxaC</i>		68	Uronate isomerase (EC 5.3.1.12)	A, B, C, 102, 710, 711
<i>uxuA</i>		98	Mannonate hydrolase (EC 4.2.1.8)	A, B, C, 106, 347
<i>uxuB</i>		98	Mannonate oxidoreductase (EC 1.1.1.57)	A, B, C, 106, 347

Continued on following page

TABLE 1—Continued

Gene symbol	Mnemonic	Map position (min) ^a	Alternate gene symbols; phenotypic trait affected ^b	Reference(s) ^c
<i>uxuR</i>		98	Regulatory gene for <i>uxuBA</i> operon	B, C
<i>valS</i>	Valine	97	<i>val-act</i> ; valyl-tRNA synthetase (EC 6.1.1.9)	A, B, C, 443, 451, 452, 1015
<i>valT</i>	Valine	17	Valine tRNA 1	B, C, 587, 1211
<i>valU</i>		52	Valine tRNA 1 (tandemly triplicated gene)	587, D
<i>valV</i>		37	Valine tRNA 2B	587
<i>valW</i>		37	Valine tRNA 2A	587
<i>weeA</i>		67	Cell elongation	265
<i>xapA</i>		52	<i>pndA</i> ; xanthosine phosphorylase	C, 582
<i>xapR</i>		52	<i>pndR</i> ; regulatory gene	C, 582
<i>xthA</i>		38	Exonuclease III	A, B, C
<i>xseA</i>		54	Exonuclease VII, large subunit	B, 187, 1131
<i>xseB</i>		10	Exonuclease VII, small subunit	1131, 1132
<i>xylA</i>	Xylose	80	D-Xylose isomerase (EC 5.3.1.5)	A, C, 132, 610, 923, 970
<i>xylB</i>	Xylose	80	Xylulokinase (EC 2.7.1.17)	A, C, 132, 923
<i>xylE</i>	Xylose	91	Xylose-proton symport	255, 256, 344, 609
<i>xylF</i>	Xylose	80	<i>xylT</i> ; xylose binding protein transport system	256, 610, 923
<i>xylR</i>	Xylose	80	Regulatory gene	A, C, 923
<i>zwf</i>	Zwischenferment	41	Glucose-6-phosphate dehydrogenase (EC 1.1.1.49)	A

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

^b Abbreviations: CoA, coenzyme A; DCCD, *N,N'*-dicyclohexylcarbodiimide; NEM, *N*-ethylmaleimide.

^c Numbers refer to Literature Cited. Letters refer to: (A) literature cited in Table 2 of reference 46; (B) literature cited in Table 1 of reference 45; (C) literature cited in Table 1 of reference 43; and personal communications from (D) Y. Brun, (E) K. Burton, (F) D. Clark, (G) J. Coleman, (H) S. Ferro-Novick, J. Sands, and J. Beckwith, (I) J. Gowrishankar, (J) B. G. Hall, (K) K. Hantke, (L) C. W. Hill, (M) P. Kuempel, (N) I. G. Old, (O) D. B. Oliver, (P) D. Oxender, (Q) R. Plapp, (R) P. Rabinovich, (S) J. M. Smith, (T) M. Volkert, (U) B. Wanner, (V) R. Webster, and (W) B. Weiss

TABLE 2. Alternate gene symbols

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
<i>acrB</i>	<i>gyrB</i>	<i>bisA</i>	<i>chlA</i>
<i>ade</i>	<i>pur</i>	<i>bisB</i>	<i>chlE</i>
<i>adth_a</i>	<i>purD</i>	<i>bisD</i>	<i>narG</i>
<i>adth_b</i>	<i>purG</i>	<i>blu</i>	<i>pgl, pgm, malP</i>
<i>aidA</i>	<i>alkA</i>	<i>brnP</i>	<i>ilvH</i>
<i>aidD</i>	<i>alkB</i>	<i>cap</i>	<i>car, crp</i>
<i>ala-act</i>	<i>alaS</i>	<i>capR</i>	<i>lon</i>
<i>ald</i>	<i>fba</i>	<i>car</i>	<i>ptsG</i>
<i>alnA</i>	<i>dadB</i>	<i>cat</i>	<i>ptsG</i>
<i>alnR</i>	<i>dadQ</i>	<i>cbr</i>	<i>fep</i>
<i>alt</i>	<i>rpoD</i>	<i>cbt</i>	<i>fep</i>
<i>amk</i>	<i>nek</i>	<i>cer</i>	<i>btuB</i>
<i>ampA</i>	<i>ampC</i>	<i>cheC</i>	<i>flaA</i>
<i>anth</i>	<i>trpE</i>	<i>cheD</i>	<i>tsr</i>
<i>apk</i>	<i>lysC</i>	<i>cheM</i>	<i>tar</i>
<i>arg + ura</i>	<i>car</i>	<i>cheX</i>	<i>cheR</i>
<i>aroR</i>	<i>aroT</i>	<i>chlC</i>	<i>narG, narH</i>
<i>asp</i>	<i>ppc</i>	<i>chlG</i>	<i>narG</i>
<i>aspB</i>	<i>glbB</i>	<i>chlI</i>	<i>narI</i>
<i>asuC</i>	<i>hisT</i>	<i>cim</i>	<i>tolA</i>
<i>asuD</i>	<i>lysS</i>	<i>cmlB</i>	<i>ompF</i>
<i>ata</i>	<i>attP22</i>	<i>cmt</i>	<i>tolM</i>
<i>att82, att434</i>	<i>attγ</i>	<i>coa</i>	<i>ompF</i>
<i>azi</i>	<i>secA</i>	<i>colE1-i</i>	<i>tolC</i>
<i>bfe</i>	<i>btuB</i>	<i>con</i>	<i>ompA, rfa</i>
<i>bglY</i>	<i>osmZ</i>	<i>cop</i>	<i>het</i>
<i>bioR</i>	<i>birA</i>	<i>Cou</i>	<i>gyrB</i>
<i>birB (bir)</i>	<i>bioP</i>	<i>cqsA</i>	<i>rrnA</i>

Continued on following page

TABLE 2—Continued

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
<i>mtcA</i>	<i>acrA</i>	<i>psuA</i>	<i>rho</i>
<i>mtcB</i>	<i>tolC</i>	<i>ptsF</i>	<i>fruA</i>
<i>muc</i>	<i>lon</i>	<i>ptsL</i>	<i>manX</i>
<i>mutD</i>	<i>dnaQ</i>	<i>ptsM</i>	<i>manX, Y, Z</i>
<i>mutR</i>	<i>mutH</i>	<i>ptsN</i>	<i>nagE</i>
<i>mutU</i>	<i>uvrD</i>	<i>ptsP</i>	<i>manY</i>
<i>nalA</i>	<i>gyrA</i>	<i>ptsX</i>	<i>manX, Y, Z</i>
<i>nalC, D</i>	<i>gyrB</i>	<i>pup</i>	<i>deoD</i>
<i>nam</i>	<i>pncA</i>	<i>pyrA</i>	<i>car</i>
<i>ncf</i>	<i>hemB</i>	<i>rad</i>	<i>uvrD</i>
<i>neaA</i>	<i>rpsQ</i>	<i>radB</i>	<i>recN</i>
<i>nic</i>	<i>nad</i>	<i>ramA</i>	<i>rpsD</i>
<i>nirA</i>	<i>fnr</i>	<i>ramB</i>	<i>rimG</i>
<i>nirR</i>	<i>fnr</i>	<i>RC</i>	<i>rel</i>
<i>nitA</i>	<i>rho</i>	<i>recL</i>	<i>uvrD</i>
<i>nitB</i>	<i>rpoB</i>	<i>refI</i>	<i>tolC</i>
<i>nmpA</i>	<i>pst, phoS, T</i>	<i>refII</i>	<i>cet</i>
<i>nmpB</i>	<i>phoR</i>	<i>relC</i>	<i>rplK</i>
<i>ntrA</i>	<i>rpoN</i>	<i>res</i>	<i>rimF</i>
<i>ntrB</i>	<i>glnL</i>	<i>resA</i>	<i>polA</i>
<i>ntrC</i>	<i>glnG</i>	<i>rglA</i>	<i>mcrA</i>
<i>nucR</i>	<i>deoR</i>	<i>rglB</i>	<i>mcrB</i>
<i>nupA</i>	<i>tsx</i>	<i>rif</i>	<i>rpoB</i>
<i>nusE</i>	<i>rpsJ</i>	<i>rimA</i>	<i>rpmH</i>
<i>old</i>	<i>fad</i>	<i>rm</i>	<i>hsd</i>
<i>ole</i>	<i>fadR</i>	<i>rnsA</i>	<i>rna</i>
<i>ompB</i>	<i>envZ, ompR</i>	<i>rnsC</i>	<i>rho</i>
<i>ompE</i>	<i>phoE</i>	<i>rodA</i>	<i>mrdB</i>
<i>osrA</i>	<i>proU</i>	<i>rodY</i>	<i>envB</i>
<i>par</i>	<i>ompC</i>	<i>ron</i>	<i>rpoB</i>
<i>paxA</i>	<i>dcd</i>	<i>rorA</i>	<i>recB</i>
<i>pbpA</i>	<i>mrdA</i>	<i>rpX</i>	<i>rps</i>
<i>pbpB</i>	<i>ftsI</i>	<i>rpy</i>	<i>rpl</i>
<i>pbpF</i>	<i>mrcB</i>	<i>rpz</i>	<i>rpm</i>
<i>pcbA</i>	<i>gyrB</i>	<i>sbcA</i>	<i>rac</i>
<i>pdeB</i>	<i>uvrD</i>	<i>sbl</i>	<i>srl</i>
<i>pdeC</i>	<i>lig</i>	<i>sdrA</i>	<i>rnH</i>
<i>pdxC</i>	<i>serC</i>	<i>sec</i>	<i>hemF</i>
<i>pdxF</i>	<i>serC</i>	<i>secC</i>	<i>rpsO</i>
<i>pdzA</i>	<i>rplT</i>	<i>secY</i>	<i>priA</i>
<i>pea</i>	<i>secA</i>	<i>seg</i>	<i>arcA</i>
<i>pel</i>	<i>manY</i>	<i>sep</i>	<i>ftsI</i>
<i>perA</i>	<i>envZ</i>	<i>sez</i>	<i>rpoA</i>
<i>pfv</i>	<i>dacA</i>	<i>sfiA</i>	<i>sulA</i>
<i>pgsB</i>	<i>lpxB</i>	<i>sfiB</i>	<i>ftsZ</i>
<i>phe-act</i>	<i>pheS</i>	<i>sfrA</i>	<i>arcA</i>
<i>phoS</i>	<i>pstS</i>	<i>sfrB</i>	<i>rfaH</i>
<i>phoT</i>	<i>pstA, B, phoU</i>	<i>sin</i>	<i>rnH</i>
<i>phoW</i>	<i>pstC</i>	<i>skp</i>	<i>hlpA</i>
<i>phs</i>	<i>rpoA</i>	<i>sof</i>	<i>dut</i>
<i>phx</i>	<i>rfa</i>	<i>som</i>	<i>rfb</i>
<i>pil</i>	<i>fim</i>	<i>spcA</i>	<i>rpsE</i>
<i>plsA</i>	<i>adk</i>	<i>spr</i>	<i>lexA</i>
<i>PMG</i>	<i>mgl</i>	<i>ssd</i>	<i>ecfB</i>
<i>pmi</i>	<i>manA</i>	<i>ssyF</i>	<i>rpsA</i>
<i>pndA</i>	<i>xapA</i>	<i>ssyG</i>	<i>infB</i>
<i>pndR</i>	<i>xapR</i>	<i>stc</i>	<i>micF</i>
<i>poaA</i>	<i>putA</i>	<i>stl</i>	<i>rpoB</i>
<i>poh</i>	<i>oriC</i>	<i>strA</i>	<i>rpsL</i>
<i>polC</i>	<i>dnaE</i>	<i>stb</i>	<i>rimH</i>
<i>pon</i>	<i>lpcB, mrc</i>	<i>stv</i>	<i>rpoB</i>
<i>popA</i>	<i>hemH</i>	<i>Su, su</i>	<i>sup</i>
<i>popB</i>	<i>hemF</i>	<i>suß</i>	<i>lysTß</i>
<i>popE</i>	<i>hemC</i>	<i>sud₂</i>	<i>rpsD</i>
<i>prd</i>	<i>fuc</i>	<i>sueB</i>	<i>prfA</i>
<i>prv</i>	<i>mutH</i>	<i>sufD</i>	<i>glyU</i>
<i>psiB</i>	<i>ugpA, B</i>	<i>sulB</i>	<i>ftsZ</i>
<i>psiC</i>	<i>ugpA, B</i>	<i>sumA</i>	<i>glyT</i>
<i>psiD</i>	<i>phnD</i>	<i>sumB</i>	<i>glyU</i>

Continued on following page

TABLE 2—Continued

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
<i>cqsB</i>	<i>rrnC</i>	<i>gpp</i>	<i>gpt</i>
<i>cqsD</i>	<i>rrnD</i>	<i>gpt</i>	<i>ptsG</i>
<i>CR</i>	<i>ptsG</i>	<i>gptB</i>	<i>manX,Z</i>
<i>cru</i>	<i>nupC</i>	<i>groE</i>	<i>mop</i>
<i>cry</i>	<i>ompR, ompF</i>	<i>groN</i>	<i>rpoB</i>
<i>csm</i>	<i>crp</i>	<i>groP</i>	<i>dnaB, dnaJ, dnaK</i>
<i>ctr</i>	<i>ptsH, ptsI</i>	<i>grpA</i>	<i>dnaB</i>
<i>cur</i>	<i>osmZ</i>	<i>grpC</i>	<i>dnaJ, dnaK</i>
<i>cxr</i>	<i>cxm</i>	<i>grpF</i>	<i>dnaK</i>
<i>cybA</i>	<i>sdhC</i>	<i>gts</i>	<i>qmeA</i>
<i>dagA</i>	<i>cycA</i>	<i>gura</i>	<i>uidA</i>
<i>dap + hom</i>	<i>asd</i>	<i>gut</i>	<i>srl</i>
<i>dar</i>	<i>uvr</i>	<i>gxu</i>	<i>gpt</i>
<i>dasC</i>	<i>rep?</i>	<i>H</i>	<i>flc</i>
<i>dasF</i>	<i>rnh</i>	<i>hag</i>	<i>flc</i>
<i>dda</i>	<i>uvrD</i>	<i>hdh</i>	<i>mop</i>
<i>deg</i>	<i>lon</i>	<i>herA</i>	<i>rnh</i>
<i>dhbB</i>	<i>bioR</i>	<i>hid</i>	<i>himA</i>
<i>dhl</i>	<i>lpd</i>	<i>himB</i>	<i>gyrB</i>
<i>dir</i>	<i>lon</i>	<i>hin</i>	<i>rpoH</i>
<i>divA</i>	<i>ftsA</i>	<i>hip</i>	<i>himD</i>
<i>divE</i>	<i>serT</i>	<i>Hpr</i>	<i>ptsH</i>
<i>dnaF</i>	<i>nrdA</i>	<i>hrbA</i>	<i>brnQ</i>
<i>dnaL</i>	<i>lig</i>	<i>hrbB,C,D</i>	<i>livG,H,J,K</i>
<i>dnaS</i>	<i>dut</i>	<i>hs</i>	<i>hsd</i>
<i>dnaW</i>	<i>adk</i>	<i>Hs</i>	<i>thrA</i>
<i>dnaY</i>	<i>argU</i>	<i>hsm</i>	<i>hsdM</i>
<i>dra</i>	<i>deoC</i>	<i>hsp</i>	<i>hsd</i>
<i>drm</i>	<i>deoB</i>	<i>hsr</i>	<i>hsdR</i>
<i>dye</i>	<i>arcA</i>	<i>hss</i>	<i>hsdS</i>
<i>eps</i>	<i>rpsE</i>	<i>htpR</i>	<i>rpoH</i>
<i>eryA</i>	<i>rplD</i>	<i>icl</i>	<i>aceA</i>
<i>eryB</i>	<i>rplV</i>	<i>ile</i>	<i>ilvA</i>
<i>eup</i>	<i>ecfB</i>	<i>ind</i>	<i>tnaA</i>
<i>exbA</i>	<i>tonB</i>	<i>ins</i>	<i>glyV, glyW</i>
<i>excC</i>	<i>tolA</i>	<i>K12</i>	<i>rpsG</i>
<i>exrA</i>	<i>lexA</i>	<i>kac</i>	<i>kdp</i>
<i>exrB</i>	<i>ssb</i>	<i>kdga</i>	<i>eda</i>
<i>fabC</i>	<i>fabB</i>	<i>kga</i>	<i>eda</i>
<i>fam</i>	<i>rpoH</i>	<i>kim</i>	<i>qin</i>
<i>far</i>	<i>fusA</i>	<i>kmt</i>	<i>ompB</i>
<i>fda</i>	<i>fba</i>	<i>lcs</i>	<i>asnS</i>
<i>fdhA</i>	<i>selA, selB</i>	<i>ldh</i>	<i>dld</i>
<i>fdhB</i>	<i>selD</i>	<i>leuK</i>	<i>hisT</i>
<i>fdhC</i>	<i>selC</i>	<i>leuX</i>	<i>leuSo, leuSp</i>
<i>fdp</i>	<i>fbp</i>	<i>lexB</i>	<i>recA</i>
<i>feuA</i>	<i>cir</i>	<i>lexC</i>	<i>ssb</i>
<i>feuB</i>	<i>fep</i>	<i>lir</i>	<i>acrA</i>
<i>fexA</i>	<i>arcA</i>	<i>lky</i>	<i>tolB</i>
<i>fii</i>	<i>tolQ, tolR</i>	<i>lop</i>	<i>ligA</i>
<i>fipA</i>	<i>trxA</i>	<i>loxB</i>	<i>attP1,P7</i>
<i>fit</i>	<i>infC</i>	<i>lps</i>	<i>rfa</i>
<i>fla</i>	<i>flg, flh, fli</i>	<i>lss</i>	<i>livR</i>
<i>flaJ</i>	<i>motA, motB</i>	<i>lstR</i>	<i>livR</i>
<i>flaF</i>	<i>fliC</i>	<i>lys + met</i>	<i>sucA, sucB</i>
<i>flb</i>	<i>flg, flh, fli</i>	<i>lysP</i>	<i>cadR</i>
<i>f1rA</i>	<i>ileR?</i>	<i>mas</i>	<i>aceB</i>
<i>f1pk</i>	<i>fruK</i>	<i>Mb</i>	<i>acrA</i>
<i>f1pr</i>	<i>fruF</i>	<i>mbl</i>	<i>acrA</i>
<i>f1dB</i>	<i>f1r</i>	<i>mec</i>	<i>dcm</i>
<i>f1sB</i>	<i>nrdB</i>	<i>meoA</i>	<i>ompC</i>
<i>gad</i>	<i>gap</i>	<i>mlpA</i>	<i>lpp</i>
<i>glmD</i>	<i>nagB</i>	<i>mni</i>	<i>manC</i>
<i>glnF</i>	<i>rpoN</i>	<i>mola</i>	<i>malM</i>
<i>gliC</i>	<i>gliSo</i>	<i>mon</i>	<i>envB</i>
<i>glu</i>	<i>ppc</i>	<i>motD</i>	<i>f1iN</i>
<i>glut</i>	<i>gliA</i>	<i>mpt</i>	<i>manX,Z</i>
<i>gly-act</i>	<i>glyS</i>	<i>mra</i>	<i>murF</i>
<i>glyD</i>	<i>gpt</i>	<i>msh</i>	<i>arcA</i>

Continued on following page

TABLE 2—Continued

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
<i>sun</i>	<i>rho</i>	<i>tpp</i>	<i>deoA</i>
<i>sup₂₀</i>	<i>rpsT</i>	<i>tre</i>	<i>Ter</i>
<i>supK</i>	<i>prfB</i>	<i>trkB</i>	<i>kefB</i>
<i>Tlrec</i>	<i>tonB</i>	<i>trkC</i>	<i>kefC</i>
<i>Tl, T5rec</i>	<i>fhuA</i>	<i>trpP</i>	<i>aroT</i>
<i>T6rec</i>	<i>tsx</i>	<i>try</i>	<i>trp</i>
<i>tabB</i>	<i>mop</i>	<i>tryp</i>	<i>trp</i>
<i>tabD</i>	<i>rpoB, rpoC</i>	<i>ts-9</i>	<i>rts</i>
<i>talA</i>	<i>alaT</i>	<i>tsl</i>	<i>lexA</i>
<i>talD</i>	<i>alaU</i>	<i>tsnC</i>	<i>trxA</i>
<i>tasC</i>	<i>aspT</i>	<i>tsu</i>	<i>rho</i>
<i>tfrA</i>	<i>lpcA</i>	<i>tss</i>	<i>asnS</i>
<i>tgl</i>	<i>ptsG</i>	<i>ttr</i>	<i>fadL</i>
<i>tgS</i>	<i>crr?</i>	<i>tut</i>	<i>ompA</i>
<i>tgtB</i>	<i>gltT</i>	<i>uar</i>	<i>prfA</i>
<i>tgtC</i>	<i>gltU</i>	<i>umg</i>	<i>ptsG</i>
<i>tgtE</i>	<i>gltV</i>	<i>umuA</i>	<i>lexA</i>
<i>thdB</i>	<i>fadR</i>	<i>umuB</i>	<i>recA</i>
<i>thyR</i>	<i>deoB, deoC</i>	<i>unc</i>	<i>atp</i>
<i>tif</i>	<i>recA</i>	<i>uraP</i>	<i>upp</i>
<i>tmr</i>	<i>fol</i>	<i>usgA</i>	<i>gntT</i>
<i>tolF</i>	<i>ompF</i>	<i>uvm</i>	<i>umu</i>
<i>tolG</i>	<i>ompA</i>	<i>uvrF</i>	<i>recF</i>
<i>tolP</i>	<i>tolQ</i>	<i>val-act</i>	<i>valS</i>
<i>tonA</i>	<i>fhuA</i>	<i>vtr</i>	<i>fabF</i>
<i>TP</i>	<i>deoA</i>	<i>xonA</i>	<i>sbcB</i>
<i>tpo</i>	<i>envZ</i>	<i>zab</i>	<i>recA</i>

although the relative positions of some genes have been determined precisely.

ACKNOWLEDGMENTS

This work was supported by National Science Foundation grant BSR-8807021. This support is gratefully acknowledged.

I thank all of the investigators, too numerous to list, who contributed to this review by sending reprints or manuscripts, by answering my questions, and by helping to resolve conflicts in the nomenclature. I am particularly grateful to those whose names are listed in the footnote to Table 1 for sending unpublished data which helped to make the map more accurate and complete. Thanks are due to Judi Ratté for typing the manuscript and to Sharon Schmiedel for making the map drawing.

LITERATURE CITED

- Aasland, R., J. Coleman, A. L. Holck, C. L. Smith, C. R. H. Raetz, and K. Kleppe. 1988. Identity of the 17-kilodalton protein, a DNA-binding protein from *Escherichia coli*, and the *firA* gene product. *J. Bacteriol.* **170**:5916–5918.
- Abdulrashid, N., and D. P. Clark. 1987. Isolation and genetic analysis of mutations allowing the degradation of furans and thiophenes by *Escherichia coli*. *J. Bacteriol.* **169**:1267–1271.
- Abraham, J. M., C. S. Freitag, J. R. Clements, and B. I. Eisenstein. 1985. An invertible element of DNA controls phase variation of type 1 fimbriae of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **82**:5724–5727.
- Adachi, T., K. Mizuuchi, R. Menzel, and M. Gellert. 1984. DNA sequence and transcription of the region upstream of the *E. coli gyrB* gene. *Nucleic Acids Res.* **12**:6389–6395.
- Adachi, T., M. Mizuuchi, E. A. Robinson, E. Appella, M. H. O'Dea, M. Gellert, and K. Mizuuchi. 1987. DNA sequence of the *E. coli gyrB* gene: application of a new sequencing strategy. *Nucleic Acids Res.* **15**:771–784.
- Aiba, H. 1985. Transcription of the *Escherichia coli* adenylate cyclase gene is negatively regulated by cAMP-cAMP receptor protein. *J. Biol. Chem.* **260**:3063–3070.
- Aiba, H., M. Kawamukai, and A. Ishihama. 1983. Cloning and promoter analysis of the *Escherichia coli* adenylate cyclase gene. *Nucleic Acids Res.* **11**:3451–3465.
- Aiba, H., K. Mori, M. Tanaka, T. Ooi, A. Roy, and A. Danchin. 1984. The complete nucleotide sequence of the adenylate cyclase gene of *Escherichia coli*. *Nucleic Acids Res.* **12**:9427–9440.
- Akiyama, M., T. Horiuchi, and M. Sekiguchi. 1987. Molecular cloning and nucleotide sequence of the *mutT* mutator of *Escherichia coli* that causes A:T to C:G transversion. *Mol. Gen. Genet.* **206**:9–16.
- Akiyama, Y., and K. Ito. 1985. The *secY* membrane component of the bacterial protein export machinery: analysis by new electrophoretic methods for integral membrane proteins. *EMBO J.* **4**:3351–3356.
- Albin, R., and P. M. Silverman. 1984. Physical and genetic structure of the *glpK-cpxA* interval of the *Escherichia coli* K-12 chromosome. *Mol. Gen. Genet.* **197**:261–271.
- Albin, R., and P. M. Silverman. 1984. Identification of the *Escherichia coli* K-12 *cpxA* locus as a single gene: construction and analysis of biologically-active *cpxA* gene fusions. *Mol. Gen. Genet.* **197**:272–279.
- Albin, R., R. Weber, and P. M. Silverman. 1986. The Cpx proteins of *Escherichia coli* K-12. Immunologic detection of the chromosomal *cpxA* gene product. *J. Biol. Chem.* **261**:4698–4705.
- Aldea, M., V. F. Maples, and S. R. Kushner. 1988. Generation of a detailed physical and genetic map of the *ilv-metE-udp* region of the *Escherichia coli* chromosome. *J. Mol. Biol.* **200**:427–438.
- Alkhimova, R. A., A. S. Mironov, and V. V. Sukhodolets. 1981. Regulation of the activity of the uridine phosphorylase of *Escherichia coli* K-12. I. Mapping of mutations for the structural gene and determination of the direction of transcription. *Sov. Genet.* **17**:1127–1133.
- Amemura, M., K. Makino, H. Shinagawa, A. Kobayashi, and A. Nakata. 1985. Nucleotide sequence of the genes involved in phosphate transport and regulation of the phosphate regulon in *Escherichia coli*. *J. Mol. Biol.* **184**:241–250.
- Amemura, M., K. Makino, H. Shinagawa, and A. Nakata. 1986. Nucleotide sequence of the *phoM* region of *Escherichia coli*: four open reading frames may constitute an operon. *J.*

- Bacteriol. 168:294-302.
18. Amemura, M., H. Shinagawa, K. Makino, N. Otsuji, and A. Nakata. 1982. Cloning of and complementation tests with alkaline phosphatase regulatory genes (*phoS* and *phoT*) of *Escherichia coli*. J. Bacteriol. 152:692-701.
 19. Amundsen, S. K., A. F. Taylor, A. M. Chaudhury, and G. R. Smith. 1986. *recD*: the gene for an essential third subunit of exonuclease V. Proc. Natl. Acad. Sci. USA 83:5558-5562.
 20. Andersen, J., N. Delihhas, K. Ikenaka, P. J. Green, O. Pines, and M. Inouye. 1987. The isolation and characterization of RNA coded by the *micF* gene in *Escherichia coli*. Nucleic Acids Res. 15:2089-2101.
 21. Andresen, P. A., I. Kaasen, O. Styrvold, G. Boulnois, and A. R. Strøm. 1988. Molecular cloning, physical mapping and expression of the *bet* genes governing the osmoregulatory choline-glycine betaine pathway of *Escherichia coli*. J. Gen. Microbiol. 134:1737-1746.
 22. Andrews, J. C., and S. Short. 1985. Genetic analysis of *Escherichia coli* oligopeptide transport mutants. J. Bacteriol. 161:484-492.
 23. Anilionis, A., P. Ostapchuk, and M. Riley. 1980. Identification of a second cryptic lambdoid prophage locus in the *E. coli* K12 chromosome. Mol. Gen. Genet. 180:479-481.
 24. Anton, I. A., and J. R. Coggins. 1988. Sequencing and over expression of the *Escherichia coli* *aroE* gene encoding shikimate dehydrogenase. Biochem. J. 249:319-326.
 25. Antonucci, T. K., L. M. Wagner, and D. L. Oxender. 1986. Cloning, expression, and nucleotide sequence of *livR*, the repressor for high-affinity branched-chain amino acid transport in *Escherichia coli*. Proteins Struct. Funct. Genet. 1: 125-133.
 26. Arikian, E., M. S. Kulkarni, D. C. Thomas, and A. Sancar. 1986. Sequences of the *E. coli* *uvrB* gene and protein. Nucleic Acids Res. 14:2637-2650.
 27. Armengod, M.-E., and E. Lambies. 1986. Overlapping arrangement of the *recF* and *dnaN* operons of *Escherichia coli*: positive and negative control sequences. Gene 43:183-196.
 28. Aronson, B. D., P. D. Ravnikar, and R. L. Somerville. 1988. Nucleotide sequence of the 2-amino-3-ketobutyrate coenzyme A ligase (*kbl*) gene of *E. coli*. Nucleic Acids Res. 16:3586.
 29. Arps, P. J., C. C. Marvel, B. C. Rubin, D. R. Tolan, E. E. Penhoet, and M. E. Winkler. 1985. Structural features of the *hisT* operon of *Escherichia coli* K-12. Nucleic Acids Res. 13:5297-5315.
 30. Arps, P. J., and M. E. Winkler. 1987. Structural analysis of the *Escherichia coli* K-12 *hisT* operon by using a kanamycin resistance cassette. J. Bacteriol. 169:1061-1070.
 31. Arps, P. J., and M. E. Winkler. 1987. An unusual genetic link between vitamin B₆ biosynthesis and tRNA pseudouridine modification in *Escherichia coli* K-12. J. Bacteriol. 169: 1071-1079.
 32. Arraj, J. A., and M. G. Marinus. 1983. Phenotypic reversal in *dam* mutants of *Escherichia coli* K-12 by a recombinant plasmid containing the *dam*⁺ gene. J. Bacteriol. 153:562-565.
 33. Arthur, H. M., and P. B. Eastlake. 1983. Transcriptional control of the *uvrD* gene of *Escherichia coli*. Gene 25: 309-316.
 34. Asada, K., S. Nakatani, and M. Takanami. 1985. Cloning of the contiguous 165-kilobase-pair region around the terminus of *Escherichia coli* K-12 DNA replication. J. Bacteriol. 163: 398-400.
 35. Asoh, S., H. Matsuzawa, F. Ishino, J. L. Strominger, M. Matsuhashi, and T. Ohta. 1986. Nucleotide sequence of the *pbpA* gene and characteristics of the deduced amino acid sequence of penicillin-binding protein 2 of *Escherichia coli* K12. Eur. J. Biochem. 160:231-238.
 36. Asoh, S., H. Matsuzawa, M. Matsuhashi, and T. Ohta. 1983. Molecular cloning and characterization of the genes (*pbpA* and *rodA*) responsible for the rod shape of *Escherichia coli* K-12: analysis of gene expression with transposon Tn5 mutagenesis and protein synthesis directed by constructed plasmids. J. Bacteriol. 154:10-16.
 37. Attfield, P. V., F. E. Benson, and R. G. Lloyd. 1985. Analysis of the *ruv* locus of *Escherichia coli* K-12 and identification of the gene product. J. Bacteriol. 164:276-281.
 38. Au, D. C.-T., and R. B. Gennis. 1987. Cloning of the *cyo* locus encoding the cytochrome *o* terminal oxidase complex of *Escherichia coli*. J. Bacteriol. 169:3237-3242.
 39. Au, D. C.-T., R. M. Lorence, and R. B. Gennis. 1985. Isolation and characterization of an *Escherichia coli* mutant lacking the cytochrome *o* terminal oxidase. J. Bacteriol. 161:123-127.
 40. Aufrère, R., M. Tempête, and J.-P. Bohin. 1986. Overlapping reading frames in *Escherichia coli*. The two promoters and the first 65 nucleotides of a gene related to the *rrnB* operon are localized in the coding sequence of *btuB*. C.R. Acad. Sci. Ser. III 303:49-54.
 41. Aufrère, R., M. Tempête, and J.-P. Bohin. 1986. Regulation of expression of the gene for vitamin B12 receptor cloned on a multicopy plasmid in *Escherichia coli*. Mol. Gen. Genet. 205:358-365.
 42. Avissar, Y. J., and S. I. Beale. 1989. Identification of the enzymatic basis for δ -aminolevulinic acid auxotrophy in a *hemA* mutant of *Escherichia coli*. J. Bacteriol. 171:2919-2924.
 43. Bachmann, B. J. 1983. Linkage map of *Escherichia coli* K-12, edition 7. Microbiol. Rev. 47:180-230.
 44. Bachmann, B. J. 1987. Linkage map of *Escherichia coli* K-12, edition 7, p. 807-877. In F. C. Neidhardt, J. Ingraham, K. B. Low, B. Magasanik, M. Schaechter, and H. E. Umbarger (ed.), *Escherichia coli* and *Salmonella typhimurium*: cellular and molecular biology, vol. 2. American Society for Microbiology, Washington, D.C.
 45. Bachmann, B. J., and K. B. Low. 1980. Linkage map of *Escherichia coli* K-12, edition 6. Microbiol. Rev. 44:1-56.
 46. Bachmann, B. J., K. B. Low, and A. L. Taylor. 1976. Recalibrated linkage map of *Escherichia coli* K-12. Bacteriol. Rev. 40:116-167.
 47. Backendorf, C., H. Spaink, A. P. Barbiero, and P. van de Putte. 1986. Structure of the *uvrB* gene of *Escherichia coli*. Homology with other DNA repair enzymes and characterization of the *uvrB5* mutation. Nucleic Acids Res. 14:2877-2890.
 48. Bäckström, D., R.-M. Sjöberg, and L. G. Lundberg. 1986. Nucleotide sequence of the structural gene for dihydroorotase of *Escherichia coli* K12. Eur. J. Biochem. 160:77-82.
 49. Baecker, P. A., C. E. Furlong, and J. Preiss. 1986. Biosynthesis of bacterial glycogen: primary structure of *Escherichia coli* ADP-glucose synthetase as deduced from the nucleotide sequence of the *glgC* gene. J. Biol. Chem. 258:5084-5088.
 50. Baecker, P. A., E. Greenberg, and J. Preiss. 1986. Biosynthesis of bacterial glycogen: primary structure of *Escherichia coli* 1,4- α -D-glucan:1,4- α -D-glucan-6- α -D-(1,4- α -D-glucano)-transferase as deduced from the nucleotide sequence of the *glgB* gene. J. Biol. Chem. 261:8738-8743.
 51. Bagg, A., and J. B. Neilands. 1985. Mapping of a mutation affecting regulation of iron uptake systems in *Escherichia coli* K-12. J. Bacteriol. 161:450-453.
 52. Bagg, A., and J. B. Neilands. 1987. Ferric uptake regulation protein acts as a repressor, employing iron (II) as a cofactor to bind the operator of an iron transport operon in *Escherichia coli*. Biochemistry 26:5471-5477.
 53. Bailly, V., and W. G. Verly. 1987. *Escherichia coli* endonuclease III is not an endonuclease but a β -elimination catalyst. Biochem. J. 242:565-572.
 54. Bakker, E. P., I. R. Booth, U. Dinnbier, W. Epstein, and A. Gajewska. 1987. Evidence for multiple K⁺ export systems in *Escherichia coli*. J. Bacteriol. 169:3743-3749.
 55. Bally, M., M. Foglino, M. Bruschi, M. Murgier, and A. Lazdunski. 1986. Nucleotide sequence of the promoter and amino-terminal encoding region of the *Escherichia coli* *pepN* gene. Eur. J. Biochem. 155:565-569.
 56. Bally, M., M. Murgier, and A. Lazdunski. 1984. Cloning and orientation of the gene encoding aminopeptidase N in *Escherichia coli*. Mol. Gen. Genet. 195:507-510.
 57. Bally, M., M. Murgier, J. Tommassen, and A. Lazdunski. 1984. Physical mapping of the gene for aminopeptidase N in

- Escherichia coli* K12. Mol. Gen. Genet. 193:190-191.
58. Bandrin, S. V., P. M. Rabinovich, and A. I. Stepanov. 1984. Three linkage groups of genes for riboflavin biosynthesis. Sov. Genet. 19:1103-1109.
 59. Bankaitis, V. A., and P. J. Bassford, Jr. 1982. Regulation of adenylate cyclase synthesis in *Escherichia coli*: studies with *cya-lac* operon and protein fusion strains. J. Bacteriol. 151:1346-1357.
 60. Bankaitis, V. A., and P. J. Bassford, Jr. 1985. Proper interaction between at least two components is required for efficient export of proteins to the *Escherichia coli* cell envelope. J. Bacteriol. 161:169-178.
 61. Banuett, F., and I. Herskowitz. 1987. Identification of polypeptides encoded by an *Escherichia coli* locus (*hflA*) that governs the lysis-lysogeny decision of bacteriophage λ . J. Bacteriol. 169:4076-4085.
 62. Banuett, F., M. A. Hoyt, L. McFarlane, H. Echols, and I. Herskowitz. 1985. *hflB*, a new *Escherichia coli* locus regulating lysogeny and the level of bacteriophage λ cII protein. J. Mol. Biol. 187:213-224.
 63. Barbier, C. S., and S. A. Short. 1985. Studies on *deo* operon regulation in *Escherichia coli*: cloning and expression of the *cytR* structural gene. Gene 36:37-44.
 64. Bardwell, J. C. A., and E. A. Craig. 1984. Major heat shock gene of *Drosophila* and the *Escherichia coli* heat-inducible *dnaK* gene are homologous. Proc. Natl. Acad. Sci. USA 81:848-852.
 65. Bardwell, J. C. A., and E. A. Craig. 1987. Eukaryotic M_{83,000} heat shock protein has a homologue in *Escherichia coli*. Proc. Natl. Acad. Sci. USA 84:5177-5181.
 66. Bardwell, J. C. A., K. Tilly, E. Craig, J. King, M. Zylicz, and C. Georgopoulos. 1986. The nucleotide sequence of the *Escherichia coli* K12 *dnaJ*⁺ gene: a gene that encodes a heat shock protein. J. Biol. Chem. 261:1782-1785.
 67. Barker, D. G., C. J. Bruton, and G. Winter. 1982. The tyrosyl tRNA synthetase from *Escherichia coli*. Complete nucleotide sequence of the structural gene. FEBS Lett. 150:419-423.
 68. Bartlett, D. H., B. B. Frantz, and P. Matsumura. 1988. Flagellar transcriptional activators FlbB and Flal; gene sequence and 5' consensus sequences of operons under FlbB and Flal control. J. Bacteriol. 170:1575-1581.
 69. Bartlett, D. H., and P. Matsumura. 1984. Identification of *Escherichia coli* region III flagellar gene products and description of two new flagellar genes. J. Bacteriol. 160:577-585.
 70. Baylor, N. W., A. L. Williams, and N. Cofie. 1983. Molecular characteristics of *ilvC* specialized transducing phages of *Escherichia coli* K-12. Mol. Gen. Genet. 191:347-352.
 71. Beall, B., and J. Lutkenhaus. 1987. Sequence analysis, transcriptional organization, and insertional mutagenesis of the *envA* gene of *Escherichia coli*. J. Bacteriol. 169:5408-5415.
 72. Beauchamp, B. B., and C. C. Richardson. 1988. A unique deoxyguanosine triphosphatase is responsible for the OptA1 phenotype of *Escherichia coli*. Proc. Natl. Acad. Sci. USA 85:2563-2567.
 73. Becerril, B., F. Valle, E. Marino, L. Riba, and F. Bolivar. 1985. Repetitive extragenic palindromic (REP) sequences in the *Escherichia coli* *gdhA* gene. Gene 37:53-62.
 74. Bech, F. W., S. T. Jørgensen, B. Diderichsen, and O. H. Karlström. 1985. Sequence of the *relB* transcription unit from *Escherichia coli* and identification of the *relB* gene. EMBO J. 4:1059-1066.
 75. Bedouelle, H. 1983. Mutations in the promoter regions of the *malEFG* and *malK-lamB* operons of *Escherichia coli* K12. J. Mol. Biol. 170:861-882.
 76. Bedouelle, H., U. Schmeissner, M. Hofnung, and M. Rosenberg. 1982. Promoters of the *malEFG* and *malK-lamB* operons in *Escherichia coli* K12. J. Mol. Biol. 161:519-531.
 77. Bedwell, D., G. Davis, M. Gosink, L. Post, M. Nomura, H. Kestler, J. M. Zengel, and L. Lindahl. 1985. Nucleotide sequence of the alpha ribosomal protein operon of *Escherichia coli*. Nucleic Acids Res. 13:3891-3903.
 78. Begg, K. J., and W. D. Donachie. 1985. Cell shape and division in *Escherichia coli*: experiments with shape and division mutants. J. Bacteriol. 163:615-622.
 79. Béjar, S., and J.-P. Bouché. 1983. Molecular cloning of the region of the terminus of *Escherichia coli* K-12 DNA replication. J. Bacteriol. 153:604-609.
 80. Béjar, S., and J.-P. Bouché. 1985. A new dispensable genetic locus of the terminus region involved in control of cell division in *Escherichia coli*. Mol. Gen. Genet. 201:146-150.
 81. Béjar, S., K. Cam, and J.-P. Bouché. 1986. Control of cell division in *Escherichia coli*. DNA sequence of *dicA* and of a second gene complementing mutation *dicA1*, *dicC*. Nucleic Acids Res. 14:6821-6833.
 82. Belfaiza, J., C. Parsot, A. Martel, C. Bouthier de la Tour, D. Margarita, G. N. Cohen, and I. Saint-Girons. 1986. Evolution in biosynthetic pathways: two enzymes catalyzing consecutive steps in methionine biosynthesis originate from a common ancestor and possess a similar regulatory region. Proc. Natl. Acad. Sci. USA 83:867-871.
 83. Belfort, M., G. Maley, J. Pederson-Lane, and F. Maley. 1983. Primary structure of the *Escherichia coli* *thyA* gene and its thymidylate synthase product. Proc. Natl. Acad. Sci. USA 80:4914-4918.
 84. Belitskii, B. R., S. T. Kulakauskas, V. V. Sukhodolets, and R. S. Shakulov. 1985. Precise mapping of the *gpp* gene involved in guanosine tetraphosphate synthesis and deletion of the *ilvC-gpp* region of *Escherichia coli* chromosome. Sov. Genet. 22:1539-1546.
 85. Bell, A. W., S. D. Buckel, J. M. Groarke, J. N. Hope, D. H. Kingsley, and M. A. Hermodsen. 1986. The nucleotide sequences of the *rbsD*, *rbsA*, and *rbsC* genes of *Escherichia coli* K12. J. Biol. Chem. 261:7652-7658.
 86. Bencini, D. A., J. E. Houghton, T. A. Hoover, K. F. Folterman, J. R. Wild, and G. A. O'Donovan. 1983. The DNA sequence of *argI* from *Escherichia coli* K12. Nucleic Acids Res. 11:8509-8518.
 87. Benson, F. E., G. T. Illing, G. J. Sharples, and R. G. Lloyd. 1988. Nucleotide sequencing of the *ruv* region of *Escherichia coli* K-12 reveals a LexA regulated operon encoding two genes. Nucleic Acids Res. 16:1541-1549.
 88. Beny, G., A. Boyen, D. Charlier, W. Lissens, A. Feller, and N. Glansdorff. 1982. Promoter mapping and selection of operator mutants by using insertion of bacteriophage Mu in the *argECBH* divergent operon of *Escherichia coli* K-12. J. Bacteriol. 151:62-67.
 89. Berg, K. L., C. L. Squires, and C. Squires. 1987. In vivo translation of a region within *rrnB* 16S rRNA gene of *Escherichia coli*. J. Bacteriol. 169:1691-1701.
 90. Bhagwat, A. S., A. Sohail, and R. J. Roberts. 1986. Cloning and characterization of the *dcm* locus of *Escherichia coli* K-12. J. Bacteriol. 166:751-755.
 91. Bhatnagar, S. K., and M. J. Bessman. 1988. Studies on the mutator gene, *mutT*, of *Escherichia coli*. Molecular cloning of the gene, purification of the gene product, and identification of a novel nucleoside triphosphatase. J. Biol. Chem. 263:8953-8957.
 92. Bialkowska-Hobrzanska, H., and D. T. Denhardt. 1984. The *rep* mutation. VI. Cloning and analysis of the functional *rep* gene of *Escherichia coli* K-12. Gene 28:93-102.
 93. Bialkowska-Hobrzanska, H., C. A. Gilchrist, and D. T. Denhardt. 1985. *Escherichia coli* *rep* gene: identification of the promoter and N terminus of the Rep protein. J. Bacteriol. 164:1004-1010.
 94. Biek, D. P., and S. N. Cohen. 1986. Identification and characterization of *recD*, a gene affecting plasmid maintenance and recombination in *Escherichia coli*. J. Bacteriol. 167:594-603. (Erratum, 168:1051.)
 95. Bilous, P. T., and J. H. Weiner. 1988. Molecular cloning and expression of the *Escherichia coli* dimethyl sulfoxide reductase operon. J. Bacteriol. 170:1511-1518.
 96. Binkley, J. P., and P. L. Kuempel. 1986. Genetic mapping in *Escherichia coli* of *tmk*, the locus for dTMP kinase. J. Bacteriol. 168:1457-1458.
 97. Birkmann, A., F. Zinoni, G. Sawers, and A. Böck. 1987. Factors affecting transcriptional regulation of the formate-

- hydrogen-lyase pathway of *Escherichia coli*. Arch. Microbiol. 148:44–51.
98. Black, P. N. 1988. The *fadL* gene product of *Escherichia coli* is an outer membrane protein required for uptake of long-chain fatty acids and involved in sensitivity to bacteriophage T2. J. Bacteriol. 170:2850–2854.
 99. Black, P. N., S. F. Kianian, C. C. DiRusso, and W. D. Nunn. 1985. Long-chain fatty acid transport in *Escherichia coli*. Cloning, mapping, and expression of the *fadL* gene. J. Biol. Chem. 260:1780–1789.
 100. Blamar, M. A., S. J. Sandler, M.-E. Armengod, L. W. Ream, and A. J. Clark. 1984. Molecular analysis of the *recF* gene of *Escherichia coli*. Proc. Natl. Acad. Sci. USA 81:4622–4626.
 101. Blanchin-Roland, S., S. Blanquet, J.-M. Schmitter, and G. Fayet. 1986. The gene for *Escherichia coli* diadenosine tetraphosphatase is located immediately clockwise to *folA* and forms an operon with *ksgA*. Mol. Gen. Genet. 205:515–522.
 102. Blanco, C., and M. Mata-Gilsinger. 1986. Identification of cyclic AMP-CRP binding sites in the intercistronic regulatory *uxaCA-exuT* region of *Escherichia coli*. FEMS Microbiol. Lett. 33:205–209.
 103. Blanco, C., and M. Mata-Gilsinger. 1986. A DNA sequence containing the control sites for the *uxaB* gene of *Escherichia coli*. J. Gen. Microbiol. 132:697–705.
 104. Blanco, C., M. Mata-Gilsinger, and P. Ritzenthaler. 1983. Construction of hybrid plasmids containing the *Escherichia coli uxaB* gene: analysis of its regulation and direction of transcription. J. Bacteriol. 153:747–755.
 105. Blanco, C., M. Mata-Gilsinger, and P. Ritzenthaler. 1985. The use of gene fusions to study the expression of *uidR*, a negative regulatory gene of *Escherichia coli* K-12. Gene 36:159–167.
 106. Blanco, C., P. Ritzenthaler, and A. Kolb. 1986. The regulatory region of the *uxuAB* operon in *Escherichia coli* K12. Mol. Gen. Genet. 202:112–119.
 107. Blanco, C., P. Ritzenthaler, and M. Mata-Gilsinger. 1985. Nucleotide sequence of a regulatory region of the *uidA* gene in *Escherichia coli* K12. Mol. Gen. Genet. 199:101–105.
 108. Blanco, C., P. Ritzenthaler, and M. Mata-Gilsinger. 1986. Negative dominant mutations of the *uidR* gene in *Escherichia coli*: genetic proof for a cooperative regulation of *uidA* expression. Genetics 112:173–182.
 109. Blasband, A. J., W. R. Macotte, Jr., and C. A. Schnaitman. 1986. Structure of the *lc* and *nmpC* outer membrane porin protein genes of lambdoid bacteriophage. J. Biol. Chem. 261:12723–12732.
 110. Bloxham, D. P., C. J. Herbert, I. G. Giles, and S. S. Ner. 1983. The use of bacteriophage M13 carrying defined fragments of the *Escherichia coli gltA* gene to determine the location and structure of the citrate synthase promoter region. Mol. Gen. Genet. 191:499–506.
 111. Bognar, A. L., C. Osborne, and B. Shane. 1987. Primary structure of the *Escherichia coli folC* gene and its folylpolyglutamate synthetase-dihydrofolate synthetase product and regulation of expression by an upstream gene. J. Biol. Chem. 262:12337–12343.
 112. Bohin, J.-P., and E. P. Kennedy. 1984. Mapping of a locus (*mdoA*) that affects the biosynthesis of membrane-derived oligosaccharides in *Escherichia coli*. J. Bacteriol. 157:956–957.
 113. Bollinger, J., C. Park, S. Harayama, and G. L. Hazelbauer. 1984. Structure of the Trg protein: homologies with and differences from other sensory transducers of *Escherichia coli*. Proc. Natl. Acad. Sci. USA 81:3287–3291.
 114. Bonnefoy, V., J.-F. Burini, G. Giordano, M.-C. Pascal, and M. Chippaux. 1987. Presence in the 'silent' terminus region of the *Escherichia coli* K12 chromosome of cryptic gene(s) encoding a new nitrate reductase. Mol. Microbiol. 1:143–150.
 115. Boos, W., C. Bantlow, D. Benner, and E. Roller. 1983. *cir*, a gene conferring resistance to colicin I maps between *mgl* and *fpk* on the *Escherichia coli* chromosome. Mol. Gen. Genet. 191:401–406.
 116. Boos, W., U. Ehmann, E. Bremer, A. Middendorf, and P. Postma. 1987. Trehalase of *Escherichia coli*. Mapping and cloning of its structural gene and identification of the enzyme as a periplasmic protein induced under high osmolarity growth conditions. J. Biol. Chem. 262:13212–13218.
 117. Boquet, P. L., C. Manoil, and J. Beckwith. 1987. Use of *TnphoA* to detect genes for exported proteins in *Escherichia coli*: identification of the plasmid-encoded gene for a periplasmic acid phosphatase. J. Bacteriol. 169:1663–1669.
 118. Borg-Olivier, S. A., D. Tarlinton, and K. D. Brown. 1987. Defective regulation of the phenylalanine biosynthetic operon in mutants of the phenylalanyl-tRNA synthetase operon. J. Bacteriol. 169:1949–1953.
 119. Bornstein-Forst, S. M., E. McFall, and S. Palchaudhuri. 1987. In vivo D-serine deaminase transcription start sites in wild-type *Escherichia coli* and in *dsdA* promoter mutants. J. Bacteriol. 169:1056–1060.
 120. Boronat, A., P. Britton, M. C. Jones-Mortimer, H. L. Kornberg, L. G. Lee, D. Murfitt, and F. Parr. 1984. Location on the *Escherichia coli* genome of a gene specifying O-acetylserine (thiol)-lyase. J. Gen. Microbiol. 130:673–685.
 121. Boros, I., É. Csordás-Tóth, A. Kiss, I. Kiss, I. Török, A. Udvardy, K. Udvardy, and P. Venetianer. 1983. Identification of two new promoters probably involved in the transcription of a ribosomal RNA gene of *Escherichia coli*. Biochim. Biophys. Acta 739:173–180.
 122. Bouché, J. P., J. P. Gelugne, J. Louarn, J. M. Louarn, and K. Kaiser. 1982. Relationship between the physical and genetic maps of a 470×10^3 base-pair region around the terminus of *Escherichia coli* K12 DNA replication. J. Mol. Biol. 154:21–23.
 123. Bouma, C. L., N. D. Meadow, E. W. Stover, and S. Roseman. 1987. II-B^{Glc}, a glucose receptor of the bacterial phosphotransferase system: molecular cloning of *ptsG* and purification of the receptor from an overproducing strain of *Escherichia coli*. Proc. Natl. Acad. Sci. USA 84:930–934.
 124. Bouvier, J., J.-C. Patte, and P. Stragier. 1984. Multiple regulatory signals in the control region of the *Escherichia coli carAB* operon. Proc. Natl. Acad. Sci. USA 81:4139–4143.
 125. Bouvier, J., C. Richaud, F. Richaud, J.-C. Patte, and P. Stragier. 1984. Nucleotide sequence and expression of the *Escherichia coli dapB* gene. J. Biol. Chem. 259:14829–14834.
 126. Boyd, A., K. Kendall, and M. I. Simon. 1983. Structure of the serine chemoreceptor in *Escherichia coli*. Nature (London) 301:623–626.
 127. Boyle, S. M., G. D. Markham, E. W. Hafner, J. M. Wright, H. Tabor, and C. W. Tabor. Expression of the cloned genes encoding the putrescine biosynthetic enzymes and methionine adenosyltransferase of *Escherichia coli*. Gene 30:129–136.
 128. Bramley, H. F., and H. L. Kornberg. 1987. Nucleotide sequence of *bglC*, the gene specifying enzyme II^{gal} of the PEP:sugar phosphotransferase system in *Escherichia coli* K12 and overexpression of the gene product. J. Gen. Microbiol. 133:563–573.
 129. Braun, V., R. Gross, W. Köster, and L. Zimmerman. 1983. Plasmid and chromosomal mutants in the iron (III)-aerobactin transport system of *Escherichia coli*. Mol. Gen. Genet. 192:131–139.
 130. Bremer, E., P. Gerlach, and A. Middendorf. 1988. Double negative and positive control of *tsx* expression in *Escherichia coli*. J. Bacteriol. 170:108–116.
 131. Breton, R., H. Sanfaçon, I. Papayannopoulos, K. Biemann, and J. Lapointe. 1986. Glutamyl-tRNA synthetase of *Escherichia coli*. Isolation and primary structure of the *gltX* gene and homology with other aminoacyl-tRNA synthetases. J. Biol. Chem. 261:10610–10617.
 132. Briggs, K. A., W. E. Lancashire, and B. S. Hartley. 1984. Molecular cloning, DNA structure and expression of the *Escherichia coli* D-xylose isomerase. EMBO J. 3:611–616.
 133. Brill, J. A., C. Quinlan-Walsh, and S. Gottesman. 1988. Fine-structure mapping and identification of two regulators of capsule synthesis in *Escherichia coli* K-12. J. Bacteriol. 170:2599–2611.
 134. Britton, P., A. Boronat, D. A. Hartley, M. C. Jones-Mortimer,

- H. L. Kornberg, and F. Parra. 1983. Phosphotransferase-mediated regulation of carbohydrate utilization in *Escherichia coli* K12: location of the *gts* and *iex* (*crr*) genes by specialized transduction. *J. Gen. Microbiol.* **129**:349-358.
135. Britton, P., L. G. Lee, D. Murfitt, A. Boronat, M. C. Jones-Mortimer, and H. L. Kornberg. 1984. Location and direction of transcription of the *ptsH* and *ptsI* genes on the *Escherichia coli* K12 genome. *J. Gen. Microbiol.* **130**:861-868.
136. Britton, P., D. Murfitt, F. Parra, M. C. Jones-Mortimer, and H. L. Kornberg. 1982. Phosphotransferase-mediated regulation of carbohydrate utilization in *Escherichia coli* K12: identification of the products of genes on the specialized transducing phages λ *iex* (*crr*) and λ *gts* (*tgs*). *EMBO J.* **1**:907-911.
137. Brody, H., A. Greener, and C. W. Hill. 1985. Excision and reintegration of the *Escherichia coli* K-12 chromosomal element ϕ 14. *J. Bacteriol.* **161**:1112-1117.
138. Brody, H., and C. W. Hill. 1988. Attachment site of the genetic element ϕ 14. *J. Bacteriol.* **170**:2040-2044.
139. Brooks, J. E., R. M. Blumenthal, and T. R. Gingeras. 1983. The isolation and characterization of the *Escherichia coli* DNA adenine methylase (*dam*) gene. *Nucleic Acids Res.* **11**:837-851.
140. Broome-Smith, J. K., A. Edelman, S. Yousif, and B. G. Spratt. 1985. The nucleotide sequences of the *ponA* and *ponB* genes encoding penicillin-binding proteins 1A and 1B of *Escherichia coli* K-12. *Eur. J. Biochem.* **147**:437-466.
141. Broome-Smith, J. K., I. Ioannidis, A. Edelman, and B. G. Spratt. 1988. Nucleotide sequences of the penicillin-binding protein 5 and 6 genes of *Escherichia coli*. *Nucleic Acids Res.* **16**:1617.
142. Brown, K., P. W. Finch, I. D. Hickson, and P. T. Emmerson. 1987. Complete nucleotide sequence of the *Escherichia coli* *argA* gene. *Nucleic Acids Res.* **15**:10586.
143. Brown, S., B. Albrechtsen, S. Pedersen, and P. Klemm. 1982. Localization and regulation of the structural gene for transcription-termination factor *rho* of *Escherichia coli*. *J. Mol. Biol.* **162**:283-298.
144. Brown, S., and M. J. Fournier. 1984. The 4.5S RNA gene of *Escherichia coli* is essential for cell growth. *J. Mol. Biol.* **178**:533-550.
145. Bruce, I., J. Hardy, and K. A. Stacey. 1984. Potentiation by purines of the growth-inhibitory effects of sulphonamides on *Escherichia coli* K-12 and the location of the gene which mediates this effect. *J. Gen. Microbiol.* **130**:2489-2495.
146. Brucker, R., R. Levitz, E. Yagil, and I. Friedberg. 1984. Complementation tests between mutations in the phosphate-specific transport region of *Escherichia coli*. *Curr. Microbiol.* **10**:303-308.
147. Brune, M., R. Schumann, and F. Wittinghofer. 1985. Cloning and sequencing of the adenylate kinase gene (*adk*) of *Escherichia coli*. *Nucleic Acids Res.* **13**:7139-7151.
148. Brusilow, W. S. A., A. C. G. Porter, and R. D. Simoni. 1983. Cloning and expression of *uncI*, the first gene of the *unc* operon of *Escherichia coli*. *J. Bacteriol.* **155**:1265-1270.
149. Bryan, S. K., and R. Moses. 1984. Map location of the *pcbA* mutation and physiology of the mutant. *J. Bacteriol.* **158**:216-221.
150. Buck, D., M. E. Spencer, and J. R. Guest. 1985. Primary structure of the succinyl-CoA synthetase of *Escherichia coli*. *Biochemistry* **24**:6245-6252.
151. Buck, D., M. E. Spencer, and J. R. Guest. 1986. Cloning and expression of the succinyl-CoA synthetase genes of *Escherichia coli* K12. *J. Gen. Microbiol.* **132**:1753-1762.
152. Buhk, H.-J., and W. Messer. 1983. The replication origin region of *Escherichia coli*: nucleotide sequence and functional units. *Gene* **24**:265-279.
153. Bulawa, C. E., and C. R. H. Raetz. 1984. Isolation and characterization of *Escherichia coli* strains defective in CDP-diglyceride hydrolase. *J. Biol. Chem.* **259**:11257-11264.
154. Burkhardt, R., and V. Braun. 1987. Nucleotide sequence of the *fhuC* and *fhuD* genes involved in iron (III) hydroxamate transport: domains in FhuC homologous to ATP-binding proteins. *Mol. Gen. Genet.* **209**:49-55.
155. Burns, D. M., and I. R. Beacham. 1986. Nucleotide sequence and transcriptional analysis of the *E. coli* *ushA* gene, encoding periplasmic UDP-sugar hydrolase (5'-nucleotidase): regulation of the *ushA* gene, and the signal sequence of its encoded protein product. *Nucleic Acids Res.* **14**:4325-4342.
156. Burton, K. 1983. Transport of nucleic acid bases into *Escherichia coli*. *J. Gen. Microbiol.* **129**:3505-3513.
157. Burton, Z. F., C. A. Gross, K. K. Watanabe, and R. R. Burgess. 1983. The operon that encodes the σ subunit of RNA polymerase also encodes ribosomal protein S21 and DNA primase in *E. coli* K12. *Cell* **32**:335-349.
158. Butler, J. S., M. Springer, J. Dondon, M. Graffe, and M. Grunberg-Manago. 1986. *Escherichia coli* protein synthesis initiation factor IF3 controls its own gene expression at the translational level *in vivo*. *J. Mol. Biol.* **192**:767-780.
159. Buvinger, W. E., K. A. Lampel, R. J. Bojanowski, and M. Riley. 1984. Location and analysis of nucleotide sequences at one end of a putative *lac* transposon in the *Escherichia coli* chromosome. *J. Bacteriol.* **159**:618-623.
160. Buxton, R. S., and L. S. Drury. 1983. Cloning and insertional inactivation of the *dye* (*sfrA*) gene, mutation of which affects sex factor F expression and dye sensitivity of *Escherichia coli* K-12. *J. Bacteriol.* **154**:1309-1314.
161. Buxton, R. S., and L. S. Drury. 1984. Identification of the dye gene product, mutational loss of which alters envelope protein composition and also affects sex factor F expression in *Escherichia coli* K-12. *Mol. Gen. Genet.* **194**:241-247.
162. Byström, A. S., and G. R. Björk. 1982. Chromosomal location and cloning of the gene (*trmD*) responsible for the synthesis of tRNA (m¹G) methyltransferase in *Escherichia coli* K-12. *Mol. Gen. Genet.* **188**:440-446.
163. Byström, A. S., and G. R. Björk. 1982. The structural gene (*trmD*) for the tRNA (m¹G) methyltransferase is part of a four polypeptide operon in *Escherichia coli* K-12. *Mol. Gen. Genet.* **188**:447-454.
164. Byström, A. S., K. J. Hjalmarsson, P. M. Wikström, and G. R. Björk. 1983. The nucleotide sequence of an *Escherichia coli* operon containing genes for the tRNA (m¹G) methyltransferase, the ribosomal proteins S16 and L19 and a 21-K polypeptide. *EMBO J.* **2**:899-905.
165. Cabrera, M., Y. Nghiem, and J. H. Miller. 1988. *mutM*, a second mutator locus in *Escherichia coli* that generates G \cdot C \rightarrow T \cdot A transversions. *J. Bacteriol.* **170**:5405-5407.
166. Caillet, J., J. A. Plumbbridge, and M. Springer. 1985. Evidence that *pheV*, a gene for tRNA^{Phe} of *E. coli* is transcribed from tandem promoters. *Nucleic Acids Res.* **13**:3699-3710.
167. Calhoun, D. H., L. Traub, J. W. Wallen, J. E. Gray, and S. K. Guterman. 1984. Location of the *rho* gene and characterization of λ *ilv-gal* derivatives of λ *ilv-rho* bacteriophage. *Mol. Gen. Genet.* **193**:205-209.
168. Calhoun, D. H., J. W. Wallen, L. Traub, J. E. Gray, and H.-F. Kung. 1985. Internal promoter in the *ilvGEDA* transcription unit of *Escherichia coli* K-12. *J. Bacteriol.* **161**:128-132.
169. Callahan, A. M., B. L. Frazier, and J. S. Parkinson. 1987. Chemotaxis in *Escherichia coli*: construction and properties of λ *tsr* transducing phage. *J. Bacteriol.* **169**:1246-1253.
170. Campbell, H. D., B. L. Rogers, and I. G. Young. 1984. Nucleotide sequence of the respiratory D-lactate dehydrogenase gene of *Escherichia coli*. *Eur. J. Biochem.* **144**:367-373.
171. Carliz, A., M. L. Ludwig, W. C. Stallings, J. A. Fee, H. M. Steinman, and D. Touati. 1988. Iron superoxide dismutase: nucleotide sequence of the gene from *Escherichia coli* K12 and correlations with crystal structures. *J. Biol. Chem.* **263**:1555-1562.
172. Carliz, A., and D. Touati. 1986. Isolation of superoxide dismutase mutants in *Escherichia coli*: is superoxide dismutase necessary for aerobic life? *EMBO J.* **5**:623-630.
173. Carlson, J., J. A. Fuchs, and J. Messing. 1984. Primary structure of the *Escherichia coli* ribonucleoside diphosphate reductase operon. *Proc. Natl. Acad. Sci. USA* **81**:4294-4297.
174. Caskey, C. T., W. C. Forrester, W. Tate, and C. D. Ward. 1984. Cloning of the *Escherichia coli* release factor 2 gene. *J.*

- Bacteriol. 158:365-368.
175. Cassan, M., C. Parsot, G. N. Cohen, and J.-C. Patte. 1986. Nucleotide sequence of *lysC* gene encoding the lysine-sensitive aspartokinase III of *Escherichia coli*. J. Biol. Chem. 261:1052-1057.
 176. Cassan, M., J. Ronceray, and J. C. Patte. 1983. Nucleotide sequence of the promoter region of the *E. coli lysC* gene. Nucleic Acids Res. 11:6157-6165.
 177. Castaño, I., and F. Bastarrachea. 1984. *glnF-lacZ* fusions in *Escherichia coli*: studies on *glnF* expression and its chromosomal orientation. Mol. Gen. Genet. 195:228-233.
 178. Castaño, I., F. Bastarrachea, and A. A. Covarrubias. 1988. *gltBDF* operon of *Escherichia coli*. J. Bacteriol. 170:821-827.
 179. Cavard, D., J. M. Pages, and C. J. Lazdunski. 1982. A protease as a possible sensor of environmental conditions in *E. coli* outer membrane. Mol. Gen. Genet. 188:508-512.
 180. Celis, R. T. F. 1982. Mapping of two loci affecting the synthesis and structure of a periplasmic protein involved in arginine and ornithine transport in *Escherichia coli* K-12. J. Bacteriol. 151:1314-1319.
 181. Cerretti, D. P., D. Dean, G. R. Davis, D. M. Bedwell, and M. Nomura. 1983. The *spc* ribosomal protein operon of *Escherichia coli*: sequence and cotranscription of the ribosomal protein genes and a protein export gene. Nucleic Acids Res. 11:2599-2616.
 182. Chakrabarti, T., Y.-M. Chen, and E. C. C. Lin. 1984. Clustering of genes for L-fucose dissimilation by *Escherichia coli*. J. Bacteriol. 157:984-986.
 183. Chanda, P. K., M. Ono, M. Kuwano, and H.-F. Kung. 1985. Cloning, sequence analysis, and expression of alteration of the mRNA stability gene (*ams*⁺) of *Escherichia coli*. J. Bacteriol. 161:446-449.
 184. Chang, C. N., W.-J. Kuang, and E. Y. Chen. 1986. Nucleotide sequence of the alkaline phosphatase gene of *Escherichia coli*. Gene 44:121-125.
 185. Chang, Y.-Y., and J. E. Cronan, Jr. 1983. Genetic and biochemical analyses of *Escherichia coli* strains having a mutation in the structural gene (*poxB*) for pyruvate oxidase. J. Bacteriol. 154:756-762.
 186. Charlier, J., and R. Sanchez. 1987. Lysyl-tRNA synthetase from *Escherichia coli* K-12. Chromatographic heterogeneity and the *lysU*-gene product. Biochem. J. 248:43-51.
 187. Chase, J. W., B. A. Rabin, J. B. Murphy, K. L. Stone, and K. R. Williams. 1986. *Escherichia coli* exonuclease VII: cloning and sequencing of the gene encoding the large subunit (*xseA*). J. Biol. Chem. 261:14929-14935.
 188. Chaudhuri, A., and A. I. Krasna. 1987. Isolation of genes required for hydrogenase synthesis in *Escherichia coli*. J. Gen. Microbiol. 133:3289-3298.
 189. Chen, Y.-M., Y. Zhu, and E. C. C. Lin. 1987. NAD-linked aldehyde dehydrogenase for aerobic utilization of L-fucose and L-rhamnose by *Escherichia coli*. J. Bacteriol. 169:3289-3294.
 190. Chen, Y.-M., Y. Zhu, and E. C. C. Lin. 1987. The organization of *fuc* regulon specifying L-fucose dissimilation in *Escherichia coli* K12 as determined by gene cloning. Mol. Gen. Genet. 210:331-337.
 191. Chesney, R. H., P. Sollitti, and D. R. Vickery. 1985. Identification of a new locus in the *Escherichia coli* cotransduction gap that represents a new genetic component of the L-asparagine utilization system. J. Gen. Microbiol. 131:2079-2085.
 192. Chiariotti, L., P. Alifano, M. S. Carlomagno, and C. B. Bruni. 1986. Nucleotide sequence of the *Escherichia coli hisD* gene and of the *Escherichia coli* and *Salmonella typhimurium hisIE* region. Mol. Gen. Genet. 203:382-388.
 193. Chiariotti, L., A. G. Nappo, M. S. Carlomagno, and C. B. Bruni. 1986. Gene structure in the histidine operon of *Escherichia coli*. Identification and nucleotide sequence of the *hisB* gene. Mol. Gen. Genet. 202:42-47.
 194. Chung, T., D.-J. Klumpp, and D. C. LaPorte. 1988. Glyoxylate bypass operon of *Escherichia coli*: cloning and determination of the functional map. J. Bacteriol. 170:386-392.
 195. Clark, D. 1984. Novel antibiotic hypersensitive mutants of *Escherichia coli*. Genetic mapping and chemical characterization. FEMS Microbiol. Lett. 21:189-195.
 196. Clark, D. P., and M. L. Rod. 1987. Regulatory mutations that allow the growth of *Escherichia coli* on butanol as carbon source. J. Mol. Evol. 25:151-158.
 197. Clarke, D. M., and P. D. Bragg. 1985. Cloning and expression of the transhydrogenase gene of *Escherichia coli*. J. Bacteriol. 162:367-373.
 198. Clarke, D. M., T. W. Loo, S. Gillam, and P. D. Bragg. 1986. Nucleotide sequence of the *pntA* and *pntB* genes encoding the pyridine nucleotide transhydrogenase of *Escherichia coli*. Eur. J. Biochem. 158:647-653.
 199. Clarke, N. D., M. Kvaal, and E. Seeberg. 1984. Cloning of *Escherichia coli* genes encoding 3-methyladenine DNA glycosylases I and II. Mol. Gen. Genet. 197:368-372.
 200. Claverie-Martin, F., M. R. Diaz-Torres, and S. R. Kushner. 1987. Analysis of the regulatory region of the protease III (*ptr*) gene of *Escherichia coli* K-12. Gene 54:185-195.
 201. Clegg, D. O., and D. E. Koshland. 1984. The role of a signaling protein in bacterial sensing: behavioral effects of increased gene expression. Proc. Natl. Acad. Sci. USA 81:5056-5060.
 202. Clegg, D. O., and D. E. Koshland, Jr. 1985. Identification of a bacterial sensing protein and effects of its elevated expression. J. Bacteriol. 162:398-405.
 203. Climie, S. C., and J. D. Friesen. 1987. Feedback regulation of the *rplJL-rpoBC* ribosomal protein operon of *Escherichia coli* requires a region of mRNA secondary structure. J. Mol. Biol. 198:371-381.
 204. Clyman, J., and R. P. Cunningham. 1987. *Escherichia coli* K-12 mutants in which viability is dependent on *recA* function. J. Bacteriol. 169:4203-4210.
 205. Coderre, P. E., and C. F. Earhart. 1984. Characterization of a plasmid carrying the *Escherichia coli* K-12 *entD*, *fepA*, *fes* and *entF* genes. FEMS Microbiol. Lett. 25:111-116.
 206. Cole, S. T. 1983. Characterization of the promoter for the LexA regulated *sula* gene of *Escherichia coli*. Mol. Gen. Genet. 189:400-404.
 207. Cole, S. T., E. Bremer, I. Hindennach, and U. Henning. 1982. Characterization of the promoters for the *ompA* gene which encodes a major outer membrane protein of *Escherichia coli*. Mol. Gen. Genet. 188:472-479.
 208. Cole, S. T., K. Eiglmeier, S. Ahmed, N. Honore, L. Elmes, W. F. Anderson, and J. H. Weiner. 1988. Nucleotide sequence and gene-polypeptide relationships of the *glpABC* operon encoding the anaerobic *sn*-glycerol-3-phosphate dehydrogenase of *Escherichia coli* K-12. J. Bacteriol. 170:2448-2456.
 209. Cole, S. T., and O. Raibaud. 1986. The nucleotide sequence of the *malT* gene encoding the positive regulator of the *Escherichia coli* maltose regulon. Gene 42:201-208.
 210. Coleman, J., and C. R. H. Raetz. 1988. First committed step of lipid A biosynthesis in *Escherichia coli*: sequence of the *lpxA* gene. J. Bacteriol. 170:1268-1274.
 211. Coleman, W. G., Jr. 1983. The *rfaD* gene codes for ADP-L-glycero-D-mannoheptose-6-epimerase. An enzyme required for lipopolysaccharide core biosynthesis. J. Biol. Chem. 258:1985-1990.
 212. Colombo, G., and J. J. Villafranca. 1986. Amino acid sequence of *Escherichia coli* glutamine synthetase deduced from the DNA nucleotide sequence. J. Biol. Chem. 261:10587-10591.
 213. Comeau, D. E., K. Ikenaka, K. Tsung, and M. Inoue. 1985. Primary characterization of the protein products of the *Escherichia coli ompB* locus: structure and regulation of synthesis of the OmpR and EnvZ proteins. J. Bacteriol. 164:578-584.
 214. Comer, M. M. 1982. Threonine tRNAs and their genes in *Escherichia coli*. Mol. Gen. Genet. 187:132-137.
 215. Conrad, C. A., G. W. Stearns III, W. E. Prater, J. A. Rheimer, and J. R. Johnson. 1984. Characterization of a *glpK* transducing phage. Mol. Gen. Genet. 193:376-378.
 216. Cooper, R. A., D. C. N. Jones, and S. Parrott. 1985. Isolation and mapping of *Escherichia coli* K12 mutants defective in

- phenylacetate degradation. *J. Gen. Microbiol.* **131**:2753–2757.
217. Cornish, E. C., V. P. Argyropoulos, J. Pittard, and B. E. Davidson. 1986. Structure of the *Escherichia coli* K12 regulatory gene *tyrR*: nucleotide sequence and sites of initiation of transcription and translation. *J. Biol. Chem.* **261**:403–410.
 218. Cornish, E. C., B. E. Davidson, and J. Pittard. 1982. Cloning and characterization of *Escherichia coli* K-12 regulator gene *tyrR*. *J. Bacteriol.* **152**:1276–1279.
 219. Cornwell, T. L., S. L. Adhya, W. S. Reznikoff, and P. A. Frey. 1987. The nucleotide sequence of the *galT* gene of *Escherichia coli*. *Nucleic Acids Res.* **15**:8116.
 220. Cortay, J.-C., F. Bleicher, C. Rieul, H. C. Reeves, and A. J. Cozzzone. 1988. Nucleotide sequence and expression of the *aceK* gene coding for isocitrate dehydrogenase kinase/phosphatase in *Escherichia coli*. *J. Bacteriol.* **170**:89–97.
 221. Coulton, J. W., P. Mason, and D. D. Allatt. 1987. *fhuC* and *fhuD* genes for iron(III)-ferrichrome transport into *Escherichia coli* K-12. *J. Bacteriol.* **169**:3844–3849.
 222. Coulton, J. W., P. Mason, D. R. Cameron, G. Carmel, R. Jean, and H. N. Rode. 1986. Protein fusions of β -galactosidase to the ferrichrome-iron receptor of *Escherichia coli* K-12. *J. Bacteriol.* **165**:181–192.
 223. Coulton, J. W., P. Mason, and M. S. DuBow. 1983. Molecular cloning of the ferrichrome-iron receptor of *Escherichia coli* K-12. *J. Bacteriol.* **156**:1315–1321.
 224. Covarrubias, A. A., and F. Bastarrachea. 1983. Nucleotide sequence of the *glnA* control region of *Escherichia coli*. *Mol. Gen. Genet.* **190**:171–175.
 225. Cox, E. C., and D. L. Horner. 1986. DNA sequence and coding properties of *mutD* (*dnaQ*) a dominant *Escherichia coli* mutator gene. *J. Mol. Biol.* **190**:113–117.
 226. Creeger, E. S., T. Schulte, and L. I. Rothfield. 1984. Regulation of membrane glycosyltransferases by the *sfrB* and *rfaH* genes of *Escherichia coli* and *Salmonella typhimurium*. *J. Biol. Chem.* **259**:3064–3069.
 227. Crofton, S., and P. P. Dennis. 1983. Cloning and orientation of the gene encoding polynucleotide phosphorylase in *Escherichia coli*. *J. Bacteriol.* **154**:58–64. (Author's correction, **156**:479.)
 228. Cronan, J. E., Jr., W.-B. Li, R. Coleman, M. Narasimhan, D. de Mendoza, and J. M. Schwab. 1988. Derived amino acid sequence and identification of active site residues of *Escherichia coli* β -hydroxydecanoyl thioester dehydratase. *J. Biol. Chem.* **263**:4641–4646.
 229. Crowell, D. N., M. S. Anderson, and C. R. H. Raetz. 1986. Molecular cloning of the genes for lipid A disaccharide synthase and UDP-*N*-acetylglucosamine acyltransferase in *Escherichia coli*. *J. Bacteriol.* **168**:152–159.
 230. Crowell, D. N., W. S. Reznikoff, and C. R. H. Raetz. 1987. Nucleotide sequence of the *Escherichia coli* gene for lipid A disaccharide synthase. *J. Bacteriol.* **169**:5727–5734.
 231. Cudny, H., J. R. Lupski, G. N. Godson, and M. P. Deutscher. 1986. Cloning, sequencing, and species relatedness of the *Escherichia coli* *cca* gene encoding the enzyme tRNA nucleotidyltransferase. *J. Biol. Chem.* **261**:6444–6449.
 232. Cunningham, P. R., and D. P. Clark. 1986. The use of suicide substrates to select mutants of *Escherichia coli* lacking enzymes of alcohol fermentation. *Mol. Gen. Genet.* **205**:487–493.
 233. Cunningham, R. P., S. M. Saporito, S. G. Spitzer, and B. Weiss. 1986. Endonuclease IV (*nfo*) mutant of *Escherichia coli*. *J. Bacteriol.* **168**:1120–1127.
 234. Cunningham, R. P., and B. Weiss. 1985. Endonuclease III (*nth*) mutants of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **82**:474–478.
 235. Dabbs, E. R. 1982. A spontaneous mutant of *Escherichia coli* with protein L24 lacking from the ribosome. *Mol. Gen. Genet.* **187**:453–458.
 236. Dabbs, E. R. 1982. Three additional loci of rifampicin dependence in *Escherichia coli*. *Mol. Gen. Genet.* **187**:519–522.
 237. Dabbs, E. R. 1983. *Escherichia coli* kasugamycin dependence arising from mutation at the *rpsI* locus. *J. Bacteriol.* **153**:709–715.
 238. Dai, D., and E. E. Ishiguro. 1988. *murH*, a new genetic locus in *Escherichia coli* involved in cell wall peptidoglycan biosynthesis. *J. Bacteriol.* **170**:2197–2201.
 239. Dairi, T., K. Inokuchi, T. Mizuno, and S. Mizushima. 1985. Positive control of transcription initiation in *Escherichia coli*. A base substitution at the Pribnow box renders *ompF* expression independent of a positive regulator. *J. Mol. Biol.* **184**:1–6.
 240. Daldal, F. 1983. Molecular cloning of the gene for phosphofructokinase-2 of *Escherichia coli* and the nature of a mutation, *pfkBI*, causing a high level of the enzyme. *J. Mol. Biol.* **168**:285–305.
 241. Daldal, F. 1984. Nucleotide sequence of gene *pfkB* encoding the minor phosphofructokinase of *Escherichia coli* K-12. *Gene* **28**:337–342.
 242. Dalrymple, B., and J. S. Mattick. 1986. Genes encoding threonine tRNA's with the anticodon CGU from *Escherichia coli* and *Pseudomonas aeruginosa*. *Biochem. Int.* **13**:547–553.
 243. Dandanell, G., and K. Hammer. 1985. Two operator sites separated by 599 base pairs are required for *deoR* repression of the *deo* operon of *Escherichia coli*. *EMBO J.* **4**:3333–3338.
 244. Daniel, J., and I. Saint-Girons. 1982. Attenuation in the threonine operon: effects of amino acids present in the presumed leader peptide in addition to threonine and isoleucine. *Mol. Gen. Genet.* **188**:225–227.
 245. Dardel, F., G. Fayat, and S. Blanquet. 1984. Molecular cloning and primary structure of the *Escherichia coli* methionyl-tRNA synthetase gene. *J. Bacteriol.* **160**:1115–1122.
 246. D'Ari, R., and O. Huisman. 1983. Novel mechanism of cell division inhibition associated with the SOS response in *Escherichia coli*. *J. Bacteriol.* **156**:243–250.
 247. Darlison, M. G., and J. R. Guest. 1984. Nucleotide sequence encoding the iron-sulfur protein subunit of the succinate dehydrogenase of *Escherichia coli*. *Biochem. J.* **223**:507–517.
 248. Darlison, M. G., M. E. Spencer, and J. R. Guest. 1984. Nucleotide sequence of the *sucA* gene encoding the 2-oxoglutarate dehydrogenase of *Escherichia coli* K12. *Eur. J. Biochem.* **141**:351–359.
 249. Dass, S. B., and R. Jayaraman. 1985. Intragenic suppression of the temperature sensitivity caused by a mutation in a gene controlling transcription (*fit*) in *Escherichia coli*. *Mol. Gen. Genet.* **198**:299–303.
 250. Dassa, E., and P. L. Boquet. 1985. Identification of the gene *appA* for the acid phosphatase (pH optimum 2.5) of *Escherichia coli*. *Mol. Gen. Genet.* **200**:68–73.
 251. Dassa, E., and M. Hofnung. 1985. Sequence of gene *malG* in *E. coli* K12: homologies between integral membrane components from binding protein-dependent transport systems. *EMBO J.* **4**:2287–2293.
 252. Datta, P., T. J. Goss, J. R. Omnass, and R. V. Patil. 1987. Covalent structure of biodegradative threonine dehydratase of *Escherichia coli*: homology with other dehydratases. *Proc. Natl. Acad. Sci. USA* **84**:393–397.
 253. Davie, E., K. Sydnor, and L. I. Rothfield. 1984. Genetic basis of minicell formation in *Escherichia coli* K-12. *J. Bacteriol.* **158**:1202–1203. (Erratum, **160**:831.)
 254. Davies, W. D., J. Pittard, and B. E. Davidson. 1985. Cloning of *aroG*, the gene coding for phospho-2-keto-3-deoxy-heptonate aldolase (phe), in *Escherichia coli* K-12, and subcloning of the *aroG* promoter and operator in a promoter-detecting plasmid. *Gene* **33**:323–331.
 255. Davis, E. O., and P. J. F. Henderson. 1987. The cloning and DNA sequence of the gene *xylE* for xylose-proton symport in *Escherichia coli* K12. *J. Biol. Chem.* **262**:13928–13932.
 256. Davis, E. O., M. C. Jones-Mortimer, and P. J. F. Henderson. 1984. Location of a structural gene for xylose-H⁺ symport at 91 min on the linkage map of *Escherichia coli* K12. *J. Biol. Chem.* **259**:1520–1525.
 257. Daws, T. D., and J. A. Fuchs. 1984. Isolation and characterization of an *Escherichia coli* mutant deficient in dTMP kinase activity. *J. Bacteriol.* **157**:440–444.
 258. Dean, G. E., R. M. Macnab, J. Stader, P. Matsumura, and C. Burks. 1984. Gene sequence and predicted amino acid se-

- quence of the *motA* protein, a membrane-associated protein required for flagellar rotation in *Escherichia coli*. J. Bacteriol. 159:991-999.
259. deBoer, P. A. J., R. E. Crossley, and L. I. Rothfield. 1988. Isolation and properties of *minB*, a complex genetic locus involved in correct placement of the division site in *Escherichia coli*. J. Bacteriol. 170:2106-2112.
 260. Debouck, C., A. Riccio, D. Schumperli, K. McKenney, J. Jeffers, C. Hughes, M. Rosenberg, M. Heusterspreute, and J. Davison. 1985. Structure of the galactokinase gene of *Escherichia coli*, the last (?) gene of the *gal* operon. Nucleic Acids Res. 13:1841-1853.
 261. DeFeyter, R. C., B. E. Davidson, and J. Pittard. 1986. Nucleotide sequence of the transcription unit containing the *aroL* and *aroM* genes from *Escherichia coli* K-12. J. Bacteriol. 165:233-239.
 262. DeFeyter, R. C., and J. Pittard. 1986. Genetic and molecular analysis of *aroL*, the gene for shikimate kinase II in *Escherichia coli* K-12. J. Bacteriol. 165:226-232.
 263. de Geus, P., I. van Die, H. Bergmans, J. Tommassen, and G. de Haas. 1983. Molecular cloning of *pldA*, the structural gene for outer membrane phospholipase of *E. coli* K12. Mol. Gen. Genet. 190:150-155.
 264. de Geus, P., H. M. Verheij, N. H. Riegman, W. P. M. Hoekstra, and G. H. de Haas. 1984. The pro- and mature forms of the *E. coli* K-12 outer membrane phospholipase A are identical. EMBO J. 3:1799-1802.
 265. de la Campa, A. G., M. Aldea, C. Hernandez-Chico, A. Tormo, and M. Vicente. 1988. Segregation of elongation potential in *Escherichia coli* mediated by the *wee* genetic system. Curr. Microbiol. 17:315-319.
 266. De Lorenzo, V., M. Herrero, F. Giovannini, and J. B. Neilands. 1988. Fur (ferric uptake regulation) protein and CAP (catabolite-activator protein) modulate transcription of *fur* gene in *Escherichia coli*. Eur. J. Biochem. 173:537-546.
 267. de Massey, B., S. Béjar, J. Louarn, J. M. Louarn, and J. P. Bouché. 1987. Inhibition of replication forks exiting the terminus region of the *Escherichia coli* chromosome occurs at two loci separated by 5 min. Proc. Natl. Acad. Sci. USA 84:1759-1763.
 268. Demerec, M., E. A. Adelberg, A. J. Clark, and P. E. Hartman. 1966. A proposal for a uniform nomenclature in bacterial genetics. Genetics 54:61-76.
 269. Denk, D., and A. Böck. 1987. L-Cysteine biosynthesis in *Escherichia coli*: nucleotide sequence and expression of the serine acetyltransferase (*cysE*) gene from the wild-type and a cysteine-excreting mutant. J. Gen. Microbiol. 133:515-525.
 270. DeReuse, H., E. Huttner, and A. Danchin. 1984. Analysis of the *ptsH-ptsI-crr* region in *Escherichia coli* K-12: evidence for the existence of a single transcriptional unit. Gene 32:31-40.
 271. DeReuse, H., A. Roy, and A. Danchin. 1985. Analysis of the *ptsH-ptsI-crr* region in *Escherichia coli* K-12: nucleotide sequence of the *ptsH* gene. Gene 35:199-207.
 272. Deutch, A. H., K. E. Rushlow, and C. J. Smith. 1984. Analysis of the *Escherichia coli* *proBA* locus by DNA and protein sequencing. Nucleic Acids Res. 12:6337-6355.
 273. Deutch, A. H., C. J. Smith, K. E. Rushlow, and P. J. Kretschmer. 1982. *Escherichia coli* *del*¹-pyrroline-5-carboxylate reductase: gene sequence, protein overproduction and purification. Nucleic Acids Res. 10:7701-7714.
 274. DeVeaux, L. C., D. S. Clevenson, C. Bradbeer, and R. J. Kadner. 1986. Identification of the BtuCED polypeptides and evidence for their role in vitamin B₁₂ transport in *Escherichia coli*. J. Bacteriol. 167:920-927.
 275. DeVeaux, L. C., J. E. Cronan, Jr., and T. L. Smith. 1989. Genetic and biochemical characterization of a mutation (*fatA*) that allows *trans* unsaturated fatty acids to replace the essential *cis* unsaturated fatty acids of *Escherichia coli*. J. Bacteriol. 171:1562-1568.
 276. DeVeaux, L. C., and R. J. Kadner. 1985. Transport of vitamin B₁₂ in *Escherichia coli*: cloning of the *btuCD* region. J. Bacteriol. 162:888-896.
 277. deWind, N., M. de Jong, M. Meijer, and A. R. Stuitje. 1985. Site-directed mutagenesis of the *Escherichia coli* chromosome near *oriC*: identification and characterization of *asnC*, a regulatory element in *E. coli* asparagine metabolism. Nucleic Acids Res. 13:8797-8811.
 278. DeFrancesco, R., S. K. Bhatnagar, A. Brown, and M. J. Bessman. 1984. The interaction of DNA polymerase III and the product of the *Escherichia coli* mutator gene, *mutD*. J. Biol. Chem. 259:5567-5573.
 279. DiRusso, C. C., and W. D. Nunn. 1985. Cloning and characterization of a gene (*fadR*) involved in regulation of fatty acid metabolism in *Escherichia coli*. J. Bacteriol. 161:583-588.
 280. Diver, W. P., N. J. Sargentini, and K. C. Smith. 1982. A mutation (*radA100*) in *Escherichia coli* that selectively sensitizes cells grown in rich medium to X- or U.V.-radiation, or methyl methanesulphonate. Int. J. Radiat. Biol. 42:339-346.
 281. Dobrynina, O. Y., T. N. Bol'shakova, and V. N. Gershanovich. 1986. The isolation and mapping of a mutation which impairs the function of the cytoplasm-specific component of the fructose transport system in *Escherichia coli*. Sov. Genet. 21:981-986.
 282. Donovan, W. P., and S. R. Kushner. 1983. Cloning and physical analysis of the *pyrF* gene (coding for orotidine-5'-phosphate decarboxylase) from *Escherichia coli* K-12. Gene 25:39-48.
 283. Downing, W. L., and P. P. Dennis. 1987. Transcription products from the *rplKAJL-rpoBC* gene cluster. J. Mol. Biol. 194:609-620.
 284. Drapeau, G. R., J. P. Chausseau, and F. Gariépy. 1983. Unusual properties of a new division mutant of *Escherichia coli*. Can. J. Microbiol. 29:694-699.
 285. Driver, R. P., and R. P. Lawther. 1985. Physical analysis of deletion mutations in the *ilvGEDA* operon of *Escherichia coli* K-12. J. Bacteriol. 162:598-606.
 286. Drury, L. S., and R. S. Buxton. 1985. DNA sequence analysis of the *dye* gene of *Escherichia coli* reveals amino acid homology between the Dye and OmpR proteins. J. Biol. Chem. 260:4236-4242.
 287. Drury, L. S., and R. S. Buxton. 1988. Identification and sequencing of the *Escherichia coli* *cet* gene which codes for an inner membrane protein, mutation of which causes tolerance of colicin E2. Mol. Microbiol. 2:109-119.
 288. Duchange, N., M. M. Zakin, P. Ferrara, I. Saint-Girons, I. Park, S. V. Tran, M.-C. Py, and G. N. Cohen. 1983. Structure of the *metJBLF* cluster in *Escherichia coli* K12. Sequence of the *metB* structural gene and of the 5'- and 3'-flanking regions of the *metBL* operon. J. Biol. Chem. 258:14868-14871.
 289. Duester, G., R. K. Campen, and W. M. Holmes. 1981. Nucleotide sequence of an *Escherichia coli* tRNA (Leu 1) operon and identification of the transcription promoter signal. Nucleic Acids Res. 9:2121-2139.
 290. Duncan, K., S. Chaudhuri, M. S. Campbell, and J. R. Coggins. 1986. The overexpression and complete amino acid sequence of *Escherichia coli* 3-dehydroquinase. Biochem. J. 238:475-483.
 291. Duncan, K., and J. R. Coggins. 1986. The *serC-aroA* operon of *Escherichia coli*. A mixed operon encoding enzymes from two different amino acid biosynthetic pathways. Biochem. J. 234:49-57.
 292. Duncan, K., A. Lewendon, and J. R. Coggins. 1984. The complete amino acid sequence of *Escherichia coli* 5-enolpyruvylshikimate 3-phosphate synthase. FEBS Lett. 170:59-63.
 293. Dunn, T. M., and R. Schleif. 1984. Deletion analysis of the *Escherichia coli* *ara* P_C and P_{BAD} promoters. J. Mol. Biol. 180:201-204.
 294. Duplay, P., H. Bedouelle, A. Fowler, I. Zabin, W. Saurin, and M. Hofnung. 1984. Sequence of the *malE* gene and of its product, the maltose-binding protein of *Escherichia coli* K12. J. Biol. Chem. 259:10606-10613.
 295. Dykstra, C., and S. R. Kushner. 1985. Physical characterization of the cloned protease III gene from *Escherichia coli* K-12. J. Bacteriol. 163:1055-1059.
 296. Dykstra, C. C., D. Prasher, and S. R. Kushner. 1984. Physical and biochemical analysis of the cloned *recB* and *recC* genes of

- Escherichia coli* K-12. J. Bacteriol. 157:21–27.
297. Easton, A. M., and S. R. Kushner. 1983. Transcription of the *uvrD* gene of *Escherichia coli* is controlled by the *lexA* repressor and by attenuation. Nucleic Acids Res. 11:8625–8640.
 298. Echols, H., C. Lu, and P. M. J. Burgers. 1983. Mutator strains of *Escherichia coli*, *mutD* and *dnaQ*, with defective exonucleolytic editing by DNA polymerase III holoenzyme. Proc. Natl. Acad. Sci. USA 80:2189–2192.
 299. Edwards, E. S., S. S. Rondeau, and J. A. DeMoss. 1983. *chlC* (*nar*) operon of *Escherichia coli* includes structural genes for α and β subunits of nitrate reductase. J. Bacteriol. 153:1513–1520.
 300. Ehrmann, M., and W. Boos. 1987. Identification of endogenous inducers of the *mal* regulon in *Escherichia coli*. J. Bacteriol. 169:3539–3545.
 301. Ehrmann, M., W. Boos, E. Ormseth, H. Schweizer, and T. J. Larson. 1987. Divergent transcription of the *sn*-glycerol-3-phosphate active transport (*glpT*) and anaerobic *sn*-glycerol-3-phosphate dehydrogenase (*glpA glpC glpB*) genes of *Escherichia coli* K-12. J. Bacteriol. 169:526–532.
 302. Eick-Helmerich, K., K. Hantke, and V. Braun. 1987. Cloning and expression of the *exbB* gene of *Escherichia coli* K-12. Mol. Gen. Genet. 206:246–251.
 303. Eiglmeier, K., W. Boos, and S. T. Cole. 1987. Nucleotide sequence and transcriptional startpoint of the *glpT* gene of *Escherichia coli*: extensive sequence homology of the glycerol-3-phosphate transport protein with components of the hexose-6-phosphate transport system. Mol. Microbiol. 1:251–258.
 304. Eisenstein, B. I., D. S. Sweet, V. Vaughn, and D. I. Friedman. 1987. Integration host factor is required for the DNA inversion that controls phase variation in *Escherichia coli*. Proc. Natl. Acad. Sci. USA 84:6506–6510.
 305. Elledge, S. J., and G. C. Walker. 1983. Proteins required for ultraviolet light and chemical mutagenesis. Identification of the products of the *umuC* locus of *Escherichia coli*. J. Mol. Biol. 164:175–192.
 306. Elseviers, D., P. Gallagher, A. Hoffman, B. Weinberg, and I. Schwartz. 1982. Molecular cloning and regulation of expression of the genes for initiation factor 3 and two aminoacyl-tRNA synthetases. J. Bacteriol. 152:357–362.
 307. Elseviers, D., L. A. Petrullo, and P. J. Gallagher. 1984. Novel *E. coli* mutants deficient in biosynthesis of 5-methylaminomethyl-2-thiouridine. Nucleic Acids Res. 12:3521–3533.
 308. Elvin, C. M., N. E. Dixon, and H. Rosenberg. 1986. Molecular cloning of the phosphate (inorganic) transport (*pit*) gene of *Escherichia coli* K-12: identification of the *pit*⁺ gene product and physical mapping of the *pit-gor* region of the chromosome. Mol. Gen. Genet. 204:477–484.
 309. Elvin, C. M., C. M. Hardy, and H. E. Rosenberg. 1985. P_i exchange mediated by the GlpT-dependent *sn*-glycerol-3-phosphate transport system in *Escherichia coli*. J. Bacteriol. 161:1054–1058.
 310. Emmerich, R. V., and I. N. Hirshfield. 1987. Mapping of the constitutive lysyl-tRNA synthetase gene of *Escherichia coli* K-12. J. Bacteriol. 169:5311–5313.
 311. Emr, S. D., S. Hanley-Way, and T. J. Silhavy. 1981. Suppressor mutations that restore export of a protein with a defective signal sequence. Cell 23:79–88.
 312. Enomoto, M., K. Oosawa, and H. Momota. 1983. Mapping of the *pin* locus coding for a site-specific recombinase that causes flagellar-phase variation in *Escherichia coli* K-12. J. Bacteriol. 156:663–668.
 313. Erni, B., and B. Zanolari. 1985. The mannose-permease of the bacterial phosphotransferase system. Gene cloning and purification of the enzyme II^{Man}/III^{Man} complex of *Escherichia coli*. J. Biol. Chem. 260:15495–15503.
 314. Erni, B., and B. Zanolari. 1986. Glucose-permease of the bacterial phosphotransferase system. Gene cloning, overproduction and amino acid sequence of enzyme II^{Glc}. J. Biol. Chem. 261:16398–16403.
 315. Erni, B., B. Zanolari, and H. P. Kocher. 1987. The mannose permease of *Escherichia coli* consists of three different proteins: amino acid sequence and function in sugar transport, sugar phosphorylation, and penetration of phage λ DNA. J. Biol. Chem. 262:5238–5247.
 316. Espion, D., K. Kaiser, and C. Dambly-Chaudiere. 1983. A third defective lambdoid prophage of *Escherichia coli* K12 defined by the λ derivative, λ qin111. J. Mol. Biol. 170:611–633.
 317. Estevenon, A.-M., B. Martin, and N. Sicard. 1985. Characterization of a mutation conferring radiation sensitivity, *ior*, located close to the gene coding for deoxycytidine deaminase in *Escherichia coli*. Mol. Gen. Genet. 200:132–137.
 318. Evans, S., and P. P. Dennis. 1985. Promoter activity and transcript mapping in the regulatory region for genes encoding ribosomal protein S15 and polynucleotide phosphorylase of *Escherichia coli*. Gene 40:15–22.
 319. Faatz, E., A. Middendorf, and E. Bremer. 1988. Cloned structural genes for the osmotically regulated binding-protein-dependent glycine betaine transport system (ProU) of *Escherichia coli* K-12. Mol. Microbiol. 2:265–279.
 320. Fayat, G., J.-F. Mayaux, C. Sacerdot, M. Fromant, M. Springer, M. Grunberg-Manago, and S. Blanquet. 1983. *Escherichia coli* phenylalanyl-tRNA synthetase operon region: evidence for an attenuation mechanism. Identification of the gene for the ribosomal protein L20. J. Mol. Biol. 171:239–261.
 321. Fecker, L., and V. Braun. 1983. Cloning and expression of the *shu* genes involved in iron(III)-hydroxamate uptake by *Escherichia coli*. J. Bacteriol. 156:1301–1314.
 322. Felzenszwalb, I., N. J. Sargentini, and K. C. Smith. 1984. Characterization of a new radiation-sensitive mutant, *Escherichia coli* K-12 *radC102*. Radiat. Res. 97:615–625.
 323. Ferone, R., S. C. Singer, M. H. Hanlon, and S. Roland. 1983. Isolation and characterization of an *E. coli* mutant affected in dihydrofolate- and folylpolyglutamate-synthetase, p. 585–589. In J. A. Blair (ed.), Chemistry and biology of pteridines. Walter de Gruyter and Co., Berlin.
 324. Ferro-Novick, S., M. Honma, and J. Beckwith. 1984. The product of gene *secC* is involved in the synthesis of exported proteins in *Escherichia coli*. Cell 38:211–217.
 325. Fiedler, W., and H. Roterling. 1985. Characterization of an *Escherichia coli* *mdoB* mutant strain unable to transfer *sn*-1-phosphoglycerol to membrane-derived oligosaccharides. J. Biol. Chem. 260:4799–4806.
 326. Finch, P., and P. T. Emmerson. 1983. Nucleotide sequence of the regulatory region of the *uvrD* gene of *Escherichia coli*. Gene 25:317–323.
 327. Finch, P. W., and P. T. Emmerson. 1984. The nucleotide sequence of the *uvrD* gene of *E. coli*. Nucleic Acids Res. 12:5789–5799.
 328. Finch, P. W., A. Storey, K. Brown, I. D. Hickson, and P. T. Emmerson. 1986. Complete nucleotide sequence of *recD*, the structural gene for the α subunit of exonuclease V of *Escherichia coli*. Nucleic Acids Res. 14:8583–8594.
 329. Finch, P. W., A. Storey, K. E. Chapman, K. Brown, I. D. Hickson, and P. T. Emmerson. 1986. Complete nucleotide sequence of the *Escherichia coli* *recB* gene. Nucleic Acids Res. 14:8573–8582.
 330. Finch, P. W., R. E. Wilson, K. Brown, I. D. Hickson, and P. T. Emmerson. 1986. Complete nucleotide sequence of *Escherichia coli* *ptr* gene encoding protease III. Nucleic Acids Res. 14:7695–7703.
 331. Finch, P. W., R. E. Wilson, K. Brown, I. D. Hickson, A. E. Tomlinson, and P. T. Emmerson. 1986. Complete nucleotide sequence of the *Escherichia coli* *recC* gene and of the *thyA-recC* intergenic region. Nucleic Acids Res. 14:4437–4451.
 332. Flamm, E. L., and R. A. Weisberg. 1983. Primary structure of the *hip* gene of *Escherichia coli* and of its product, the β subunit of integration host factor. J. Mol. Biol. 183:117–128.
 333. Fleming, T. P., M. S. Nahlik, and M. A. McIntosh. 1983. Regulation of enterobactin iron transport in *Escherichia coli*: characterization of *ent::Mu* d(Ap⁺ *lac*) operon fusions. J. Bacteriol. 156:1171–1177.

334. Fleming, T. P., M. S. Nahlik, J. B. Neilands, and M. A. McIntosh. 1985. Physical and genetic characterization of cloned enterobactin genomic sequences from *Escherichia coli* K-12. *Gene* 34:47-54.
335. Flower, A. M., and C. S. McHenry. 1986. The adjacent *dnaZ* and *dnaX* genes of *Escherichia coli* are contained within one continuous open reading frame. *Nucleic Acids Res.* 14:8091-8101.
336. Foglino, M., S. Gharbi, and A. Lazdunski. 1986. Nucleotide sequence of the *pepN* gene encoding aminopeptidase N of *Escherichia coli*. *Gene* 49:303-309.
337. Fognini-Lefebvre, N., J. C. Lazzarone, and R. Portalier. 1987. *tolA*, *tolB* and *excC*, three cistrons involved in the control of pleiotropic release of periplasmic proteins by *Escherichia coli* K12. *Mol. Gen. Genet.* 209:391-395.
338. Forster, J. W., and P. Strike. 1985. Organization and control of the *Escherichia coli uvrC* gene. *Gene* 35:71-82.
339. Forster, J. W., and P. Strike. 1988. Analysis of the regulatory elements of the *Escherichia coli uvrC* gene by construction of operon fusions. *Mol. Gen. Genet.* 211:531-537.
340. Fotheringham, I. G., S. A. Dacey, P. P. Taylor, T. J. Smith, M. G. Hunter, M. E. Finlay, S. B. Primrose, D. M. Parker, and R. M. Edwards. 1986. The cloning and sequence analysis of the *aspC* and *tyrB* genes from *Escherichia coli* K-12. *Biochem. J.* 234:593-604.
341. Fournier, M. J., and H. Ozeki. 1985. Structure and organization of the transfer ribonucleic acid genes of *Escherichia coli* K-12. *Microbiol. Rev.* 49:379-397.
342. Fouts, K. E., T. Wasie-Gilbert, D. K. Willis, A. J. Clark, and S. D. Barbour. 1983. Genetic analysis of transposon-induced mutations of the *rac* prophage in *Escherichia coli* K-12 which affect expression and function of *recE*. *J. Bacteriol.* 156:718-726.
343. François, V., J. Louarn, and J.-M. Louarn. 1989. The terminus of the *Escherichia coli* chromosome is flanked by several polar replication pause sites. *Mol. Microbiol.* 3:995-1002.
344. Francoz, E., and E. Dassa. 1988. 3' end of the *malEFG* operon in *E. coli*: localization of the transcription termination site. *Nucleic Acids Res.* 16:4097-4109.
345. Freedman, R., B. Gibson, D. Donovan, K. Biemann, S. Eisenbeis, J. Parker, and P. Schimmel. 1985. Primary structure of histidine-tRNA synthetase and characterization of *hisS* transcripts. *J. Biol. Chem.* 260:10063-10068.
346. Freitag, C. S., J. M. Abraham, J. R. Clements, and B. I. Eisenstein. 1985. Genetic analysis of the phase variation control of expression of type 1 fimbriae in *Escherichia coli*. *J. Bacteriol.* 162:668-675.
347. Freitag, C. S., and B. I. Eisenstein. 1983. Genetic mapping and transcriptional orientation of the *fimD* gene. *J. Bacteriol.* 156:1052-1058.
348. Freundlieb, S., and W. Boos. 1986. α -Amylase of *Escherichia coli*, mapping and cloning of the structural gene, *malS*, and identification of its product as a periplasmic protein. *J. Biol. Chem.* 261:2946-2953.
349. Friden, P., J. Donegan, J. Mullen, P. Tsui, M. Freundlich, L. Eoyang, R. Weber, and P. M. Silverman. 1985. The *ilvB* locus of *Escherichia coli* K-12 is an operon encoding both subunits of acetohydroxy acid synthase I. *Nucleic Acids Res.* 13:3979-3993.
350. Friden, P., T. Newman, and M. Freundlich. 1982. Nucleotide sequence of the *ilvB* promoter-regulatory region: a biosynthetic operon controlled by attenuation and cyclic AMP. *Proc. Natl. Acad. Sci. USA* 79:6156-6160.
351. Friedrich, M. J., L. C. DeVaux, and R. J. Kadner. 1986. Nucleotide sequence of the *btuCED* genes involved in vitamin B₁₂ transport in *Escherichia coli* and homology with components of periplasmic-binding-protein-dependent transport systems. *J. Bacteriol.* 167:928-934.
352. Friedrich, M. J., and R. J. Kadner. 1987. Nucleotide sequence of the *uhp* region of *Escherichia coli*. *J. Bacteriol.* 169:3556-3563.
353. Froschauer, S., and J. Beckwith. 1984. The nucleotide sequence of the gene for *malF* protein, an inner membrane component of the maltose transport system of *Escherichia coli*. Repeated DNA sequences are found in the *malE-malF* intercistronic region. *J. Biol. Chem.* 259:10896-10903.
354. Fujita, N., T. Miwa, S. Ishijima, K. Izui, and H. Katsuki. 1984. The primary structure of phosphoenolpyruvate carboxylase of *Escherichia coli*. Nucleotide sequence of the *ppc* gene and deduced amino acid sequence. *J. Biochem.* 95:909-916.
355. Fukada, R., A. Nishimura, and H. Serizawa. 1988. Genetic mapping of the *Escherichia coli* gene for the stringent starvation protein and its dispensability for normal cell growth. *Mol. Gen. Genet.* 211:515-519.
356. Fukuda, R., R. Yano, T. Fukui, T. Hase, A. Ishihama, and H. Matsubara. 1985. Cloning of the *Escherichia coli* gene for the stringent starvation protein. *Mol. Gen. Genet.* 201:151-157.
357. Gallagher, P. J., I. Schwartz, and D. Elseviers. 1984. Genetic mapping of *pheU*, an *Escherichia coli* gene for phenylalanine tRNA. *J. Bacteriol.* 158:762-763.
358. Ganong, B. R., and C. R. H. Raetz. 1983. pH-sensitive CDP-diglyceride synthetase mutants of *Escherichia coli*: phenotypic suppression by mutations at a second site. *J. Bacteriol.* 153:731-738.
359. Garcia, G. M., P. K. Mar, D. A. Mullin, J. R. Walker, and N. E. Prather. 1986. The *E. coli dnaY* gene encodes an arginine transfer RNA. *Cell* 45:453-459.
360. Garcíarrubio, A., E. Lozoya, A. Covarrubias, and F. Bolívar. 1983. Structural organization of the genes that encode two glutamate synthase subunits of *Escherichia coli*. *Gene* 26:165-170.
361. Gardel, C., S. Benson, J. Hunt, S. Michaelis, and J. Beckwith. 1987. *secD*, a new gene involved in protein export in *Escherichia coli*. *J. Bacteriol.* 169:1286-1290.
362. Garnant, M. K., and G. V. Stauffer. 1984. Construction and analysis of plasmids containing the *Escherichia coli serB* gene. *Mol. Gen. Genet.* 193:72-75.
363. Garrett, S., R. K. Taylor, and T. J. Silhavy. 1983. Isolation and characterization of chain-terminating nonsense mutations in a porin regulator gene, *envZ*. *J. Bacteriol.* 156:62-69.
364. Garrett, S., R. K. Taylor, T. J. Silhavy, and M. L. Berman. 1985. Isolation and characterization of $\Delta ompB$ strains of *Escherichia coli* by a general method based on gene fusions. *J. Bacteriol.* 162:840-844.
365. Garrido-Pertierra, A., and R. A. Cooper. 1983. Evidence for two distinct pyruvate kinase genes in *Escherichia coli* K-12. *FEBS Lett.* 162:420-422.
366. Gayda, R. C., P. E. Stevens, R. Hewick, J. M. Schoemaker, W. J. Dreyer, and A. Markovitz. 1985. Regulatory region of the heat shock-inducible *capR* (*lon*) gene: DNA and protein sequences. *J. Bacteriol.* 162:271-275.
367. Geerse, R. H., C. R. Ruig, A. R. J. Schuitema, and P. W. Postma. 1986. Relationship between pseudo-HPr and the PEP: fructose phosphotransferase system in *Salmonella typhimurium* and *Escherichia coli*. *Mol. Gen. Genet.* 203:435-444.
368. Gemmill, R. M., J. W. Jones, G. W. Haughn, and J. M. Calvo. 1983. Transcription initiation sites of the leucine operons of *Salmonella typhimurium* and *Escherichia coli*. *J. Mol. Biol.* 170:39-59.
369. George, A. M., and S. B. Levy. 1983. Gene in the major cotransduction gap of the *Escherichia coli* K-12 linkage map required for the expression of chromosomal resistance to tetracycline and other antibiotics. *J. Bacteriol.* 155:541-548.
370. George, S. E., and T. Melton. 1986. Cloning and molecular characterization of *csm* mutations allowing expression of catabolite-repressible operons in the absence of exogenous cyclic AMP. *J. Bacteriol.* 166:533-540.
371. Georgiou, C. D., H. Fang, and R. B. Gennis. 1987. Identification of the *cydC* locus required for expression of the functional form of the cytochrome *d* terminal oxidase complex in *Escherichia coli*. *J. Bacteriol.* 169:2107-2112.
372. Gerdes, K., F. W. Bech, S. T. Jorgensen, A. Løbner-Olesen, P. B. Rasmussen, T. Atlung, L. Boe, O. Karlstrom, S. Molin, and K. von Meyenburg. 1986. Mechanism of postreplicational

- killing by the *hok* gene product of the *parB* system of plasmid R1 and its homology with the *relF* gene product of the *E. coli* *relB* operon. *EMBO J.* 5:2023–2029.
373. Ghisotti, D., S. Zangrossi, and G. Sironi. 1983. An *Escherichia coli* gene required for bacteriophage P2- λ interference. *J. Virol.* 48:616–626.
 374. Gjaever, H. M., O. B. Styrvoid, I. Kassen, and A. R. Strøm. 1988. Biochemical and genetic characterization of osmoregulatory trehalose synthesis in *Escherichia coli*. *J. Bacteriol.* 170:2841–2849.
 375. Gilbert, I., M. Llagostera, and J. Barbé. 1988. Regulation of *ubiG* gene expression in *Escherichia coli*. *J. Bacteriol.* 170:1346–1349.
 376. Gilchrist, C. A., and D. T. Denhardt. 1987. *Escherichia coli* *rep* gene: sequence of the gene, the encoded helicase, and its homology with *uvrD*. *Nucleic Acids Res.* 15:465–475.
 377. Gill, D. R., G. F. Hatfull, and G. P. C. Salmond. 1986. A new cell division operon in *Escherichia coli*. *Mol. Gen. Genet.* 205:134–145.
 378. Gilson, E., J.-M. Clément, D. Brutlag, and M. Hofnung. 1984. A family of dispersed repetitive extragenic palindromic DNA sequences in *E. coli*. *EMBO J.* 3:1417–1421.
 379. Gilson, E., H. Nikaido, and M. Hofnung. 1982. Sequence of the *malK* gene in *E. coli* K12. *Nucleic Acids Res.* 10:7449–7458.
 380. Gilson, E., J.-P. Rousset, A. Charbit, D. Perrin, and M. Hofnung. 1986. *malM*, a new gene of the maltose regulon in *Escherichia coli* K12. I. *malM* is the last gene of the *malK-lamB* operon and encodes a periplasmic protein. *J. Mol. Biol.* 191:303–311.
 381. Goldberg, E. B., T. Arbel, J. Chen, R. Karpel, G. A. Mackie, S. Schuldiner, and E. Padan. 1987. Characterization of a Na^+/H^+ antiporter gene of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* 84:2615–2619.
 382. Goldman, R. C., T. J. Bolling, W. E. Kohlbrenner, Y. Kim, and J. L. Fox. 1986. Primary structure of CTP: CMP-3-deoxy-D-manno-octulosonate cytidylyl-transferase (CMP-KDO synthetase) from *Escherichia coli*. *J. Biol. Chem.* 261:15831–15835.
 383. Goldman, R. C., and W. E. Kohlbrenner. 1985. Molecular cloning of the structural gene coding for CTP: CMP-3-deoxy-manno-octulosonate cytidylyltransferase from *Escherichia coli* K-12. *J. Bacteriol.* 163:256–261.
 384. Goncharoff, P., and B. P. Nichols. 1984. Nucleotide sequence of *Escherichia coli* *pabB* indicates a common evolutionary origin of *p*-aminobenzoate synthetase and anthranilate synthetase. *J. Bacteriol.* 159:57–62.
 385. Goosen, N., and P. van de Putte. 1984. Hek: an *Escherichia coli* function involved in functional expression of the *kil* gene of bacteriophage Mu. *Mol. Gen. Genet.* 196:170–172.
 386. Gopalakrishnan, A. S., Y.-C. Chen, M. Temkin, and W. Dowhan. 1986. Structure and expression of the gene locus encoding the phosphatidylglycerophosphate synthase of *Escherichia coli*. *J. Biol. Chem.* 261:1329–1338.
 387. Gordon, G., R. C. Gayda, and A. Markovitz. 1984. Sequence of the regulatory region of *ompT*, the gene specifying major outer membrane protein *a* (3b) of *Escherichia coli* K-12: implications for regulation and processing. *Mol. Gen. Genet.* 193:414–421.
 388. Goss, T. J., and P. Datta. 1984. *Escherichia coli* K-12 mutation that inactivates biodegradative threonine dehydratase by transposon Tn5 insertion. *J. Bacteriol.* 158:826–831.
 389. Goss, T. J., and P. Datta. 1985. Molecular cloning and expression of the biodegradative threonine dehydratase gene (*tdc*) of *Escherichia coli* K12. *Mol. Gen. Genet.* 201:308–314.
 390. Gottesman, S., P. Trisler, and A. Torres-Cabassa. 1985. Regulation of capsular polysaccharide synthesis in *Escherichia coli* K-12: characterization of three regulatory genes. *J. Bacteriol.* 162:1111–1119.
 391. Gough, J. A., and N. E. Murray. 1983. Sequence diversity among related genes for recognition of specific targets in DNA molecules. *J. Mol. Biol.* 166:1–19.
 392. Gowrishankar, J. 1985. Identification of osmoreponsive genes in *Escherichia coli*: evidence for participation of potassium and proline transport systems in osmoregulation. *J. Bacteriol.* 164:434–445.
 393. Gowrishankar, J. 1986. *proP*-mediated proline transport also plays a role in *Escherichia coli* osmoregulation. *J. Bacteriol.* 166:331–333.
 394. Gowrishankar, J., P. Jayashree, and K. Rajkumari. 1986. Molecular cloning of an osmoregulatory locus in *Escherichia coli*: increased *proU* gene dosage results in enhanced osmotolerance. *J. Bacteriol.* 168:1197–1204.
 395. Gowrishankar, J., and J. Pittard. 1982. Molecular cloning of *pheR* in *Escherichia coli* K-12. *J. Bacteriol.* 152:1–6.
 396. Grabau, C., and J. E. Cronan, Jr. 1984. Molecular cloning of the gene (*poxB*) encoding the pyruvate oxidase of *Escherichia coli*, a lipid-activated enzyme. *J. Bacteriol.* 160:1088–1092.
 397. Grabau, C., and J. E. Cronan, Jr. 1986. Nucleotide sequence and deduced amino acid sequence of *Escherichia coli* pyruvate oxidase, a lipid-activated flavoprotein. *Nucleic Acids Res.* 14:5449–5460.
 398. Grafstrom, R. H., and R. H. Hoess. 1983. Cloning of *mutH* and identification of the gene product. *Gene* 22:245–253.
 399. Grafstrom, R. H., and R. H. Hoess. 1987. Nucleotide sequence of the *Escherichia coli* *mutH* gene. *Nucleic Acids Res.* 15:3073–3083.
 400. Green, G. N., J. E. Kranz, and R. B. Gennis. 1984. Cloning the *cyd* locus coding for the cytochrome *d* complex of *E. coli*. *Gene* 32:99–106.
 401. Green, G. N., R. G. Kranz, R. M. Lorence, and R. B. Gennis. 1984. Identification of subunit I as the cytochrome *b*₅₅₈ component of the cytochrome *d* terminal oxidase complex of *Escherichia coli*. *J. Biol. Chem.* 259:7994–7997.
 402. Green, G. N., R. M. Lorence, and R. B. Gennis. 1986. Specific overproduction and purification of the cytochrome *b*₅₅₈ component of the cytochrome *d* complex from *Escherichia coli*. *Biochemistry* 25:2309–2314.
 403. Green, P. J., and M. Inouye. 1984. Roles of the 5' leader region of the *ompA* mRNA. *J. Mol. Biol.* 176:431–442.
 404. Greenberg, J. T., and B. Demple. 1986. Glutathione in *Escherichia coli* is dispensable for resistance to H_2O_2 and gamma radiation. *J. Bacteriol.* 168:1026–1029.
 405. Greene, R. C., J. H. Krueger, and J. R. Johnson. 1982. Localization of the *metJBLF* gene cluster of *Escherichia coli* in λ met transducing phage. *Mol. Gen. Genet.* 187:401–404.
 406. Greene, R. C., and A. A. Smith. 1984. Insertion mutagenesis of the *metJBLF* gene cluster of *Escherichia coli* K-12: evidence for a *metBL* operon. *J. Bacteriol.* 159:767–769.
 407. Greer, S., and R. N. Perham. 1986. Glutathione reductase from *Escherichia coli*: cloning and sequence analysis of the gene and relationship to other flavoprotein disulfide oxidoreductases. *Biochemistry* 25:2736–2742.
 408. Griggs, D. W., B. B. Tharp, and J. Konisky. 1987. Cloning and promoter identification of the iron-regulated *cir* gene of *Escherichia coli*. *J. Bacteriol.* 169:5343–5352.
 409. Grisolia, V., M. S. Carlomagno, A. G. Nappo, and C. B. Bruni. 1985. Cloning, structure and expression of the *Escherichia coli* K-12 *hisC* gene. *J. Bacteriol.* 164:1317–1323.
 410. Grisolia, V., A. Riccio, and C. B. Bruni. 1983. Structure and function of the internal promoter (*hisBp*) of the *Escherichia coli* K-12 histidine operon. *J. Bacteriol.* 155:1288–1296.
 411. Grodberg, J., and J. J. Dunn. 1988. *ompT* encodes the *Escherichia coli* outer membrane protease that cleaves T7 RNA polymerase during purification. *J. Bacteriol.* 170:1245–1253.
 412. Grodberg, J., M. D. Lundigan, D. L. Toledo, W. F. Mangel, and J. J. Dunn. 1988. Complete nucleotide sequence and deduced amino acid sequence of the *ompT* gene of *Escherichia coli* K-12. *Nucleic Acids Res.* 16:1209.
 413. Grogan, D. W., and J. E. Cronan, Jr. 1983. Use of lambda phasmids for deletion mapping of non-selectable markers cloned in plasmids. *Gene* 22:75–83.
 414. Grogan, D. W., and J. E. Cronan, Jr. 1984. Cloning and manipulation of the *Escherichia coli* cyclopropane fatty acid synthase gene: physiological aspects of enzyme overproduc-

- tion. *J. Bacteriol.* **158**:286–295.
415. Grogan, D. W., and J. E. Cronan, Jr. 1984. Genetic characterization of the *Escherichia coli* cyclopropane fatty acid (*cfa*) locus and neighboring loci. *Mol. Gen. Genet.* **196**:367–372.
 416. Grossman, A. D., J. W. Erickson, and C. A. Gross. 1984. The *htpR* gene product of *E. coli* is a sigma factor for heat-shock promoters. *Cell* **38**:383–390.
 417. Grossman, A. D., Y.-N. Zhou, C. Gross, J. Heilig, G. E. Christie, and R. Calendar. 1985. Mutations in the *rpoH* (*htpR*) gene of *Escherichia coli* K-12 phenotypically suppress a temperature-sensitive mutant defective in the σ^{70} subunit of RNA polymerase. *J. Bacteriol.* **161**:939–943.
 418. Grothe, S., R. L. Krogsrud, D. J. McClellan, J. L. Milner, and J. M. Wood. 1986. Proline transport and osmotic stress response in *Escherichia coli* K-12. *J. Bacteriol.* **166**:253–259.
 419. Guarneros, G., G. Machado, P. Guzman, and E. Garay. 1987. Genetic and physical location of the *Escherichia coli* *rap* locus, which is essential for growth of bacteriophage lambda. *J. Bacteriol.* **169**:5188–5192.
 420. Guest, J. R., J. S. Miles, R. E. Roberts, and S. A. Woods. 1985. The fumarase genes of *Escherichia coli*: location of the *fumB* gene and discovery of a new gene (*fumC*). *J. Gen. Microbiol.* **131**:2971–2984.
 421. Guest, J. R., and R. E. Roberts. 1983. Cloning, mapping, and expression of the fumarase gene of *Escherichia coli* K-12. *J. Bacteriol.* **153**:588–596.
 422. Guest, J. R., R. E. Roberts, and P. E. Stephens. 1983. Hybrid plasmids containing the pyruvate dehydrogenase complex genes and gene-DNA relationships in the 2 to 3 minute region of the *Escherichia coli* chromosome. *J. Gen. Microbiol.* **129**:671–680.
 423. Guest, J. R., R. E. Roberts, and R. J. Wilde. 1984. Cloning of the aspartase gene (*aspA*) of *Escherichia coli*. *J. Gen. Microbiol.* **130**:1271–1278.
 424. Guilloton, M., and F. Karst. 1987. Isolation and characterization of mutants of *Escherichia coli* lacking inducible cyanase. *J. Gen. Microbiol.* **133**:645–653.
 425. Hackett, J., R. Misra, and P. Reeves. 1983. The TolC protein of *Escherichia coli* K12 is synthesized in a precursor form. *FEBS Lett.* **156**:307–310.
 426. Hackett, J., and P. Reeves. 1983. Primary structure of the *tolC* gene that codes for an outer membrane protein of *Escherichia coli* K12. *Nucleic Acids Res.* **11**:6487–6495.
 427. Hackett, N. R., and P. D. Bragg. 1983. Membrane cytochromes of *Escherichia coli* mutants. *J. Bacteriol.* **154**:719–727.
 428. Hagervall, T. G., and G. R. Björk. 1984. Genetic mapping and cloning of the gene (*trmC*) responsible for the synthesis of tRNA (mnm⁵s²U) methyl transferase. *Mol. Gen. Genet.* **196**:201–207.
 429. Hall, B. G. 1982. Chromosomal mutation for citrate utilization by *Escherichia coli* K-12. *J. Bacteriol.* **151**:269–273.
 430. Hall, B. G., P. W. Betts, and J. C. Wootton. 1989. DNA sequence analysis of artificially evolved *ebg* enzyme and *ebg* repressor genes. *Genetics* **123**:635–648.
 431. Haller, B. L., and J. A. Fuchs. 1984. Mapping of *trxB*, a mutation responsible for reduced thioredoxin reductase activity. *J. Bacteriol.* **159**:1060–1062.
 432. Hamann, A., D. Bossemeyer, and E. P. Bakker. 1987. Physical mapping of the K⁺ transport *trkA* gene of *Escherichia coli* and overproduction of the TrkA protein. *J. Bacteriol.* **169**:3138–3145.
 433. Hanatani, M., H. Yazyu, S. Shiota-Niijima, Y. Moriya, H. Kanazawa, M. Futai, and T. Tsuchiya. 1984. Physical and genetic characterization of the melibiose operon and identification of the gene products in *Escherichia coli*. *J. Biol. Chem.* **259**:1807–1812.
 434. Hansen, E. B., F. G. Hansen, and K. von Meyenburg. 1982. The nucleotide sequence of the *dnaA* gene and the first part of the *dnaN* gene of *Escherichia coli* K-12. *Nucleic Acids Res.* **10**:7373–7385.
 435. Hansen, F. G., E. B. Hansen, and T. Atlung. 1985. Physical mapping and nucleotide sequence of the *rnpA* gene that encodes the protein component of ribonuclease P in *Escherichia coli*. *Gene* **38**:85–93.
 436. Hantke, K. 1983. Identification of an iron uptake system specific for coprogen and rhodotorulic acid in *Escherichia coli* K12. *Mol. Gen. Genet.* **191**:301–306.
 437. Hantke, K. 1984. Cloning of the repressor protein gene of iron-regulated systems in *Escherichia coli* K12. *Mol. Gen. Genet.* **197**:337–341.
 438. Hantke, K. 1987. Ferrous iron transport mutants in *Escherichia coli* K12. *FEMS Microbiol. Lett.* **44**:53–57.
 439. Hantke, K. 1987. Selection procedure for deregulated iron transport mutants (*fur*) in *Escherichia coli* K12: *fur* not only affects iron transport. *Mol. Gen. Genet.* **210**:135–139.
 440. Harayama, S., J. Bollinger, T. Iino, and G. L. Hazelbauer. 1983. Characterization of the *mgl* operon of *Escherichia coli* by transposon mutagenesis and molecular cloning. *J. Bacteriol.* **153**:408–415.
 441. Harayama, S., P. Engstrom, H. Wolf-Watz, T. Iino, and G. L. Hazelbauer. 1982. Cloning of *trg*, a gene for a sensory transducer in *Escherichia coli*. *J. Bacteriol.* **152**:372–383.
 442. Harkness, R. E., and E. E. Ishiguro. 1983. Temperature-sensitive autolysis-defective mutants of *Escherichia coli*. *J. Bacteriol.* **155**:15–21.
 443. Härtlein, M., R. Frank, and D. Madern. 1987. Nucleotide sequence of *Escherichia coli* valyl-tRNA synthetase gene *valS*. *Nucleic Acids Res.* **15**:9081.
 444. Härtlein, M., and D. Madern. 1987. Molecular cloning and nucleotide sequence of the gene for *Escherichia coli* leucyl-tRNA. *Nucleic Acids Res.* **15**:10199–10210.
 445. Härtlein, M., D. Madern, and R. Leberman. 1987. Cloning and characterization of the gene for *Escherichia coli* seryl-tRNA synthetase. *Nucleic Acids Res.* **15**:1005–1017.
 446. Harvey, S., C. W. Hill, C. Squires, and C. L. Squires. 1988. Loss of the spacer loop sequence from the *rrnB* operon in the *Escherichia coli* K-12 subline that bears the *relA1* mutation. *J. Bacteriol.* **170**:1235–1238.
 447. Haughn, G. W., C. H. Squires, M. DeFelice, C. T. Largo, and J. M. Calvo. 1985. Unusual organization of the *ilvIH* promoter of *Escherichia coli*. *J. Bacteriol.* **163**:186–198.
 448. Hauser, C. A., and G. W. Hatfield. 1983. Nucleotide sequence of the *ilvB* multivalent attenuator region of *Escherichia coli* K-12. *Nucleic Acids Res.* **11**:127–139.
 449. Hays, J. B., and B. E. Korba. 1985. Apparent alteration in properties of *arl* mutants of *Escherichia coli*. *J. Mol. Biol.* **182**:611–612.
 450. Hayzer, D. J. 1983. Sub-cloning of the wild-type *proAB* region of the *Escherichia coli* genome. *J. Gen. Microbiol.* **129**:3215–3225.
 451. Heck, J. D., and G. W. Hatfield. 1988. Valyl-tRNA synthetase gene of *Escherichia coli* K12. Molecular genetic characterization. *J. Biol. Chem.* **263**:857–867.
 452. Heck, J. D., and G. W. Hatfield. 1988. Valyl-tRNA synthetase gene of *Escherichia coli* K12. Primary structure and homology within a family of aminoacyl-tRNA synthetases. *J. Biol. Chem.* **263**:868–877.
 453. Hediger, M. A., D. F. Johnson, D. P. Nierlich, and I. Zabin. 1985. DNA sequence of the lactose operon: the *lacA* gene and the transcriptional termination region. *Proc. Natl. Acad. Sci. USA* **82**:6414–6418.
 454. Heitman, J., and P. Model. 1987. Site-specific methylases induce the SOS DNA repair response in *Escherichia coli*. *J. Bacteriol.* **169**:3243–3250.
 455. Heller, K., and R. J. Kadner. 1985. Nucleotide sequence of the gene for the vitamin B₁₂ receptor protein in the outer membrane of *Escherichia coli*. *J. Bacteriol.* **161**:904–908.
 456. Hellinga, H. W., and P. R. Evans. 1985. Nucleotide sequence and high-level expression of the major *Escherichia coli* phosphofructokinase. *Eur. J. Biochem.* **149**:363–373.
 457. Hershey, H. V., R. Gutstein, and M. W. Taylor. 1982. Cloning and restriction map of the *E. coli apt* gene. *Gene* **19**:89–92.
 458. Hershey, H. V., and M. W. Taylor. 1986. Nucleotide sequence and deduced amino acid sequence of *Escherichia coli* adenine phosphoribosyltransferase and comparison with other analogs.

- gous enzymes. *Gene* **43**:287–293.
459. Hickson, I. D., H. M. Arthur, D. Bramhill, and P. T. Emmer-son. 1983. The *E. coli* *uvrD* gene product is DNA helicase II. *Mol. Gen. Genet.* **190**:265–270.
 460. Hidaka, M., M. Akiyama, and T. Horiuchi. 1988. A consensus sequence of three DNA replication terminus sites on the *E. coli* chromosome is highly homologous to the *terR* sites of the R6K plasmid. *Cell* **55**:467–475.
 461. Higgins, C. F., C. J. Dorman, D. A. Stirling, L. Waddell, I. R. Booth, G. May, and E. Bremer. 1988. A physiological role for DNA supercoiling in the osmotic regulation of gene expression in *S. typhimurium* and *E. coli*. *Cell* **52**:569–584.
 462. Highton, P. J., Y. Chang, W. R. Marcotte, Jr., and C. A. Schnaitman. 1985. Evidence that the outer membrane porin protein gene *nmpC* of *Escherichia coli* K-12 lies within the defective *qsr'* prophage. *J. Bacteriol.* **162**:256–262.
 463. Hill, T. M., J. M. Henson, and P. L. Kuempel. 1987. The terminus region of the *Escherichia coli* chromosome contains two separate loci that exhibit polar inhibition of replication. *Proc. Natl. Acad. Sci. USA* **84**:1754–1758.
 464. Hill, T. M., B. J. Kopp, and P. L. Kuempel. 1988. Termination of DNA replication in *Escherichia coli* requires a *trans*-acting factor. *J. Bacteriol.* **170**:662–668.
 465. Hill, T. M., A. J. Pelletier, M. L. Tecklenburg, and P. L. Kuempel. 1988. Identification of the DNA sequence from the *E. coli* terminus region that halts replication forks. *Cell* **55**:459–466.
 466. Hill, T. M., M. L. Tecklenburg, A. J. Pelletier, and P. L. Kuempel. 1989. *tus*, the *trans*-acting gene required for termination of DNA replication in *Escherichia coli*, encodes a DNA-binding protein. *Proc. Natl. Acad. Sci. USA* **86**:1593–1597.
 467. Hirschman, J., P.-K. Wong, K. Sei, J. Keener, and S. Kustu. 1985. Products of nitrogen regulatory genes *ntrA* and *ntrC* of enteric bacteria activate *gluA* transcription *in vitro*: evidence that the *ntrA* product is a σ factor. *Proc. Natl. Acad. Sci. USA* **82**:7525–7529.
 468. Hogarth, B. G., and C. F. Higgins. 1983. Genetic organization of the oligopeptide permease (*opp*) locus of *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **153**:1548–1551.
 469. Holck, A., and K. Kleppe. 1988. Cloning and sequencing of the gene for the DNA-binding 17K protein of *Escherichia coli*. *Gene* **67**:117–124.
 470. Holowachuk, E. W., and J. D. Friesen. 1982. Isolation of a recombinant lambda phage carrying *nusA* and surrounding region of the *Escherichia coli* chromosome. *Mol. Gen. Genet.* **187**:248–253.
 471. Homma, H., T. Kobayashi, N. Chiba, K. Karasawa, H. Mizushima, I. Kudo, K. Inoue, H. Ikeda, M. Sekiguchi, and S. Nojima. 1984. The DNA sequence encoding *pldA* gene, the structural gene for detergent-resistant phospholipase A of *E. coli*. *J. Biochem.* **96**:1655–1664.
 472. Homma, H., T. Kobayashi, Y. Ito, I. Kudo, K. Inoue, H. Ikeda, M. Sekiguchi, and S. Nojima. 1983. Identification and cloning of the gene coding for lysophospholipase *L*₂ of *E. coli* K-12. *J. Biochem.* **94**:2079–2081.
 473. Höög, J.-O., H. von Bahr-Lindström, H. Jörnvall, and A. Holmgren. 1986. Cloning and expression of the glutaredoxin (*grx*) gene of *Escherichia coli*. *Gene* **43**:13–21.
 474. Hoover, T. A., W. D. Roof, K. F. Foltermann, G. A. O'Donovan, D. A. Bencini, and J. R. Wild. 1983. Nucleotide sequence of the structural gene (*pyrB*) that encodes the catalytic polypeptide of aspartate transcarbamoylase of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **80**:2462–2466.
 475. Hope, J. N., A. W. Bell, M. A. Hermodson, and J. M. Groarke. 1986. Ribokinase from *Escherichia coli* K12. Nucleotide sequence and overexpression of the *rbsK* gene and purification of ribokinase. *J. Biol. Chem.* **261**:7663–7668.
 476. Hopkins, J. D., M. Clements, and M. Syvanen. 1983. New class of mutations in *Escherichia coli* (*uup*) that affect precise excision of insertion elements and bacteriophage Mu growth. *J. Bacteriol.* **153**:384–389.
 477. Horiuchi, T., T. Nagasawa, K. Takano, and M. Sekiguchi. 1987. A newly discovered tRNA^{Asp} gene (*aspV*) of *Escherichia coli* K12. *Mol. Gen. Genet.* **206**:356–357.
 478. Horowitz, H., and T. Platt. 1982. A termination site for *Lac I* transcription is between the CAP site and the *lac* promoter. *J. Biol. Chem.* **257**:11740–11746.
 479. Houlberg, U., B. Hove-Jensen, B. Jochimsen, and P. Nygaard. 1983. Identification of the enzymatic reactions encoded by the *purG* and *purI* genes of *Escherichia coli*. *J. Bacteriol.* **154**:1485–1488.
 480. Hove-Jensen, B. 1983. Chromosomal location of the gene encoding phosphoribosylpyrophosphate synthetase in *Escherichia coli*. *J. Bacteriol.* **154**:177–184.
 481. Hove-Jensen, B. 1985. Cloning and characterization of the *prs* gene encoding phosphoribosylpyrophosphate synthetase of *Escherichia coli*. *Mol. Gen. Genet.* **201**:269–276.
 482. Hove-Jensen, B., K. W. Harlow, C. J. King, and R. L. Switzer. 1986. Phosphoribosylpyrophosphate synthetase of *Escherichia coli*. Properties of the purified enzyme and primary structure of the *prs* gene. *J. Biol. Chem.* **261**:6765–6771.
 483. Howard, P. K., J. Shaw, and A. J. Otsuka. 1985. Nucleotide sequence of the *birA* gene encoding the biotin operon repressor and biotin holoenzyme synthetase functions of *Escherichia coli*. *Gene* **35**:321–331.
 484. Hrebenda, J., H. Heleszko, K. Brozostek, and J. Bielecki. 1985. Mutation affecting resistance of *Escherichia coli* K12 to nalidixic acid. *J. Gen. Microbiol.* **131**:2285–2292.
 485. Hsu, L. M., H. J. Klee, J. Zagorski, and M. J. Fournier. 1984. Structure of an *Escherichia coli* tRNA operon containing linked genes for arginine, histidine, leucine, and proline tRNAs. *J. Bacteriol.* **158**:934–942.
 486. Hsu, L. M., J. Zagorski, and M. J. Fournier. 1984. Cloning and sequence analysis of the *Escherichia coli* 4.5S RNA gene. *J. Mol. Biol.* **178**:509–531.
 487. Hsu, L. M., J. Zagorski, Z. Wang, and M. J. Fournier. 1985. *Escherichia coli* 6S RNA gene is part of a dual function transcription unit. *J. Bacteriol.* **161**:1162–1170.
 488. Hudson, G. S., and B. E. Davidson. 1984. Nucleotide sequence and transcription of the phenylalanine and tyrosine operons of *Escherichia coli* K-12. *J. Mol. Biol.* **180**:1023–1051.
 489. Hugouvieux-Cotte-Pattat, N., and J. Robert-Baudouy. 1982. Determination of the transcription direction of the *exuT* gene in *Escherichia coli* K-12: divergent transcription of the *exuT-uxaCA* operons. *J. Bacteriol.* **151**:480–484.
 490. Hugouvieux-Cotte-Pattat, N., and J. Robert-Baudouy. 1983. Determination of the transcription direction of the *uxaB* gene, in *Escherichia coli* K12. *Mol. Gen. Genet.* **189**:334–336.
 491. Hui, I., K. Maltman, R. Little, S. Hastrup, M. Johnsen, N. Fiil, and P. Dennis. 1982. Insertions of transposon Tn5 into ribosomal protein RNA polymerase operons. *J. Bacteriol.* **152**:1022–1032.
 492. Hull, E. P., M. E. Spencer, D. Wood, and J. R. Guest. 1983. Nucleotide sequence of the promoter region of the citrate synthase gene (*gltA*) of *Escherichia coli*. *FEBS Lett.* **156**:366–370.
 493. Hunt, C. L., V. Colless, M. T. Smith, D. O. Molasky, M. S. Malo, and R. E. Loughlin. 1987. Lambda transducing phage and clones carrying genes of the *cysJIHDC* gene cluster of *Escherichia coli* K-12. *J. Gen. Microbiol.* **333**:2707–2717.
 494. Hunt, T. P., and B. Magasanik. 1985. Transcription of *glnA* by purified *Escherichia coli* components: core RNA polymerase and the products of *glnF*, *glnG*, and *glnL*. *Proc. Natl. Acad. Sci. USA* **82**:8453–8457.
 495. Husain, I., and A. Sancar. 1987. Photoreactivation in *phr* mutants of *Escherichia coli* K-12. *J. Bacteriol.* **169**:2367–2372.
 496. Husain, I., B. Van Houten, D. C. Thomas, and A. Sancar. 1986. Sequences of *Escherichia coli* *uvrA* gene and protein reveal two potential ATP binding sites. *J. Biol. Chem.* **261**:4895–4901.
 497. Hussain, K., E. J. Elliot, and G. P. C. Salmond. 1987. The ParD mutant of *Escherichia coli* also carries a *gyrA*_{am} mutation. The complete sequence of *gyrA*. *Mol. Microbiol.* **1**:259–273.

498. Ichihara, S., T. Suzuki, M. Suzuki, and S. Mizushima. 1986. Molecular cloning and sequencing of the *sppA* gene and characterization of the encoded protease IV, a signal peptide peptidase, of *Escherichia coli*. J. Biol. Chem. 261:9405-9411.
499. Icho, T., C. E. Bulawa, and C. R. H. Raetz. 1985. Molecular cloning and sequencing of the gene for CDP-diglyceride hydrolase of *Escherichia coli*. J. Biol. Chem. 260:12092-12098.
500. Icho, T., and C. R. H. Raetz. 1983. Multiple genes for membrane-bound phosphatases in *Escherichia coli* and their action on phospholipid precursors. J. Bacteriol. 153:722-730.
501. Icho, T., C. P. Sparrow, and C. R. H. Raetz. 1985. Molecular cloning and sequencing of the gene for CDP-diglyceride synthetase of *Escherichia coli*. J. Biol. Chem. 260:12078-12083.
502. Iida, A., S. Harayama, T. Iino, and G. L. Hazelbauer. 1984. Molecular cloning and characterization of genes required for ribose transport and utilization in *Escherichia coli* K-12. J. Bacteriol. 158:674-682.
503. Iida, K., Y. Hirota, and U. Schwarz. 1983. Mutants of *Escherichia coli* defective in penicillin-insensitive murein DD-endopeptidase. Mol. Gen. Genet. 189:215-221.
504. Iino, T., Y. Komeda, K. Kutsukake, R. M. Macnab, P. Matsumura, J. S. Parkinson, M. I. Simon, and S. Yamaguchi. 1988. New unified nomenclature for the flagellar genes of *Escherichia coli* and *Salmonella typhimurium*. Microbiol. Rev. 52:533-535.
505. Innis, M. A., M. Tokunaga, M. E. Williams, J. M. Loranger, S.-Y. Chang, S. Chang, and H. C. Wu. 1984. Nucleotide sequence of the *Escherichia coli* prolipoprotein signal peptidase (*lsp*) gene. Proc. Natl. Acad. Sci. USA 81:3708-3712.
506. Inokuchi, K., H. Furukawa, K. Nakamura, and S. Mizushima. 1984. Characterization by deletion mutagenesis *in vitro* of the promoter region of *ompF*, a positively regulated gene of *Escherichia coli*. J. Mol. Biol. 178:653-668.
507. Inokuchi, K., N. Mutoh, S. Matsuyama, and S. Mizushima. 1982. Primary structure of the *ompF* gene that codes for a major outer membrane protein of *Escherichia coli* K-12. Nucleic Acids Res. 10:6957-6968.
508. Irino, N., K. Nakayama, and H. Nakayama. 1986. The *recQ* gene of *Escherichia coli* K12: primary structure and evidence for SOS regulation. Mol. Gen. Genet. 205:298-304.
509. Ishii, S., E. Hatada, T. Maekawa, and F. Imamoto. 1984. Molecular cloning and nucleotide sequencing of the *nusB* gene of *E. coli*. Nucleic Acids Res. 12:4987-4995.
510. Ishii, S., M. Ihara, T. Maekawa, Y. Nakamura, H. Uchida, and F. Imamoto. 1984. The nucleotide sequence of the cloned *nusA* gene and its flanking region of *Escherichia coli*. Nucleic Acids Res. 12:3333-3342.
511. Ishii, S., K. Kuroki, and F. Imamoto. 1984. tRNA^{Met} gene in the leader region of the *nusA* operon in *Escherichia coli*. Proc. Natl. Acad. Sci. USA 81:409-413.
512. Ishino, Y., H. Shinagawa, K. Makino, M. Amemura, and A. Nakata. 1987. Nucleotide sequence of the *iap* gene, responsible for alkaline phosphatase isozyme conversion in *Escherichia coli*, and identification of the gene product. J. Bacteriol. 169:5429-5433.
513. Ishino, Y., H. Shinagawa, K. Makino, S. Tsunasawa, F. Sakiyama, and A. Nakata. 1986. Nucleotide sequence of the *lig* gene and primary structure of DNA ligase of *Escherichia coli*. Mol. Gen. Genet. 204:1-7.
514. Isono, S., S. Thamm, M. Kitakawa, and K. Isono. 1985. Cloning and nucleotide sequencing of the genes for ribosomal proteins S9 (*rpsI*) and L13 (*rplM*) of *Escherichia coli*. Mol. Gen. Genet. 198:279-282.
515. Istúriz, T., E. Palmero, and J. Vitelli-Flores. 1986. Mutations affecting gluconate catabolism in *Escherichia coli*. Genetic mapping of the locus for the thermosensitive gluconokinase. J. Gen. Microbiol. 132:3209-3219.
516. Ito, K., D. P. Cerretti, H. Nashimoto, and M. Nomura. 1984. Characterization of an amber mutation in the structural gene for ribosomal protein L15, which impairs the expression of the protein export gene, *secY*, in *Escherichia coli*. EMBO J. 3:2319-2324.
517. Ito, K., M. Wittekind, M. Nomura, K. Shiba, T. Yura, A. Miura, and H. Nashimoto. 1983. A temperature-sensitive mutant of *E. coli* exhibiting slow processing of exported proteins. Cell 32:789-797.
518. Iuchi, S., and E. C. C. Lin. 1987. The *narL* gene product activates the nitrate reductase operon and represses the fumarate reductase and trimethylamine *N*-oxide reductase operons in *Escherichia coli*. Proc. Natl. Acad. Sci. USA 84:3901-3905.
519. Iuchi, S., and E. C. C. Lin. 1988. *arcA* (*dye*), a global regulatory gene in *Escherichia coli* mediating repression of enzymes in aerobic pathways. Proc. Natl. Acad. Sci. USA 85:1888-1892.
520. Iwakura, M., Y. Shimura, and K. Tsuda. 1982. Isolation of DNA fragment containing *phoS* gene of *Escherichia coli*. J. Biochem. 92:615-622.
521. Jackson, B. J., J.-P. Bohin, and E. P. Kennedy. 1984. Biosynthesis of membrane-derived oligosaccharides: characterization of *mdoB* mutants defective in phosphoglycerol transferase I activity. J. Bacteriol. 160:976-981.
522. Jackson, R. H., A. Cornish-Bowden, and J. A. Cole. 1981. Prosthetic groups of the NADH-dependent nitrite reductase from *Escherichia coli* K12. Biochem. J. 193:861-867.
523. Jagadeeswaran, P., C. R. Ashman, S. Roberts, and J. Langenberg. 1984. Nucleotide sequence and analysis of deletion mutants of the *Escherichia coli* *gpt* gene in plasmids. Gene 31:309-313.
524. Janda, I., M. Kitakawa, and K. Isono. 1985. Gene *rpmF* for ribosomal protein L32 and gene *rimJ* for a ribosomal protein acetylating enzyme are located near *pyrC* (23.4 min) in *Escherichia coli*. Mol. Gen. Genet. 201:433-436.
525. Jaurin, B., T. Grundström, and S. Normark. 1982. Sequence elements determining *ampC* promoter strength in *E. coli*. EMBO J. 1:875-881.
526. Jayaraman, P. S., T. C. Peakman, S. J. W. Busby, R. V. Quinary, and J. A. Cole. 1987. Location and sequence of the promoter of the gene for the NADH-dependent nitrite reductase of *Escherichia coli* and its regulation by oxygen, the Fnr protein and nitrite. J. Mol. Biol. 196:781-788.
527. Jefferson, R. A., S. M. Burgess, and D. Hersh. 1986. β -Glucuronidase from *Escherichia coli* as a gene-fusion marker. Proc. Natl. Acad. Sci. USA 83:8447-8451.
528. Jenkins, L. S., and W. D. Nunn. 1987. Genetic and molecular characterization of the genes involved in short-chain fatty acid degradation in *Escherichia coli*: the *ato* system. J. Bacteriol. 169:42-52.
529. Jenkins, L. S., and W. D. Nunn. 1987. Regulation of the *ato* operon by the *atoC* gene in *Escherichia coli*. J. Bacteriol. 169:2096-2102.
530. Jensen, K. F., J. N. Larsen, L. Schack, and A. Sivertsen. 1984. Studies on the structure and expression of *Escherichia coli* *pyrC*, *pyrD* and *pyrF* using the cloned genes. Eur. J. Biochem. 140:343-352.
531. Johann, S., and S. M. Hinton. 1987. Cloning and nucleotide sequence of the *chdD* locus. J. Bacteriol. 169:1911-1916.
532. Johnson, D. I., and R. L. Somerville. 1983. Evidence that repression mechanisms can exert control over the *thr*, *leu*, and *ilv* operons of *Escherichia coli* K-12. J. Bacteriol. 155:49-55.
533. Johnson, D. I., and R. L. Somerville. 1984. New regulatory genes involved in the control of transcription initiation at the *thr* and *ilv* promoters in *Escherichia coli* K-12. Mol. Gen. Genet. 195:70-76.
534. Johnson, M. E., and K. V. Rajagopalan. 1987. Involvement of *chlA*, *E*, *M*, and *N* loci in *Escherichia coli* molybdopterin biosynthesis. J. Bacteriol. 169:117-125.
535. Jones, C. A., and I. B. Holland. 1984. Inactivation of essential division genes *ftsA*, *ftsZ*, suppresses mutations at *sfiB*, a locus mediating division inhibition during the SOS response in *E. coli*. EMBO J. 3:1181-1186.
536. Jones, C. J., M. Homma, and R. M. Macnab. 1987. Identification of proteins of the outer (L and P) rings of the flagellar

- basal body of *Escherichia coli*. J. Bacteriol. 169:1489-1492.
537. Jones, H. M., C. M. Brajkovich, and R. P. Gunsalus. 1983. In vivo 5' terminus and length of the mRNA for the proton-translocating ATPase (*unc*) operon of *Escherichia coli*. J. Bacteriol. 155:1279-1287.
 538. Jones, H. M., and R. P. Gunsalus. 1985. Transcription of the *Escherichia coli* fumarate reductase genes (*frdABCD*) and their coordinate regulation by oxygen, nitrate, and fumarate. J. Bacteriol. 164:1100-1109.
 539. Jordan, P. M., B. I. A. Mgbeje, A. F. Alwan, and S. D. Thomas. 1987. Nucleotide sequence of *hemD*, the second gene in the *hem* operon of *Escherichia coli* K-12. Nucleic Acids Res. 15:10583.
 540. Jordan, P. M., B. I. A. Mgbeje, S. D. Thomas, and A. F. Alwan. 1988. Nucleotide sequence for the *hemD* gene of *Escherichia coli* encoding uroporphyrinogen III synthase and initial evidence for a *hem* operon. Biochem. J. 249:613-616.
 541. Josephsen, J., K. Hammer-Jespersen, and T. D. Hansen. 1983. Mapping of the gene for cytidine deaminase (*cdd*) in *Escherichia coli* K-12. J. Bacteriol. 154:72-75.
 542. Junker, D. E., Jr., L. A. Rokeach, D. Ganea, A. Chiaramello, and J. W. Zyskind. 1986. Transcription termination within the *Escherichia coli* origin of DNA replication. Mol. Gen. Genet. 203:101-109.
 543. Kadner, R. J., and D. M. Shattuck-Eidens. 1983. Genetic control of the hexose phosphate transport system of *Escherichia coli*: mapping of deletion and insertion mutations in the *uhp* region. J. Bacteriol. 155:1052-1061.
 544. Kagawa, H., N. Ono, M. Enomoto, and Y. Komeda. 1984. Bacteriophage chi sensitivity and motility of *Escherichia coli* and *Salmonella typhimurium* Fla⁻ mutants possessing the hook structure. J. Bacteriol. 157:649-654.
 545. Kaiser, K. 1980. The origin of Q-independent derivatives of phage λ . Mol. Gen. Genet. 179:547-554.
 546. Kalman, L. V., and R. P. Gunsalus. 1988. The *frdR* gene of *Escherichia coli* globally regulates several operons involved in anaerobic growth in response to nitrate. J. Bacteriol. 170:623-629.
 547. Kalnins, A., K. Otto, U. R  ther, and B. M  ller-Hill. 1983. Sequence of the *lacZ* gene of *Escherichia coli*. EMBO J. 2:593-597.
 548. Kamholz, J., J. Keyhani, and J. S. Gots. 1986. Molecular cloning and characterization of the *purE* operon of *Escherichia coli*. Gene 44:55-62.
 549. Kamio, Y., C.-K. Lin, M. Regue, and H. C. Wu. 1985. Characterization of the *ileS-lsp* operon in *Escherichia coli*. Identification of an open reading frame upstream of the *ileS* gene and potential promoter(s) for the *ileS-lsp* operon. J. Biol. Chem. 260:5616-5620.
 550. Kanaya, S., and R. J. Crouch. 1983. DNA sequence of the gene coding for *Escherichia coli* ribonuclease H. J. Biol. Chem. 258:1276-1281.
 551. Kano, Y., M. Wada, T. Nagase, and F. Imamoto. 1986. Genetic characterization of the gene *hupB* encoding the HU-1 protein of *Escherichia coli*. Gene 45:37-44.
 552. Kano, Y., S. Yoshino, M. Wada, K. Yokoyama, M. Nobuhara, and F. Imamoto. 1985. Molecular cloning and nucleotide sequence of the HU-1 gene of *Escherichia coli*. Mol. Gen. Genet. 201:360-362.
 553. Kao, C., E. Gumbs, and L. Snyder. 1987. Cloning and characterization of the *Escherichia coli* *lit* gene, which blocks bacteriophage T4 late gene expression. J. Bacteriol. 169:1232-1238.
 554. Kao, C., and L. Snyder. 1988. The *lit* gene product which blocks bacteriophage T4 late gene expression is a membrane protein encoded by a cryptic DNA element, e14. J. Bacteriol. 170:2056-2062.
 555. Kaplan, J. B., and B. P. Nichols. 1983. Nucleotide sequence of *Escherichia coli* *pabA* and its evolutionary relationship to *trp(G)D*. J. Mol. Biol. 168:451-468.
 556. Karibian, D., G. P. F. Michel, and J. Starka. 1985. The EnvC phenotype and its expression in various *Escherichia coli* K12 strains. FEMS Microbiol. Lett. 27:319-324.
 557. Karube, I., M. Tomiyama, and A. Kikuchi. 1984. Molecular cloning and physical mapping of the *hyd* gene of *Escherichia coli* K-12. FEMS Microbiol. Lett. 25:165-168.
 558. Kasian, P. A., B. E. Davidson, and J. Pittard. 1986. Molecular analysis of the promoter operator region of the *Escherichia coli* K-12 *tyrP* gene. J. Bacteriol. 167:556-561.
 559. Kasian, P. A., and J. Pittard. 1984. Construction of a *tyrP-lac* operon fusion strain and its use in the isolation and analysis of mutants derepressed for *tyrP* expression. J. Bacteriol. 160:175-183.
 560. Kataoka, H., and M. Sekiguchi. 1985. Molecular cloning and characterization of the *alkB* gene of *Escherichia coli*. Mol. Gen. Genet. 198:263-269.
 561. Kataoka, H., Y. Yamamoto, and M. Sekiguchi. 1983. A new gene (*alkB*) of *Escherichia coli* that controls sensitivity to methyl methane sulfonate. J. Bacteriol. 153:1301-1307.
 562. Kato, J.-I., H. Suzuki, and Y. Hirota. 1984. Overlapping of the coding regions for α and γ components of penicillin-binding protein 1b in *Escherichia coli*. Mol. Gen. Genet. 196:449-457.
 563. Katsukake, K., T. Nakao, and T. Iino. 1985. A gene for DNA invertase and an invertible DNA in *Escherichia coli* K-12. Gene 34:343-350.
 564. Kawakami, K., Y. H. J  nsson, G. R. Bj  rk, H. Ikeda, and Y. Nakamura. 1988. Chromosomal location and structure of the operon encoding peptide-chain-release factor 2 of *Escherichia coli*. Proc. Natl. Acad. Sci. USA 85:5620-5624.
 565. Kawamoto, S., S. Tokuyama, K. Aoyama, S. Yashima, and Y. Eguchi. 1984. Genetic mapping of cold resistance gene of *Escherichia coli*. Agric. Biol. Chem. 48:2067-2071.
 566. Keng, T., T. A. Webster, R. T. Sauer, and P. Schimmel. 1982. Gene for *Escherichia coli* glycyl-tRNA synthetase has tandem subunit coding regions in the same reading frame. J. Biol. Chem. 257:12503-12508.
 567. Kikuchi, A., E. Flamm, and R. A. Weisberg. 1985. An *Escherichia coli* mutant unable to support site-specific recombination of bacteriophage λ . J. Mol. Biol. 183:129-140.
 568. Kilstrup, M., L. M. Meng, J. Neuhaard, and P. Nygaard. 1989. Genetic evidence for a repressor of synthesis of cytosine deaminase and purine biosynthesis enzymes in *Escherichia coli*. J. Bacteriol. 171:2124-2127.
 569. Kirby, T. W., B. R. Hindenach, and R. C. Greene. 1986. Regulation of in vivo transcription of the *Escherichia coli* K-12 *metJBLF* gene cluster. J. Bacteriol. 165:671-677.
 570. Kitagawa, Y., E. Akaboshi, H. Shinagawa, T. Horii, H. Ogawa, and T. Kato. 1985. Structural analysis of the *umu* operon required for inducible mutagenesis in *Escherichia coli*. Proc. Natl. Acad. Sci. USA 82:4336-4340.
 571. Klein, J., B. Henrich, and R. Plapp. 1986. Cloning and expression of the *pepD* gene of *Escherichia coli*. J. Gen. Microbiol. 132:2337-2343.
 572. Klemm, P. 1984. The *fimA* gene encoding the type 1 fimbrial subunit of *Escherichia coli*: nucleotide sequence and primary structure of the protein. Eur. J. Biochem. 143:395-399.
 573. Klemm, P. 1986. Two regulatory *fim* genes, *fimB* and *fimE*, control the phase variation of type 1 fimbriae in *Escherichia coli*. EMBO J. 5:1389-1393.
 574. Klemm, P., and G. Christiansen. 1987. Three *fim* genes required for the regulation of length and mediation of adhesion of *Escherichia coli* type 1 fimbriae. Mol. Gen. Genet. 208:439-445.
 575. Klemm, P., B. J. J  rgensen, I. van Die, H. de Ree, and H. Bergmans. 1985. The *fim* genes responsible for synthesis of type 1 fimbriae in *Escherichia coli*, cloning and genetic organization. Mol. Gen. Genet. 199:410-414.
 576. Klumpp, D. J., D. W. Plank, L. J. Bowdin, C. S. Stueland, T. Chung, and D. C. LaPorte. 1988. Nucleotide sequence of *aceK*, the gene encoding isocitrate dehydrogenase kinase/phosphatase. J. Bacteriol. 170:2763-2769.
 577. Knott, V., D. J. Blake, and G. G. Brownlee. 1989. Completion of the detailed restriction map of the *E. coli* genome by the isolation of overlapping cosmid clones. Nucleic Acids Res. 17:5901-5912.
 578. Knott, V., D. J. G. Rees, Z. Cheng, and G. G. Brownlee. 1988.

- Randomly picked cosmid clones overlap the *pyrB* and *oriC* gap in the physical map of the *E. coli* chromosome. *Nucleic Acids Res.* **16**:2601–2612.
579. Kobayashi, T., I. Kudo, H. Homma, K. Karasawa, K. Inoue, H. Ikeda, and S. Nojima. 1985. Gene organization of *pldA* and *pldB*, the structural genes for detergent-resistant phospholipase A and lysophospholipase L_2 of *Escherichia coli*. *J. Biochem.* **98**:1007–1016.
 580. Kobayashi, T., I. Kudo, K. Karasawa, H. Mizushima, K. Inoue, and S. Nojima. 1985. Nucleotide sequence of the *pldB* gene and characteristics of deduced amino acid sequence of lysophospholipase L_2 in *Escherichia coli*. *J. Biochem.* **98**:1017–1025.
 581. Koch, C., J. Vandekerckhove, and R. Kahmann. 1988. *Escherichia coli* host factor for site-specific DNA inversion: cloning and characterization of the *fis* gene. *Proc. Natl. Acad. Sci. USA* **85**:4237–4241.
 582. Kocharyan, S. M., and M. A. Melkumyan. 1986. Genetic study of *Escherichia coli* K-12 mutants defective for structural and regulatory genes of second purine nucleoside phosphorylase. *Sov. Genet.* **22**:963–972.
 583. Kodaira, M., S. B. Biswas, and A. Kornberg. 1983. The *dnaX* gene encodes the DNA polymerase III holoenzyme τ subunit, precursor of the γ subunit, the *dnaZ* gene product. *Mol. Gen. Genet.* **192**:80–86.
 584. Kohara, Y., K. Akiyama, and K. Isono. 1987. The physical map of the whole *E. coli* chromosome: application of a new strategy for *re. coli* analysis and sorting of a large genomic library. *Cell* **50**:495–508.
 585. Kolodner, R., R. A. Fishel, and M. Howard. 1985. Genetic recombination of bacterial plasmid DNA: effect of *recF* pathway mutations on plasmid recombination in *Escherichia coli*. *J. Bacteriol.* **163**:1060–1066.
 586. Komeda, Y. 1986. Transcriptional control of flagellar genes in *Escherichia coli* K-12. *J. Bacteriol.* **168**:1315–1318.
 587. Komine, Y., T. Adachi, H. Inokuchi, and H. Ozeki. 1990. Genomic organization and physical mapping of the transfer RNA genes in *Escherichia coli* K12. *J. Mol. Biol.* **212**:579–598.
 588. Koop, A. H., M. Hartley, and S. Bourgeois. 1984. Analysis of the *cya* locus of *Escherichia coli*. *Gene* **28**:133–146.
 589. Kornberg, H. 1986. The roles of HPr and FPr in the utilization of fructose by *Escherichia coli*. *FEBS Lett.* **194**:12–15.
 590. Kornberg, H. L., and C. M. Elvin. 1987. Location and function of *fruC*, a gene involved in the regulation of fructose utilization by *Escherichia coli*. *J. Gen. Microbiol.* **133**:341–346.
 591. Köster, W., and V. Braun. 1986. Iron hydroxamate transport of *Escherichia coli*: nucleotide sequence of the *fhuB* gene and identification of the protein. *Mol. Gen. Genet.* **204**:435–442.
 592. Kraft, R., and L. A. Leinwand. 1987. Sequence of the complete P protein gene and part of the M protein gene from the histidine transport operon of *Escherichia coli* compared to that of *Salmonella typhimurium*. *Nucleic Acids Res.* **15**:8568.
 593. Kren, B., and J. A. Fuchs. 1987. Characterization of the *ftsB* gene as an allele of the *nrdB* gene in *Escherichia coli*. *J. Bacteriol.* **169**:14–18.
 594. Kren, B., D. Parsell, and J. A. Fuchs. 1988. Isolation and characterization of an *Escherichia coli* K-12 mutant deficient in glutaredoxin. *J. Bacteriol.* **170**:308–315.
 595. Krickler, M., and B. Hall. 1984. Directed evolution of cellobiose utilization in *Escherichia coli* K12. *Mol. Biol. Evol.* **1**:171–182.
 596. Krickler, M., and B. Hall. 1987. Biochemical genetics of the cryptic gene system for cellulose utilization in *Escherichia coli* K12. *Genetics* **115**:419–429.
 597. Krikos, A., N. Mutoh, A. Boyd, and M. I. Simon. 1983. Sensory transducers of *E. coli* are composed of discrete structural and functional domains. *Cell* **33**:615–622.
 598. Krueger, J. H., S. J. Elledge, and G. C. Walker. 1983. Isolation and characterization of Tn5 insertion mutations in the *lexA* gene of *Escherichia coli*. *J. Bacteriol.* **153**:1368–1378.
 599. Kuchino, Y., F. Mori, and S. Nishimura. 1985. Structure and transcription of the tRNA^{Pro} gene from *Escherichia coli*. *Nucleic Acids Res.* **13**:3213–3220.
 600. Kumamoto, C. A., and J. Beckwith. 1983. Mutations in a new gene, *secB*, cause defective porin localization in *Escherichia coli*. *J. Bacteriol.* **154**:253–260.
 601. Kumamoto, C. A., and J. Beckwith. 1985. Evidence for specificity at an early step in protein export in *Escherichia coli*. *J. Bacteriol.* **163**:267–274.
 602. Kumar, A., C. E. Larsen, and J. Preiss. 1986. Biosynthesis of bacterial glycogen. Primary structure of *Escherichia coli* ADP-glucose: α -1,4-glucan, 4-glucosyltransferase as deduced from the nucleotide sequence of the *glgA* gene. *J. Biol. Chem.* **261**:16256–16259.
 603. Kumura, K., and M. Sekiguchi. 1984. Identification of the *uvrD* gene product of *Escherichia coli* as DNA helicase II and its induction by DNA-damaging agents. *J. Biol. Chem.* **259**:1560–1565.
 604. Kuo, S. C., and D. E. Koshland, Jr. 1986. Sequence of the *flaA* (*cheC*) locus of *Escherichia coli* and discovery of a new gene. *J. Bacteriol.* **166**:1007–1012.
 605. Kuramitsu, S., K. Inoue, T. Ogawa, H. Ogawa, and H. Kagamiyama. 1985. Aromatic amino acid aminotransferase of *Escherichia coli*: nucleotide sequence of the *tyrB* gene. *Biochem. Biophys. Res. Commun.* **133**:134–139.
 606. Kuramitsu, S., T. Ogawa, H. Ogawa, and H. Kagamiyama. 1985. Branched chain amino acid aminotransferase of *Escherichia coli*: nucleotide sequence of the *ilvE* gene and the deduced amino acid sequence. *J. Biochem.* **97**:993–999.
 607. Kuramitsu, S., S. Okuno, T. Ogawa, H. Ogawa, and H. Kagamiyama. 1985. Aspartate aminotransferase of *Escherichia coli*: nucleotide sequence of the *aspC* gene. *J. Biochem.* **97**:1259–1262.
 608. Kurihara, T., and Y. Nakamura. 1983. Cloning of the *nusA* gene of *Escherichia coli*. *Mol. Gen. Genet.* **190**:189–195.
 609. Kurose, N., K. Murata, and A. Kimura. 1985. An *Escherichia coli* mutant having altered D-xylose uptake activity and cloning of a gene for D-xylose uptake. *Agric. Biol. Chem.* **49**:2597–2603.
 610. Kurose, N., K. Murata, and A. Kimura. 1987. Cloning of the D-xylose uptake gene linked to the *xylA* gene in *Escherichia coli*. *Agric. Biol. Chem.* **51**:2575–2578.
 611. Kusser, W., and E. E. Ishiguro. 1987. Suppression of mutations conferring penicillin tolerance by interference with the stringent control mechanism of *Escherichia coli*. *J. Bacteriol.* **169**:4396–4398.
 612. Kuwajima, G., J.-I. Asaka, T. Fujiwara, T. Fujiwara, K. Node, and E. Kondo. 1986. Nucleotide sequence of the *hag* gene encoding flagellin of *Escherichia coli*. *J. Bacteriol.* **168**:1479–1483.
 613. Landick, R., and D. L. Oxender. 1985. The complete nucleotide sequences of the *Escherichia coli* LIV-BP and LS-BP genes. *J. Biol. Chem.* **260**:8257–8261.
 614. Landick, R., V. Vaughn, E. T. Lau, R. A. VanBogelen, J. W. Erickson, and F. C. Neidhardt. 1984. Nucleotide sequence of the heat shock regulatory gene of *E. coli* suggests its protein product may be a transcription factor. *Cell* **38**:175–182.
 615. LaPorte, D. C., and T. Chung. 1985. A single gene codes for the kinase and phosphatase which regulate isocitrate dehydrogenase. *J. Biol. Chem.* **260**:15291–15297.
 616. LaPorte, D. C., P. E. Thorsness, and D. E. Koshland, Jr. 1985. Compensatory phosphorylation of isocitrate dehydrogenase. A mechanism for adaptation to the intracellular environment. *J. Biol. Chem.* **260**:10563–10568.
 617. Larsen, J. E. L., B. Albrechtsen, and P. Valentin-Hansen. 1987. Analysis of the terminator region after the *deoCABD* operon of *Escherichia coli* K-12 using a new class of single copy number operon-fusion vectors. *Nucleic Acids Res.* **15**:5125–5140.
 618. Larsen, J. N., and K. F. Jensen. 1985. Nucleotide sequence of the *pyrD* gene of *Escherichia coli* and characterization of the flavoprotein dihydroorotate dehydrogenase. *Eur. J. Biochem.* **151**:59–65.
 619. Larson, T. J., M. Ehrmann, and W. Boos. 1983. Periplasmic

- glycerophosphodiesterase of *Escherichia coli*, a new enzyme of the *glp* regulon. *J. Biol. Chem.* **258**:5425-5432.
620. Larson, T. J., D. N. Ludtke, and R. M. Bell. 1984. *sn*-Glycerol-3-phosphate auxotrophy of *plsB* strains of *Escherichia coli*: evidence that a second mutation, *plsX*, is required. *J. Bacteriol.* **160**:711-717.
 621. Lathe, R., H. Buc, J.-P. Lecocq, and E. K. F. Bautz. 1980. Prokaryotic histone-like protein interacting with RNA polymerase. *Proc. Natl. Acad. Sci. USA* **77**:3548-3552.
 622. Laviña, M., A. P. Pugsley, and F. Moreno. 1986. Identification, mapping, cloning, and characterization of a gene (*sbmA*) required for microcin B17 action on *Escherichia coli* K12. *J. Gen. Microbiol.* **132**:1685-1693.
 623. Lawther, R. P., R. C. Wek, J. M. Lopes, R. Pereira, B. E. Taillon, and G. W. Hatfield. 1987. The complete nucleotide sequence of the *ilvGMEDA* operon of *Escherichia coli* K-12. *Nucleic Acids Res.* **15**:2137-2155.
 624. Lazzaroni, J.-C., N. Fognini-Lefebvre, and R. C. Portalier. 1986. Cloning of the *lkyB* (*tolB*) gene of *Escherichia coli* K12 and characterization of its product. *Mol. Gen. Genet.* **204**:285-288.
 625. Lazzaroni, J.-C., and R. C. Portalier. 1981. Genetic and biochemical characterization of periplasmic-leaky mutants of *Escherichia coli* K-12. *J. Bacteriol.* **145**:1351-1358.
 626. Lech, K. F., C. H. Lee, R. R. Isberg, and M. Syvanen. 1985. New gene in *Escherichia coli* K-12 (*drpA*): does its product play a role in RNA synthesis? *J. Bacteriol.* **162**:117-123.
 627. Lee, C. A., M. J. Fournier, and J. Beckwith. 1985. *Escherichia coli* 6S RNA is not essential for growth or protein secretion. *J. Bacteriol.* **161**:1156-1161.
 628. Lee, C. A., and M. H. Saier, Jr. 1983. Mannitol-specific enzyme II of the bacterial phosphotransferase system. III. The nucleotide sequence of the permease gene. *J. Biol. Chem.* **258**:10761-10767.
 629. Lee, J. H., P. Patel, P. Sankar, and K. T. Sundaram. 1985. Isolation and characterization of mutant strains of *Escherichia coli* altered in H₂ metabolism. *J. Bacteriol.* **162**:344-352.
 630. Lee, N., W. Gielow, R. Martin, E. Hamilton, and A. Fowler. 1986. The organization of the *araBAD* operon of *Escherichia coli*. *Gene* **47**:231-244.
 631. Lee, S.-H., P. Kanda, R. C. Kennedy, and J. R. Walker. 1987. Relation of the *Escherichia coli* *dnaX* gene to its two products—the τ and γ subunits of DNA polymerase III holoenzyme. *Nucleic Acids Res.* **15**:7663-7675.
 632. Leinfelder, W., K. Forchhammer, F. Zinoni, G. Sawers, M.-A. Mandrand-Berthelot, and A. Böck. 1988. *Escherichia coli* genes whose products are involved in selenium metabolism. *J. Bacteriol.* **170**:540-546.
 633. Leinfelder, W., E. Zehelein, M.-A. Mandrand-Berthelot, and A. Böck. 1988. Gene for a novel tRNA species that accepts L-serine and cotranslationally inserts selenocysteine. *Nature (London)* **331**:723-725.
 634. Lemaire, H.-G., and B. Müller-Hill. 1986. Nucleotide sequences of the *galE* gene and the *galT* gene of *E. coli*. *Nucleic Acids Res.* **14**:7705-7711.
 635. LeMotte, P. K., and G. C. Walker. 1985. Induction and autoregulation of *ada*, a positively acting element regulating the response of *Escherichia coli* K-12 to methylating agents. *J. Bacteriol.* **161**:888-895.
 636. Leung, H. B., and V. L. Schramm. 1984. The structural gene for AMP nucleosidase. Mapping, cloning and overproduction of the enzyme. *J. Biol. Chem.* **259**:6972-6978.
 637. Levin, H. L., and H. K. Schachman. 1985. Regulation of aspartate transcarbamoylase synthesis in *Escherichia coli*: analysis of deletion mutations in the promoter region of the *pyrBI* operon. *Proc. Natl. Acad. Sci. USA* **82**:4643-4647.
 638. Levitz, R., I. Friedberg, R. Brucker, A. Fux, and E. Yagil. 1985. The effect of the locus *pstB* on phosphate binding in the phosphate specific transport (PST) system of *Escherichia coli*. *Mol. Gen. Genet.* **200**:118-122.
 639. Levitz, R., A. Klar, N. Sar, and E. Yagil. 1984. A new locus in the phosphate specific transport (PST) region of *Escherichia coli*. *Mol. Gen. Genet.* **197**:98-103.
 640. Leyh, T. S., J. C. Taylor, and G. D. Markham. 1988. The sulfate activation locus of *Escherichia coli* K12: cloning, genetic, and enzymatic characterization. *J. Biol. Chem.* **263**:2409-2416.
 641. Li, C., H. D. Peck, Jr., and A. E. Przybyla. 1987. Cloning of the 3'-phosphoadenylyl sulfate reductase and sulfite reductase genes from *Escherichia coli* K-12. *Gene* **53**:227-234.
 642. Li, J.-M., H. Umanoff, R. Proenca, C. S. Russell, and S. D. Cosloy. 1988. Cloning of the *Escherichia coli* K-12 *hemB* gene. *J. Bacteriol.* **170**:1021-1025.
 643. Li, S., T. Rabi, and J. A. DeMoss. 1985. Delineation of two distinct regulatory domains in the 5' region of the *nar* operon of *Escherichia coli*. *J. Bacteriol.* **164**:25-32.
 644. Li, S. F., and J. A. DeMoss. 1987. Promoter region of the *nar* operon of *Escherichia coli*: nucleotide sequence and transcription initiation signals. *J. Bacteriol.* **169**:4614-4620.
 645. Liebbe, H., and G. Hatfull. 1985. The sequence of the distal end of the *E. coli* ribosomal RNA *rrnE* operon indicates conserved features are shared by *rrn* operons. *Nucleic Acids Res.* **13**:5515-5525.
 646. Lightner, V. A., R. M. Bell, and P. Modrich. 1983. The DNA sequences encoding *plsB* and *dgk* loci of *Escherichia coli*. *J. Biol. Chem.* **258**:10856-10861.
 647. Liljestrand-Golden, C. A., and J. R. Johnson. 1984. Physical organization of the *metJB* component of the *Escherichia coli* K-12 *metJBLF* gene cluster. *J. Bacteriol.* **157**:413-419.
 648. Liljeström, P. L., and P. Liljeström. 1987. Nucleotide sequence of the *mela* gene, coding for α -galactosidase in *Escherichia coli* K-12. *Nucleic Acids Res.* **15**:2213-2220.
 649. Lim, C.-J., D. Geraghty, and J. A. Fuchs. 1985. Cloning and nucleotide sequence of the *trxA* gene of *Escherichia coli* K-12. *J. Bacteriol.* **163**:311-316.
 650. Lim, C.-J., B. Haller, and J. A. Fuchs. 1985. Thioredoxin is the bacterial protein encoded by *fip* that is required for filamentous bacteriophage ϕ 1 assembly. *J. Bacteriol.* **161**:799-802.
 651. Lim, D., J. D. Oppenheim, T. Eckhardt, and W. K. Maas. 1987. Nucleotide sequence of the *argR* gene of *Escherichia coli* K-12 and isolation of its product, the arginine repressor. *Proc. Natl. Acad. Sci. USA* **84**:6697-6701.
 652. Lin, R.-J., M. Capage, and C. W. Hill. 1984. A repetitive DNA sequence, *rhs*, responsible for duplications within the *Escherichia coli* K-12 chromosome. *J. Mol. Biol.* **177**:1-18.
 653. Lin, R.-J., and C. W. Hill. 1983. Mapping the *xyl*, *mtl*, and *lct* loci in *Escherichia coli* K-12. *J. Bacteriol.* **156**:314-316.
 654. Lindström, P. H. R., D. Stüber, and G. R. Björk. 1985. Genetic organization and transcription from the gene (*trmA*) responsible for synthesis of tRNA (uracil-5)-methyltransferase by *Escherichia coli*. *J. Bacteriol.* **164**:3117-3123.
 655. Link, C. D., and A. M. Reiner. 1983. Genotypic exclusion: a novel relationship between the ribitol-arabitol and galactitol genes of *E. coli*. *Mol. Gen. Genet.* **189**:337-339.
 656. Liu, J., D. M. Burns, and I. R. Beacham. 1986. Isolation and sequence analysis of the gene (*cpdB*) encoding periplasmic 2'3'-cyclic phosphodiesterase. *J. Bacteriol.* **165**:1002-1010.
 657. Lloyd, R. G., and C. Buckman. 1985. Identification and genetic analysis of *sbcC* mutations in commonly used *recBC sbcB* strains of *Escherichia coli* K-12. *J. Bacteriol.* **164**:836-844.
 658. Lloyd, R. G., S. M. Picksley, and C. Prescott. 1983. Inducible expression of a gene specific to the RecF pathway for recombination in *Escherichia coli* K12. *Mol. Gen. Genet.* **190**:162-167.
 659. Løbner-Olesen, A., T. Atlung, and K. V. Rasmussen. 1987. Stability and replication control of *Escherichia coli* minichromosomes. *J. Bacteriol.* **169**:2835-2842.
 660. Loenen, W. A. M., A. S. Daniel, H. D. Braymer, and N. E. Murray. 1987. Organization and sequence of the *hsd* genes of *Escherichia coli* K-12. *J. Mol. Biol.* **198**:159-170.
 661. Loewen, P. C. 1984. Isolation of catalase-deficient *Escherichia coli* mutants and genetic mapping of *katE*, a locus that affects catalase activity. *J. Bacteriol.* **157**:622-626.

662. Loewen, P. C., and B. L. Triggs. 1984. Genetic mapping of *katF*, a locus that with *katE* affects the synthesis of a second catalase species in *Escherichia coli*. *J. Bacteriol.* **160**:668–675.
663. Loewen, P. C., B. L. Triggs, C. S. George, and B. E. Hrabarchuk. 1985. Genetic mapping of *katG*, a locus that affects synthesis of the bifunctional catalase-oxidase hydroperoxidase I in *Escherichia coli*. *J. Bacteriol.* **162**:661–667.
664. Lopes, J. M., and R. P. Lawther. 1986. Analysis and comparison of the internal promoter, pE, of the *ilvGMEDA* operon from *Escherichia coli* K-12 and *Salmonella typhimurium*. *Nucleic Acids Res.* **14**:2779–2798.
665. Lopez, J., and R. E. Webster. 1985. *fipB* and *fipC*: two bacterial loci required for morphogenesis of the filamentous bacteriophage ϕ 1. *J. Bacteriol.* **163**:900–905.
666. Lopilato, J., S. Bortner, and J. Beckwith. 1986. Mutations in a new chromosomal gene of *Escherichia coli* K-12, *pcnB*, reduce plasmid copy number of pBR322 and its derivatives. *Mol. Gen. Genet.* **205**:285–290.
667. Lopilato, J. E., J. L. Garwin, S. D. Emr, T. J. Silhavy, and J. R. Beckwith. 1984. D-Ribose metabolism in *Escherichia coli* K-12: genetics, regulation, and transport. *J. Bacteriol.* **158**:665–673.
668. Lovett, S. T., and A. J. Clark. 1984. Genetic analysis of the *recJ* gene of *Escherichia coli* K-12. *J. Bacteriol.* **157**:190–196.
669. Lovett, S. T., and A. J. Clark. 1985. Cloning of the *Escherichia coli* *recJ* chromosomal region and identification of its encoded proteins. *J. Bacteriol.* **162**:280–285.
670. Lu, M.-F., and H. E. Umbarger. 1987. Effects of deletion and insertion mutations in the *ilvM* gene of *Escherichia coli*. *J. Bacteriol.* **169**:600–604.
671. Ludtke, D., J. Bernstein, C. Hamilton, and A. Torriani. 1984. Identification of the *phoM* gene product and its regulation in *Escherichia coli* K-12. *J. Bacteriol.* **159**:19–25.
672. Lundberg, L. G., O. H. Karlström, and P. O. Nyman. 1983. Isolation and characterization of the *dut* gene of *Escherichia coli*. II. Restriction enzyme mapping and analysis of polypeptide products. *Gene* **22**:127–131.
673. Lundberg, L. G., H.-O. Thoresson, O. H. Karlström, and P. O. Nyman. 1983. Nucleotide sequence of the structural gene for dUTPase of *Escherichia coli* K-12. *EMBO J.* **2**:967–971.
674. Lundrigan, M. D., L. C. DeVeaux, B. J. Mann, and R. J. Kadner. 1987. Separate regulatory systems for the repression of *metE* and *btuB* by vitamin B12 in *Escherichia coli*. *Mol. Gen. Genet.* **206**:401–407.
675. Lundrigan, M. D., and C. F. Earhart. 1984. Gene *envY* of *Escherichia coli* K-12 affects thermoregulation of major porin expression. *J. Bacteriol.* **157**:262–268.
676. Lundrigan, M. D., and R. J. Kadner. 1986. Nucleotide sequence of the gene for the ferrienterochelin receptor *fepA* in *Escherichia coli*: homology among outer membrane receptors which interact with TonB. *J. Biol. Chem.* **261**:10797–10801.
677. Lupski, J. R., A. A. Ruiz, and G. N. Godson. 1984. Promotion, termination and anti-termination in the *rpsU-dnaG-rpoD* macromolecular synthesis operon of *E. coli* K-12. *Mol. Gen. Genet.* **195**:391–401.
678. Lynn, S. P., C. E. Bauer, K. Chapman, and J. F. Gardner. 1985. Identification and characterization of mutants affecting transcription termination at the threonine operon attenuator. *J. Mol. Biol.* **183**:529–541.
679. MacDonald, H., and J. Cole. 1985. Molecular cloning and functional analysis of the *cysG* and *nirB* genes of *Escherichia coli* K12, two closely-linked genes required for NADH-dependent nitrite reductase activity. *Mol. Gen. Genet.* **200**:328–334.
680. MacDonald, H., N. R. Pope, and J. A. Cole. 1985. Isolation, characterization and complementation analysis of *nirB* mutants of *Escherichia coli* deficient only in NADH-dependent nitrite reductase activity. *J. Gen. Microbiol.* **131**:2771–2782.
681. Mackie, G. A. 1986. Structure of the DNA distal to the gene for ribosomal protein S20 in *Escherichia coli* K12: presence of a strong terminator and an IS1 element. *Nucleic Acids Res.* **14**:6965–6981.
682. MacNeil, T., G. P. Roberts, D. MacNeil, and B. Tyler. 1982. The products of *glnL* and *glnG* are bifunctional regulatory proteins. *Mol. Gen. Genet.* **188**:325–333.
683. Magota, K., N. Otsuji, T. Miki, T. Horiuchi, S. Tsunasawa, J. Kondo, F. Sakiyama, M. Amemura, T. Morita, H. Shinagawa, and A. Nakata. 1984. Nucleotide sequence of the *phoS* gene, the structural gene for the phosphate-binding protein of *Escherichia coli*. *J. Bacteriol.* **157**:909–917.
684. Maguin, E., H. Brody, C. W. Hill, and R. D'Ari. 1986. SOS-associated division inhibition gene *sfiC* is part of excisable element ϵ 14 in *Escherichia coli*. *J. Bacteriol.* **168**:464–466.
685. Mahadevan, S., A. E. Reynolds, and A. Wright. 1987. Positive and negative regulation of the *bgl* operon in *Escherichia coli*. *J. Bacteriol.* **169**:2570–2578.
686. Mahajan, S. K., N. B. Vartak, and A. R. Datta. 1988. A new pleiotropic mutation causing defective carbohydrate uptake in *Escherichia coli* K-12: isolation, mapping, and preliminary characterization. *J. Bacteriol.* **170**:2568–2574.
687. Mahan, M. J., and L. N. Csonka. 1983. Genetic analysis of the *proBA* genes of *Salmonella typhimurium*: physical and genetic analyses of the cloned *proB*⁺*A*⁺ genes of *Escherichia coli* and of a mutant allele that confers proline overproduction and enhanced osmotolerance. *J. Bacteriol.* **156**:1249–1262.
688. Maiden, M. C. J., M. C. Jones-Mortimer, and P. J. F. Henderson. 1988. The cloning, DNA sequence, and overexpression of the gene *araE* coding for arabinose-proton symport in *Escherichia coli* K12. *J. Biol. Chem.* **263**:8003–8010.
689. Makaroff, C. A., and H. Zalkin. 1985. Regulation of *Escherichia coli* *purF*: analysis of the control region of a *pur* regulon gene. *J. Biol. Chem.* **260**:10378–10387.
690. Maki, H., T. Horiuchi, and M. Sekiguchi. 1983. Structure and expression of the *dnaQ* mutator and the RNase H genes of *Escherichia coli*: overlap of the promoter regions. *Proc. Natl. Acad. Sci. USA* **80**:7137–7141.
691. Makino, K., H. Shinagawa, M. Amemura, and A. Nakata. 1986. Nucleotide sequence of the *phoB* gene, the positive regulatory gene for the phosphate regulon of *Escherichia coli* K-12. *J. Mol. Biol.* **190**:37–44.
692. Makino, K., H. Shinagawa, M. Amemura, and A. Nakata. 1986. Nucleotide sequence of the *phoR* gene, a regulatory gene for the phosphate regulon of *Escherichia coli*. *J. Mol. Biol.* **192**:549–556.
693. Makino, K., H. Shinagawa, and A. Nakata. 1982. Cloning and characterization of the alkaline phosphatase positive regulator gene (*phoB*) of *Escherichia coli*. *Mol. Gen. Genet.* **187**:181–186.
694. Makino, K., H. Shinagawa, and A. Nakata. 1984. Cloning and characterization of the alkaline phosphatase positive regulatory gene (*phoM*) of *Escherichia coli*. *Mol. Gen. Genet.* **195**:381–390.
695. Makino, K., H. Shinagawa, and A. Nakata. 1985. Regulation of the phosphate regulon of *Escherichia coli* K-12: regulation and role of the regulatory gene *phoR*. *J. Mol. Biol.* **184**:231–240.
696. Malakooti, J., K. Yoshibumi, and P. Matsumura. 1989. DNA sequence analysis, gene product identification, and localization of flagellar motor components of *Escherichia coli*. *J. Bacteriol.* **171**:2728–2734.
697. Malcolm, B. A., and J. F. Kirsch. 1985. Site-directed mutagenesis of aspartate aminotransferase from *E. coli*. *Biochem. Biophys. Res. Commun.* **132**:915–921.
698. Mandrand-Berthelot, M.-A., P. Ritzenthaler, and M. Mata-Gilsinger. 1984. Construction and expression of hybrid plasmids containing the structural gene of the *Escherichia coli* K-12 3-deoxy-2-oxo-D-gluconate transport system. *J. Bacteriol.* **160**:600–606.
699. March, P. E., J. Ahnn, and M. Inouye. 1985. The DNA sequence of the gene (*rnc*) encoding ribonuclease III of *Escherichia coli*. *Nucleic Acids Res.* **13**:4677–4685.
700. March, P. E., and M. Inoue. 1985. Characterization of the *lep* operon of *Escherichia coli*. Identification of the promoter and the gene upstream of the signal peptidase I gene. *J. Biol.*

- Chem. 260:7206-7213.
701. March, P. E., and M. Inouye. 1985. GTP-binding membrane protein of *Escherichia coli* with sequence homology to initiation factor 2 and elongation factors Tu and G. *Proc. Natl. Acad. Sci. USA* 82:7500-7504.
 702. Marek, L. E., and J. M. Henson. 1987. Cloning and expression of the *Escherichia coli* K-12 *sad* gene. *J. Bacteriol.* 170:991-994.
 703. Margison, G. P., D. P. Cooper, and J. Brennand. 1985. Cloning of the *E. coli* O⁶-methylguanine and methylphosphotriester methyltransferase gene using a functional DNA repair assay. *Nucleic Acids Res.* 13:1939-1952.
 704. Margolin, P., L. Zumstein, R. Sternglanz, and J. C. Wang. 1985. The *Escherichia coli* *supX* locus is *topA*, the structural gene for DNA topoisomerase I. *Proc. Natl. Acad. Sci. USA* 82:5437-5441.
 705. Markham, G. D., J. DeParasis, and J. Gatmaitan. 1984. The sequence of *metK*, the structural gene for S-adenosylmethionine synthetase in *Escherichia coli*. *J. Biol. Chem.* 259:14505-14507.
 706. Marsh, L., and G. C. Walker. 1985. Cold sensitivity induced by overproduction of UmuDC in *Escherichia coli*. *J. Bacteriol.* 162:155-161.
 707. Maruyama, M., T. Horiuchi, H. Maki, and M. Sekiguchi. 1983. A dominant (*mutD5*) and a recessive (*dnaQ49*) mutator of *Escherichia coli*. *J. Mol. Biol.* 167:757-771.
 708. Marvel, C. C., P. J. Arps, B. C. Rubin, H. O. Kammen, E. E. Penhoet, and M. E. Winkler. 1985. *hisT* is part of a multigene operon in *Escherichia coli* K-12. *J. Bacteriol.* 161:60-71.
 709. Masai, H., M. W. Bond, and K.-I. Arai. 1986. Cloning of the *Escherichia coli* gene for primosomal protein i: the relationship to *dnaT*, essential for chromosomal DNA replication. *Proc. Natl. Acad. Sci. USA* 83:1256-1260.
 710. Mata-Gilsinger, M., and P. Ritzenthaler. 1983. Physical mapping of the *exuT* and *uxaC* operators by use of *exu* plasmids and generation of deletion mutants in vitro. *J. Bacteriol.* 155:973-982.
 711. Mata-Gilsinger, M., P. Ritzenthaler, and C. Blanco. 1983. Characterization of the operator sites of the *exu* regulon in *Escherichia coli* K-12 by operator-constitutive mutations and repressor titration. *Genetics* 105:829-842.
 712. Matsui, M., A. Oka, M. Takanami, S. Yasuda, and Y. Hirota. 1985. Sites of DNA protein-binding in the replication origin of the *Escherichia coli* K-12 chromosome. *J. Mol. Biol.* 184:529-533.
 713. Matsumoto, Y., K. Shigesada, M. Hirano, and M. Imai. 1986. Autogenous regulation of the gene for transcription termination factor Rho in *Escherichia coli*: localization and function of its attenuators. *J. Bacteriol.* 166:945-958.
 714. Matsumura, P., J. J. Rydel, R. Linzmeier, and D. Vacante. 1984. Overexpression and sequence of the *Escherichia coli* *cheY* gene and biochemical activities of the *CheY* protein. *J. Bacteriol.* 160:36-41.
 715. Matsuzawa, H., S. Ushimaya, Y. Koyama, and T. Ohta. 1984. *Escherichia coli* K-12 *tolZ* mutants tolerant to colicins E2, E3, D, Ia, and Ib: defect in generation of the electrochemical proton gradient. *J. Bacteriol.* 160:733-739.
 716. May, G., E. Faatz, M. Villarejo, and E. Bremer. 1986. Binding protein dependent transport of glycine betaine and its osmotic regulation in *Escherichia coli*. *Mol. Gen. Genet.* 205:225-233.
 717. Mayaux, J.-F., G. Fayat, M. Fromant, M. Springer, M. Grunberg-Manago, and S. Blanquet. 1983. Structural and transcriptional evidence for related *thrS* and *infC* expression. *Proc. Natl. Acad. Sci. USA* 80:6152-6156.
 718. McAlister-Henn, L., M. Blaber, R. A. Bradshaw, and S. J. Nisco. 1987. Complete nucleotide sequence of the *Escherichia coli* gene encoding malate dehydrogenase. *Nucleic Acids Res.* 15:4993.
 719. McCaman, M. T., and J. D. Gabe. 1986. The nucleotide sequence of the *pepN* gene and its over-expression in *Escherichia coli*. *Gene* 48:145-153.
 720. McCaman, M. T., and J. D. Gabe. 1986. Sequence of the promoter and 5' coding region of *pepN*, and the amino terminus of peptidase N from *Escherichia coli* K-12. *Mol. Gen. Genet.* 204:108-152.
 721. McCaman, M. T., A. McPartland, and M. R. Villarejo. 1982. Genetics and regulation of peptidase N in *Escherichia coli* K-12. *J. Bacteriol.* 152:848-854.
 722. McCarthy, J. E. G., H. U. Schairer, and W. Sebald. 1985. Translational initiation frequency of *atp* genes from *Escherichia coli*: identification of an intercistronic sequence that enhances translation. *EMBO J.* 4:519-526.
 723. McFall, E., and M. C. Heincz. 1983. Identification and control of synthesis of the *dsdC* activator protein. *J. Bacteriol.* 153:872-877.
 724. McFall, E., and L. Runkel. 1983. DNA sequences of the D-serine deaminase control region and the N-terminal portion of the gene. *J. Bacteriol.* 154:1508-1512.
 725. McPherson, M. J., A. J. Baron, D. J. C. Pappin, and J. C. Wootton. 1984. Respiratory nitrate reductase of *Escherichia coli*. Sequence identification of the large subunit gene. *FEBS Lett.* 177:260-264.
 726. McPherson, M. J., and J. C. Wootton. 1983. A complete nucleotide sequence of the *Escherichia coli* *gdhA* gene. *Nucleic Acids Res.* 11:5257-5266.
 727. Mechulam, Y., S. Blanquet, and G. Fayat. 1987. Dual level control of the *Escherichia coli* *pheST-himA* operon expression. tRNA^{Phe}-dependent attenuation and transcriptional operator-repressor control by *himA* and the SOS network. *J. Mol. Biol.* 197:453-470.
 728. Mechulam, Y., G. Fayat, and S. Blanquet. 1985. Sequence of the *E. coli* *pheST* operon and identification of the *himA* gene. *J. Bacteriol.* 163:787-791.
 729. Mechulam, Y., M. Fromant, P. Mellot, P. Plateau, S. Blanchin-Roland, G. Fayat, and S. Blanquet. 1985. Molecular cloning of the *Escherichia coli* gene for diadenosine 5', 5'''-P¹, P⁴-tetraphosphate pyrophosphohydrolase. *J. Bacteriol.* 164:63-69.
 730. Meek, D. W., and R. S. Hayward. 1984. Nucleotide sequence of the *rpoA-rplQ* DNA of *Escherichia coli*: a second regulatory binding site for protein S4? *Nucleic Acids Res.* 12:5813-5821.
 731. Meier, U., and H. Mayer. 1985. Genetic location of genes encoding enterobacterial common antigen. *J. Bacteriol.* 163:756-762.
 732. Menzel, R., and M. Gellert. 1987. Fusions of the *Escherichia coli* *gyrA* and *gyrB* control regions to the galactokinase gene are inducible by coumermycin treatment. *J. Bacteriol.* 169:1272-1278.
 733. Menzel, R., and M. Gellert. 1987. Modulation of transcription by DNA supercoiling: a deletion analysis of the *Escherichia coli* *gyrA* and *gyrB* promoters. *Proc. Natl. Acad. Sci. USA* 84:4185-4189.
 734. Michaeli, S., M. Mevarech, and E. Z. Ron. 1984. Regulatory region of the *metA* gene of *Escherichia coli* K-12. *J. Bacteriol.* 160:1158-1162.
 735. Michaeli, S., and E. Z. Ron. 1984. The *metC* gene in *Escherichia coli* K-12: isolation and studies of relatedness in Enterobacteriaceae. *FEMS Microbiol. Lett.* 22:31-35.
 736. Middendorf, A., H. Schweizer, J. Vreemann, and W. Boos. 1984. Mapping the markers in the *his-gyrA* region of *Escherichia coli*. *Mol. Gen. Genet.* 197:175-181.
 737. Miles, J. S., and J. R. Guest. 1984. Complete nucleotide sequence of the fumarase gene *fumA*, of *Escherichia coli*. *Nucleic Acids Res.* 12:3631-3642.
 738. Miles, J. S., and J. R. Guest. 1984. Nucleotide sequence and transcriptional start point of the phosphomannose isomerase gene (*manA*) of *Escherichia coli*. *Gene* 32:41-48.
 739. Miles, J. S., and J. R. Guest. 1987. Subgenes expressing single lipoyl domains of the pyruvate dehydrogenase complex of *Escherichia coli*. *J. Biochem.* 245:869-874.
 740. Millar, G., and J. R. Coggins. 1986. The complete amino acid sequence of 3-dehydroquinate synthase of *Escherichia coli* K12. *FEBS Lett.* 200:11-17.
 741. Miller, K. W., and H. C. Wu. 1987. Cotranscription of the isoleucyl-tRNA synthetase (*ileS*) and prolipoprotein signal

- peptidase (*lsp*) genes: fine-structure mapping of the *lsp* internal promoter. *J. Biol. Chem.* **262**:389–393.
742. Miranda-Ríos, J., R. Sanchez-Pescador, M. Urdea, and A. A. Covarrubias. 1987. The complete nucleotide sequence of the *glnALG* operon of *Escherichia coli* K12. *Nucleic Acids Res.* **15**:2757–2770.
 743. Misra, R., and P. Reeves. 1985. Molecular characterization of the *Stc*[−] mutation of *Escherichia coli* K-12. *Gene* **40**:337–342.
 744. Mitra, S., B. C. Pal, and R. S. Foote. 1982. O⁶-Methylguanine-DNA methyltransferase in wild-type and *ada* mutants of *Escherichia coli*. *J. Bacteriol.* **152**:534–537.
 745. Mizuno, T., M.-Y. Chou, and M. Inouye. 1983. DNA sequence of the promoter region of the *ompC* gene and the amino acid sequence of the signal peptide of pro-OmpC protein of *Escherichia coli*. *FEBS Lett.* **151**:159–164.
 746. Mizuno, T., M.-Y. Chou, and M. Inouye. 1983. A comparative study on the genes for three porins of the *Escherichia coli* outer membrane: DNA sequence of the osmoregulated *ompC* gene. *J. Biol. Chem.* **258**:6932–6940.
 747. Mizuno, T., M.-Y. Chou, and M. Inouye. 1984. A unique mechanism regulating gene expression: translational inhibition by a complementary RNA transcript (micRNA). *Proc. Natl. Acad. Sci. USA* **81**:1966–1970.
 748. Mizuno, T., and S. Mizushima. 1987. Isolation and characterization of deletion mutants of *ompR* and *envZ*, regulatory genes for expression of the outer membrane proteins OmpC and OmpF in *Escherichia coli*. *J. Biochem.* **101**:387–396.
 749. Mizuno, T., E. T. Wurtzel, and M. Inouye. 1982. Osmoregulation of gene expression. II. DNA sequence of the *envZ* gene of the *ompB* operon of *Escherichia coli* and characterization of its gene product. *J. Biol. Chem.* **257**:13692–13698.
 750. Mizusawa, S., D. Court, and S. Gottesman. 1983. Transcription of the *sula* gene and expression by *lexA*. *J. Mol. Biol.* **171**:337–343.
 751. Moffat, K. G., and A. Mackinnon. 1985. Cloning of the *Escherichia coli* K-12 *guaC* gene following its transposition into the RP4::Mu cointegrate. *Gene* **40**:141–143.
 752. Mogi, T., H. Yamamoto, T. Nakao, I. Yamato, and Y. Anraku. 1986. Genetic and physical characterization of *putP*, the proline carrier gene of *Escherichia coli* K12. *Mol. Gen. Genet.* **202**:35–41. (Erratum, **204**:362.)
 753. Morimyo, M. 1988. Isolation and characterization of methyl viologen-sensitive mutants of *Escherichia coli* K-12. *J. Bacteriol.* **170**:2136–2142.
 754. Morita, T., M. Amemura, K. Makino, H. Shinagawa, K. Magota, N. Otsuji, and A. Nakata. 1983. Hyperproduction of phosphate-binding protein, *phoS*, and pre-*phoS* proteins in *Escherichia coli* carrying a cloned *phoS* gene. *Eur. J. Biochem.* **130**:427–435.
 755. Morona, R., and U. Henning. 1986. New locus (*ttr*) in *Escherichia coli* K-12 affecting sensitivity to bacteriophage T2 and growth on oleate as the sole carbon source. *J. Bacteriol.* **168**:534–540.
 756. Morona, R., and P. Reeves. 1982. A new locus, *stc*, which affects the phenotype of *tolC* mutants of *Escherichia coli* K-12. *Mol. Gen. Genet.* **187**:335–341.
 757. Morris, P. W., J. P. Binkley, J. M. Henson, and P. L. Kuempel. 1985. Cloning and location of the *dgsA* gene of *Escherichia coli*. *J. Bacteriol.* **163**:785–786.
 758. Motamedi, H., Y. Lee, and F. J. Schmidt. 1984. Tandem promoters preceding the gene for the M1 RNA component of *Escherichia coli* ribonuclease P. *Proc. Natl. Acad. Sci. USA* **81**:3959–3963.
 759. Moyed, H. S., and K. P. Bertrand. 1983. *hipA*, a newly recognized gene of *Escherichia coli* K-12 that affects frequency of persistence after inhibition of murein synthesis. *J. Bacteriol.* **155**:768–775.
 760. Moyed, H. S., and S. H. Broderick. 1986. Molecular cloning and expression of *hipA*, a gene of *Escherichia coli* K-12 that affects frequency of persistence after inhibition and murein synthesis. *J. Bacteriol.* **166**:399–403.
 761. Mullin, D. A., C. L. Woldringh, J. M. Henson, and J. R. Walker. 1983. Cloning of the *Escherichia coli* *dnaZX* region and identification of its products. *Mol. Gen. Genet.* **192**:73–79.
 762. Murakami, H., K. Kita, and Y. Anraku. 1984. Cloning of *cybB*, the gene for cytochrome *b561* of *Escherichia coli* K12. *Mol. Gen. Genet.* **198**:1–6.
 763. Murakami, H., K. Kita, H. Oya, and Y. Anraku. 1984. Chromosomal location of the *Escherichia coli* cytochrome *b556* gene, *cybA*. *Mol. Gen. Genet.* **196**:1–5.
 764. Murakami, H., K. Kita, H. Oya, and Y. Anraku. 1985. The *Escherichia coli* cytochrome *b556* gene, *cybA*, is assignable as *sdhC* in the succinate dehydrogenase gene cluster. *FEMS Microbiol. Lett.* **30**:307–311.
 765. Murakami, Y., T. Nagata, W. Schwarz, C. Wada, and T. Yura. 1985. Novel *dnaG* mutation in a *dnaP* mutant of *Escherichia coli*. *J. Bacteriol.* **162**:830–832.
 766. Muramatsu, T., K. Nishikawa, F. Nemoto, Y. Kuchino, S. Nishimura, T. Miyazawa, and S. Yokoyama. 1988. Codon and amino-acid specificities of a transfer RNA are both converted by a single post-transcriptional modification. *Nature (London)* **336**:179–181.
 767. Murray, N. E., J. A. Gough, B. Suri, and T. A. Bickle. 1982. Structural homologies among type I restriction-modification systems. *EMBO J.* **1**:535–539.
 768. Mutoh, N., and M. I. Simon. 1986. Nucleotide sequence corresponding to five chemotaxis genes in *Escherichia coli*. *J. Bacteriol.* **165**:161–166.
 769. Nagase, T., S. Ishii, and F. Imamoto. 1988. Differential transcriptional control of the two tRNA^{Met} genes of *Escherichia coli* K-12. *Gene* **67**:49–57.
 770. Nahlik, M. S., T. P. Fleming, and M. A. McIntosh. 1987. Cluster of genes controlling synthesis and activation of 2,3-dihydroxybenzoic acid in production of enterobactin in *Escherichia coli*. *J. Bacteriol.* **169**:4163–4170.
 771. Naito, S., T. Kitani, T. Ogawa, T. Okazaki, and H. Uchida. 1984. *Escherichia coli* mutants suppressing replication-defective mutations of the ColE1 plasmid. *Proc. Natl. Acad. Sci. USA* **81**:550–554.
 772. Nakabeppu, Y., H. Kondo, S. I. Kawabata, S. Iwanaga, and M. Sekiguchi. 1985. Purification and structure of the intact Ada regulatory protein of *Escherichia coli* K12, O⁶-methylguanine-DNA methyltransferase. *J. Biol. Chem.* **260**:7281–7288.
 773. Nakabeppu, Y., H. Kondo, and M. Sekiguchi. 1984. Cloning and characterization of the *alkA* gene of *Escherichia coli* that encodes 3-methyladenine DNA glycosylase II. *J. Biol. Chem.* **259**:13723–13729.
 774. Nakabeppu, Y., T. Miyata, H. Kondo, S. Iwanaga, and M. Sekiguchi. 1984. Structure and expression of the *alkA* gene of *Escherichia coli* involved in adaptive response to alkylating agents. *J. Biol. Chem.* **259**:13730–13736.
 775. Nakamura, M., I. N. Maruyama, M. Soma, J.-I. Kato, H. Suzuki, and Y. Hirota. 1983. On the process of cellular division in *Escherichia coli*: nucleotide sequence of the gene for penicillin-binding protein 3. *Mol. Gen. Genet.* **191**:1–9.
 776. Nakamura, Y., and S. Mizusawa. 1985. In vivo evidence that the *nusA* and *infB* genes of *E. coli* are part of the same multi-gene operon which encodes at least four proteins. *EMBO J.* **4**:527–532.
 777. Nakao, T., I. Yamato, and Y. Anraku. 1987. Nucleotide sequence of *putP*, the proline carrier gene of *Escherichia coli* K12. *Mol. Gen. Genet.* **208**:70–75.
 778. Nakao, T., I. Yamato, and Y. Anraku. 1987. Nucleotide sequence of *putC*, the regulatory region for the *put* regulon of *Escherichia coli* K12. *Mol. Gen. Genet.* **210**:364–368.
 779. Nakata, A., M. Amemura, and H. Shinagawa. 1984. Regulation of the phosphate regulon in *Escherichia coli* K-12: regulation of the negative regulatory gene *phoU* and identification of the gene product. *J. Bacteriol.* **159**:979–985.
 780. Nakata, A., H. Shinagawa, and M. Amemura. 1982. Cloning of alkaline phosphatase isozyme gene (*iap*) of *Escherichia coli*. *Gene* **19**:313–319.
 781. Nakayama, H., K. Nakayama, R. Nakayama, N. Irino, Y. Nakayama, and P. C. Hanawalt. 1984. Isolation and genetic

- characterization of a thymineless death-resistant mutant of *Escherichia coli* K12: identification of a new mutation (*recQ1*) that blocks the RecF recombination pathway. *Mol. Gen. Genet.* 195:474-480.
782. Nakayama, K., N. Irino, and H. Nakayama. 1985. The *recQ* gene of *Escherichia coli* K12: molecular cloning and isolation of insertion mutants. *Mol. Gen. Genet.* 200:266-271.
 783. Nakayama, N., N. Arai, M. W. Bond, Y. Kaziro, and K.-I. Arai. 1984. Nucleotide sequence of *dnaB* and the primary structure of the *dnaB* protein from *Escherichia coli*. *J. Biol. Chem.* 259:97-101.
 784. Nakayama, N., M. W. Bond, A. Miyajima, J. Kabori, and K.-I. Arai. 1987. Structure of *Escherichia coli* *dnaC*. Identification of a cysteine residue possibly involved in association with *dnaB* protein. *J. Biol. Chem.* 262:10475-10480.
 785. Nara, F., S.-I. Matsuyama, T. Mizuno, and S. Mizushima. 1986. Molecular analysis of mutant *ompR* genes exhibiting different phenotypes as to osmoregulation of the *ompF* and *ompC* genes of *Escherichia coli*. *Mol. Gen. Genet.* 202:194-199.
 786. Narasimhan, M. L., J. L. Lampi, and J. E. Cronan, Jr. 1986. Genetic and biochemical characterization of an *Escherichia coli* K-12 mutant deficient in acyl-coenzyme A thioesterase II. *J. Bacteriol.* 165:911-917.
 787. Nashimoto, H., and H. Uchida. 1985. DNA sequencing of the *Escherichia coli* ribonuclease III gene and its mutations. *Mol. Gen. Genet.* 201:25-29.
 788. Nasoff, M. S., H. V. Baker II, and R. E. Wolf, Jr. 1984. DNA sequence of the *Escherichia coli* gene, *gnd*, for 6-phosphogluconate dehydrogenase. *Gene* 27:253-264.
 789. Navre, M., and H. K. Schachman. 1983. Synthesis of aspartate transcarbamoylase in *Escherichia coli*: transcriptional regulation of the *pyrB-pyrI* operon. *Proc. Natl. Acad. Sci. USA* 80:1207-1211.
 790. Nazos, P. M., T. K. Antonucci, R. Landick, and D. L. Oxender. 1986. Cloning and characterization of *livH*, the structural gene encoding a component of the leucine transport system in *Escherichia coli*. *J. Bacteriol.* 166:565-573.
 791. Nazos, P. M., M. M. Mayo, T.-Z. Su, J. J. Anderson, and D. L. Oxender. 1985. Identification of *livG*, a membrane-associated component of the branched-chain amino acid transport in *Escherichia coli*. *J. Bacteriol.* 163:1196-1202.
 792. Neidhardt, F. C., R. A. VanBogelin, and E. T. Lau. 1983. Molecular cloning and expression of a gene that controls the high-temperature regulon of *Escherichia coli*. *J. Bacteriol.* 153:597-603.
 793. Neidhardt, F. C., V. Vaughn, T. A. Phillips, and P. L. Bloch. 1983. Gene-protein index of *Escherichia coli* K-12. *Microbiol. Rev.* 47:231-284.
 794. Nelson, S. O., J. Lengeler, and P. W. Postman. 1984. Role of III^{Glc} of the phosphoenol pyruvate-glucose phosphotransferase system in inducer exclusion in *Escherichia coli*. *J. Bacteriol.* 160:360-364.
 795. Ner, S. S., V. Bhayana, A. W. Bell, I. G. Giles, H. W. Duckworth, and D. P. Bloxham. 1983. Complete sequence of the *gltA* gene encoding citrate synthase in *Escherichia coli*. *Biochemistry* 22:5243-5249.
 796. Nersisyan, A. A., I. L. Mett, Z. R. Badalyan, A. V. Kochikyan, A. L. Mett, A. M. Kocharyan, S. M. Kocharyan, and V. A. Sakanyan. 1986. Restriction mapping of recombinant plasmids carrying the genes of arginine biosynthesis from *Escherichia coli* K-12. *Sov. Genet.* 22:805-809.
 797. Nersisyan, A. A., Y. A. Fedorova, and E. M. Khurges. 1986. Cloning of *Escherichia coli* genes for proline biosynthesis. *Sov. Genet.* 22:1493-1500.
 798. Nettleton, C. J., C. Bull, T. O. Baldwin, and J. A. Fee. 1984. Isolation of the *Escherichia coli* iron superoxide dismutase gene: evidence that intracellular superoxide concentration does not regulate oxygen-dependent synthesis of the manganese superoxide dismutase. *Proc. Natl. Acad. Sci. USA* 81:4970-4973.
 799. Neuwald, A. F., and G. V. Stauffer. 1985. DNA sequence and characterization of the *Escherichia coli* *serB* gene. *Nucleic Acids Res.* 13:7025-7039.
 800. Nghiem, Y., M. Cabrera, C. G. Cupples, and J. H. Miller. 1988. The *mutY* gene: a mutator locus in *Escherichia coli* that generates G \rightarrow C \rightarrow T \rightarrow A transversions. *Proc. Natl. Acad. Sci. USA* 85:2709-2713.
 801. Nielson, J., B. B. Jørgensen, K. von Meyenburg, and F. G. Hansen. 1984. The promoters of the *atp* operon of *Escherichia coli* K12. *Mol. Gen. Genet.* 193:64-71.
 802. Nilsson, O., A. Åberg, T. Lundqvist, and B.-M. Sjöberg. 1988. Nucleotide sequence of the gene coding for the large subunit of ribonucleotide reductase of *Escherichia coli*. *Correction.* *Nucleic Acids Res.* 16:4174.
 803. Nohno, T., Y. Kasai, and T. Saito. 1988. Cloning and sequencing of the *Escherichia coli* *chlEN* operon involved in molybdopter biosynthesis. *J. Bacteriol.* 170:4097-4102.
 804. Nohno, T., and T. Saito. 1987. Two transcriptional start sites found in the promoter region of *Escherichia coli* glutamine permease operon, *glnHPQ*. *Nucleic Acids Res.* 15:2777.
 805. Nohno, T., T. Saito, and J.-S. Hong. 1986. Cloning and complete nucleotide sequence of the *Escherichia coli* glutamine permease operon (*glnHPQ*). *Mol. Gen. Genet.* 205:260-269.
 806. Nomura, T., H. Aiba, and A. Ishihama. 1985. Transcriptional organization of the convergent overlapping *dnaQ-rnh* genes of *Escherichia coli*. *J. Biol. Chem.* 260:7122-7125.
 807. Nonet, M. L., C. C. Marvel, and D. R. Tolan. 1987. The *hisT-purF* region of the *Escherichia coli* K-12 chromosome. Identification of additional genes of the *hisT* and *purF* operons. *J. Biol. Chem.* 262:12209-12217.
 808. Norris, V., T. Alliotte, A. Jaffé, and R. D'Ari. 1986. DNA replication termination in *Escherichia coli* *parB* (a *dnaG* allele), *parA*, and *gyrB* mutants affected in DNA distribution. *J. Bacteriol.* 168:494-504.
 809. Nowlan, S. F., and E. R. Kantrowitz. 1983. Identification of a trans-acting regulatory factor involved in the control of the pyrimidine pathway in *E. coli*. *Mol. Gen. Genet.* 192:264-271.
 810. Nüesch, J., and D. Schümperli. 1984. Structural and functional organization of the *gpt* gene region of *Escherichia coli*. *Gene* 32:243-249.
 811. Nyunoya, H., and C. J. Lusty. 1983. The *carB* gene of *Escherichia coli*: a duplicated gene coding for the large subunit of carbamoyl-phosphate synthetase. *Proc. Natl. Acad. Sci. USA* 80:4629-4633.
 812. Odovetskaya, E. R., and S. P. Sineokii. 1987. Isolation and genetic study of the bacterial mutations *gpr* blocking the replication of certain lambdoid phages. *Sov. Genet.* 23:432-440.
 813. Ogawa, T., G. G. Pickett, T. Kogoma, and A. Kornberg. 1984. RNase H confers specificity in the *dnaA*-dependent initiation of replication at the unique origin of the *Escherichia coli* chromosome in vivo and in vitro. *Proc. Natl. Acad. Sci. USA* 81:1040-1044.
 814. Ohki, M., F. Tamura, S. Nishimura, and H. Uchida. 1986. Nucleotide sequence of the *Escherichia coli* *dnaJ* gene and purification of the gene product. *J. Biol. Chem.* 261:1778-1781.
 815. Ohmori, H., M. Kimura, T. Nagata, and Y. Sakakibara. 1984. Structural analysis of the *dnaA* and *danN* genes of *Escherichia coli*. *Gene* 28:159-170.
 816. Ohsumi, M., T. Sekiya, S. Nishimura, and M. Ohki. 1983. Nucleotide sequence of the regulatory region of *malB* operons in *E. coli*. *J. Biochem.* 94:243-247.
 817. Ohta, A., T. Obara, Y. Asami, and I. Shibuya. 1985. Molecular cloning of the *cls* gene responsible for cardiolipin synthesis in *Escherichia coli* and phenotypic consequences of its amplification. *J. Bacteriol.* 163:506-514.
 818. Ohta, Y., K. Watanabe, and A. Kimura. 1985. Complete nucleotide sequence of the *E. coli* N-acetylneuraminatase lyase. *Nucleic Acids Res.* 13:8843-8852.
 819. Oka, A., H. Sasaki, K. Sugimoto, and M. Takami. 1984. Sequence organization of replication origin of the *Escherichia coli* K-12 chromosome. *J. Mol. Biol.* 176:443-458.
 820. Oka, A., K. Sugimoto, H. Sasaki, and M. Takanami. 1982. An

- in vitro method generating base substitutions in preselected regions of plasmid DNA: application to structural analysis of the replication origin of the *Escherichia coli* K-12 chromosome. *Gene* 19:59-69.
821. Okamoto, K., and M. Freundlich. 1986. Mechanism for the autogenous control of the *crp* operon: transcriptional inhibition by a divergent RNA transcript. *Proc. Natl. Acad. Sci. USA* 83:5000-5004.
 822. Old, I. G., M. G. Hunter, D. T. R. Wilson, S. M. Knight, C. A. Weatherston, and R. E. Glass. 1988. Cloning and characterization of the genes for the two homocysteine transmethyases of *Escherichia coli*. *Mol. Gen. Genet.* 211:78-87.
 823. Oliver, D. B. 1985. Identification of five new essential genes involved in the synthesis of a secreted protein in *Escherichia coli*. *J. Bacteriol.* 161:285-291.
 824. Oliver, G., G. Gosset, R. Sanchez-Pescador, E. Lozoya, L. M. Ku, N. Flores, B. Becerril, F. Valle, and F. Bolivar. 1987. Determination of the sequence nucleotide for the glutamate synthase structural genes of *Escherichia coli*. *Gene* 60:1-11.
 825. Ostrowski, J., G. Jagura-Burdzy, and N. M. Kredich. 1987. DNA sequences of the *cysB* regions of *Salmonella typhimurium* and *Escherichia coli*. *J. Biol. Chem.* 262:5999-6005.
 826. Otsuji, N., T. Soejima, S. Maki, and H. Shinagawa. 1982. Cloning of colicin E1 tolerant *tolC* (*mtcB*) gene of *Escherichia coli* K12 and identification of its gene product. *Mol. Gen. Genet.* 187:30-36.
 827. Overbeeke, N., H. Bergmans, F. vanMansfeld, and B. Lugtenberg. 1983. Complete nucleotide sequence of *phoE*, the structural gene for the phosphate limitation inducible outer membrane pore protein of *Escherichia coli* K12. *J. Mol. Biol.* 163:513-532.
 828. Overduin, P., W. Boos, and J. Tommassen. 1988. Nucleotide sequence of the *ugp* genes of *Escherichia coli* K-12: homology to the maltose system. *Mol. Microbiol.* 2:767-775.
 829. Ozenberger, B. A., M. S. Nahlik, and M. A. McIntosh. 1987. Genetic organization of multiple *fep* genes encoding ferric enterobactin transport functions in *Escherichia coli*. *J. Bacteriol.* 169:3638-3646.
 830. Palchaudhuri, S., V. Patel, and E. McFall. 1988. DNA sequence of the D-serine deaminase activator gene. *J. Bacteriol.* 170:330-334.
 831. Palva, E. T., P. Saris, and T. J. Silhavy. 1985. Gene fusions to the *pTsm/pel* locus of *Escherichia coli*. *Mol. Gen. Genet.* 199:427-433.
 832. Park, W., I. Takase, S. Tamaki, I.-N. Jin, F. Ishino, and M. Matsushashi. 1985. Cloning of the gene of *Escherichia coli* mutant penicillin-binding protein 5 that has no penicillin-releasing activity. *Agric. Biol. Chem.* 49:881-883.
 833. Parker, J. 1984. Identification of the *purC* gene product of *Escherichia coli*. *J. Bacteriol.* 157:712-717.
 834. Parker, L. L., and B. G. Hall. 1990. Characterization and nucleotide sequence of the cryptic *cel* operon of *E. coli* K12. *Genetics* 124:455-471.
 835. Parra, F., M. C. Jones-Mortimer, and H. L. Kornberg. 1983. Phosphotransferase-mediated regulation of carbohydrate utilization in *Escherichia coli* K12: the nature of the *lex* (*crr*) and *gsr* (*tgs*) mutations. *J. Gen. Microbiol.* 129:337-348.
 836. Parsot, C., P. Cossart, I. Saint-Girons, and G. N. Cohen. 1983. Nucleotide sequence of *thrC* and of the termination region of the threonine operon in *Escherichia coli* K12. *Nucleic Acids Res.* 11:7331-7345.
 837. Pascal, M.-C., J.-F. Burini, and M. Chippaux. 1984. Regulation of the trimethylamine N-oxide (TMAO) reductase in *Escherichia coli*: analysis of *Tor::Mud1* operon fusion. *Mol. Gen. Genet.* 195:351-355.
 838. Pauza, C. D., M. J. Karels, M. Navre, and H. K. Schachman. 1982. Genes encoding *Escherichia coli* aspartate transcarbamoylase: the *pyrB-pyrI* operon. *Proc. Natl. Acad. Sci. USA* 79:4020-4024.
 839. Pecher, A., H. P. Blaschkowski, K. Knappe, and A. Böck. 1982. Expression of pyruvate-formate lyase of *Escherichia coli* from the cloned structural gene. *Arch. Microbiol.* 132:365-371.
 840. Pecher, A., F. Zinoni, and A. Böck. 1985. The seleno-peptide of formic dehydrogenase (formate hydrogen-lyase linked) from *Escherichia coli*: genetic analysis. *Arch. Microbiol.* 141:359-363.
 841. Pedersen, S., J. Skouv, M. Kajitani, and A. Ishihama. 1984. Transcriptional organization of the *rpsA* operon of *Escherichia coli*. *Mol. Gen. Genet.* 196:135-140.
 842. Pelletier, A. J., T. M. Hill, and P. L. Kuempel. 1988. Location of sites that inhibit progression of replication forks in the terminus region in *Escherichia coli*. *J. Bacteriol.* 170:4293-4298.
 843. Perry, K. L., S. J. Elledge, B. B. Mitchell, L. Marsh, and G. C. Walker. 1985. *umuDC* and *mucAB* operons whose products are required for UV light- and chemical-induced mutagenesis: UmuD, MucA, and LexA proteins share homology. *Proc. Natl. Acad. Sci. USA* 82:4331-4335.
 844. Pettigrew, D. W., D.-P. Ma, C. A. Conrad, and J. R. Johnson. 1988. *Escherichia coli* glycerol kinase. Cloning and sequencing of the *glpK* gene and the primary structure of the enzyme. *J. Biol. Chem.* 263:135-139.
 845. Pettis, G. S., and M. A. McIntosh. 1987. Molecular characterization of the *Escherichia coli* enterobactin cistron *entF* and coupled expression of *entF* and the *fes* gene. *J. Bacteriol.* 169:4154-4162.
 846. Phillips, G. J., and S. R. Kushner. 1987. Determination of the nucleotide sequence for the exonuclease I structural gene (*sbcB*) of *Escherichia coli* K-12. *J. Biol. Chem.* 262:455-459.
 847. Phillips, G. J., D. C. Prasher, and S. R. Kushner. 1988. Physical and biochemical characterization of cloned *sbcB* and *xonA* mutations from *Escherichia coli* K-12. *J. Bacteriol.* 170:2089-2094.
 848. Phillips, T. A., V. Vaughn, P. L. Bloch, and F. C. Neidhardt. 1987. Gene-protein index of *Escherichia coli* K-12, edition 2, p. 919-966. In F. C. Neidhardt, J. L. Ingraham, K. B. Low, B. Magasanik, M. Schaechter, and H. E. Umbarger (ed.), *Escherichia coli* and *Salmonella typhimurium*: cellular and molecular biology, vol. 2. American Society for Microbiology, Washington, D.C.
 849. Pichersky, E., L. D. Gottlieb, and J. F. Hess. 1984. Nucleotide sequence of the triose phosphate isomerase gene of *Escherichia coli*. *Mol. Gen. Genet.* 195:314-320.
 850. Pickett, C. L., L. Hayes, and C. F. Earhart. 1984. Molecular cloning of the *Escherichia coli* K-12 *entACGBE* genes. *FEMS Microbiol. Lett.* 24:77-80.
 851. Picksley, S. M., S. J. Morton, and R. G. Lloyd. 1985. The *recN* locus of *Escherichia coli* K12: molecular analysis and identification of the gene product. *Mol. Gen. Genet.* 201:301-307.
 852. Pierce, J. R., and C. F. Earhart. 1986. *Escherichia coli* K-12 envelope proteins specifically required for ferrienterobactin uptake. *J. Bacteriol.* 166:930-936.
 853. Pierce, J. R., C. L. Pickett, and C. F. Earhart. 1983. Two *fep* genes are required for ferrienterochelin uptake in *Escherichia coli* K-12. *J. Bacteriol.* 155:330-336.
 854. Piette, J., R. Cunin, A. Boyen, D. Charlier, M. Crabeel, F. Van Vliet, N. Glansdorff, C. Squires, and C. L. Squires. 1982. The regulatory region of the divergent *argECBH* operon in *Escherichia coli* K-12. *Nucleic Acids Res.* 10:8031-8048.
 855. Piette, J., R. Cunin, F. Van Vliet, D. Charlier, M. Crabeel, Y. Ota, and N. Glansdorff. 1982. Homologous control sites and DNA transcription starts in the related *argF* and *argI* genes of *Escherichia coli* K12. *EMBO J.* 1:853-857.
 856. Piette, J., H. Nyunoya, C. J. Lusty, R. Cunin, G. Weyens, M. Crabeel, D. Charlier, N. Glansdorff, and A. Piérard. 1984. DNA sequence of the *carA* gene and the control region of *carAB*: tandem promoters, respectively controlled by arginine and the pyrimidines, regulate the synthesis of carbamoyl-phosphate synthetase in *Escherichia coli* K-12. *Proc. Natl. Acad. Sci. USA* 81:4134-4138.
 857. Pinkham, J. L., and T. Platt. 1983. The nucleotide sequence of the *rho* gene of *E. coli* K-12. *Nucleic Acids Res.* 11:3531-3545.
 858. Plamann, M. D., W. D. Rapp, and G. V. Stauffer. 1983.

- Escherichia coli* K12 mutants defective in the glycine cleavage enzyme system. *Mol. Gen. Genet.* 192:15–20.
859. Plamann, M. D., and G. V. Stauffer. 1983. Characterization of the *Escherichia coli* gene for serine hydroxymethyltransferase. *Gene* 22:9–18.
 860. Plamann, M. D., L. T. Stauffer, M. L. Urbanowski, and G. V. Stauffer. 1983. Complete nucleotide sequence of the *E. coli* *glyA* gene. *Nucleic Acids Res.* 11:2065–2075.
 861. Plasterk, R. H. A., A. Brinkman, and P. van de Putte. 1983. DNA inversions in the chromosome of *Escherichia coli* and in bacteriophage Mu: relationship to other site-specific recombination systems. *Proc. Natl. Acad. Sci. USA* 80:5355–5358.
 862. Plasterk, R. H. A., and P. van de Putte. 1985. The invertible P-DNA segment in the chromosome of *Escherichia coli*. *EMBO J.* 4:237–242.
 863. Plate, C. A., S. A. Seely, and T. G. Laffler. 1986. Evidence for a protonmotive force related regulatory system in *Escherichia coli* and its effects on lactose transport. *Biochemistry* 25: 6127–6132.
 864. Plumbridge, J. 1987. Organization of the *Escherichia coli* chromosome between genes *glnS* and *glnU*. *Mol. Gen. Genet.* 209:618–620.
 865. Plumbridge, J. A., F. Deville, C. Sacerdot, H. U. Petersen, Y. Cenatiempo, A. Cozzzone, M. Grunberg-Manago, and J. W. B. Hershey. 1985. Two translational initiation sites in the *infB* gene are used to express initiation factor IF2 α and IF2 β in *Escherichia coli*. *EMBO J.* 4:223–229.
 866. Plumbridge, J. A., J. G. Howe, M. Springer, D. Touati-Schwartz, J. W. B. Hershey, and M. Grunberg-Manago. 1982. Cloning and mapping of a gene for translation initiation factor IF2 in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* 79: 5033–5037.
 867. Plumbridge, J. A., and M. Springer. 1982. *Escherichia coli* phenylalanyl-tRNA synthetase operon: transcription studies of wild-type and mutated operons on multicopy plasmids. *J. Bacteriol.* 152:661–668.
 868. Plumbridge, J. A., and M. Springer. 1983. Organization of the *Escherichia coli* chromosome around the genes for translation initiation factor IF2 (*infB*) and a transcription termination factor (*nusA*). *J. Mol. Biol.* 167:227–243.
 869. Polayes, D. A., P. W. Rice, and J. E. Dahlberg. 1988. DNA polymerase I activity in *Escherichia coli* is influenced by spot 42 RNA. *J. Bacteriol.* 170:2083–2088.
 870. Pon, C. L., R. A. Calogero, and C. O. Gualerzi. 1988. Identification, cloning, nucleotide sequence and chromosomal map location of *hns*, the structural gene of *Escherichia coli* DNA-binding protein H-NS. *Mol. Gen. Genet.* 212: 199–202.
 871. Poon, A. P. W., and T. S. Dhillon. 1986. Temperate coliphage HK253: attachment site and restricted transduction of *proAB* mutants of *Escherichia coli* K-12. *J. Virol.* 60:317–319.
 872. Porter, A. C. G., W. S. A. Brusilow, and R. D. Simoni. 1983. Promoter for the *unc* operon of *Escherichia coli*. *J. Bacteriol.* 155:1271–1278.
 873. Portier, C., and P. Regnier. 1984. Expression of the *rspO* and *pnp* genes: structural analysis of a DNA fragment carrying their control regions. *Nucleic Acids Res.* 12:6091–6102.
 874. Postle, K., and R. F. Good. 1983. DNA sequence of the *Escherichia coli* *tonB* gene. *Proc. Natl. Acad. Sci. USA* 80:5235–5239.
 875. Postle, K., and R. F. Good. 1985. A bidirectional rho-independent transcription terminator between the *E. coli* *tonB* gene and an opposing gene. *Cell* 41:577–585.
 876. Poulsen, P., F. Bonekamp, and K. F. Jensen. 1984. Structure of the *Escherichia coli* *pyrE* operon and control of *pyrE* expression by a UTP modulated intercistronic attenuation. *EMBO J.* 3:1783–1790.
 877. Poulsen, P., K. F. Jensen, P. Valentin-Hansen, P. Carlsson, and L. G. Lundberg. 1983. Nucleotide sequence of the *Escherichia coli* *pyrE* gene and of the DNA in front of the protein-coding region. *Eur. J. Biochem.* 135:223–229.
 878. Pramanik, A., S. J. Wertheimer, J. J. Schwartz, and I. Schwartz. 1986. Expression of *Escherichia coli* *infC*: identification of a promoter in an upstream *thrS* coding sequence. *J. Bacteriol.* 168:746–751.
 879. Prasher, D., D. A. Kasunic, and S. R. Kushner. 1983. Physical and genetic characterization of the cloned *sbvB* (exonuclease I) region of the *Escherichia coli* genome. *J. Bacteriol.* 153: 903–908.
 880. Prather, N. E., B. H. Mims, and E. J. Murgola. 1983. *supG* and *supL* in *Escherichia coli* code for mutant lysine tRNAs. *Nucleic Acids Res.* 11:8283–8286.
 881. Pratt, D., and S. Subramani. 1983. Nucleotide sequence of the *Escherichia coli* xanthine-guanine phosphoribosyl transferase gene. *Nucleic Acids Res.* 11:8817–8823.
 882. Pressler, U., H. Staudenmaier, L. Zimmermann, and V. Braun. 1988. Genetics of the iron dicitrate transport system of *Escherichia coli*. *J. Bacteriol.* 170:2716–2724.
 883. Prody, C. A., and J. B. Neillands. 1984. Genetic and biochemical characterization of the *Escherichia coli* K-12 *fhuB* mutation. *J. Bacteriol.* 157:874–880.
 884. Pugsley, A. P., F. Moreno, and V. deLorenzo. 1986. Microcin-E492-insensitive mutants of *Escherichia coli* K12. *J. Gen. Microbiol.* 132:3253–3259.
 885. Raftery, L. A., and M. Yarus. 1985. Site-specific mutagenesis of *Escherichia coli* *gltT* yields a weak, glutamic acid-inserting ochre suppressor. *J. Mol. Biol.* 184:343–345.
 886. Raji, A., D. J. Zabel, C. S. Laufer, and R. E. Depew. 1985. Genetic analysis of mutations that compensate for loss of *Escherichia coli* DNA topoisomerase I. *J. Bacteriol.* 162: 1173–1179.
 887. Raleigh, E. A., R. Trimarchi, and H. Revel. 1989. Genetic and physical mapping of the *mcrA* (*rflA*) and *mcrB* (*rflB*) loci of *Escherichia coli* K-12. *Genetics* 122:279–296.
 888. Raleigh, E. A., and G. Wilson. 1986. *Escherichia coli* K-12 restricts DNA containing 5-methylcytosine. *Proc. Natl. Acad. Sci. USA* 83:9070–9074.
 889. Ralling, G., and T. Linn. 1984. Relative activities of the transcriptional regulatory sites in the *rplKAJLrpoBC* gene cluster of *Escherichia coli*. *J. Bacteriol.* 158:279–285.
 890. Ravi, R. S., S. Sozhamannan, and K. Dharmalingam. 1985. Transposon mutagenesis and genetic mapping of the *rglA* and *rglB* loci of *Escherichia coli*. *Mol. Gen. Genet.* 198:390–392.
 891. Ravnkar, P. D., and R. L. Somerville. 1986. Localization of the structural gene for threonine dehydrogenase in *Escherichia coli*. *J. Bacteriol.* 168:434–436.
 892. Ravnkar, P. D., and R. L. Somerville. 1987. Structural and functional analysis of a cloned segment of *Escherichia coli* DNA that specifies proteins of a C₄ pathway of serine biosynthesis. *J. Bacteriol.* 169:4716–4721.
 893. Ray, A., and D. Apirion. 1982. Characterization of DNA from the *rne* gene of *Escherichia coli*: uniqueness of the *rne* DNA. *Biochem. Biophys. Res. Commun.* 107:1361–1367.
 894. Ream, L. W., and A. J. Clark. 1983. Cloning and deletion mapping of the *recF* *dnaN* region of the *Escherichia coli* chromosome. *Plasmid* 10:101–110.
 895. Reed, R. E., and S. Altman. 1983. Repeated sequences and open reading frames in the 3' flanking region of the gene for the RNA subunit of *Escherichia coli* ribonuclease P. *Proc. Natl. Acad. Sci. USA* 80:5359–5363.
 896. Reed, R. E., M. F. Baer, C. Guerrier-Takada, H. Donis-Keller, and S. Altman. 1982. Nucleotide sequence of the gene encoding the RNA subunit (M1 RNA) of ribonuclease P from *Escherichia coli*. *Cell* 30:627–636.
 897. Regnier, P., M. Grunberg-Manago, and C. Portier. 1987. Nucleotide sequence of the *pnp* gene of *Escherichia coli* encoding polynucleotide phosphorylase: homology of the primary structure of the protein with the RNA-binding domain of ribosomal protein S1. *J. Biol. Chem.* 262:63–68.
 898. Regnier, P., and C. Portier. 1986. Initiation, attenuation and RNaseIII processing of transcripts from the *Escherichia coli* operon encoding ribosomal protein S15 and polynucleotide phosphorylase. *J. Mol. Biol.* 187:23–32.
 899. Regue, M., J. Remenick, M. Tokunaga, G. A. Mackie, and H. C. Wu. 1984. Mapping of the lipoprotein signal peptidase gene (*lsp*). *J. Bacteriol.* 158:632–635.

900. Rehemtulla, A., S. K. Kadam, and K. E. Sanderson. 1986. Cloning and analysis of the *sfrB* (sex factor repression) gene of *Escherichia coli* K-12. *J. Bacteriol.* **166**:651-657.
901. Reiss, J., A. Kleinhofs, and W. Klingmüller. 1987. Cloning of seven differently complementing DNA fragments with *chl* functions from *Escherichia coli* K12. *Mol. Gen. Genet.* **206**: 352-355.
902. Reitzer, L. J., and B. Magasanik. 1985. Expression of *glnA* in *Escherichia coli* is regulated at tandem promoters. *Proc. Natl. Acad. Sci. USA* **82**:1979-1983.
903. Renkichi, T., T. Mukai, M. Aoyagi, and K. Hori. 1984. Nucleotide sequence of the gene for *Escherichia coli* ribosomal protein (*rpsO*). *Mol. Gen. Genet.* **197**:225-229.
904. Reynolds, A. E., J. Felton, and A. Wright. 1981. Insertion of DNA activates the cryptic *bgl* operon in *E. coli* K12. *Nature (London)* **293**:625-629.
905. Reynolds, A. E., S. Mahadevan, S. F. J. LeGrice, and A. Wright. 1984. Enhancement of bacterial gene expression by insertion elements or by mutation in a CAP-cAMP binding site. *J. Mol. Biol.* **191**:85-95.
906. Richardson, K. K., J. Fostel, and T. R. Skopek. 1983. Nucleotide sequence of the xanthine guanine phosphoribosyl transferase gene of *E. coli*. *Nucleic Acids Res.* **11**:8809-8816.
907. Richaud, C., W. Higgins, D. Mengin-Lecreux, and P. Stragier. 1987. Molecular cloning, characterization, and chromosomal localization of *dapF*, the *Escherichia coli* gene for diaminopimelate epimerase. *J. Bacteriol.* **169**:1454-1459.
908. Richaud, C., F. Richaud, C. Martin, C. Haziza, and J.-C. Patte. 1984. Regulation of expression and nucleotide sequence of the *Escherichia coli* *dapD* gene. *J. Biol. Chem.* **259**:14824-14828.
909. Richaud, F., C. Richaud, P. Ratet, and J.-C. Patte. 1986. Chromosomal location and nucleotide sequence of the *Escherichia coli* *dapA* gene. *J. Bacteriol.* **166**:297-300.
910. Rieul, C., F. Bleicher, B. Duclos, J.-C. Cortay, and A. J. Cozzzone. 1988. Nucleotide sequence of the *aceA* gene coding for isocitrate lyase in *Escherichia coli*. *Nucleic Acids Res.* **16**:5689.
911. Riley, M., and N. Glansdorff. 1983. Cloning the *Escherichia coli* *argD* gene specifying acetylornithine δ -transaminase. *Gene* **24**:335-339.
912. Roberts, R. E., C. I. Leinhard, C. G. Gaines, J. M. Smith, and J. R. Guest. 1988. Genetic and molecular characterization of the *guaC-nadC-aroP* region of *Escherichia coli* K-12. *J. Bacteriol.* **170**:463-467.
913. Robinson, A. C., D. J. Kenan, G. F. Hatfull, N. F. Sullivan, R. Spiegelberg, and W. Donachie. 1984. DNA sequence and transcriptional organization of essential cell division genes *ftsQ* and *ftsA* of *Escherichia coli*: evidence for overlapping transcriptional units. *J. Bacteriol.* **160**:546-555. (Erratum **161**: 1238, 1985.)
914. Robinson, A. C., D. J. Kenan, J. Sweeney, and W. D. Donachie. 1986. Further evidence for overlapping transcriptional units in an *Escherichia coli* cell envelope-cell division gene cluster: DNA sequence and transcriptional organization of the *ddl ftsQ* region. *J. Bacteriol.* **167**:809-817.
915. Rocha, M., M. Vazquez, A. Garciarrubio, and A. A. Covarrubias. 1985. Nucleotide sequence of the *glnA-glnL* intercistronic region of *Escherichia coli*. *Gene* **37**:91-99.
916. Rogers, M. J., T. Ohgi, J. Plumbridge, and D. Söll. 1988. Nucleotide sequence of the *Escherichia coli* *nagE* and *nagB* genes: the structural genes for the N-acetylglucosamine transport protein of the bacterial phosphoenolpyruvate: sugar phosphotransferase system and for glucosamine-6-phosphate deaminase. *Gene* **62**:197-207.
917. Rojo, F., J. A. Ayala, M. A. dePedro, and D. Vazquez. 1984. Analysis of the different molecular forms of penicillin-binding protein 1B in *Escherichia coli* *ponB* mutants lysogenized with special transducing λ (*ponB*+) bacteriophages. *Eur. J. Biochem.* **144**:571-576.
918. Roland, K. L., F. E. Powell, and C. L. Turnbough, Jr. 1985. Role of translation and attenuation in the control of *pyrBI* operon expression in *Escherichia coli* K-12. *J. Bacteriol.* **163**:991-999.
919. Rolfes, R. J., and H. Zalkin. 1988. *Escherichia coli* gene *purR* encoding a repressor protein for purine nucleotide synthesis. *J. Biol. Chem.* **263**:19653-19661.
920. Rondeaux, S. S., P.-Y. Hsu, and J. A. DeMoss. 1984. Construction in vitro of a cloned *nar* operon from *Escherichia coli*. *J. Bacteriol.* **159**:159-166.
921. Roof, W. D., K. F. Foltermann, and J. R. Wild. 1982. The organization and regulation of the *pyrBI* operon in *E. coli* includes a Rho-independent attenuator sequence. *Mol. Gen. Genet.* **187**:391-400.
922. Rosenberg, H. 1987. Phosphate transport in prokaryotes, p. 205-246. In B. P. Rosen and S. Silver (ed.), *Ion transport in prokaryotes*. Academic Press, Inc., New York.
923. Rosenfeld, S. A., P. E. Stevis, and N. W. Y. Ho. 1984. Cloning and characterization of the *xyl* genes from *Escherichia coli*. *Mol. Gen. Genet.* **194**:410-415.
924. Ross, T. K., E. C. Achberger, and H. D. Braymer. 1987. Characterization of the *Escherichia coli* modified cytosine restriction (*mcrB*) gene. *Gene* **61**:277-289.
925. Ross, T. K., and H. D. Braymer. 1987. Localization of a genetic region involved in *McrB* restriction by *Escherichia coli* K-12. *J. Bacteriol.* **169**:1757-1759.
926. Rostas, K., S. J. Morton, S. M. Pickley, and R. G. Lloyd. 1987. Nucleotide sequence and LexA regulation of the *Escherichia coli* *recN* gene. *Nucleic Acids Res.* **15**:5041-5049.
927. Rowen, L., J. A. Kobori, and S. Scherer. 1982. Cloning of bacterial DNA replication genes in bacteriophage λ . *Mol. Gen. Genet.* **187**:501-509.
928. Rowland, G. C., P. M. Giffard, and I. R. Booth. 1984. Genetic studies of the *phs* locus of *Escherichia coli*, a mutation causing pleiotropic lesions in metabolism and pH homeostasis. *FEBS Lett.* **173**:295-300.
929. Rowland, G. C., P. M. Giffard, and I. R. Booth. 1985. *phs* locus of *Escherichia coli*, a mutation causing pleiotropic lesions in metabolism, is an *rpoA* allele. *J. Bacteriol.* **164**: 972-975.
930. Roy, A., and A. Danchin. 1982. The *cya* locus of *Escherichia coli* K12: organization and gene products. *Mol. Gen. Genet.* **188**:465-471.
931. Roy, A., and A. Danchin. 1983. Regulation of adenylate cyclase synthesis: nucleotide sequence of the control region. *EMBO J.* **2**:791-797.
932. Rule, G. S., E. A. Pratt, C. C. Q. Chin, F. Wold, and C. Ho. 1985. Overproduction and nucleotide sequence of the respiratory D-lactate dehydrogenase of *Escherichia coli*. *J. Bacteriol.* **161**:1059-1068.
933. Rupprecht, K. R., G. Gordon, M. Lundrigan, R. C. Gayda, A. Markovitz, and C. Earhart. 1983. *ompT*: *Escherichia coli* K-12 structural gene for protein *a* (3b). *J. Bacteriol.* **153**: 1104-1106.
934. Russel, M., and A. Holmgren. 1988. Construction and characterization of glutaredoxin-negative mutants of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **85**:990-994.
935. Russel, M., and P. Model. 1983. A bacterial gene, *fip*, required for filamentous bacteriophage ϕ 1 assembly. *J. Bacteriol.* **154**: 1064-1076.
936. Russel, M., and P. Model. 1984. Characterization of the cloned *fip* gene and its product. *J. Bacteriol.* **157**:526-532.
937. Russel, M., and P. Model. 1985. Direct cloning of the *trxB* gene that encodes thioredoxin reductase. *J. Bacteriol.* **163**: 238-242.
938. Russel, M., and P. Model. 1985. Thioredoxin is required for filamentous phage assembly. *Proc. Natl. Acad. Sci. USA* **82**:29-33.
939. Russel, M., and P. Model. 1988. Sequence of thioredoxin reductase from *Escherichia coli*. Relationship to other flavoprotein disulfide oxidoreductases. *J. Biol. Chem.* **263**:9015-9019.
940. Ryals, J., R.-Y. Hsu, M. N. Lipsett, and H. Bremer. 1982. Isolation of single-site *Escherichia coli* mutants deficient in thiamine and 4-thiouridine syntheses: identification of a *nuvC* mutant. *J. Bacteriol.* **151**:899-904.

941. Rydén, M., J. Murphy, R. Martin, L. Isaksson, and J. Gallant. 1986. Mapping and complementation studies of the gene for release factor 1. *J. Bacteriol.* **168**:1066–1069.
942. Rydén, S. M., and L. Isaksson. 1984. A temperature-sensitive mutant of *Escherichia coli* that shows enhanced misreading of UAG/A and increased efficiency for some tRNA nonsense suppressors. *Mol. Gen. Genet.* **193**:38–45.
943. Sabe, H., T. Miwa, T. Kodaki, K. Izui, S. Hiraga, and H. Katsuki. 1984. Molecular cloning of the phosphoenolpyruvate carboxylase gene, *ppc*, of *Escherichia coli*. *Gene* **31**:279–283.
944. Sadosky, A. B., A. Davidson, R.-J. Lin, and C. W. Hill. 1989. *rhs* gene family of *Escherichia coli* K-12. *J. Bacteriol.* **171**:636–642.
945. Saffen, D. W., K. A. Presper, T. L. Doering, and S. Roseman. 1987. Sugar transport by the bacterial phosphotransferase system. Molecular cloning and structural analysis of the *Escherichia coli* *ptsH*, *ptsI* and *crr* genes. *J. Biol. Chem.* **262**:16241–16253.
946. Saint-Girons, I., N. Duchange, G. N. Cohen, and M. M. Zakin. 1984. Structure and autoregulation of the *metJ* regulatory gene in *Escherichia coli*. *J. Biol. Chem.* **259**:14282–14285.
947. Saint-Girons, I., N. Duchange, M. M. Zakin, I. Park, D. Margarita, P. Ferrara, and G. N. Cohen. 1983. Nucleotide sequence of *metF*, the *E. coli* structural gene for 5-10 methylene tetrahydrofolate reductase and of its control region. *Nucleic Acids Res.* **11**:6723–6732.
948. Saint-Girons, I., and D. Margarita. 1985. Evidence for an internal promoter in the *Escherichia coli* threonine operon. *J. Bacteriol.* **161**:461–462.
949. Saito, M., A. Tsugawa, K. Egawa, and Y. Nakamura. 1986. Revised sequence of the *nusA* gene of *Escherichia coli* and identification of *nusA11* (ts) and *nusA1* mutations which cause changes in a hydrophobic amino acid cluster. *Mol. Gen. Genet.* **205**:380–382.
950. Sak, B. D., A. Eisenstark, and D. Touati. 1989. Exonuclease III and the catalase hydropoxidase II in *Escherichia coli* are both regulated by the *katF* gene product. *Proc. Natl. Acad. Sci. USA* **86**:3271–3275.
951. Sakakibara, Y. 1988. The *dnaK* gene of *Escherichia coli* functions in initiation of chromosome replication. *J. Bacteriol.* **170**:972–979.
952. Sakamoto, H., N. Kimura, and Y. Shimura. 1983. Processing of transcription products of the gene encoding the RNA component of RNase P. *Proc. Natl. Acad. Sci. USA* **80**:6187–6191.
953. Sakumi, K., Y. Nakabeppu, Y. Yamamoto, S.-I. Kawabata, S. Iwanaga, and M. Sekiguchi. 1986. Purification and structure of 3-methyladenine-DNA glycosylase I of *Escherichia coli*. *J. Biol. Chem.* **261**:15761–15766.
954. Salmond, G. P. C., and S. Plakidou. 1984. Genetic analysis of essential genes in the *ftsE* region of the *Escherichia coli* genetic map and identification of a new cell division gene *ftsS*. *Mol. Gen. Genet.* **197**:304–308.
955. Sammartano, L. J., R. W. Tuveson, and R. Davenport. 1986. Control of sensitivity to inactivation by H₂O₂ and broad-spectrum near-UV radiation by the *Escherichia coli* *katF* locus. *J. Bacteriol.* **168**:13–21.
956. Sancar, G. B., A. Sancar, and W. D. Rupp. 1984. Sequences of the *urrC* gene and protein. *Nucleic Acids Res.* **12**:4593–4608.
957. Sancar, G. B., F. W. Smith, M. C. Lorence, C. S. Rupert, and A. Sancar. 1984. Sequences of the *Escherichia coli* photolyase gene and protein. *J. Biol. Chem.* **259**:6033–6038.
958. Sancar, G. B., F. W. Smith, and A. Sancar. 1983. Identification and amplification of the *E. coli* *phr* gene product. *Nucleic Acids Res.* **11**:6667–6678.
959. Sanderson, K. E., and J. R. Roth. 1988. Linkage map of *Salmonella typhimurium*, edition VII. *Microbiol. Rev.* **52**:485–532.
960. Sands, J. F., H. S. Cummings, C. Sacerdot, L. Dondon, M. Grunberg-Manago, and J. W. B. Hershey. 1987. Cloning and mapping of *infA*, the gene for protein synthesis initiation factor If1. *Nucleic Acids Res.* **15**:5157–5168.
961. Sanfacon, H., S. Levasseur, P. H. Roy, and J. Lapointe. 1983. Cloning of the gene for *Escherichia coli* glutamyl-tRNA synthetase. *Gene* **22**:175–180.
962. Sankar, P., J. H. Lee, and K. T. Shanmugam. 1985. Cloning of hydrogenase genes and fine structure of an operon essential for H₂ metabolism in *Escherichia coli*. *J. Bacteriol.* **162**:353–360.
963. Sargentini, N. J., and K. C. Smith. 1983. characterization of an *Escherichia coli* mutant (*radB101*) sensitive to γ and uv radiation, and methyl methanesulfonate. *Radiat. Res.* **93**:461–478.
964. Sargentini, N. J., and K. C. Smith. 1988. Genetic and phenotypic analyses indicating occurrence of the *recN262* and *radB101* mutations of the same locus in *Escherichia coli*. *J. Bacteriol.* **170**:2392–2394.
965. Sasaki, M., T. Fujiyoshi, K. Shimada, and Y. Takagi. 1982. Fine structure of the *recB* and *recC* gene region of *Escherichia coli*. *Biochem. Biophys. Res. Commun.* **109**:414–422.
966. Sasarman, A., A. Nepveu, Y. Echelard, J. Dymetrszyn, M. Drolet, and C. Goyer. 1987. Molecular cloning and sequencing of the *hemD* gene of *Escherichia coli* K-12 and preliminary data on the Uro operon. *J. Bacteriol.* **169**:4257–4262.
967. Sastry, S. S., and R. Jayaraman. 1984. Nitrofurantoin-resistant mutants of *Escherichia coli*: isolation and mapping. *Mol. Gen. Genet.* **196**:379–380.
968. Sauer, M., K. Hantke, and V. Braun. 1987. Ferric-coprogen receptor FhuE of *Escherichia coli*: processing and sequence common to all TonB-dependent outer membrane receptor proteins. *J. Bacteriol.* **169**:2044–2049.
969. Schäffer, S., K. Hantke, and V. Braun. 1985. Nucleotide sequence of the iron regulatory gene *fur*. *Mol. Gen. Genet.* **200**:110–113.
970. Schellenberg, G. D., A. Sarthy, A. E. Larson, M. P. Backer, J. W. Crabb, M. Lidstrom, B. D. Hall, and C. E. Furlong. 1984. Xylose isomerase from *Escherichia coli*. Characterization of the protein and the structural gene. *J. Biol. Chem.* **259**:6826–6832.
971. Scheuermann, R., S. Tam, P. M. J. Burgers, C. Lu, and H. Echols. 1983. Identification of the ϵ -subunit of *Escherichia coli* DNA polymerase III holoenzyme as the *dnaQ* gene product: a fidelity subunit for DNA replication. *Proc. Natl. Acad. Sci. USA* **80**:7085–7089.
972. Schmidt, M. G., E. E. Rollo, J. Grodberg, and D. B. Oliver. 1988. Nucleotide sequence of the *secA* gene and *secA*(Ts) mutations preventing protein export in *Escherichia coli*. *J. Bacteriol.* **170**:3404–3414.
973. Schnetz, K., C. Toloczky, and B. Rak. 1987. β -Glucoside (*bgl*) operon of *Escherichia coli* K-12: nucleotide sequence, genetic organization, and possible evolutionary relationship to regulatory components of two *Bacillus subtilis* genes. *J. Bacteriol.* **169**:2579–2590.
974. Schnier, J., M. Kitakawa, and K. Isono. 1986. The nucleotide sequence of an *Escherichia coli* chromosomal region containing the genes of ribosomal proteins S6, S18, L9 and an open reading frame. *Mol. Gen. Genet.* **204**:126–132.
975. Scholle, A., J. Vreeman, V. Blank, A. Nold, W. Boos, and M. D. Manson. 1987. Sequence of the *mgIB* gene from *Escherichia coli* K12: comparison of wild-type and mutant galactose chemoreceptors. *Mol. Gen. Genet.* **208**:247–253.
976. Schwartz, I., R. Klotsky, D. Elseviers, P. J. Gallagher, M. Krauskopf, M. A. Q. Siddiqui, J. F. H. Wong, and B. A. Roe. 1983. Molecular cloning and sequencing of *pheU*, a gene for *Escherichia coli* tRNA^{Phe}. *Nucleic Acids Res.* **11**:4379–4389.
977. Schweizer, H., and W. Boos. 1983. Cloning of the *ugp* region containing the structural genes for the *pho* regulon-dependent *sn*-glycerol-3-phosphate transport system of *Escherichia coli*. *Mol. Gen. Genet.* **192**:177–186.
978. Schweizer, H., and W. Boos. 1984. Characterization of the *ugp* region containing the genes for the *phoB* dependent *sn*-glycerol-3-phosphate transport system of *Escherichia coli*. *Mol. Gen. Genet.* **197**:161–168.
979. Schweizer, H., W. Boos, and T. J. Larson. 1985. Repressor for the *sn*-glycerol-3-phosphate regulon of *Escherichia coli* K-12:

- cloning of the *glpR* gene and identification of its product. J. Bacteriol. 161:563-566.
980. Schweizer, H., and T. J. Larson. 1987. Cloning and characterization of the aerobic *sn*-glycerol-3-phosphate dehydrogenase structural gene *glpD* of *Escherichia coli* K-12. J. Bacteriol. 169:507-513.
 981. Schweizer, H., G. Sweet, and T. J. Larson. 1986. Physical and genetic structure of the *glpD-malT* interval of the *Escherichia coli* chromosome. Mol. Gen. Genet. 202:488-492.
 982. Scripture, J. B., and R. W. Hogg. 1983. The nucleotide sequences defining the signal peptides of the galactose-binding protein and the arabinose-binding protein. J. Biol. Chem. 258:10853-10855.
 983. Scripture, J. B., C. Voelker, S. Miller, R. T. O'Donnell, L. Polgar, J. Rade, B. F. Horazdovsky, and R. H. Hogg. 1987. High-affinity L-arabinose transport operon. Nucleotide sequence and analysis of gene products. J. Mol. Biol. 197:37-46.
 984. Searles, L. L., J. W. Jones, M. J. Fournier, N. Grambow, B. Tyler, and J. M. Calvo. 1986. *Escherichia coli* B/r *leuK* mutant lacking pseudouridine synthase I activity. J. Bacteriol. 166:341-345.
 985. Sedivy, J. M., F. Daldal, and D. G. Fraenkel. 1984. Fructose biphosphatase of *Escherichia coli*: cloning of the structural gene and preparation of a chromosomal deletion. J. Bacteriol. 158:1048-1053.
 986. Serizawa, H., and R. Fukuda. 1987. Structure of the gene for the stringent starvation protein of *Escherichia coli*. Nucleic Acids Res. 15:1153-1163.
 987. Seufert, W., and W. Messer. 1987. Start sites for bidirectional *in vitro* DNA replication inside the replication origin, *oriC*, of *Escherichia coli*. EMBO J. 6:2469-2472.
 988. Sever, I. S., E. S. Kalyaeva, and O. N. Danilevskaya. 1982. Mutations slowing down degradation of the $\beta\beta'$ subunits of *Escherichia coli* RNA polymerase. Sov. Genet. 18:965-971.
 989. Shaibe, E., E. Metzger, and Y. S. Halpern. 1985. Metabolic pathway for the utilization of L-arginine, L-ornithine, agmatine, and putrescine as nitrogen sources in *Escherichia coli*. J. Bacteriol. 163:933-937.
 990. Sharma, R. C., N. J. Sargentini, and K. C. Smith. 1983. New mutation (*mmrA1*) in *Escherichia coli* K-12 that affects minimal medium recovery and postreplication repair after UV irradiation. J. Bacteriol. 154:743-747.
 991. Sharma, S., W. Dowhan, and R. E. Moses. 1982. Molecular structure of the *uvrC* gene of *Escherichia coli*: identification of DNA sequences required for transcription of the *uvrC* gene. Nucleic Acids Res. 10:5209-5221.
 992. Sharma, S., T. F. Stark, W. G. Beattie, and R. E. Moses. 1986. Multiple control elements for the *uvrC* gene unit of *Escherichia coli*. Nucleic Acids Res. 14:2301-2318.
 993. Shattuck-Eidens, D. M., and R. J. Kadner. 1983. Molecular cloning of the *uhp* region and evidence for a positive activator for expression of the hexose phosphate transport system of *Escherichia coli*. J. Bacteriol. 155:1062-1070.
 994. Shaw, D. J., and J. R. Guest. 1982. Amplification and product identification of the *fnr* gene of *Escherichia coli*. J. Gen. Microbiol. 128:2221-2228.
 995. Shaw, D. J., and J. R. Guest. 1982. Nucleotide sequence of the *fnr* gene and primary structure of the Fnr protein of *Escherichia coli*. Nucleic Acids Res. 10:6119-6130.
 996. Shaw, D. J., J. R. Guest, R. Meganathan, and R. Bentley. 1982. Characterization of *Escherichia coli* *men* mutants defective in conversion of *o*-succinylbenzoate to 1,4-dihydroxy-2-naphthoate. J. Bacteriol. 152:1132-1137.
 997. Shaw, D. J., E. C. Robinson, R. Meganathan, R. Bentley, and J. R. Guest. 1983. Recombinant plasmids containing menaquinone biosynthetic genes of *Escherichia coli*. FEMS Microbiol. Lett. 17:63-67.
 998. Shepard, D., R. W. Oberfelder, M. M. Welch, and C. S. McHenry. 1984. Determination of the precise location and orientation of the *Escherichia coli* *dnaE* gene. J. Bacteriol. 158:455-459.
 999. Shiba, K., K. Ito, Y. Nakamura, J. Dondon, and M. Grunberg-Manago. 1986. Altered translation initiation factor 2 in cold-sensitive *ssyG* mutant affects protein export in *Escherichia coli*. EMBO J. 5:3001-3006.
 1000. Shiba, K., K. Ito, and T. Yura. 1984. Mutation that suppresses the protein export defect of the *secY* mutation and causes cold-sensitive growth of *Escherichia coli*. J. Bacteriol. 160:696-701.
 1001. Shiba, K., K. Ito, and T. Yura. 1986. Suppressors of the *secY24* mutation: identification and characterization of additional *ssy* genes in *Escherichia coli*. J. Bacteriol. 166:849-856.
 1002. Shiba, K., K. Ito, T. Yura, and D. P. Cerretti. 1984. A defined mutation in the protein export gene within the *spc* ribosomal protein operon of *Escherichia coli*: isolation and characterization of a new temperature-sensitive *secY* mutant. EMBO J. 3:631-635.
 1003. Shimamoto, T., H. Yazyu, M. Futai, and T. Tsuchiya. 1984. Nucleotide sequence of the promoter region of the melibiose operon of *Escherichia coli*. Biochem. Biophys. Res. Commun. 121:41-46.
 1004. Shimmin, L. C., D. Vanderwel, R. E. Harkness, B. R. Currie, A. Galloway, and E. E. Ishiguro. 1984. Temperature-sensitive β -lactam-tolerant mutants of *Escherichia coli*. J. Gen. Microbiol. 130:1315-1323.
 1005. Shinagawa, H., T. Kato, T. Ise, K. Makino, and A. Nakata. 1983. Cloning and characterization of the *umu* operon responsible for inducible mutagenesis in *Escherichia coli*. Gene 23:167-174.
 1006. Shinagawa, H., K. Makino, and A. Nakata. 1983. Regulation of the *pho* regulon in *Escherichia coli* K-12. Genetic and physiological regulation of the positive regulatory gene *phoB*. J. Mol. Biol. 168:477-488.
 1007. Short, S. A., and J. T. Singer. 1984. Studies on *deo* operon regulation in *Escherichia coli*: cloning and expression of the *deoR* structural gene. Gene 31:205-211.
 1008. Shultz, J., M. A. Hermodson, C. C. Garner, and K. M. Herrmann. 1984. The nucleotide sequence of the *aroF* gene of *Escherichia coli* and the amino acid sequence of the encoded protein, the tyrosine-sensitive 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase. J. Biol. Chem. 259:9655-9661.
 1009. Shultz, J., T. J. Silhavy, M. L. Berman, N. Fill, and S. D. Emr. 1982. A previously unidentified gene in the *spc* operon of *Escherichia coli* K12 specifies a component of the protein export machinery. Cell 31:227-235.
 1010. Shurvinton, C. E., R. G. Lloyd, F. E. Benson, and P. V. Attfield. 1984. Genetic analysis and molecular cloning of the *Escherichia coli* *ruv* gene. Mol. Gen. Genet. 194:322-329.
 1011. Shuttleworth, H., J. Taylor, and N. Minton. 1986. Sequence of the gene for alkaline phosphatase from *Escherichia coli* JM83. Nucleic Acids Res. 14:8689.
 1012. Sirko, A. E., M. Zatyka, and M. D. Hulanicka. 1987. Identification of the *Escherichia coli* *cysM* gene encoding O-acetylserine sulphydrylase B by cloning with mini-mu-*lac* containing a plasmid replicon. J. Gen. Microbiol. 133:2719-2725.
 1013. Skjold, A. C., and D. H. Ezekiel. 1982. Analysis of lambda insertions in the fucose utilization region of *Escherichia coli* K-12: use of λ *fuc* and *argA* transducing bacteriophages to partially order the fucose utilization genes. J. Bacteriol. 152:120-125.
 1014. Skjold, A. C., and D. H. Ezekiel. 1982. Regulation of D-arabinose utilization in *Escherichia coli* K-12. J. Bacteriol. 152:521-523.
 1015. Skogman, S. G., and J. Nilsson. 1984. Molecular cloning and characterization of the gene for *Escherichia coli* valyl-tRNA synthetase. Gene 30:219-226.
 1016. Slocum, M. K., and J. S. Parkinson. 1983. Genetics of methyl-accepting chemotaxis proteins in *Escherichia coli*: organization of the *tar* region. J. Bacteriol. 155:565-577.
 1017. Slocum, M. K., and J. S. Parkinson. 1985. Genetics of methyl-accepting chemotaxis proteins in *Escherichia coli*: null phenotypes of the *tar* and *tap* genes. J. Bacteriol. 163:586-594.

1018. Smiley, B. L., J. R. Lupski, P. S. Svec, R. McMacken, and G. N. Godson. 1982. Sequences of the *Escherichia coli* *dnaG* primase gene and regulation of its expression. *Proc. Natl. Acad. Sci. USA* **79**:4550-4554.
1019. Smirnov, Y. V., and A. F. Lisenkov. 1986. Construction of the hybrid *crp-lac* operon and investigation of the role of the CRP-cAMP complex in its regulation in *Escherichia coli*. *Sov. Genet.* **22**:432-438.
1020. Smith, A. A., and R. C. Greene. 1984. Cloning of the methionine regulatory gene, *metJ*, of *Escherichia coli* K12 and identification of its product. *J. Biol. Chem.* **259**:14279-14281.
1021. Smith, C. L., J. G. Encome, A. Schutt, S. Klco, and C. R. Cantor. 1987. A physical map of the *Escherichia coli* K12 genome. *Science* **236**:1448-1453.
1022. Smith, J. M., and H. A. Daum III. 1986. Nucleotide sequence of the *purM* gene encoding 5'-phosphoribosyl-5-aminimidazole synthetase of *Escherichia coli* K12. *J. Biol. Chem.* **261**:10632-10636.
1023. Smith, J. M., and H. A. Daum III. 1987. Identification and nucleotide sequence of a gene encoding 5'-phosphoribosylglycinamide transformylase in *Escherichia coli* K12. *J. Biol. Chem.* **262**:10565-10569.
1024. Sodergren, E. J., and J. A. DeMoss. 1988. *narI* region of the *Escherichia coli* nitrate reductase (*nar*) operon contains two genes. *J. Bacteriol.* **170**:1721-1729.
1025. Son, H. S., and S. G. Rhee. 1987. Cascade control of *Escherichia coli* glutamine synthetase. Purification and properties of P_{II} protein and nucleotide sequence of its structural gene. *J. Biol. Chem.* **262**:8690-8695.
1026. Sparrow, C. P., and C. R. H. Raetz. 1983. A *trans*-acting regulatory mutation that causes overproduction of phosphatidylserine synthase in *Escherichia coli*. *J. Biol. Chem.* **258**:9963-9967.
1027. Spears, P. A., D. Schauer, and P. E. Orndorff. 1986. Metastable regulation of type 1 piliation in *Escherichia coli* and isolation and characterization of a phenotypically stable mutant. *J. Bacteriol.* **168**:179-185.
1028. Spencer, M. E., M. G. Darlison, P. E. Stephens, I. K. Duckenfield, and J. R. Guest. 1984. Nucleotide sequence of the *sucB* gene encoding the dihydrolipoamide succinyltransferase of *Escherichia coli* K12 and homology with the corresponding acetyltransferase. *Eur. J. Biochem.* **141**:361-374.
1029. Spencer, M. E., and J. R. Guest. 1985. Transcription analysis of the *sucAB*, *aceEF* and *lpd* genes of *Escherichia coli*. *Mol. Gen. Genet.* **200**:145-154.
1030. Spitzer, E. D., H. E. Jimenez-Billini, and B. Weiss. 1988. β -Alanine auxotrophy associated with *dfp*, a locus affecting DNA synthesis in *Escherichia coli*. *J. Bacteriol.* **170**:872-876.
1031. Spitzer, E. D., and B. Weiss. 1985. The *dfp* gene of *Escherichia coli* K-12, a locus affecting DNA synthesis, codes for a flavoprotein. *J. Bacteriol.* **164**:994-1003.
1032. Spratt, S. K., P. N. Black, M. M. Ragozzino, and W. D. Nunn. 1984. Cloning, mapping and expression of genes involved in the fatty acid-degradative multienzyme complex of *Escherichia coli*. *J. Bacteriol.* **158**:535-542.
1033. Spring, K. J., P. G. Jerlström, D. M. Burns, and I. R. Beacham. 1986. L-Asparaginase genes in *Escherichia coli*: isolation of mutants and characterization of the *ansA* gene and its protein product. *J. Bacteriol.* **166**:135-142.
1034. Springer, M., M. Graffe, J. S. Butler, and M. Grunberg-Manago. 1986. Genetic definition of the translational operator of the threonine-tRNA ligase gene in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **83**:4384-4388.
1035. Springer, M., J.-F. Mayaux, G. Fayat, J. A. Plumbbridge, M. Graffe, S. Blanquet, and M. Grunberg-Manago. 1985. Attenuation control of the *Escherichia coli* phenylalanyl-tRNA synthetase operon. *J. Mol. Biol.* **181**:467-478.
1036. Springer, M., M. Trudel, M. Graffe, J. Plumbbridge, G. Fayat, J. F. Mayaux, C. Sacerdot, S. Blanquet, and M. Grunberg-Manago. 1983. *Escherichia coli* phenylalanyl-tRNA synthetase operon is controlled by attenuation *in vivo*. *J. Mol. Biol.* **171**:263-279.
1037. Squires, C. H., M. DeFelice, J. Devereux, and J. M. Calvo. 1983. Molecular structure of *ilvIH* and its evolutionary relationship to *ilvG* in *Escherichia coli* K-12. *Nucleic Acids Res.* **11**:5299-5313.
1038. Stader, J., P. Matsumura, D. Uacante, G. E. Dean, and R. M. Macnab. 1986. Nucleotide sequence of the *Escherichia coli* *motB* gene and site-limited incorporation of its product into the cytoplasmic membrane. *J. Bacteriol.* **166**:244-252.
1039. Stauffer, G. V., M. D. Plamann, and L. T. Stauffer. 1981. Construction and expression of hybrid plasmids containing the *Escherichia coli* *glyA* gene. *Gene* **14**:63-72.
1040. Stauffer, L. T., M. D. Plamann, and G. V. Stauffer. 1986. Cloning and characterization of the glycine-cleavage enzyme system of *Escherichia coli*. *Gene* **44**:219-226.
1041. Steege, D. A. 1983. A nucleotide change in the anticodon of an *Escherichia coli* serine transfer RNA results in *supD*⁻ amber suppression. *Nucleic Acids Res.* **11**:3823-3832.
1042. Steinem, A.-L., and E. Seeberg. 1986. Nucleotide sequence of the *tag* gene from *Escherichia coli*. *Nucleic Acids Res.* **14**:3763-3772.
1043. Stephens, P. E., M. G. Darlison, H. M. Lewis, and J. R. Guest. 1983. The pyruvate dehydrogenase complex of *Escherichia coli* K12. Nucleotide sequence encoding the dihydrolipoamide acetyltransferase component. *Eur. J. Biochem.* **133**:481-489.
1044. Stephens, P. E., H. M. Lewis, M. G. Darlison, and J. R. Guest. 1983. Nucleotide sequence of the lipoamide dehydrogenase gene of *Escherichia coli* K12. *Eur. J. Biochem.* **135**:519-527.
1045. Stewart, V., R. Landick, and C. Yanofsky. 1986. Rho-dependent transcription termination in the tryptophanase operon leader region of *Escherichia coli* K-12. *J. Bacteriol.* **166**:217-223.
1046. Stewart, V., and J. Parales, Jr. 1988. Identification and expression of genes *narL* and *narX* of the *nar* (nitrate reductase) locus in *Escherichia coli* K-12. *J. Bacteriol.* **170**:1589-1597.
1047. Stoker, K., L. F. Oltman, and A. H. Stouthamer. 1988. Partial characterization of an electrophoretically labile hydrogenase activity of *Escherichia coli* K-12. *J. Bacteriol.* **170**:1220-1226.
1048. Stoker, N. G., J. K. Broome-Smith, A. Edelman, and B. G. Spratt. 1983. Organization and subcloning of the *dacA-rodA-pbpA* cluster of cell shape genes in *Escherichia coli*. *J. Bacteriol.* **155**:847-853.
1049. Stoker, N. G., J. M. Pratt, and B. G. Spratt. 1983. Identification of the *rodA* gene product of *Escherichia coli*. *J. Bacteriol.* **155**:854-859.
1050. Stokes, H. W., P. W. Betts, and B. G. Hall. 1985. Sequence of the *ebgA* gene of *Escherichia coli*: comparison with the *lacZ* gene. *Mol. Biol. Evol.* **2**:469-477.
1051. Stokes, H. W., and B. G. Hall. 1985. Sequence of the *ebgR* gene of *Escherichia coli*: evidence that the EBG and LAC operons are descended from a common ancestor. *Mol. Biol. Evol.* **2**:478-483.
1052. Stoner, C., and R. Schleif. 1983. The *araE* low affinity L-arabinose transport promoter. Cloning, sequence, transcription start site and DNA binding sites of regulatory proteins. *J. Mol. Biol.* **171**:369-381.
1053. Storts, D. R., and A. Markovitz. 1988. Construction and characterization of mutations in *hupB*, the gene encoding HU- β (HU-1) in *Escherichia coli* K-12. *J. Bacteriol.* **170**:1541-1547.
1054. Stragier, P., O. Danos, and J.-C. Patte. 1983. Regulation of diaminopimelate decarboxylase synthesis in *Escherichia coli*. II. Nucleotide sequence of the *lysA* gene and its regulatory region. *J. Mol. Biol.* **168**:321-331.
1055. Stragier, P., and J.-C. Patte. 1983. Regulation of diaminopimelate decarboxylase synthesis in *Escherichia coli*. III. Nucleotide sequence and regulation of the *lysR* gene. *J. Mol. Biol.* **168**:333-350.
1056. Stragier, P., F. Richaud, F. Borne, and J.-C. Patte. 1983. Regulation of diaminopimelate decarboxylase synthesis in *Escherichia coli*. I. Identification of a *lysR* gene encoding an activator of the *lysA* gene. *J. Mol. Biol.* **168**:307-320.
1057. Stuitje, A. R., N. deWind, J. C. van der Spek, T. H. Pors, and

- M. Meijer. 1986. Dissection of promoter sequences involved in transcriptional activation of the *Escherichia coli* replication origin. *Nucleic Acids Res.* **14**:2333-2344.
1058. Styrvold, O. B., P. Falkenberg, B. Landfald, M. W. Eshoo, T. Bjørnsen, and A. R. Strøm. 1986. Selection, mapping, and characterization of osmoregulatory mutants of *Escherichia coli* blocked in the choline-glycine betaine pathway. *J. Bacteriol.* **165**:856-863.
1059. Sullivan, N. F., and W. D. Donachie. 1984. Overlapping functional units in a cell division gene cluster in *Escherichia coli*. *J. Bacteriol.* **158**:1198-1201.
1060. Sullivan, N. F., and W. D. Donachie. 1984. Transcriptional organization within an *Escherichia coli* cell division gene cluster: direction of transcription of the cell separation gene *envA*. *J. Bacteriol.* **160**:724-732.
1061. Sun, T.-P., and R. E. Webster. 1986. *fli*, a bacterial locus required for filamentous phage infection and its relation to colicin-tolerant *tolA* and *tolB*. *J. Bacteriol.* **165**:107-115.
1062. Sun, T.-P., and R. E. Webster. 1987. Nucleotide sequence of a gene cluster involved in entry of E colicins and single-stranded DNA of infecting filamentous bacteriophages into *Escherichia coli*. *J. Bacteriol.* **169**:2667-2674.
1063. Sung, Y.-C., P. M. Anderson, and J. A. Fuchs. 1987. Characterization of high-level expression and sequencing of the *Escherichia coli* K-12 *cynS* gene encoding cyanase. *J. Bacteriol.* **169**:5224-5230.
1064. Sung, Y.-C., D. Parsell, P. M. Anderson, and J. A. Fuchs. 1987. Identification, mapping, and cloning of the gene encoding cyanase in *Escherichia coli* K-12. *J. Bacteriol.* **169**:2639-2642.
1065. Surin, B. P., D. A. Jans, A. L. Fimmel, D. C. Shaw, G. B. Cox, and H. Rosenberg. 1984. Structural gene for the phosphate-repressible phosphate-binding protein of *Escherichia coli* has its own promoter: complete nucleotide sequence of the *phoS* gene. *J. Bacteriol.* **157**:772-778.
1066. Surin, B. P., H. Rosenberg, and G. B. Cox. 1985. Phosphate-specific transport system of *Escherichia coli*: nucleotide sequence and gene-polypeptide relationships. *J. Bacteriol.* **161**:189-198.
1067. Sutherland, P., and L. McAlister-Henn. 1985. Isolation and expression of the *Escherichia coli* gene encoding malate dehydrogenase. *J. Bacteriol.* **163**:1074-1077.
1068. Suzuki, H., H. Kumagai, T. Echigo, and T. Tochikura. 1988. Molecular cloning of *Escherichia coli* K-12 *ggt* and rapid isolation of γ -glutamyltranspeptidase. *Biochem. Biophys. Res. Commun.* **150**:33-38.
1069. Suzuki, H., H. Kumagai, and T. Tochikura. 1987. Isolation, genetic mapping, and characterization of *Escherichia coli* K-12 mutants lacking γ -glutamyltranspeptidase. *J. Bacteriol.* **169**:3926-3931.
1070. Suzuki, T., A. Itoh, S. Ichihara, and S. Mizushima. 1987. Characterization of the *sppA* gene coding for protease IV, a signal peptide peptidase of *Escherichia coli*. *J. Bacteriol.* **169**:2523-2528.
1071. Swindle, J., J. Ajioka, D. Dawson, R. Myers, D. Carroll, and C. Georgopoulos. 1984. The nucleotide sequence of the *Escherichia coli* K12 *nusB* (*groNB*) gene. *Nucleic Acids Res.* **12**:4977-4985.
1072. Szybalski, E. H., and W. Szybalski. 1982. A physical map of the *Escherichia coli* *bio* operon. *Gene* **19**:93-103.
1073. Tabata, S., A. Oka, K. Sugimoto, M. Takanami, S. Yasuda, and Y. Hirota. 1983. The 245 base-pair *oriC* sequence of the *E. coli* chromosome directs bidirectional replication at an adjacent region. *Nucleic Acids Res.* **11**:2617-2626.
1074. Tabor, C. W., and H. Tabor. 1987. The *speEspeD* operon of *Escherichia coli*. Formation and processing of a proenzyme form of S adenosylmethionine decarboxylase. *J. Biol. Chem.* **262**:16037-16040.
1075. Tabor, C. W., H. Tabor, and Q.-W. Xie. 1986. Spermidine synthase of *Escherichia coli*: localization of the *speE* gene. *Proc. Natl. Acad. Sci. USA* **83**:6040-6044.
1076. Takase, I., F. Ishino, M. Wachi, H. Kamada, M. Doi, S. Asoh, H. Matsuzawa, T. Ohta, and M. Matsushashi. 1987. Genes encoding two lipoproteins in the *leuS-dacA* region of the *Escherichia coli* chromosome. *J. Bacteriol.* **169**:5692-5699.
1077. Takata, R., T. Mukai, M. Aoyagi, and K. Hori. 1984. Nucleotide sequence of the gene for *Escherichia coli* ribosomal protein S15 (*rpsO*). *Mol. Gen. Genet.* **197**:225-229.
1078. Takata, R., T. Mukai, and K. Hori. 1985. Attenuation and processing of RNA from the *rpsO-pnp* transcription unit of *Escherichia coli*. *Nucleic Acids Res.* **13**:7289-7297.
1079. Takebe, Y., and Y. Kaziro. 1982. In vitro construction of the *tufB-lacZ* fusion: analysis of the regulatory mechanism of *tufB* promoter. *Mol. Gen. Genet.* **187**:355-363.
1080. Takeda, Y., and H. Avila. 1986. Structure and gene expression of the *E. coli* Mn-superoxide dismutase gene. *Nucleic Acids Res.* **14**:4577-4589.
1081. Tamura, F., S. Nishimura, and M. Ohki. 1984. The *E. coli* *divE* mutation, which differentially inhibits synthesis of certain proteins, is in tRNA^{Ser}. *EMBO J.* **3**:1103-1107.
1082. Taschner, P. E. M., J. G. J. Verest, and C. L. Woldringh. 1987. Genetic and morphological characterization of *fisB* and *nrdB* mutants of *Escherichia coli*. *J. Bacteriol.* **169**:19-25.
1083. Taucher-Scholz, G., and H. Hoffmann-Berling. 1983. Identification of the gene for DNA helicase II of *Escherichia coli*. *Eur. J. Biochem.* **137**:573-580.
1084. Taylor, J. L., J. R. Bedbrook, F. J. Grant, and A. Kleinhofs. 1983. Reconstitution of plant nitrate reductase by *Escherichia coli* extracts and the molecular cloning of the *chlA* gene of *Escherichia coli* K12. *J. Mol. Appl. Genet.* **2**:261-271.
1085. Taylor, R. K., S. Garrett, E. Sodergren, and T. J. Silhavy. 1985. Mutations that define the promoter of *ompF*, a gene specifying a major outer membrane porin protein. *J. Bacteriol.* **162**:1054-1060.
1086. Taylor, W. E., D. B. Straus, A. D. Grossman, Z. F. Burton, C. A. Gross, and R. R. Burgess. 1984. Transcription from a heat-inducible promoter causes heat shock regulation of the sigma subunit of *E. coli* RNA polymerase. *Cell* **38**:371-381.
1087. Teo, I., B. Sedgwick, M. W. Kilpatrick, T. V. McCarthy, and T. Lindahl. 1986. The intracellular signal for induction of resistance to alkylating agents in *E. coli*. *Cell* **45**:315-324.
1088. Teslyar, G. E., and G. M. Shavlovskii. 1983. Localization of genes coding cyclohexolase [cyclohydrolase] II and riboflavin synthase on the *Escherichia coli* K-12 chromosome. *Cytol. Genet.* **17**(5):57-59.
1089. Thomas, M. S., and W. T. Drabble. 1984. Molecular cloning and characterization of the *gua* regulatory region of *Escherichia coli* K12. *Mol. Gen. Genet.* **195**:238-245.
1090. Thomas, M. S., and W. T. Drabble. 1985. Nucleotide sequence and organization of the *gua* promoter region of *Escherichia coli*. *Gene* **36**:45-53.
1091. Thomas, S. D., and P. M. Jordan. 1986. Nucleotide sequence of the *hemC* locus encoding porphobilinogen deaminase of *Escherichia coli* K12. *Nucleic Acids Res.* **14**:6215-6226.
1092. Thorbjarnardóttir, S., T. Dingermann, T. Rafner, Ó. S. Andrésson, D. Söll, and G. Eggertsson. 1985. Leucine tRNA family of *Escherichia coli*: nucleotide sequence of the *supP*(Am) suppressor gene. *J. Bacteriol.* **161**:219-222.
1093. Thorbjarnardóttir, S., H. Uemura, T. Dingermann, T. Rafner, S. Thorsteinsdóttir, D. Söll, and G. Eggertsson. 1985. *Escherichia coli* *supH* suppressor: temperature-sensitive missense suppression caused by an anticodon change in tRNA^{Ser}. *J. Bacteriol.* **161**:207-211.
1094. Tiedeman, A., and J. M. Smith. 1985. Nucleotide sequence of the *guaB* locus encoding IMP dehydrogenase of *Escherichia coli* K12. *Nucleic Acids Res.* **13**:1303-1316.
1095. Tiedeman, A. A., J. Keyhani, J. Kamholz, H. A. Daum III, J. S. Gots, and J. M. Smith. 1989. Nucleotide sequence analysis of the *purEK* operon encoding 5' phosphoribosyl-5-aminoimidazole carboxylase of *Escherichia coli* K-12. *J. Bacteriol.* **171**:205-212.
1096. Tiedeman, A. A., and J. M. Smith. 1984. Isolation and characterization of regulatory mutations affecting the expression of the *guaBA* operon of *Escherichia coli* K-12. *Mol. Gen. Genet.* **195**:77-82.
1097. Tiedeman, A. A., J. M. Smith, and H. Zalkin. 1985. Nucleo-

- tide sequence of the *guaA* gene encoding GMP synthetase of *Escherichia coli* K12. *J. Biol. Chem.* **260**:8676–8679.
1098. Tobe, T., K. Ito, and T. Yura. 1984. Isolation and physical mapping of temperature-sensitive mutants defective in heat-shock induction of proteins in *Escherichia coli*. *Mol. Gen. Genet.* **195**:10–16.
 1099. Tobe, T., N. Kusakawa, and T. Yura. 1987. Suppression of *rpoH* (*htpR*) mutations of *Escherichia coli*: heat shock response in *suha* revertants. *J. Bacteriol.* **169**:4128–4134.
 1100. Tobey, K. L., and G. A. Grant. 1986. The nucleotide sequence of the *serA* gene of *Escherichia coli* and the amino acid sequence of the encoded protein, D-3-phosphoglycerate dehydrogenase. *J. Biol. Chem.* **261**:12179–12183.
 1101. Tobin, J. F., and R. F. Schleif. 1987. Positive regulation of the *Escherichia coli* rhamnose operon is mediated by the products of tandemly repeated regulatory genes. *J. Mol. Biol.* **196**:789–799.
 1102. Tokunaga, M., J. M. Loranger, S.-Y. Chang, M. Regue, S. Chang, and H. C. Wu. 1985. Identification of prolipoprotein signal peptidase and genomic organization of the *lsp* gene in *Escherichia coli*. *J. Biol. Chem.* **260**:5610–5615.
 1103. Tomasiewicz, H. G., and C. S. McHenry. 1987. Sequence analysis of the *Escherichia coli* *dnaE* gene. *J. Bacteriol.* **169**:5735–5744.
 1104. Tomioka, S., T. Nikaido, T. Miyakawa, and M. Matsushashi. 1983. Mutation of the *N*-acetylmuramyl-L-alanine amidase gene of *Escherichia coli*. *J. Bacteriol.* **156**:463–465.
 1105. Tommassen, J., P. Hiemstra, P. Overduin, and B. Lugtenberg. 1984. Cloning of *phoM*, a gene involved in regulation of the synthesis of phosphate limitation inducible proteins in *Escherichia coli* K-12. *Mol. Gen. Genet.* **195**:190–194.
 1106. Tommassen, J., M. Koster, and P. Overduin. 1987. Molecular analysis of the promoter region of the *Escherichia coli* K-12 *phoE* gene. Identification of an element, upstream from the promoter, required for the efficient expression of *phoE* protein. *J. Mol. Biol.* **198**:633–641.
 1107. Torres-Cabassa, A. S., and S. Gottesman. 1987. Capsule synthesis in *Escherichia coli* K-12 is regulated by proteolysis. *J. Bacteriol.* **169**:981–989.
 1108. Torrey, T. A., T. Atlung, and T. Kogoma. 1984. *dnaA* suppressor (*dasF*) mutants of *Escherichia coli* are stable DNA replication (*sdrA/rnh*) mutants. *Mol. Gen. Genet.* **196**:350–355.
 1109. Touati, D. 1983. Cloning and mapping of the manganese superoxide dismutase gene (*sodA*) of *Escherichia coli* K-12. *J. Bacteriol.* **155**:1078–1087.
 1110. Touati, E., E. Dassa, and P. L. Bouquet. 1986. Pleiotropic mutations in *appR* reduce pH 2.5 acid phosphatase expression and restore succinate utilization in CRP-deficient strains of *Escherichia coli*. *Mol. Gen. Genet.* **202**:257–264.
 1111. Treat, M. L., M. L. Weaver, M. R. Emmett, and J. R. Johnson. 1984. Mutagenesis of the *metJBLF* gene cluster with transposon Tn5: localization of the *metF* transcription unit. *Mol. Gen. Genet.* **193**:370–375.
 1112. Triggs-Raine, B. L., and P. C. Loewen. 1987. Physical characterization of *katG*, encoding catalase HPI of *Escherichia coli*. *Gene* **52**:121–128.
 1113. Trisler, P., and S. Gottesman. 1984. *lon* transcriptional regulation of genes necessary for capsular polysaccharide synthesis in *Escherichia coli* K-12. *J. Bacteriol.* **160**:184–191.
 1114. Trun, N. J., and T. J. Silhavy. 1987. Characterization and *in vivo* cloning of *prlC*, a suppressor of signal sequence mutations in *Escherichia coli* K12. *Genetics* **116**:513–521.
 1115. Tse-Dinh, Y.-C., and J. C. Wang. 1986. Complete nucleotide sequence of the *topA* gene encoding *Escherichia coli* DNA topoisomerase I. *J. Mol. Biol.* **191**:321–331.
 1116. Tsuchido, T., R. A. VanBogelen, and F. C. Neidhardt. 1986. Heat shock response in *Escherichia coli* influences cell division. *Proc. Natl. Acad. Sci. USA* **83**:6959–6963.
 1117. Tucker, S. D., and E. J. Murgola. 1985. Sequence analysis of the *glyW* region in *Escherichia coli*. *Biochimie* **67**:1053–1057.
 1118. Tuggle, C. K., and J. A. Fuchs. 1986. Regulation of the operon encoding ribonucleotide reductase in *Escherichia coli*: evidence for both positive and negative control. *EMBO J.* **5**:1077–1085.
 1119. Turnbough, C. L., Jr., K. L. Hicks, and J. P. Donahue. 1983. Attenuation control of *pyrBI* operon expression in *Escherichia coli* K-12. *Proc. Natl. Acad. Sci. USA* **80**:368–372.
 1120. Turnbough, C. L., Jr., K. H. Kerr, W. R. Funderburg, J. P. Donahue, and F. E. Powell. 1987. Nucleotide sequence and characterization of the *pyrF* operon of *Escherichia coli* K12. *J. Biol. Chem.* **262**:10239–10245.
 1121. Uemura, H., S. Thorbjarnardóttir, V. Gamulin, J. Yano, O. S. Andrésson, D. Söhl, and G. Eggertsson. 1985. *supN* ochre suppressor gene in *Escherichia coli* codes for tRNA^{Lys}. *J. Bacteriol.* **163**:1288–1289.
 1122. Ueno-Nishio, S., S. Mango, L. J. Reitzer, and B. Magasanik. 1984. Identification and regulation of the *glnL* operator-promoter of the complex *glnALG* operon of *Escherichia coli*. *J. Bacteriol.* **160**:379–384.
 1123. Ulrich, A. K., D. de Mendoza, J. L. Garwin, and J. E. Cronan, Jr. 1983. Genetic and biochemical analyses of *Escherichia coli* mutants altered in the temperature regulation of membrane lipid composition. *J. Bacteriol.* **154**:221–230.
 1124. Urbanowski, M. L., L. T. Stauffer, L. S. Plamann, and G. V. Stauffer. 1987. A new methionine locus, *metR*, that encodes a *trans*-acting protein required for activation of *metE* and *metH* in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **169**:1391–1397.
 1125. Utsumi, R., Y. Nakamoto, M. Kawakumai, M. Himeno, and T. Komano. 1982. Involvement of cyclic AMP and its receptor protein in filamentation of an *Escherichia coli* *fic* mutant. *J. Bacteriol.* **151**:807–812.
 1126. Valentin-Hansen, P. 1982. Tandem CRP binding sites in the *deo* operon of *Escherichia coli* K-12. *EMBO J.* **1**:1049–1054.
 1127. Valentin-Hansen, P., K. Hammer, J. E. L. Larsen, and I. Svendsen. 1984. The internal regulated promoter of the *deo* operon of *Escherichia coli* K-12. *Nucleic Acids Res.* **12**:5211–5224.
 1128. Valentin-Hansen, P., K. Hammer-Jespersen, F. Boetius, and I. Svendsen. 1984. Structure and function of the intercistronic regulatory *deoC-deoA* element of *Escherichia coli* K-12. *EMBO J.* **3**:179–183.
 1129. Valentin-Hansen, P., P. Højrup, and S. Short. 1985. The primary structure of the *deoR* repressor from the *Escherichia coli* K-12. *Nucleic Acids Res.* **13**:5927–5936.
 1130. Valentin-Hansen, P., J. E. L. Larson, P. Højrup, S. A. Short, and C. S. Barbier. 1986. Nucleotide sequence of the CytR regulatory gene of *E. coli* K-12. *Nucleic Acids Res.* **14**:2215–2228.
 1131. Vales, L. D., B. A. Rabin, and J. W. Chase. 1982. Subunit structure of *Escherichia coli* exonuclease VII. *J. Biol. Chem.* **257**:8799–8805.
 1132. Vales, L. D., B. A. Rabin, and J. W. Chase. 1983. Isolation and preliminary characterization of *Escherichia coli* mutants deficient in exonuclease VII. *J. Bacteriol.* **155**:1116–1122.
 1133. Vallari, D. S., and C. O. Rock. 1985. Isolation and characterization of *Escherichia coli* pantothenate permease (*panF*) mutants. *J. Bacteriol.* **164**:136–142.
 1134. Vallari, D. S., and C. O. Rock. 1987. Isolation and characterization of temperature-sensitive pantothenate kinase (*coaA*) mutants of *Escherichia coli*. *J. Bacteriol.* **169**:5795–5800.
 1135. Valle, F., B. Becerril, E. Chen, P. Seeburg, H. Heyneker, and F. Bolivar. 1984. Complete nucleotide sequence of the glutamate dehydrogenase gene from *Escherichia coli* K-12. *Gene* **27**:193–199.
 1136. Valle, F., E. Sanvicente, P. Seeburg, A. Covarrubias, R. L. Rodriguez, and F. Bolivar. 1983. Nucleotide sequence of the promoter and amino-terminal coding region of the glutamate dehydrogenase structural gene of *Escherichia coli*. *Gene* **23**:199–209.
 1137. VanBogelen, R. A., V. Vaughn, and F. C. Neidhardt. 1983. Gene for heat-inducible lysyl-tRNA synthetase (*lysU*) maps near *cadA* in *Escherichia coli*. *J. Bacteriol.* **153**:1066–1068.
 1138. van Buul, C. P. J. J., and P. H. van Knippenberg. 1985. Nucleotide sequence of the *ksgA* gene of *Escherichia coli*:

- comparison of methyltransferases effecting dimethylation of adenosine in ribosomal RNA. *Gene* 38:65-72.
1139. van de Putte, P., R. Plasterk, and A. Kuijpers. 1984. A *Mu* *gin* complementing function and an invertible DNA region in *Escherichia coli* K-12 are situated on the genetic element *e14*. *J. Bacteriol.* 158:517-522.
 1140. van Sluis, C. A., G. F. Moolenaar, and C. Backendorf. 1983. Regulation of the *uvrC* gene of *Escherichia coli* K12: localization and characterization of a damage-inducible promoter. *EMBO J.* 2:2313-2318.
 1141. Van Vliet, F., R. Cunin, A. Jacobs, J. Piette, D. Gigot, M. Lauwereys, A. Piérard, and N. Glansdorff. 1984. Evolutionary divergence of genes for ornithine and aspartate carbamoyl-transferases—complete sequence and mode of regulation of the *Escherichia coli* *argF* gene; comparison of *argF* with *argI* and *pyrB*. *Nucleic Acids Res.* 12:6277-6289.
 1142. Varshney, U., T. Hutcheon, and J. H. van de Sande. 1988. Sequence analysis, expression and conservation of *Escherichia coli* uracil DNA glycosylase and its gene (*ung*). *J. Biol. Chem.* 263:7776-7784.
 1143. Vimr, E. R., and F. A. Troy. 1985. Identification of an inducible catabolic system for sialic acids (*nan*) in *Escherichia coli*. *J. Bacteriol.* 164:845-853.
 1144. Vogel, R. F., K.-D. Entian, and D. Mecke. 1987. Cloning and sequence of the *mdh* structural gene of *Escherichia coli* coding for malate dehydrogenase. *Arch. Microbiol.* 149:36-42.
 1145. Volkert, M. R., D. C. Nguyen, and K. C. Beard. 1986. *Escherichia coli* gene induction by alkylation treatment. *Genetics* 112:11-26.
 1146. von Meyenburg, K., B. B. Jorgensen, J. Nielsen, and F. G. Hansen. 1982. Promoters of the *atp* operon coding for the membrane-bound ATP synthase of *Escherichia coli* mapped by Tn10 insertion mutations. *Mol. Gen. Genet.* 188:240-248.
 1147. Wachi, M., M. Doi, S. Tamaki, W. Park, S. Nakajima-Iijima, and M. Matsushashi. 1987. Mutant isolation and molecular cloning of *mre* genes, which determine cell shape, sensitivity to mecillinam, and amount of penicillin-binding proteins in *Escherichia coli*. *J. Bacteriol.* 169:4935-4940.
 1148. Wackett, L. P., B. L. Wanner, C. P. Venditti, and C. T. Walsh. 1987. Involvement of the phosphate regulon and the *psiD* locus in carbon-phosphorus lyase activity of *Escherichia coli* K-12. *J. Bacteriol.* 169:1753-1756.
 1149. Wada, A., and T. Sako. 1987. Primary structures of and genes for new ribosomal proteins A and B in *Escherichia coli*. *J. Biochem.* 101:817-820.
 1150. Wahab, S. Z., R. Elford, and W. M. Holmes. 1989. Nucleotide sequence of the *Escherichia coli* tRNA₃^{Leu} gene. *Gene* 81:193-194.
 1151. Wakayama, Y., M. Takagi, and K. Yano. 1984. Gene responsible for protecting *Escherichia coli* from sodium dodecyl sulfate and toluidine blue plus light. *J. Bacteriol.* 159:527-532.
 1152. Walker, J. E., N. J. Gay, M. Saraste, and A. N. Eberle. 1984. DNA sequence around the *Escherichia coli* *unc* operon. Completion of the sequence of a 17 kilobase segment containing *asnA*, *oriC*, *unc*, *glmS* and *phoS*. *Biochem. J.* 224:799-815.
 1153. Wallace, B. J., and S. R. Kushner. 1984. Genetic and physical analysis of the thioredoxin (*trxA*) gene of *Escherichia coli* K-12. *Gene* 32:399-408.
 1154. Wang, J. C., and K. Becherer. 1983. Cloning of the gene *topA* encoding for DNA topoisomerase I and the physical mapping of the *cysB-topA-trp* region of *Escherichia coli*. *Nucleic Acids Res.* 11:1773-1790.
 1155. Wang, M.-D., L. Liu, B. Wang, and C. M. Berg. 1987. Cloning and characterization of the *Escherichia coli* K-12 alanine-valine transaminase (*avtA*) gene. *J. Bacteriol.* 169:4228-4234.
 1156. Wanner, B. L. 1987. Control of *phoR*-dependent bacterial alkaline phosphatase clonal variation by the *phoM* region. *J. Bacteriol.* 169:900-903. (Erratum, 169:3866.)
 1157. Wanner, B. L., and B.-D. Chang. 1987. The *phoBR* operon in *Escherichia coli* K-12. *J. Bacteriol.* 169:5569-5574.
 1158. Wanner, B. L., S. Wieder, and R. McSharry. 1981. Use of bacteriophage transposon *Mu dl* to determine the orientation for three *proC*-linked phosphate-starvation-inducible (*psi*) genes in *Escherichia coli* K-12. *J. Bacteriol.* 146:93-101.
 1159. Wanner, B. L., M. R. Wilmes, and E. Hunter. 1988. Molecular cloning of the wild-type *phoM* operon in *Escherichia coli* K-12. *J. Bacteriol.* 170:279-288.
 1160. Watson, N., and D. Apirion. 1985. Molecular cloning of the gene for the RNA-processing enzyme RNase III of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* 82:849-853.
 1161. Waugh, R., and D. Boxer. 1986. Pleiotropic hydrogenase mutants of *Escherichia coli* K12: growth in the presence of nickel can restore hydrogenase activity. *Biochimie* 68:157-166.
 1162. Webster, C., K. Kempesell, I. Booth, and S. Busby. 1987. Organization of the regulatory region of the *Escherichia coli* melibiose operon. *Gene* 59:253-263.
 1163. Weiss, B., and R. P. Cunningham. 1985. Genetic mapping of *nth*, a gene affecting endonuclease III (thymine glycol-DNA glycosylase) in *Escherichia coli* K-12. *J. Bacteriol.* 162:607-610.
 1164. Weiss, D. L., D. I. Johnson, H. L. Weith, and R. L. Somerville. 1986. Structural analysis of the *ileR* locus of *Escherichia coli* K12. *J. Biol. Chem.* 261:9966-9971.
 1165. Wek, R. C., and G. W. Hatfield. 1986. Nucleotide sequence and *in vivo* expression of the *ilvY* and *ilvC* genes in *Escherichia coli* K12. Transcription from divergent overlapping promoters. *J. Biol. Chem.* 261:2441-2450.
 1166. Wek, R. C., and G. W. Hatfield. 1986. Examination of the internal promoter, P_E, in the *ilvGMEDA* operon of *E. coli* K-12. *Nucleic Acids Res.* 14:2763-2777.
 1167. Wek, R. C., C. A. Hauser, and G. W. Hatfield. 1985. The nucleotide sequence of the *ilvBN* operon of *Escherichia coli*: sequence homologies of the acetohydroxy acid synthase isozyme. *Nucleic Acids Res.* 13:3995-4010.
 1168. Welch, M. M., and C. S. McHenry. 1982. Cloning and identification of the product of the *dnaE* gene of *Escherichia coli*. *J. Bacteriol.* 152:351-356.
 1169. Weng, M., C. A. Makaroff, and H. Zalkin. 1986. Nucleotide sequence of *Escherichia coli* *pyrG* encoding CTP synthetase. *J. Biol. Chem.* 261:5568-5574.
 1170. Werthheimer, S. J., R.-A. Klotsky, and I. Schwartz. 1988. Transcriptional patterns for the *thrS-infC-rpLT* operon of *Escherichia coli*. *Gene* 63:309-320.
 1171. Westh Hansen, S. V., N. Jensen, and A. Munch-Petersen. 1987. Studies on the sequence and structure of the *Escherichia coli* K-12 *nupG* gene. *Eur. J. Biochem.* 168:385-391.
 1172. Weston, L. A., and R. J. Kadner. 1987. Identification of Uhp polypeptides and evidence for their role in exogenous induction of the sugar phosphate transport system of *Escherichia coli* K-12. *J. Bacteriol.* 169:3546-3555.
 1173. Wild, J., J. Hennig, M. Lobočka, W. Walczak, and T. Klopotoski. 1985. Identification of the *dadX* gene coding for the predominant isozyme of alanine racemase in *Escherichia coli* K12. *Mol. Gen. Genet.* 198:315-322.
 1174. Wilde, R. J., and J. R. Guest. 1986. Transcript analysis of the citrate synthase and succinate dehydrogenase genes of *Escherichia coli* J. *Gen. Microbiol.* 132:3239-3251.
 1175. Williams, N., D. K. Fox, C. Shea, and S. Roseman. 1986. Pel, the protein that permits λ DNA penetration of *Escherichia coli*, is encoded by a gene in *ptsM* and is required for mannose utilization by the phosphotransferase system. *Proc. Natl. Acad. Sci. USA* 83:8934-8938.
 1176. Willis, D. K., K. E. Fouts, S. D. Barbour, and A. J. Clark. 1983. Restriction nuclease and enzymatic analysis of transposon-induced mutations of the *rac* prophage which affect expression and function of *recE* in *Escherichia coli*. *J. Bacteriol.* 156:727-736.
 1177. Willis, D. K., L. H. Satin, and A. J. Clark. 1985. Mutation-dependent suppression of *recB21 recC22* by a region cloned from the *rac* prophage of *Escherichia coli* K-12. *J. Bacteriol.* 162:1166-1172.
 1178. Willis, H. R., P. T. Chan, and C. L. Turnbough, Jr. 1987.

- Nucleotide sequence and expression of the *pyrC* gene of *Escherichia coli* K-12. *J. Bacteriol.* **169**:3051-3058.
1179. Willis, R. K., T. Brown, and B. A. Roe. 1986. Nucleotide sequence of *pheW*; a third gene for *E. coli* tRNA^{Phe}. *Nucleic Acids Res.* **14**:5937.
 1180. Woisetschlager, M., A. Hoedel-Neuhofer, and G. Hoegenauer. 1988. Localization of the *kdsA* gene with the aid of the physical map of the *Escherichia coli* chromosome. *J. Bacteriol.* **170**:5382-5384.
 1181. Woisetschlager, M., and G. Hoegenauer. 1987. The *kdsA* gene coding for 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase in part of an operon in *Escherichia coli*. *Mol. Gen. Genet.* **207**:369-373.
 1182. Wold, M. S., and R. McMacken. 1982. Regulation of expression of the *Escherichia coli* *dnaG* gene and amplification of the *dnaG* primase. *Proc. Natl. Acad. Sci. USA* **79**:4907-4911.
 1183. Wolfe, P. B., W. Wickner, and J. M. Goodman. 1983. Sequence of the leader peptidase gene of *Escherichia coli* and the orientation of leader peptidase in the bacterial envelope. *J. Biol. Chem.* **258**:12073-12080.
 1184. Wood, D., M. G. Darlison, R. J. Wilde, and J. R. Guest. 1984. Nucleotide sequence encoding the flavoprotein and hydrophobic subunits of the succinate dehydrogenase of *Escherichia coli*. *Biochem. J.* **222**:519-534.
 1185. Wookey, P., and H. Rosenberg. 1978. Involvement of inner and outer membrane components in the transport of iron and in colicin B action in *Escherichia coli*. *J. Bacteriol.* **133**:661-666.
 1186. Wookey, P. J., J. Pittard, S. M. Forrest, and B. E. Davidson. 1984. Cloning of the *tyrP* gene and further characterization of the tyrosine-specific transport system in *Escherichia coli* K-12. *J. Bacteriol.* **160**:169-174.
 1187. Wu, L. F., and M.-A. Mandrand-Berthelot. 1986. Genetic and physiological characterization of new *Escherichia coli* mutants impaired in hydrogenase activity. *Biochimie* **68**:167-179.
 1188. Wu, L.-F., and M.-A. Mandrand-Berthelot. 1987. Characterization of the product of the cloned *fdhF* gene of *Escherichia coli*. *J. Gen. Microbiol.* **133**:2421-2426.
 1189. Wu, L. F., and M.-A. Mandrand-Berthelot. 1987. Regulation of the *fdhF* gene encoding the selenopolypeptide for benzyl viologen-linked formate dehydrogenase in *Escherichia coli*. *Mol. Gen. Genet.* **209**:129-134.
 1190. Wu, T.-H., D. L. Wood, P. L. Stein, and M. M. Comer. 1984. Transcription of a gene cluster coding for two aminoacyl-tRNA synthetases and an initiation factor in *Escherichia coli*. *J. Mol. Biol.* **173**:177-209.
 1191. Wurtzel, E. T., M.-Y. Chou, and M. Inouye. 1982. Osmoregulation of gene expression. I. DNA sequence of the *ompR* gene of the *ompB* operon of *Escherichia coli* and characterization of its gene product. *J. Biol. Chem.* **257**:13685-13691.
 1192. Yamada, H., M. Kitagawa, M. Kawakami, and S. Mizushima. 1984. The gene coding for lipoprotein signal peptidase (*lspA*) and that for isoleucyl-tRNA synthetase (*ileS*) constitute a cotranscriptional unit in *Escherichia coli*. *FEBS Lett.* **171**:245-248.
 1193. Yamada, M., and M. H. Saier, Jr. 1987. Physical and genetic characterization of the glucitol operon in *Escherichia coli*. *J. Bacteriol.* **169**:2990-2994.
 1194. Yamada, M., and M. H. Saier, Jr. 1987. Glucitol-specific enzymes of the phosphotransferase system in *Escherichia coli*. *J. Biol. Chem.* **262**:5455-5463.
 1195. Yamagata, H., K. Daishima, and S. Mizushima. 1983. Cloning and expression of a gene coding for the prolipoprotein signal peptidase of *Escherichia coli*. *FEBS Lett.* **158**:301-304.
 1196. Yamagata, H., N. Taguchi, K. Daishima, and S. Mizushima. 1983. Genetic characterization of a gene for prolipoprotein signal peptidase in *Escherichia coli*. *Mol. Gen. Genet.* **192**:10-14.
 1197. Yamagishi, J.-I., H. Yoshida, M. Yamayoshi, and S. Nakamura. 1986. Nalidixic acid-resistant mutations of the *gyrB* gene of *Escherichia coli*. *Mol. Gen. Genet.* **204**:367-373.
 1198. Yamamoto, Y., T. Ogawa, H. Shinagawa, T. Nakayama, H. Matsuo, and H. Ogawa. 1986. Determination of the initiation sites of transcription and translation of the *uvrD* gene of *Escherichia coli*. *J. Biochem.* **99**:1579-1590.
 1199. Yamao, F., H. Inokuchi, A. Cheng, H. Ozeki, and D. Söll. 1982. *Escherichia coli* glutamyl-tRNA synthetase. I. Isolation and DNA sequence of the *glnS* gene. *J. Biol. Chem.* **257**:11639-11643.
 1200. Yang, J., and J. Pittard. 1987. Molecular analysis of the regulatory region of the *Escherichia coli* *tyrB* gene. *J. Bacteriol.* **169**:4710-4715.
 1201. Yang, S.-Y., J. Li, X.-Y. He, S. D. Cosloy, and H. Schulz. 1988. Evidence that the *fadB* gene of the *fadAB* operon of *Escherichia coli* encodes 3-hydroxyacyl-coenzyme A (CoA) epimerase, Δ^3 -cis- Δ^2 -trans-enoyl-CoA isomerase, and enoyl-CoA hydratase in addition to 3-hydroxyacyl-CoA dehydrogenase. *J. Bacteriol.* **170**:2543-2548.
 1202. Yang, S. Y., and H. Schulz. 1983. The large subunit of the fatty acid oxidation complex from *Escherichia coli* is a multifunctional polypeptide. Evidence for the existence of a fatty acid oxidation operon (*fadAB*) in *Escherichia coli*. *J. Biol. Chem.* **258**:9780-9785.
 1203. Yazyu, H., S. Shiota-Niia, T. Shimamoto, H. Kanazawa, M. Futai, and T. Tsuchiya. 1985. Nucleotide sequence of the *melB* gene and characteristics of deduced amino acid sequence of the melibiose carrier in *Escherichia coli*. *J. Biol. Chem.* **259**:4320-4326.
 1204. Yerkes, J., L. P. Casson, A. K., Honkanen, and G. C. Walker. 1984. Anaerobiosis induces expression of *ant*, a new *Escherichia coli* locus with a role in anaerobic electron transport. *J. Bacteriol.* **158**:180-186.
 1205. Yi, Q.-M., and J. Lutkenhaus. 1985. The nucleotide sequence of the essential cell-division gene *ftsZ* of *Escherichia coli*. *Gene* **36**:241-247.
 1206. Yi, Q.-M., S. Rockenbach, J. E. Ward, Jr., and J. Lutkenhaus. 1985. Structure and expression of the cell-division genes *ftsQ*, *ftsA*, and *ftsZ*. *J. Mol. Biol.* **184**:399-412.
 1207. Yin, K.-C., A. Blinkowa, and J. R. Walker. 1986. Nucleotide sequence of the *Escherichia coli* replication gene *dnaZX*. *Nucleic Acids Res.* **14**:6541-6550.
 1208. Yoshida, H., T. Kojima, J. Yamagishi, and S. Nakamura. 1988. Quinolone-resistant mutations of the *gyrA* gene of *Escherichia coli*. *Mol. Gen. Genet.* **211**:1-7.
 1209. Yoshikawa, A., S. Isono, A. Sheback, and K. Isono. 1987. Cloning and nucleotide sequencing of the genes *rimI* and *rimJ* which encode enzymes acetylating ribosomal proteins S18 and S5 of *Escherichia coli* K12. *Mol. Gen. Genet.* **209**:481-488.
 1210. Yoshimura, M., H. Inokuchi, and H. Ozeki. 1984. Identification of transfer RNA suppressors in *Escherichia coli*. IV. Amber suppressor Su⁺6 a double mutant of a new species of leucine tRNA. *J. Mol. Biol.* **177**:627-644.
 1211. Yoshimura, M., M. Kimura, M. Ohno, H. Inokuchi, and H. Ozeki. 1984. Identification of transfer RNA suppressors in *Escherichia coli*. III. Ochre suppressor of lysine tRNA. *J. Mol. Biol.* **177**:609-625.
 1212. Yu, F., H. Yamada, K. Daishima, and S. Mizushima. 1984. Nucleotide sequence of the *lspA* gene, the structural gene for lipoprotein signal peptidase of *Escherichia coli*. *FEBS Lett.* **173**:264-268.
 1213. Yura, T., T. Tobe, K. Ito, and T. Osawa. 1984. Heat shock regulatory gene (*htrP*) of *Escherichia coli* is required for growth at high temperature but is dispensable at low temperature. *Proc. Natl. Acad. Sci. USA* **81**:6803-6807.
 1214. Zakin, M. M., N. Duchange, P. Ferrara, and G. N. Cohen. 1983. Nucleotide sequence of the *metL* gene of *Escherichia coli*. Its product, the bifunctional aspartokinase II-homoserine dehydrogenase II, and the bifunctional product of the *thrA* gene, aspartokinase I-homoserinedehydrogenase-I, derive from a common ancestor. *J. Biol. Chem.* **158**:3028-3031.
 1215. Zengel, J. M., R. H. Archer, and L. Lindahl. 1984. The nucleotide sequence of the *Escherichia coli* *fus* gene, coding for elongation factor G. *Nucleic Acids Res.* **12**:2181-2192.
 1216. Zhang, J., and M. P. Deutscher. 1988. Cloning, characteriza-

- tion, and effects of overexpression of the *Escherichia coli* *rnd* gene encoding RNase D. *J. Bacteriol.* **170**:522–527.
1217. **Zhu, Y., and E. C. C. Lin.** 1988. A mutant *crp* allele that differentially activates the operons of the *fuc* regulon in *Escherichia coli*. *J. Bacteriol.* **170**:2352–2358.
1218. **Zimmerman, L., K. Hantke, and V. Braun.** 1984. Exogenous induction of the iron dicitrate transport system of *Escherichia coli* K-12. *J. Bacteriol.* **159**:271–277.
1219. **Zinkewich-Péotti, K., and J. M. Fraser.** 1988. New locus for exopolysaccharide overproduction in *Escherichia coli* K-12. *J. Bacteriol.* **170**:1405–1407.
1220. **Zinoni, F., A. Birkmann, W. Leinfelder, and A. Böck.** 1987. Cotranslational insertion of selenocysteine into formate dehydrogenase from *Escherichia coli* directed by a UGA codon. *Proc. Natl. Acad. Sci. USA* **84**:3156–3160.
1221. **Zinoni, F., A. Birkmann, T. C. Stadtman, and A. Böck.** 1986. Nucleotide sequence and expression of the selenocysteine-containing polypeptide of formate dehydrogenase (formate-hydrogen-lyase-linked) from *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **83**:4650–4654.
1222. **Zurawski, G., and S. M. Zurawski.** 1985. Structure of the *Escherichia coli* S10 ribosomal protein operon. *Nucleic Acids Res.* **13**:4521–4526.