

Functions of the Gene Products of *Escherichia coli*

MONICA RILEY

Marine Biological Laboratory, Woods Hole, Massachusetts 02543

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INTRODUCTION

A substantial fraction of the genes and open reading frames of *Escherichia coli*, in the neighborhood of half the estimated whole, have been identified and mapped to either a genetic map (76) or a physical map (163, 1058a, 1377, 1378, 1380, 1381). The products of most of these genes have been identified, and main cellular functions of many products are known. Sequencing projects are yielding sequences of large continuous segments of the genome (see, e.g., references 331 and 1810). Some of the genes defined by sequence as open reading frames are presumed to have functions similar to those of known genes of similar sequence. These presumptions of function will have to be tested by experiment. Other open reading frames have unique sequence not similar to other sequences in current data banks (331, 1810). Therefore there are overlapping sets of genes of *E. coli*, some mapped, some sequenced, some with known function, and some not.

The sequence of the entire *E. coli* genome is expected to be in hand in a few years. It may be useful, then, at this intermediate juncture to step back and look with perspective at the sum of what we know today about the genetic determination of the *E. coli* cell and its physiological functions. This compilation essentially updates an earlier classification of *E. coli* genes and gene products by metabolic and physiological categories (710).

When all of the genes of the *E. coli* chromosome and the function of each gene product are known, we will have before us a list of all the genetic and biochemical ingredients that together make up a functioning and self-perpetuating free-living organism. Further in the future, we will under-

stand all of the complex interrelated regulation systems that allow the genes and gene products to carry out their functions in a coordinated way, making it possible for the cell not only to live and perpetuate itself but also to adapt appropriately to changing circumstances.

For the present, we can ask, "How far have we come, and how far have we yet to go in the task of understanding completely the genetic determination of the biology of a single cell?" *E. coli* is a useful tool in this connection not because it is among the simplest of free-living organisms (other bacteria have smaller genomes and more limited biochemistry) but because more is known both genetically and biochemically about *E. coli* than about any other single-celled organism.

The aim of this article is to summarize present knowledge of the gene products of *E. coli* and their functions in the cell. Three sources were used as the starting point for this compilation. One is the listing and bibliography of *E. coli* genes, phenotypes, and gene products prepared by Barbara Bachmann and based on the literature through mid-1988 (76). Another is a set of data on genes kindly provided by Kenneth E. Rudd and his associate, Gerard Bouffard, constituting a subset of the physical map and sequence data assembled in the course of constructing data bases of the genome of *E. coli* (163, 1377, 1380). Finally, the primary literature was consulted directly, often with the aid of the Medline data base, with emphasis on the last 6 years.

DATA BASE OF GENES AND GENE PRODUCTS

I have assembled a database, EcoGeneFunction, in Microsoft Foxpro2 (MS-DOS) with the following information: gene name, synonyms, gene product (or a phenotype), for enzymes the EC number for the class of enzyme and the reaction catalyzed, the categories of cellular function(s) of the gene product, the type of gene (e.g., regulatory, coding

* Corresponding author. Electronic mail address: mriley@ohm.mbl.edu.

for an enzyme), literature references, and information on duplicate or redundant gene products. An electronic version of the data base suitable for distribution will be prepared and will be available either on a DOS diskette or at the gopher of the Marine Biological Laboratory on crane.mbl.edu. Kindly contact me for more information.

Selection of Genes

All of the genes and gene products listed in the most recent Bachmann genetic map (76) are included in this data base (although some of the names are now synonyms). To maintain continuity with past compilations, all genes listed in the 1990 Bachmann map are retained. No entry in that work is excluded, even though information on the products of some of the genes was limited to a description of a mutant phenotype. In time, no doubt many of the early descriptions will be replaced by more precise definitions. Added to the Bachmann list are new genes identified after that compilation. These genes are treated differently. In this case new genes are included only if their gene products or cellular roles have been delineated well enough to support classification of the cellular function of the gene product. Thus recently reported open reading frames and genes whose products have not yet been well defined are not included here.

There were 1,403 listings in the 1990 Bachmann compilation. Some of the entries were redundant, such as some suppressor genes and the corresponding tRNA designations. In the data base described here, these double entries are reduced to one entry each. Also, *rrn* loci are not listed; only their component RNA genes are given. Some genes do not appear in their original position in the list because they have been renamed or redefined, and two genes, *pyrS* and *guaR*, have been removed. After these revisions, the Bachmann compilation was reduced to 1,356 genes of which 23 represent sites that generate no gene product (2 Ori, 4 Ter, 4 Rhs, and 13 phage attachment sites).

To this group were added 361 newly characterized genes, some derived from Rudd's EcoGene6 data base (1379, 1380) and some derived from recent literature. The new genes that were added were those for which the gene product has been, at least in gross terms, identified. No open reading frames whose function was identified only through sequence similarity were included. A total of 1,717 gene products are listed in Table 2, collected through 1992.

Gene Names

For the sake of consistency, the gene names used in Table 2 are the same as those used by Rudd (1377-1379). Older, synonymous gene names are given, including the cumulative list of designations given in the most recent genetic map (76).

Functional Categories

The gene products were categorized according to their function, by using the classification system of cell functions shown in Table 1. (The right-hand column of numbers of genes in Table 1 does not apply to the immediate discussion but will be covered in the section, Apportionment of Resources.) This classification scheme is arbitrary; there is of course no single, correct way to catalog cellular functions

and structures as they relate to gene products. What is presented here is only one version from many possible. However flawed it may be, the scheme will serve the purpose of providing an interim overview. The categories are sufficiently small that rearrangement into other schemes for other purposes should not be too difficult.

Some of the arbitrary elements of the scheme stem from the fact that some categories emphasize structure and some emphasize function, leading to some imprecision and overlap. For instance, the outer and inner membranes and the murein sacculus are structural elements of the cell, classified in the category Cell Structure. However, some of the enzymes for synthesis of peptidoglycans could have been put instead into the category of Macromolecule Synthesis. In the opposite direction, there are constituents of the cell membrane that could have been classified as structural elements but, since they carry out important cell processes, were classified by function instead. Some of these are porins that function as channels for traverse of small molecules in and out of the cell, outer membrane proteins that respond to the osmotic strength of the surrounding milieu, or components of the electron transport system. Such membrane components were placed in various categories for cellular processes and metabolic function rather than in the category Cell Structure. Clearly, the classification scheme used in this exercise did not avoid such ambiguities, and the assignments of gene products were arbitrary, perhaps even idiosyncratic.

Ambiguity of classification also occurs with all enzymes that perform more than one metabolic role. Some enzymes play several quite different metabolic roles. Carbamyl phosphate synthase, for example, catalyzes a reaction used in both pyrimidine synthesis and arginine synthesis. The product of the *trxB* gene, the enzyme ribonucleotide reductase, not only reduces ribonucleotides to deoxyribonucleotides but also reduces sulfate ions and methionine sulfoxide and carries out general sulfide reduction. Therefore, in classifying gene products, it was sometimes necessary to make arbitrary decisions. In the data base EcoGeneFunction, up to four different roles for gene products were assigned when appropriate. One role was arbitrarily chosen as the primary assignment, and others were defined as subsidiary. Only one of these assignments of function was used to establish the organization of the data that is presented in Table 2.

Another factor of complexity is that the metabolic role of a reaction may depend on environmental and nutritional conditions. As an example, glycerol kinase can function as the first enzyme in the utilization of externally supplied glycerol as a carbon source, but in another context glycerol kinase carries out an essential early step in the pathway of fatty acid synthesis, supplying glycerol 3-phosphate as a needed intermediate. Therefore, whether the role of glycerol kinase is catabolic or synthetic depends on whether the cell is growing on glycerol as a carbon source and whether it is actively synthesizing fatty acids *de novo*. Similarly, the reaction catalyzed by acetate kinase can be a reaction in the final steps of metabolism of glucose fermentation or can be an early step in the utilization of acetate as a carbon source. In the first case we would call this a reaction of fermentation, whereas in the second case it would be a degradative reaction.

To determine the major function of a gene product, one might look to the regulatory organization of genes in the cell as a true measure of the relatedness of gene functions and the primary cellular function of gene products. However, this approach is not used for this data base since some operons are composed of member genes that seem only

TABLE 1. Classification of *E. coli* gene products

Category of function	No. of genes
I. Intermediary metabolism	
A. Degradation	175
B. Central intermediary metabolism	54
C. Respiration (aerobic and anaerobic)	55
D. Fermentation	39
E. ATP-proton motive force interconversion.....	9
F. Broad regulatory functions	43
II. Biosynthesis of small molecules	
A. Amino acids	
1. Glutamate family/nitrogen assimilation	23
2. Aspartate family, pyruvate family	53
3. Glycine-serine family/sulfur metabolism.....	17
4. Aromatic amino acid family	24
5. Histidine	9
B. Nucleotides	
1. Purine ribonucleotides	20
2. Pyrimidine ribonucleotides	11
3. 2'-Deoxyribonucleotides	7
4. Salvage and interconversions	19
C. Sugars and sugar nucleotides	13
D. Cofactors, prosthetic groups, electron carriers	
1. Biotin	8
2. Folic acid	9
3. Lipoate	2
4. Molybdopterin	5
5. Pantothenate	4
6. Pyridoxine	4
7. Pyridine nucleotides	5
8. Thiamine	11
9. Riboflavin	3
10. Thioredoxin, glutaredoxin, and glutathione	5
11. Menaquinone and ubiquinones	15
12. Heme and porphyrins	11
E. Fatty acids and lipids	35
F. Polyamines	6
III. Macromolecule metabolism	
A. Synthesis and modification	
1. Ribosomal and "stable" RNAs	25
2. Ribosomal proteins and their modification.....	64
3. Ribosomes and their maturation and modification	8
4. tRNAs, aminoacyl-tRNA synthetases and their modification.....	133
5. RNA synthesis, modification, and DNA transcription	19
6. Basic proteins	4
7. DNA replication, restriction/modification, recombination, and repair	99
8. Proteins (translation and modification).....	22
9. Polysaccharides (cytoplasmic).....	5
B. Degradation of macromolecules	
1. RNA	12
2. DNA	8
3. Proteins	20
IV. Cell structure	
A. Membrane components	20
B. Murein sacculus.....	36
C. Surface polysaccharides and antigens	35
D. Surface structures	50

Continued

TABLE 1—Continued

Category of function	No. of genes
V. Cellular processes	
A. Transport/binding proteins	216
B. Cell division	33
C. Chemotaxis and mobility	15
D. Protein secretion	19
E. Osmotic adaptation	21
VI. Other functions	
A. Cryptic genes	31
B. Phage-related functions and prophages.....	31
C. Colicin-related functions.....	16
D. Plasmid-related functions	5
E. Drug/analog sensitivity	35
F. Radiation sensitivity	4
G. DNA sites	20
H. Adaptations to atypical conditions	20

remotely connected in metabolic terms. One example is the operon containing *pdxA*, which codes for an enzyme in the pathway of pyridoxine synthesis; *ksgA*, which codes for a methyltransferase that acts on RNA; *apaG*, a gene of unknown function; and *apaH*, the gene for diadenosine tetraphosphatase (1344). Another mixed operon contains the *pdxB* gene; *asd'* (a homolog of an aspartate semialdehyde dehydrogenase gene); *hisT*, the gene which codes for a tRNA modification enzyme pseudouridine synthase; and *dedA*, a gene which codes for a membrane protein (1440). Yet another example is the operon containing *serC*, which codes for 3-phosphoserine aminotransferase, an enzyme in the pathway of serine synthesis; and *aroA*, which codes for 5-enolpyruvylshikimate 3-phosphate synthase, an enzyme in the pathway of synthesis of aromatic amino acids (412). A goal for information systems will be to connect information on regulatory relationships among genes and gene products with representations of the biochemistry of *E. coli*. The classification scheme of Table 1 does not yet make use of regulatory relationships.

Gene Products and Phenotypes

The information available in the cited literature for the genes in Table 2 is not all of the same type. The level of our understanding of *E. coli* gene products is extremely variable from gene to gene. For some, the gene product has been well characterized physically and biochemically and the function in the cell is well understood. For others, the gene product has been identified but its role in the cell is not fully understood. For some, tentative function assignments have been made on the basis of sequence similarities. For still others, a gene is defined only broadly by a mutant phenotype. Phenotypic descriptions of organisms carrying either mutant or wild-type alleles do not always reveal the identity of the underlying gene product. For instance, drug resistance can be conferred by a mutant ribosomal protein, a mutant RNA polymerase subunit, or a mutant transport component. The root cause of radiation sensitivity or resistance or high rates of spontaneous mutation can reside in any one of several DNA repair processes. Complex phenotypes are often difficult to penetrate. Clearly, as mutants and gene products are defined more precisely and information on the metabolic function of gene products becomes more exact,

some of the assignments of category of function made in this compilation will have to be changed to be more nearly correct.

Citations

The focus of the bibliography provided here is the gene product rather than the gene. Primary literature citations have been collected in the cumulative lists compiled by Bachmann over the years (75, 76) for many *E. coli* genes, with a focus on their genetic map positions. More recently, citations have been collected on physical maps and sequences of *E. coli* genes in a number of data bases, including the review by Danchin (1058a) and in the work of Rudd (163, 1377, 1378, 1380, 1381) and others. In Table 2 the citations focus on the function of the gene product. There is some overlap with other bibliographies, as when the sequence gives most of the information we have on the function of the gene product and in the cases when little work has been reported since isolation and mapping of mutant alleles many years ago.

There is great unevenness in the extent and depth of knowledge of the many gene products of *E. coli*. The present state of knowledge about any given gene product ranges from having full biochemical characterization and X-ray patterns of the molecular structure to the other extreme, having only a phenotype connected to the gene with no indication of the nature of the gene product. Between these extremes are many states. For some enzymes, known for decades, the catalyzed reactions have been studied in detail and activators and inhibitors and their sites of action are known; for some other enzymes, sequences have been determined and directed mutagenesis has given information on biochemical interactions of individual amino acid residues at catalytic sites, binding sites, and regulatory sites. Other enzymes have not yet been isolated or purified, and the main source of information about the properties of the protein is the nucleotide sequence of the gene and its translated amino acid sequence. For still others, neither gene nor enzyme has been isolated, and a metabolic or cellular process has been assigned to the gene by reasoning from the properties of mutants. The same unevenness in the state of knowledge is found for other cellular components.

In some cases, little research as been done over the years and the citations collected in cumulative reviews by Bachmann (75, 76) remain the most pertinent. In other cases, there is a large literature and the few citations in Table 2 (arbitrarily no more than three per entry) constitute only a sample of a large literature and are not intended to be inclusive.

APPORTIONMENT OF *E. COLI* GENETIC RESOURCES

Table 2 shows the broad outlines of the apportionment of *E. coli* genetic resources to different kinds of cellular activities or cell substance (keeping in mind that there is a degree of ambiguity and arbitrary choice in the classification system applied). The numbers of genes located in each category are shown in the righthand column of Table 1. The percentage of genes listed here that are devoted to each of the main categories of functions is summarized in Table 3.

In the category of small-molecule metabolism, the number of gene products concerned with degradation and with interconversion of metabolites is relatively large. This seems

to reflect the versatility of *E. coli* in its ability to derive energy and building blocks from many different starting compounds by using separate specialized pathways that each feed into the main central degradation pathways. As to biosynthesis, the number of genes required to specify enzymes for biosynthesis of small molecules is of the same order as the number of genes used in degradative pathways and intermediary metabolism (Table 3).

The number of gene products devoted to the metabolism of macromolecules is larger than the number devoted to any one of the small-molecule categories but smaller than the sum of the two major small-molecule categories (Table 3). On the whole there are no surprises here in the balance of genetic resources devoted to small and large molecules, even though the sample of *E. coli* genes and gene products analyzed here may constitute only half or less of the total number.

Within the category of metabolism of macromolecules, tRNAs and their amino acid synthetases require relatively large proportions of the coding functions of *E. coli* so far identified. The size of the tRNA category is a consequence of the redundancy of the code and also of many instances of replicate tRNA genes. The next largest component in macromolecule metabolism is that of DNA replication, recombination, repair and restriction/modification, reflecting the importance of the care, maintenance, and promulgation of hereditary material.

As this catalog has been arranged, a smaller number of genes encode structural materials of the cell, although, as noted above, some structural elements have been classified by their function; therefore the category of genes encoding components of cell structure is reduced in size. In the category of cellular functions as defined here, a large fraction is that of transport proteins (including a few other binding proteins of various functions). The size of this group emphasizes the importance of the gateways between the exterior environment and the interior of the cell. This group of genes encodes the molecules that transport specific molecules into the cell, excrete other molecules, and maintain a balance of such critical ions as sodium and potassium.

The last group in Table 1 is a catchall. Only modest numbers of genes have been assigned to these "other-function" categories. Genes of cryptic operons are listed here, as are genes related to external genetic elements such as phages and plasmids and also the DNA sites for which there is no gene product. The genes described as conferring sensitivity to drugs or radiation or as being involved in adaptation to atypical conditions are genes that may well be reclassified into more definitive categories when the identity and mechanism of action of their gene products are more clearly defined.

DISTRIBUTION OF TYPES OF GENES

Table 4 classifies the genes listed here by type of gene product, if that has been determined, or notes them as known at the level of phenotype only if the gene product has not been determined. Despite the massive research attention *E. coli* receives from a large number of scientists, the category of genes known only by phenotype remains very large, about 15% of the total. One hopes that members of this class will receive concentrated attention in the future so that their cellular functions can be better understood and the category of genes defined only by phenotypes can shrink toward zero.

Among the various types of gene products that have been

TABLE 2. *E. coli* genes grouped by function

Gene	Synonym	Gene product and description	Reference(s)
I. Intermediary metabolism			
A. Degradation			
<i>aceE</i>	<i>aceE1</i>	Pyruvate dehydrogenase (decarboxylase component) (EC 1.2.4.1)	556
<i>aceF</i>	<i>aceE2</i>	Pyruvate dehydrogenase (dihydrolipoyltransacetylase component) (EC 2.3.1.12)	1389, 1447, 1448
<i>ackA</i>		Acetate kinase activity (EC 2.7.2.1)	1037, 1714
<i>ackB</i>		Acetate kinase activity (EC 2.7.2.1)	1233
<i>adi</i>		Arginine decarboxylase, degradative periplasmic glucose-1-phosphatase (EC 3.1.3.10)	1544
<i>agp</i>			1286
<i>amyA</i>		α -Amylase (EC 3.2.1.1)	1308
<i>ansA</i>		Cytoplasmic L-asparaginase I (EC 3.5.1.1); isozyme	743
<i>ansB</i>		Cytoplasmic L-asparaginase II (EC 3.5.1.1); isozyme	154, 742
<i>appA</i>		pH 2.5 acid phosphatase (EC 3.1.3.2); exopolyphosphatase (EC 3.6.1.11)	337, 338
<i>araA</i>		L-Arabinose isomerase (EC 5.3.1.4)	898, 946
<i>araB</i>		Ribulokinase (EC 2.7.1.16)	898, 946
<i>araC</i>		Activator and repressor protein for <i>ara</i>	897, 975, 1069
<i>araD</i>		L-Ribulosephosphate 4-epimerase (EC 5.1.3.4)	898
<i>asu</i>		Asparagine utilization, as sole nitrogen source	258
<i>atoA</i>		Acetyl-CoA:acetoacetyl-CoA transferase (EC 2.8.3.-) β -subunit	741, 1237
<i>atoB</i>		Acetyl-CoA acetyltransferase (EC 2.3.1.9)	741, 1237
<i>atoC</i>		Positive regulator of <i>ato</i>	740, 741, 1237
<i>atoD</i>		Acetyl-CoA:acetoacetyl-CoA transferase (EC 2.8.3.-) α -subunit?	741, 1237
<i>cadA</i>		Lysine decarboxylase (EC 4.1.1.18)	1066, 1720
<i>cadC</i>		Transcriptional activator of <i>cad</i> operon	1720
<i>cxm</i>	<i>cxr</i>	Methylglyoxal biosynthesis	806
<i>cynR</i>		<i>cyn</i> operon positive regulator	40, 1571
<i>cynS</i>	<i>cnt</i>	Cyanate aminohydrolase (EC 3.5.5.3), cyanase	40, 578, 959
<i>dadA</i>	<i>dadR</i>	D-Amino acid dehydrogenase subunit (EC 1.4.99.1)	1752
<i>dadB</i>	<i>alnA</i>	D-Amino acid dehydrogenase subunit (EC 1.4.99.1)	481
<i>dadQ</i>	<i>alnR</i>	Regulator of <i>dad</i> regulon	481
<i>dgd</i>		D-Galactose dehydrogenase (EC 1.1.1.48)	967
<i>dgoA</i>		2-Oxo-3-deoxygalactonate 6-phosphate aldolase (EC 4.1.2.21)	298
<i>dgoD</i>		Galactonate dehydratase (EC 4.2.1.6)	298
<i>dgoK</i>		2-Oxo-3-deoxygalactonate kinase (EC 2.7.1.58)	298
<i>dgoR</i>		Regulator of <i>dgo</i> operon	298
<i>dgt</i>		Deoxyguanosine triphosphate triphosphohydrolase (EC 3.1.5.1)	1305, 1306, 1780
<i>dsdA</i>		D-Serine deaminase (EC 4.2.1.14)	1018-1020
<i>dsdC</i>		Activator for <i>dsdA</i>	1216
<i>eda</i>	<i>kdgA, kga</i>	2-Keto-3-deoxygluconate 6-phosphate aldolase (EC 4.1.2.14); 2-keto-4-hydroxyglutarate aldolase (EC 4.1.3.16)	419, 1235
<i>edd</i>		Phosphogluconate dehydratase (EC 4.2.1.12)	419
<i>eno</i>		Enolase (EC 4.2.1.11)	714
<i>eutB</i>		Ethanolamine-ammonia lyase heavy chain (EC 4.3.1.7)	749, 750, 1177
<i>eutC</i>		Ethanolamine-ammonia lyase light chain (EC 4.3.1.7)	749, 750, 1177
<i>exuR</i>		Negative regulator of <i>exu</i> regulon, <i>exuT</i> , <i>uxaAC</i> , and <i>uxuB</i>	142
<i>fadA</i>		Thiolase I (EC 2.3.1.16)	1796
<i>fadB</i>	<i>oldA, oldB</i>	3-Hydroxyhydroxyacyl-CoA dehydrogenase (EC 1.1.1.35), 3-hydroxyacyl-CoA epimerase (EC 5.1.2.3), $\delta(3)-cis-\delta(2)-trans$ -enoyl-CoA isomerase (EC 5.3.3.8)	1795, 1797
<i>fadD</i>	<i>oldD</i>	Enoyl-CoA-hydrolase (crotonase) (EC 4.2.1.17)	135
<i>fadE</i>		Acyl-CoA synthetase (EC 6.2.1.3)	270, 1204
<i>fadH</i>		Electron transport flavoprotein (ETF) of β -oxidation	1806
<i>fatA</i>		2,4-Dienoyl-CoA reductase (EC 1.3.1.34)	378
<i>fba</i>	<i>ald, fda</i>	Utilization of <i>trans</i> -unsaturated fatty acids	17, 592, 1138
<i>fruK</i>	<i>fpk</i>	Fructose-bisphosphate aldolase, class II (EC 4.1.2.13)	1194
<i>fruL</i>		Fructose-1-phosphate kinase (EC 2.7.1.56)	736
<i>fruR</i>	<i>fruC, shl</i>	<i>fruR</i> leader peptide	513, 736, 890
<i>fruS</i>		Repressor of <i>fru</i> operon	153
<i>fucA</i>	<i>fucC, prd</i>	Regulator of <i>fucA</i> and <i>fucF</i>	250, 1827
<i>fucI</i>		L-Fuculose-1-phosphate aldolase (EC 4.1.2.17)	250
<i>fucK</i>		L-Fucose isomerase (EC 5.3.1.-)	250
<i>fucO</i>		L-Fuculokinase (EC 2.7.1.51)	250
<i>fucR</i>		L-1,2-Propanediol oxidoreductase (EC 1.1.1.77)	295
		Positive regulator of the <i>fuc</i> operon	251, 987

Continued on following page

TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>galK</i>	<i>galA</i>	Galactokinase (EC 2.7.1.6)	1691
<i>galM</i>		Aldose-1-epimerase (mutarotase) (EC 5.1.3.3)	1032
<i>galR</i>	<i>Rgal</i>	Repressor of <i>galETK</i> operon	326
<i>galS</i>		Second <i>gal</i> repressor	1727
<i>gapA</i>	<i>gad</i>	Glyceraldehyde-3-phosphate dehydrogenase A (EC 1.2.1.12)	638, 713
<i>gapB</i>		Glyceraldehyde 3-phosphate dehydrogenase B (EC 1.2.1.12)	18, 398
<i>garA</i>		Glucarate utilization	1349
<i>garB</i>		Glucarate utilization	1349
<i>gatC</i>		Regulator of <i>gat</i>	905
<i>gatD</i>		Galactitol-1-phosphate dehydrogenase	368, 905
<i>gcd</i>		Glucose dehydrogenase (EC 1.1.99.17)	278
<i>gcl</i>		Glyoxylate carboligase (EC 4.1.1.47)	236
<i>gcvA</i>		Positive regulator of <i>gcv</i>	1760
<i>gcvH</i>	<i>gcv</i>	H protein of glycine cleavage complex, carrier of aminomethyl moiety (EC 1.4.4.2)	1263, 1535, 1538
<i>gcvP</i>		Glycine decarboxylase, P protein of glycine cleavage system (EC 1.4.4.2)	1263, 1538
<i>gcvT</i>		T protein (tetrahydrofolate dependent) of glycine cleavage system	1263, 1538
<i>glc</i>		Malate synthase G (EC 4.1.3.2)	1670
<i>glk</i>		Glucokinase (EC 2.7.1.2)	318
<i>glpQ</i>		Glycerophosphodiester diesterase (EC 3.1.4.46)	881, 1628
<i>gntR</i>		Regulator of <i>edd</i> ; transport and phosphorylation of gluconate	74, 280
<i>gntV</i>		Gluconokinase, thermosensitive	280, 719
<i>gpm</i>		Phosphoglyceromutase (EC 2.7.5.3)	162
<i>gurB</i>	<i>crp?</i>	Utilization of methyl-β-D-glucuronide; <i>crp?</i>	1549
<i>gurC</i>		Utilization of methyl-β-D-glucuronide	1549
<i>gurD</i>		Utilization of methyl-β-D-glucuronide	1549
<i>hga</i>		2-Keto-4-hydroxyglutarate aldolase (EC 4.1.3.16)	1235
<i>kba</i>		Ketose-bisphosphate aldolase (EC 4.1.2.13)	1243
<i>kdgK</i>		Ketodeoxygluconokinase (EC 2.7.1.45)	1285
<i>kdgR</i>		Regulator of <i>kdgK</i> , <i>kdgT</i> , and <i>eda</i>	1285
<i>lacA</i>	<i>a, lacAc</i>	Galactoside acetyltransferase (EC 2.3.1.18)	43
<i>lacI</i>	<i>i</i>	Repressor of the <i>lac</i> operon	805, 826
<i>lacZ</i>	<i>z</i>	β-D-Galactosidase (EC 3.2.1.23)	511
<i>mac</i>		Maltose acetyltransferase, broad specificity (EC 2.3.1.-)	173
<i>malM</i>	<i>molA</i>	Periplasmic protein of <i>mal</i> operon	536, 1370
<i>malP</i>	<i>malA</i>	Maltodextrin phosphorylase (EC 2.4.1.1)	1432
<i>malQ</i>	<i>malA</i>	Amylomaltase (EC 2.4.1.25)	1300
<i>malS</i>		α-Amylase (EC 3.2.1.1)	1435
<i>malT</i>	<i>malA</i>	Positive regulator of <i>mal</i> regulon	1435
<i>malY</i>		Enzyme that may degrade or block biosynthesis of endogenous <i>mal</i> inducer	1324
<i>malZ</i>		Maltodextrin glucosidase (EC 3.2.1.20)	1435
<i>manC</i>	<i>mni</i>	D-Mannose isomerase regulation; utilization of D-lyxose	1542
<i>maoA</i>	<i>tynA</i>	Tyramine oxidase (EC 1.4.3.4)	1131, 1791
<i>melA</i>	<i>mel-7</i>	α-Galactosidase (EC 3.2.1.22)	944, 1134, 1283
<i>melR</i>		Regulator of melibiose operon	1724
<i>mtlC</i>		Regulator for <i>mtl</i> 906, 907, 1506	
<i>mtlD</i>		Mannitol-1-phosphate dehydrogenase (EC 1.1.1.17)	1608
<i>nlp</i>	<i>sfs7</i>	<i>crp</i> *-dependent stimulation of <i>malPQ</i> and <i>lacZ</i> , similar to <i>Ner</i> protein of phage Mu?	265
<i>pac</i>		Penicillin acylase, detaches phenylacetate residue	104, 1072
<i>pat</i>		Putrescine aminotransferase activity	1293
<i>pfkA</i>		6-Phosphofructokinase I (EC 2.7.1.11)	379, 380, 851
<i>pfkB</i>		6-Phosphofructokinase II; suppressor of <i>pfkA</i> (EC 2.7.1.11)	73, 579
<i>pga</i>		Penicillin G acylase (EC 3.5.1.11)	261, 1182
<i>pgi</i>		Glucosephosphate isomerase (EC 5.3.1.9)	488
<i>pgk</i>		Phosphoglycerate kinase (EC 2.7.2.3)	1151
<i>pgm</i>		Phosphoglucomutase (EC 5.4.2.2)	1286
<i>phnD</i>	<i>psiD</i>	Carbon-phosphorus lyase	1009, 1075, 1713
<i>phnF</i>		Utilization of phosphorus-containing compounds	1075, 1713
<i>phnG</i>		Utilization of phosphorus-containing compounds	1009, 1075, 1713
<i>phnH</i>		Utilization of phosphorus-containing compounds, C-P lyase component?	1009, 1075, 1713
<i>phnI</i>		Utilization of phosphorus-containing compounds	1009, 1075, 1713
<i>phnJ</i>		Utilization of phosphorus-containing compounds, C-P lyase component?	1009, 1075, 1713

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>phnK</i>		Utilization of phosphorus-containing compounds, C-P lyase component?	1009, 1075, 1713
<i>phnL</i>		Utilization of phosphorus-containing compounds, probable regulator	1009, 1075, 1713
<i>phnM</i>		Utilization of phosphorus-containing compounds	1009, 1075, 1713
<i>phnN</i>		Utilization of phosphorus-containing compounds	1009, 1075, 1713
<i>phnO</i>		Utilization of phosphorus-containing compounds, probably a regulator	1009, 1075, 1713
<i>phnP</i>		Utilization of phosphorus-containing compounds, C-P lyase component?	1009, 1075, 1713
<i>phoA</i>		Alkaline phosphatase (EC 3.1.3.1)	372
<i>phoP</i>		Response regulator for <i>phoA</i> (sensor, <i>phoQ</i>)	570, 783
<i>phoQ</i>		Sensor for <i>phoP</i> , histidine protein kinase	783
<i>poaR</i>		Regulation of proline oxidase production	290
<i>poxA</i>		Regulator for <i>poxB</i>	1671
<i>poxB</i>		Pyruvate oxidase (EC 1.2.2.2)	554, 1706
<i>ppr</i>		Propionate metabolism	1518
<i>psiF</i>		Induced by phosphate starvation	1074, 1712
<i>pta</i>		Phosphotransacetylase (EC 2.3.1.8) activity	580, 1296
<i>putA</i>	<i>poaA</i>	Proline dehydrogenase (EC 1.5.99.8)	1767
<i>pykA</i>		Pyruvate kinase II, glucose stimulated (EC 2.7.1.40)	1059, 1664
<i>pykF</i>		Pyruvate kinase I (formerly F), fructose stimulated (EC 2.7.1.40)	1183, 1514
<i>rbsK</i>		Ribokinase (EC 2.7.1.15)	37, 662
<i>rbsR</i>		Regulator for <i>rbs</i>	983
<i>rhaA</i>		L-Rhamnose isomerase (EC 5.3.1.14)	78
<i>rhaB</i>		Rhamnulokinase (EC 2.7.1.5)	78
<i>rhaD</i>		Rhamnulosephosphate aldolase (EC 4.1.2.19)	78
<i>rhaR</i>	<i>rhaC</i>	Positive regulator for <i>rha</i>	1623, 1624
<i>rhaS</i>	<i>rhaC</i>	Positive regulator for <i>rha</i>	1623
<i>rpiA</i>		Ribosephosphate isomerase (EC 5.3.1.6), constitutive	1498
<i>sdaA</i>		L-Serine deaminase (EC 4.2.1.13)	1018, 1562, 1563
<i>sdaB</i>		L-Serine deaminase, L-SD2 (EC 4.2.1.13)	1562
<i>srlD</i>	<i>gutD, sbl</i>	Glucitol (sorbitol)-6-phosphate dehydrogenase (EC 1.1.1.140)	1788
<i>srlM</i>	<i>gutM</i>	Glucitol operon activator	1788
<i>srlR</i>	<i>gutR</i>	Regulator for <i>srl</i>	1788
<i>tdcA</i>	<i>tdc</i>	Threonine dehydratase (EC 4.2.1.16)	1452
<i>tdcB</i>		Threonine dehydratase, catabolic (EC 4.2.1.16)	549, 650, 1452
<i>tdcR</i>		Threonine dehydratase operon activator protein	1451
<i>tdh</i>		Threonine dehydrogenase (EC 1.1.1.103)	62, 307, 441
<i>thdA</i>		Sulfone and sulfoxide oxidase activity	754
<i>thdC</i>		Protection against furans and thiophenes	754
<i>thdD</i>		Protection against furans and thiophenes	754
<i>thdF</i>		Thiophene and furan oxidation	14
<i>tmaA</i>	<i>ind</i>	Tryptophanase (EC 4.1.99.1)	1625
<i>tmaL</i>		Tryptophanase leader peptide	544
<i>treC</i>		Amylotrehalase	155
<i>udk</i>		Uridine/cytidine kinase (EC 2.7.1.48)	1662
<i>udp</i>		Uridine phosphorylase (EC 2.4.2.3)	183, 1082
<i>uidA</i>	<i>gurA</i>	β -D-Glucuronidase (EC 3.2.1.31)	140
<i>uidR</i>		Regulator for <i>uid</i>	140
<i>uxaA</i>		Altronate hydrolase (EC 4.2.1.7)	1275
<i>uxaB</i>		Altronate oxidoreductase (EC 1.1.1.58)	141
<i>uxaC</i>		Uronate isomerase (EC 5.3.1.12)	1170
<i>uxuA</i>		Mannonate hydrolase (EC 4.2.1.8)	142
<i>uxuB</i>		Mannonate oxidoreductase (EC 1.1.1.57)	142
<i>uxuR</i>		Regulator of <i>uxuBA</i> operon	142
<i>xapA</i>	<i>pndA</i>	Xanthosine phosphorylase (EC 2.4.2.1)	124
<i>xapR</i>	<i>pndR</i>	Regulator for <i>xapA</i>	210
<i>xylA</i>		D-Xylose isomerase (EC 5.3.1.5)	96, 1366
<i>xylB</i>		Xylulokinase (EC 2.7.1.17)	156, 1366
<i>xylR</i>		Regulator for <i>xyl</i>	1366
B. Central intermediary metabolism			
<i>aceA</i>	<i>icl</i>	Isocitrate lyase (EC 4.1.3.1)	3, 821, 1375
<i>aceB</i>	<i>mas</i>	Malate synthase A (EC 4.1.3.2)	211, 212, 1036
<i>aceK</i>		Isocitrate dehydrogenase kinase/phosphatase (EC 2.7.1.116)	700, 819, 878

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>acn</i>		Aconitase (EC 4.2.1.3)	1296
<i>ahpC</i>		Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	1552
<i>ahpF</i>		Alkyl hydroperoxide reductase, F52a subunit; detoxification of hydroperoxides	1552
<i>appY</i>		Regulatory protein affecting <i>appA</i> and other genes	68
<i>cynT</i>		Carbonic anhydrase (EC 4.2.1.1)	40, 578
<i>dprA</i>		Dihydropteridine reductase (EC 1.6.99.7)	567, 1678
<i>fbp</i>	<i>fdp</i>	Fructose-1,6-bisphosphatase (EC 3.1.3.11)	592
<i>fumA</i>		Fumarase A, aerobic isozyme (EC 4.2.1.2)	1656, 1769
<i>fumB</i>		Fumarase B, anaerobic isozyme (EC 4.2.1.2)	109, 575, 1769
<i>fumC</i>		Fumarase C, isozyme (EC 4.2.1.2)	956, 1656, 1769
<i>gabC</i>		Regulator for <i>gabPDT</i>	1076
<i>gabD</i>		Succinate-semialdehyde dehydrogenase (EC 1.2.1.24), NADP-dependent activity	95, 1076
<i>gabT</i>		Aminobutyrate aminotransferase (EC 2.6.1.19) activity	95, 1076
<i>gadA</i>	<i>gadS</i>	Glutamate decarboxylase isozyme (EC 4.1.1.15)	1500
<i>gadB</i>		Glutamate decarboxylase isozyme (EC 4.1.1.15)	1500
<i>glmS</i>		L-Glutamine:D-fructose-6-phosphate aminotransferase (EC 2.6.1.16)	77, 468, 1655
<i>gltA</i>	<i>glut</i>	Citrate synthase (EC 4.1.3.7)	38, 392, 1013
<i>gnd</i>		Gluconate-6-phosphate dehydrogenase, decarboxylating (EC 1.1.1.44)	224
<i>gpsA</i>		<i>sn</i> -Glycerol-3-phosphate dehydrogenase [NAD(P) ⁺] (EC 1.1.1.94)	416
<i>grx</i>		Small dithiol protein required for glutathione-dependent ribonucleotide reductase	1254, 1387, 1407
<i>hdhA</i>		NAD-dependent 7- α -hydroxysteroid dehydrogenase (EC 1.1.1.159), dehydroxylation of bile acids	1804
<i>icdC'</i>	<i>icd</i>	Isocitrate dehydrogenase, NADP ⁺ specific (EC 1.1.1.42), chromosomal fragment	218, 684, 685
<i>icdE</i>	<i>icd</i>	Isocitrate dehydrogenase, NADP ⁺ specific (EC 1.1.1.42), chromosome-e14 hybrid	636, 684, 685
<i>iclR</i>		Repressor of <i>aceBA</i> operon	300, 1150, 1572
<i>kbl</i>		2-Amino-3-ketobutyrate CoA ligase (glycine acetyltransferase) (EC 2.3.1.29)	1115, 1116
<i>lpdA</i>	<i>lpd, dhl</i>	Lipoamide dehydrogenase (NADH) (EC 1.8.1.4); component of pyruvate and 2-oxodehydrogenase complexes; L-protein of glycine cleavage complex	26, 1538
<i>maeA</i>	<i>sfc</i>	NAD-linked malic enzyme? (EC 1.1.1.38)	296
<i>mdh</i>		Malate dehydrogenase (EC 1.1.1.37)	1685
<i>metK</i>		Methionine adenosyltransferase (EC 2.5.1.6) (AdoMet synthetase); methyl and propylamine donor, corepressor of <i>met</i> genes	143, 1420
<i>mog</i>	<i>chlG, bisD</i>	Required for the efficient incorporation of molybdate in molybdoproteins	644
<i>nadR</i>		Probable <i>nad4B</i> transcriptional regulator	1379
<i>nanA</i>		<i>N</i> -Acetylneuraminate lyase (aldolase) (EC 4.1.3.3)	10, 11
<i>pckA</i>	<i>pck</i>	Phosphoenolpyruvate carboxykinase (EC 4.1.1.49)	541
<i>pgl</i>	<i>blu</i>	6-Phosphogluconolactonase (EC 3.1.1.31)	855
<i>ppa</i>		Inorganic pyrophosphatase (EC 3.6.1.1)	865, 866
<i>ppc</i>	<i>asp, glu</i>	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	1606, 1607
<i>ppsA</i>	<i>pps</i>	Phosphoenolpyruvate synthase (EC 2.7.9.2)	1236
<i>prr</i>		γ -Aminobutyraldehyde (pyrroline) dehydrogenase activity	1293
<i>sad</i>		Succinate-semialdehyde dehydrogenase (EC 1.2.1.16), NAD dependent	1024
<i>snoB</i>		Reduces activity of <i>Rhizobium</i> NifA in <i>E. coli</i> , probably by increased rate of degradation and by inactivation	675
<i>snoC</i>		Increases rate of degradation of <i>Rhizobium</i> NifA in <i>E. coli</i>	675
<i>sucA</i>	(<i>lys + met</i>)	2-Oxoglutarate dehydrogenase (decarboxylase component) (EC 1.2.4.2)	628
<i>sucB</i>	(<i>lys + met</i>)	2-Oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase component) (EC 2.3.1.61)	628, 1209
<i>sucC</i>		Succinyl-CoA synthetase (EC 6.2.1.5), β subunit	1007
<i>sucD</i>		Succinyl-CoA synthetase (EC 6.2.1.5), α subunit	1007
<i>tesB</i>		Thioesterase II (EC 3.1.2.-)	1137
<i>tkt</i>		Transketolase (EC 2.2.1.1)	752
<i>tpiA</i>		Triosephosphate isomerase (EC 5.3.1.1)	136, 1271
<i>trxB</i>		Thioredoxin reductase	856, 1297

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>ugpQ</i>		Glycerophosphodiester phosphodiesterase, cytosolic (EC 3.1.4.46)	1628
<i>zwf</i>		Glucose-6-phosphate dehydrogenase (EC 1.1.1.49)	1372, 1373
C. Respiration (aerobic and anaerobic)			
<i>appB</i>		Probable third cytochrome oxidase, subunit	337
<i>appC</i>		Probable third cytochrome oxidase, subunit	337
<i>cybB</i>		Cytochrome <i>b</i> ₅₆₁	1090, 1142, 1160
<i>cybC</i>		Cytochrome <i>b</i> ₅₆₂	1090, 1142, 1160
<i>cydA</i>		Cytochrome <i>d</i> terminal oxidase, polypeptide subunit I (EC 1.10.3.-)	303, 605, 1156
<i>cydB</i>		Cytochrome <i>d</i> terminal oxidase, polypeptide subunit II (EC 1.10.3.-)	303, 605, 1156
<i>cydC</i>		Cytochrome <i>d</i> terminal oxidase, possible heme <i>d</i> component	363, 522
<i>cydD</i>		Cytochrome <i>d</i> activity, Zn sensitive	411, 1156, 1272
<i>cyaA</i>		Cytochrome <i>o</i> ubiquinol oxidase subunit II (EC 1.10.3.-)	257, 303, 1143
<i>cyoB</i>		Cytochrome <i>o</i> ubiquinol oxidase subunit I (EC 1.10.3.-)	255, 1091, 1143
<i>cyoC</i>		Cytochrome <i>o</i> ubiquinol oxidase subunit III (EC 1.10.3.-)	255, 257, 1091
<i>cyoD</i>		Cytochrome <i>o</i> ubiquinol oxidase operon protein CyoD	255, 257, 1091
<i>cyoE</i>		Cytochrome <i>o</i> ubiquinol oxidase operon protein CyoE	255, 257, 1091
<i>dmsA</i>		Anaerobic dimethyl sulfoxide reductase chain A	216, 1403
<i>dmsB</i>		Anaerobic dimethyl sulfoxide reductase chain B	1369, 1402, 1403
<i>dmsC</i>		Anaerobic dimethyl sulfoxide reductase chain C	1403
<i>fdx</i>		[2Fe-2S] ferredoxin, electron carrier protein	1582
<i>fdaA</i>		Flavodoxin	1198
<i>fre</i>	<i>frtD, fadI, fsrC</i>	Ferrisiderophore reductase; flavin reductase (NADPH:flavin oxidoreductase) (EC 1.6.8.1)	1521
<i>glpA</i>		<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), large subunit (EC 1.1.99.5)	282, 724, 881
<i>glpB</i>		<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit (EC 1.1.99.5)	282, 724, 881
<i>glpC</i>		<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), small subunit (EC 1.1.99.5)	282, 724, 881
<i>glpD</i>	<i>glyD</i>	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (aerobic) (EC 1.1.99.5)	71, 724
<i>glpE</i>		Protein of <i>glp</i> regulon	724
<i>glpG</i>		Protein of <i>glp</i> regulon	1450
<i>glpR</i>		Repressor of the <i>glp</i> operon	264, 724, 881
<i>hmp</i>		Hemoprotein (EC 1.6.99.7); ferrisiderophore reductase activity	46, 466, 1677
<i>hyaA</i>		Hydrogenase-1 small subunit (EC 1.18.99.1)	1070, 1071, 1298
<i>hyaB</i>		Hydrogenase-1 large subunit (EC 1.18.99.1)	1070, 1071, 1298
<i>hyaC</i>		Membrane-spanning protein of <i>hya</i> operon?	1070, 1071, 1298
<i>hyaD</i>		Processing of HyaA and HyaB proteins	1070, 1071, 1298
<i>hyaE</i>		Processing of HyaA and HyaB proteins	1070, 1071, 1298
<i>hyaF</i>		Nickel incorporation into hydrogenase-1 proteins	1070, 1071, 1298
<i>hydA</i>		Hydrogenase 1 activity	945
<i>katC</i>		Catalase activity	922
<i>katE</i>		Catalase hydroperoxidase HPII(III) (EC 1.11.1.6)	5, 349, 1690
<i>katG</i>		Catalase-peroxidase hydroperoxidase HPI(I) (EC 1.11.1.6)	5, 979, 1636
<i>narG</i>	<i>chlC, narC</i>	Nitrate reductase (EC 1.7.99.4), α subunit	144, 408
<i>narH</i>	<i>chlC</i>	Nitrate reductase (EC 1.7.99.4), β subunit	144, 408
<i>narI</i>	<i>chlI</i>	Cytochrome <i>b</i> (NR), nitrate reductase (EC 1.7.99.4), γ subunit	144, 408
<i>narJ</i>	<i>chlC</i>	Nitrate reductase (EC 1.7.99.4), δ subunit, assembly function	144, 408
<i>ndh</i>		Respiratory NADH dehydrogenase (EC 1.6.99.3)	591, 707, 1516
<i>nirB</i>	<i>nirD</i>	Nitrite reductase [NAD(P)H] subunit (EC 1.6.6.4)	599
<i>nirC</i>		Nitrite reductase activity	599
<i>nirD</i>		Nitrate reductase [NAD(P)H] subunit (EC 1.6.6.4)	599
<i>pntA</i>		Pyridine nucleotide transhydrogenase (EC 1.6.1.1), α subunit	8, 1629
<i>pntB</i>		Pyridine nucleotide transhydrogenase (EC 1.6.1.1), β subunit	8, 1629
<i>sdhA</i>		Succinate dehydrogenase (EC 1.3.99.1), flavoprotein subunit	1084, 1765
<i>sdhB</i>		Succinate dehydrogenase (EC 1.3.99.1), iron sulfur protein	335, 1084
<i>sdhC</i>	<i>cybA</i>	Succinate dehydrogenase (EC 1.3.99.1), cytochrome <i>b</i> ₅₅₆	1084, 1126
<i>sdhD</i>		Succinate dehydrogenase (EC 1.3.99.1), hydrophobic subunit	1084, 1765
<i>sodA</i>		Superoxide dismutase, manganese (EC 1.15.1.1)	122, 458, 1295
<i>sodB</i>		Superoxide dismutase, iron (EC 1.15.1.1)	122, 458, 1295
<i>torA</i>		Trimethylamine <i>N</i> -oxide reductase (EC 1.6.6.9)	1493, 1494
<i>torR</i>		Regulator for <i>torA</i>	1234

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
D. Fermentation			
<i>acd</i>		Acetaldehyde-CoA dehydrogenase	272
<i>act</i>		Pyruvate formate-lyase-activating enzyme	1424
<i>adhE</i>	<i>ana</i>	CoA-linked acetaldehyde dehydrogenase and alcohol dehydrogenase; pyruvate-formate-lyase deactivase (EC 1.1.1.1)	546, 580, 803
<i>adhR</i>		Regulator for <i>acd</i> and <i>adhE</i>	273
<i>ald</i>		Aldehyde dehydrogenase, NAD linked (EC 1.2.1.3)	252, 634
<i>aldH</i>		Aldehyde dehydrogenase, prefers NADP over NAD (EC 1.2.1.3)	616
<i>ldd</i>	<i>ldh</i>	D-Lactate dehydrogenase, NADH independent (EC 1.1.1.28)	1642
<i>fdhF</i>		Selenopolypeptide subunit of formate dehydrogenase H (part of formate hydrogen-lyase complex) (EC 1.2.1.2)	244, 615, 1830
<i>fdnG</i>		Formate dehydrogenase-N, nitrate inducible, major subunit (EC 1.2.1.2)	117, 118, 931
<i>fdnH</i>		Formate dehydrogenase-N, nitrate inducible, iron-sulfur subunit (EC 1.2.1.2)	118, 931
<i>fdnI</i>		Formate dehydrogenase-N, nitrate inducible, cytochrome <i>b</i> ₅₅₆ (Fdn) subunit (EC 1.2.1.2)	118, 931
<i>fhlA</i>		Formate hydrogen-lyase transcriptional activator for <i>fdhF</i> , <i>hyc</i> , and <i>hyp</i> operons	1041, 1367, 1433
<i>fhlB</i>		Regulator for formate hydrogen-lyase (FHL complex)	1041, 1367
<i>frdA</i>		Fumarate reductase (EC 1.3.99.1), flavoprotein subunit	291
<i>frdB</i>		Fumarate reductase (EC 1.3.99.1), iron-sulfur protein subunit	291, 1016, 1738
<i>frdC</i>		Fumarate reductase (EC 1.3.99.1), membrane anchor polypeptide	291
<i>frdD</i>		Fumarate reductase (EC 1.3.99.1), membrane anchor polypeptide	291
<i>hybA</i>		Small subunit of hydrogenase-2, probable iron-sulfur protein (EC 1.18.99.1)	149, 1297
<i>hybB</i>		Hydrogenase-2 activity	1297
<i>hybC</i>		Large subunit, hydrogenase-2 (EC 1.18.99.1)	1297
<i>hybD</i>		Hydrogenase-2 activity	1297
<i>hybG</i>		Pleiotrophic regulator of hydrogenase genes	1297
<i>hycA</i>		Transcriptional repression of <i>hyc</i> and <i>hyp</i> operons	1297, 1423
<i>hycB</i>		Probable small subunit of hydrogenase-3, iron-sulfur protein (part of formate hydrogen-lyase [FHL] complex) (EC 1.18.99.1)	1297, 1423
<i>hycC</i>		Membrane-spanning protein of hydrogenase 3 (part of FHL complex) (EC 1.18.99.1)	1297, 1423
<i>hycD</i>		Membrane-spanning protein of hydrogenase 3 (part of FHL complex) (EC 1.18.99.1)	1297, 1423
<i>hycE</i>		Probable large subunit of hydrogenase 3 (part of FHL complex) (EC 1.18.99.1)	945, 1297, 1423
<i>hycF</i>		Probable iron-sulfur protein of hydrogenase 3 (part of FHL complex) (EC 1.18.99.1)	1297, 1423
<i>hycG</i>		Hydrogenase activity	1297, 1423
<i>hycH</i>		Processing of large subunit (HycE) of hydrogenase 3 (part of the FHL complex)	1297, 1423
<i>hydG</i>		Regulation of hydrogenase 3 activity	945, 1550
<i>hydH</i>		Regulation of hydrogenase 3 activity	945, 1550
<i>hydL</i>	<i>hup?</i>	Probable member of <i>hyb</i> operon; pleiotrophic effects	
<i>hypA</i>		Pleiotrophic effects on three hydrogenase isozymes	945, 997, 1297
<i>hypB</i>	<i>hydB</i> <i>hydE</i>	Pleiotrophic effects on three hydrogenase isozymes	945, 997
<i>hypC</i>		Pleiotrophic effects on three hydrogenase isozymes	945, 997
<i>hypD</i>		Pleiotrophic effects on three hydrogenase isozymes	945, 997
<i>lctD</i>	<i>lct</i>	L-Lactate dehydrogenase (EC 1.1.1.27)	393
<i>pfl</i>		Pyruvate formate-lyase (EC 2.3.1.54)	820, 1426
E. ATP-proton motive force interconversion			
<i>atpA</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), F1 sector, α subunit	925, 1683
<i>atpB</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), F0 sector, subunit a	926, 1682
<i>atpC</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), F1 sector, ϵ subunit	879, 1065
<i>atpD</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), F1 sector, β subunit	899
<i>atpE</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), F0 sector, subunit c; DCCD ^a -binding protein	464, 478, 537
<i>atpF</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), F0 sector, subunit b	1051
<i>atpG</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), F1 sector, γ subunit	681
<i>atpH</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), F1 sector, δ subunit	438
<i>atpI</i>	<i>unc</i>	Membrane-bound ATP synthase (EC 3.6.1.34), subunit?	1436

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
F. Broad regulatory functions			
<i>ada</i>		Bifunctional gene product: O6-methylguanine-DNA methyltransferase (EC 2.1.1.-); transcription activator/repressor	12, 125, 1319
<i>arcA</i>	<i>dye, fexA, msp, cpxC, sfrA, seg</i>	Negative response regulator of genes in aerobic pathways, (sensor for <i>arcB</i> and <i>cpxA</i>)	304, 723, 726
<i>arcB</i>		Aerobic respiration sensor protein; histidine protein kinase/phosphatase, sensor for <i>arcA</i> (EC 2.7.1.-)	725, 728
<i>barA</i>		Sensor-regulator for an uncharacterized bacterial adaptive response	1135
<i>cpxA</i>	<i>ecfB, ssd, eup</i>	Probable inner membrane sensor protein (histidine protein kinase), acting on <i>arcA</i> , energy coupling factor, F-pilin formation (EC 2.7.1.-)	1723
<i>creB</i>	<i>yjjE, ORF2</i>	Catabolic regulation response regulator	966, 1223
<i>creC</i>	<i>phoN</i>	Catabolite repression sensor (histidine protein kinase); alternative sensor for <i>pho</i> regulon (EC 2.7.1.-)	1712
<i>crp</i>	<i>cap, csm</i>	Cyclic AMP receptor protein	631, 632, 1503
<i>cyaA</i>		Adenylyl cyclase (EC 4.6.1.1)	1245
<i>cytR</i>		Regulator for <i>deo</i> operon, <i>udp</i> , <i>cdd</i> , <i>tsx</i> , <i>nupC</i> , and <i>nupG</i>	90, 1240, 1504
<i>envZ</i>	<i>ompB, perA, tpo</i>	Response regulator for <i>ompC</i> and <i>ompF</i> (protein kinase/phosphatase sensor; regulates outer membrane protein biosynthesis) (EC 2.7.1.-)	696, 1721
<i>era</i>		GTP-binding protein	545, 910
<i>fexB</i>		FexA (ArcA) phenotype affected	911
<i>fnr</i>	<i>nirA, nirR, frdB</i>	Regulatory gene for nitrite and nitrate reductases, hydrogenase, and fumarate reductase	437, 1515, 1634
<i>fur</i>		Ferric iron uptake; negative regulator	604, 1725
<i>gppA</i>	<i>gpp</i>	Guanosine pentaphosphate activity	106
<i>kdpD</i>	<i>kac</i>	High-affinity potassium transport system; regulator (sensor)	1146, 1269, 1701
<i>lctZ</i>	<i>lct*</i>	Pleiotrophic effects on components of respiratory chain	305
<i>lexA</i>	<i>spr, exrA, umuA</i>	Regulator for SOS (<i>lexA</i>) regulon	949
<i>lon</i>	<i>tsl</i>		
	<i>capR, muc, deg, dir</i>	DNA-binding, ATP-dependent protease La; heat shock protein (EC 3.4.21.53)	373
<i>narL</i>	<i>frdR, narR</i>	Pleiotrophic regulation of electron transport and fermentation: <i>nar</i> , <i>frd</i> , <i>dms</i> , and <i>tor</i> genes (sensor for <i>narX</i>)	421, 727, 1212
<i>narQ</i>		Sensor for nitrate reductase system, putative protein histidine kinase	260
<i>narX</i>	<i>narR</i>	Nitrate sensor, probable histidine protein kinase acts on <i>narL</i> (EC 2.7.1.-)	260, 285, 420
<i>ntrL</i>		Nitrogen-regulatory protein	25
<i>ompR</i>	<i>ompB, cry, knt</i>	Response regulator (sensor for <i>envZ</i>) affecting transcription of <i>ompC</i> and <i>ompF</i> ; outer membrane protein synthesis	188, 696, 1721
<i>oxyR</i>			
<i>oxyS</i>	<i>momR</i>	Activator, hydrogen peroxide-inducible genes	152, 1602, 1603
<i>phoB</i>	<i>R_c, phoT</i>	RNA, a pleiotropic regulator	737
<i>phoR</i>	<i>nmpB, phoR1, R1pho</i>	Positive regulator for <i>pho</i> regulon, (sensor for <i>phoR</i>)	1010, 1712
		Positive and negative regulatory gene for <i>pho</i> regulon, sensor protein (2.7.1.-)	1010, 1712, 1786
<i>pus</i>		Effect of suppressors on <i>relB</i> mutations	384
<i>relA</i>	<i>RC</i>	Regulation of RNA synthesis; stringent factor; ATP:GTP 3'-pyrophotransferase (EC 2.7.6.5)	1442, 1782
<i>relB</i>	<i>RC</i>	Regulation of RNA synthesis; stringent factor	1107
<i>relX</i>		Control of synthesis of guanosine 5'-diphosphate 3'-diphosphate	1219
<i>rpoD</i>	<i>alt</i>	RNA polymerase (EC 2.7.7.6), σ^{70} subunit; regulation of proteins induced at high temperatures	502, 1700
<i>rpoH</i>	<i>fam, hin, htpR</i>	RNA polymerase (EC 2.7.7.6), σ^{32} subunit; regulation of proteins induced at high temperatures	739, 1133, 1658
<i>rpoN</i>	<i>ntrA, glnF</i>	RNA polymerase (EC 2.7.7.6), σ^{60} subunit, nitrogen and fermentation regulation	1326
<i>rpoS</i>	<i>katF, appR, csi2</i>	RNA polymerase (EC 2.7.7.6), putative sigma subunit; affects expression of pH 2.5 acid phosphatase, and biosynthesis of catalase hydroperoxidase HPII(III) and exonuclease III	622, 875, 1634
<i>soxR</i>		Regulation of superoxide response regulon	458, 562
<i>soxS</i>		Regulation of superoxide response regulon	458
<i>spf</i>		Spot 42 RNA, inhibition of DNA synthesis	1334
<i>sspA</i>	<i>pog, ssp</i>	Stringent starvation protein; affects gene expression, also expression of late genes of phage P1	491, 1755

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>suhA</i>		Induction of heat shock genes	1622
<i>uspT</i>		Putative histidine protein kinase (sensor) for universal stress protein	1176
II. Biosynthesis of small molecules			
A. Amino acids			
1. Glutamate family/nitrogen assimilation			
<i>argA</i>	<i>argB, arg1, arg2</i>	Amino acid acetyltransferase; <i>N</i> -acetylglutamate synthase (EC 2.3.1.1)	194
<i>argB</i>	<i>argC</i>	Acetylglutamate kinase (EC 2.7.2.8)	170, 432, 547
<i>argC</i>	<i>argH, arg2</i>	<i>N</i> -Acetyl- γ -glutamylphosphate reductase (EC 1.2.1.38)	170, 432, 547
<i>argD</i>	<i>argG, arg1</i>	Acetylornithine δ -aminotransferase (EC 2.6.1.11)	495, 1341, 1684
<i>argE</i>	<i>argA, arg4</i>	Acetylornithine deacetylase (EC 3.5.1.16)	1064
<i>argF</i>	<i>argD, arg5</i>	Ornithine carbamoyltransferase (EC 2.1.3.3)	276, 547, 674
<i>argG</i>	<i>argE, arg6</i>	Argininosuccinate synthetase (EC 6.3.4.5)	547
<i>argH</i>	<i>argF, arg7</i>	Argininosuccinate lyase (EC 4.3.2.1)	170, 432
<i>argI</i>		Ornithine carbamoyltransferase (EC 2.1.3.3)	854, 1087, 1812
<i>argR</i>	<i>xerA, Rarg</i>	Repressor of <i>arg</i> regulon; <i>cer</i> -mediated site specific recombination	1546, 1618
<i>gdhA</i>		NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	1055
<i>glnR</i>		Glutamine synthetase (EC 6.3.1.2)	67, 1327, 1487
<i>glnB</i>		Regulatory protein P-II for glutamine synthetase	67
<i>glnG</i>	<i>ntrC, glnT</i>	Response regulator for <i>gln</i> (sensor for <i>glnL</i>) (nitrogen regulator I [NRI])	1726
<i>glnL</i>	<i>ntrB, glnR</i>	Histidine protein kinase sensor for <i>glnG</i> regulator (nitrogen regulator II [NRII]) (EC 2.7.1.-)	67, 1327
<i>gltB</i>	<i>aspB</i>	Glutamate synthase, large subunit (EC 1.4.1.13)	227, 228, 550
<i>gltD</i>	<i>aspB</i>	Glutamate synthase, small subunit (EC 1.4.1.13)	227, 228, 550
<i>gltF</i>		Regulator	227, 228
<i>gltH</i>		Glutamate synthesis	1022
<i>proA</i>	<i>pro1</i>	γ -Glutamylphosphate reductase (EC 1.2.1.41)	610, 1455
<i>proB</i>	<i>pro2</i>	γ -Glutamate kinase (EC 2.7.2.11)	610, 1455
<i>proC</i>	<i>pro3, pro2</i>	Pyroline-5-carboxylate reductase (EC 1.5.1.2)	374, 610
<i>uspA</i>		Universal stress protein	1176
2. Aspartate family, pyruvate family			
<i>alr</i>		Alanine racemase (EC 5.1.1.1); isozyme	1707, 1746
<i>asd</i>	(<i>dap</i> + <i>hom</i>)	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	782
<i>asnA</i>		Asparagine synthetase A (EC 6.3.1.1)	643
<i>asnB</i>		Asparagine synthetase B (EC 6.3.5.4)	682, 1453
<i>asnC</i>		Regulator for <i>asnA</i> , <i>asnC</i> , and <i>gidA</i>	827
<i>aspA</i>		Aspartate ammonia-lyase (aspartase) (EC 4.3.1.1)	453, 1128
<i>aspC</i>	<i>aat</i>	Aspartate aminotransferase (EC 2.6.1.1)	333, 770, 1798
<i>avtA</i>	<i>avt</i>	Alanine- α -ketoisovalerate transaminase, transaminase C (EC 2.6.1.66)	1710
<i>azl</i>		Regulation of <i>ilv</i> and <i>leu</i> genes; azaleucine resistance	1265
<i>dapA</i>		Dihydrodipicolinate synthase (EC 4.2.1.52)	863, 1337
<i>dapB</i>		Dihydrodipicolinate reductase (EC 1.3.1.26)	168
<i>dapC</i>		Tetrahydrodipicolinate succinylase	205
<i>dapD</i>		Succinyldiaminopimelate transaminase (EC 2.6.1.17)	205
<i>dapE</i>	<i>msgB, dapB</i>	<i>N</i> -Succinyldiaminopimelate deacylase (EC 3.5.1.18)	167, 1774
<i>dapF</i>		Diaminopimelate epimerase (EC 5.1.1.7)	635, 870, 1336
<i>ileR</i>	<i>avr, flrA?</i>	Negative regulator for <i>thr</i> and <i>ilv</i> operons	1730
<i>ilvA</i>	<i>ile</i>	Threonine deaminase (EC 4.2.1.16)	428, 676, 1585
<i>ilvB</i>		Acetolactate synthase I (EC 4.1.3.18), valine sensitive, large subunit	484, 1728, 1735
<i>ilvC</i>	<i>ilvA</i>	Ketol-acid reductoisomerase (EC 1.1.1.86)	1733
<i>ilvD</i>	<i>ilvE</i>	Dihydroxyacid dehydratase (EC 4.2.1.9)	676
<i>ilvE</i>	<i>ilvC, ilvJ</i>	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	711, 769
<i>ilvH</i>	<i>brnP</i>	Acetolactate synthase III (EC 4.1.3.18), valine sensitive, small subunit	1332, 1333, 1728
<i>ilvI</i>		Acetolactate synthase III (EC 4.1.3.18), valine sensitive, large subunit	1332, 1728
<i>ilvO</i>		<i>ilvGEDA</i> operon leader peptide	246, 1735

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>ilvN</i>		Acetolactate synthase I (EC 4.1.3.18), valine sensitive, small subunit	484, 1728, 1735
<i>ilvR</i>		Positive regulator for <i>thr</i> and <i>ilv</i> operons	744
<i>ilvY</i>		Positive regulator for <i>ilvC</i>	1733, 1734
<i>ilvL</i>		<i>ilvB</i> operon leader peptide	485, 1735
<i>leuA</i>		α -Isopropylmalate synthase (EC 4.1.3.12)	517, 1507
<i>leuB</i>		β -Isopropylmalate dehydrogenase (EC 1.1.1.85)	853
<i>leuC</i>		α -Isopropylmalate isomerase subunit (EC 4.2.1.33)	492
<i>leuD</i>		α -Isopropylmalate isomerase subunit (EC 4.2.1.33)	492
<i>leuJ</i>	<i>ftr</i>	Regulator for <i>leu</i> and <i>ilv</i> operons	1171
<i>leuL</i>		<i>leu</i> operon leader peptide	94, 798
<i>leuO</i>		Probable activator protein for <i>leuABCD</i> operon	623
<i>lrp</i>	<i>livR, lss, lstR, mbl, oppI</i>	Regulator for leucine (or <i>lrp</i>) regulon and high-affinity branched-chain amino acid transport system regulatory gene; binds upstream of <i>lysU</i>	449, 950, 951
<i>lysA</i>		Diaminopimelate decarboxylase (EC 4.1.1.20)	253, 1557
<i>lysC</i>	<i>apk</i>	Aspartokinase III (EC 2.7.2.4)	274
<i>lysR</i>		Positive regulator for <i>lys</i>	623
<i>metA</i>	<i>met₃</i>	Homoserine transsuccinylase (EC 2.3.1.46)	409, 1362
<i>metB</i>	<i>met-1, met₁</i>	Cystathionine γ -synthase (EC 4.2.99.9)	657, 1029, 1371
<i>metC</i>		Cystathionine γ -lyase (EC 4.4.1.1)	657, 1029, 1371
<i>metE</i>	<i>metB₁₂</i>	Tetrahydropteroylglutamate methyltransferase (EC 2.1.1.14)	267
<i>metF</i>	<i>met-2, met₂</i>	5,10-Methylenetetrahydrofolate reductase (EC 1.7.99.5)	1398
<i>metH</i>		B ₁₂ -dependent homocysteine-N5-methyltetrahydrofolate transmethylase, repressor of <i>metE</i> and <i>metF</i> (EC 2.1.1.13)	85
<i>metJ</i>		Repressor of all <i>met</i> genes but <i>metF</i>	1252
<i>metL</i>	<i>metM</i>	Aspartokinase II (EC 2.7.2.4), homoserine dehydrogenase II (EC 1.1.1.3)	1231
<i>metR</i>		Regulator for <i>metE</i> and <i>metH</i>	1043
<i>mraA</i>		D-Alanine carboxypeptidase	1094
<i>thrA</i>		Aspartokinase I (EC 2.7.2.4), homoserine dehydrogenase I (EC 1.1.1.3)	1252
<i>thrB</i>	<i>HS, thrD</i>	Homoserine kinase (EC 2.7.1.39)	302, 1400
<i>thrC</i>		Threonine synthase (EC 4.2.99.2)	1232
<i>thrL</i>		<i>thr</i> operon leader peptide	330, 504
3. Glycine-serine family/sulfur metabolism			
<i>cysB</i>		Positive regulator for cysteine regulon	1012, 1100
<i>cysC</i>		Adenosine 5'-phosphosulfate kinase (EC 2.7.1.25)	928, 929
<i>cysD</i>		ATP:sulfate adenylyltransferase (EC 2.7.7.4), subunit	927-929
<i>cysE</i>		Serine acetyltransferase (EC 2.3.1.30)	1745
<i>cysH</i>		Phosphoadenylsulfate reductase (EC 2.8.2.-)	845, 1201
<i>cysI</i>	<i>cysQ</i>	Sulfite reductase (EC 1.8.1.2), α subunit	1201
<i>cysJ</i>	<i>cysP</i>	Sulfite reductase flavoprotein (EC 1.8.1.2) β subunit	1200, 1201
<i>cysK</i>	<i>cysE</i>	O-Acetylserine sulfhydrylase A (EC 4.2.99.8)	1206
<i>cysM</i>		O-Acetylserine sulfhydrylase B (EC 4.2.99.8)	1206, 1495, 1496
<i>cysN</i>		ATP-sulfurylase (ATP:sulfate adenylyltransferase) (EC 2.7.7.4), subunit	927-929
<i>cysP</i>		Thiosulfate binding protein	671
<i>cysQ</i>	<i>amt, amtA</i>	Affects pool of 3'-phosphoadenoside 5'-phosphosulfate in pathway of sulfite synthesis; protein	1153, 1716, 1717
<i>glyA</i>		Serine hydroxymethyltransferase (EC 2.1.2.1)	48, 1555, 1556
<i>sbaA</i>		Regulation of serine and branched-chain amino acid metabolism	328
<i>serA</i>		D-3-Phosphoglycerate dehydrogenase (EC 1.1.1.95)	1440, 1443
<i>serB</i>		Phosphoserine phosphatase (EC 3.1.3.3)	1659
<i>serC</i>	<i>pdxC, pdxF</i>	3-Phosphoserine aminotransferase (EC 2.6.1.52)	412, 868
4. Aromatic amino acid family			
<i>aroA</i>		5-Enolpyruvylshikimate-3-phosphate synthetase (EC 2.5.1.19)	39, 1210, 1488
<i>aroB</i>		Dehydroquinate synthase (EC 4.6.1.3)	811
<i>aroC</i>		Chorismate synthase (EC 4.6.1.4)	239, 1741
<i>aroD</i>		5-Dehydroquinate dehydratase (EC 4.2.1.10)	242, 811, 812
<i>aroE</i>		Dehydroshikimate reductase (EC 1.1.1.25)	51
<i>aroF</i>		Phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP synthetase, tyrosine repressible) (EC 4.1.2.15)	1317

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>aroG</i>		Phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP synthetase, phenylalanine repressible) (EC 4.1.2.15)	345, 1539
<i>aroH</i>		Phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP synthetase, tryptophan repressible) (EC 4.1.2.15)	678, 1316, 1317
<i>aroI</i>		Member of <i>aroI</i> operon	529
<i>aroK</i>		Shikimate kinase I (EC 2.7.1.71)	977
<i>aroL</i>		Shikimate kinase II (EC 2.7.1.71)	358, 613
<i>aroM</i>		Regulated by <i>aroR</i>	358
<i>pheA</i>		Chorismate mutase (EC 5.4.99.5) and P-prephenate dehydratase (EC 4.2.1.51)	508, 509, 1152
<i>pheM</i>		<i>phe</i> leader peptide	
<i>pheR</i>		Regulator for <i>pheA</i>	508
<i>trpA</i>	<i>try, tryp-2</i>	Tryptophan synthase (EC 4.2.1.20), A protein	200, 1179, 1391
<i>trpB</i>	<i>tryp-1</i>	Tryptophan synthase (EC 4.2.1.20), B protein	200, 414, 1391
<i>trpC</i>	<i>tryp-3</i>	<i>N</i> -(5-Phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) and indole-3-glycerolphosphate synthetase (EC 4.1.1.48)	1758
<i>trpD</i>	<i>tryE</i>	Glutamine amidotransferase (EC 4.1.3.27) and phosphoribosylanthranilate transferase (EC 2.4.2.18)	665, 1484
<i>trpE</i>	<i>anth, tryD, tryp-4</i>	Anthranilate synthase (EC 4.1.3.27)	630, 1483
<i>trpL</i>		<i>trp</i> operon leader peptide	873, 1352
<i>trpR</i>	<i>Rtry</i>	Regulator for <i>trp</i> operon and <i>aroH</i> ; <i>trp</i> aporepressor	63, 817, 849
<i>tyrA</i>		Chorismate mutase T (EC 5.4.99.5) and prephenate dehydrogenase (EC 1.3.1.12)	1030, 1652, 1653
<i>tyrB</i>		Tyrosine aminotransferase (EC 2.6.1.57), tyrosine repressible	1467
5. Histidine			
<i>hisA</i>		<i>N</i> -(5'-Phospho-L-ribosyl-formimino)-5-amino-1-(5'-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	221
<i>hisB</i>		Imidazoleglycerolphosphate dehydratase (EC 4.2.1.19) and histidinol phosphate phosphatase (EC 3.1.3.15)	221
<i>hisC</i>		Histidinol-phosphate aminotransferase (EC 2.6.1.9)	221
<i>hisD</i>		L-Histidinol:NAD ⁺ oxidoreductase (EC 1.1.1.23)	221, 753
<i>hisF</i>		Cyclase	505, 542
<i>hisG</i>		ATP phosphoribosyltransferase (EC 2.4.2.17)	221
<i>hisH</i>		Amidotransferase (EC 2.4.2.-)	221
<i>hisI</i>	<i>hisE</i>	Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) and phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	221
<i>hisL</i>		<i>his</i> operon leader peptide	235
B. Nucleotides			
1. Purine ribonucleotides			
<i>adk</i>	<i>plsA, dnaW</i>	Adenylate kinase (EC 2.7.4.3) activity; pleiotropic effects on glycerol-3-phosphate acyltransferase activity	1364, 1365, 1399
<i>fadR</i>	<i>ole, thdB</i>	Negative regulator for <i>fad</i> regulon, and positive activator of <i>fabA</i>	54, 387, 626
<i>gmk</i>	<i>spoR, kguA</i>	Guanylate kinase (EC 2.7.4.8)	518, 1782
<i>guaA</i>	<i>gua_b</i>	GMP synthetase (EC 6.3.5.2)	1621
<i>guaB</i>	<i>gua_a</i>	IMP dehydrogenase (EC 1.1.1.205)	44
<i>guaC</i>		GMP reductase (EC 1.6.6.8)	44
<i>ndk</i>		Nucleoside diphosphate kinase (EC 2.7.4.6)	591
<i>prs</i>		Phosphoribosylpyrophosphate synthetase (EC 2.7.6.1)	169, 668
<i>purA</i>	<i>ade_k, Ad₄</i>	Adenylosuccinate synthetase (EC 6.3.4.4)	394, 960, 1502
<i>purB</i>	<i>ade_n</i>	Adenylosuccinate lyase (EC 4.3.2.2)	611
<i>purC</i>	<i>ade_g</i>	Phosphoribosylaminoimidazole-succinocarboxamide synthetase (EC 6.3.2.6) = SAICAR synthetase	1619
<i>purD</i>	<i>adth_a</i>	Phosphoribosylglycinamide synthetase (EC 6.3.4.13), = GAR synthetase	9, 1475
<i>purE</i>	<i>ade₃, ade_f, Pur₂</i>	Phosphoribosylaminoimidazole carboxylase, = AIR carboxylase (EC 4.1.1.21), catalytic subunit	1078, 1620, 1719
<i>purF</i>	<i>ade_{u,b}, purC</i>	Amidophosphoribosyltransferase (EC 2.4.2.14) = PRPP amidotransferase	1061, 1404
<i>purH</i>	<i>ade_i</i>	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.1.3) = AICAR formyltransferase	9, 471
<i>purK</i>		Phosphoribosylaminoimidazole carboxylase = AIR carboxylase (EC 4.1.1.21), CO ₂ -fixing subunit	1078, 1620, 1719

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>purL</i>	<i>purI</i>	Phosphoribosylformyl-glycineamide synthetase = FGAM synthetase (EC 6.3.5.3); homologous to <i>purG</i> of <i>S. typhimurium</i>	1430
<i>purM</i>	<i>purG</i>	Phosphoribosylaminoimidazole synthetase = AIR synthetase (EC 6.3.3.1); homologous to <i>purl</i> of <i>S. typhimurium</i>	1501
<i>purN</i>		5'-Phosphoribosyl-glycinamide (GAR) transformylase (EC 2.1.2.2)	708, 709
<i>purR</i>		Repressor for <i>pur</i> regulon, <i>glyA</i>	808, 1537, 1759
2. Pyrimidine ribonucleotides			
<i>carA</i>	<i>pyrA, cap, (arg + ura)</i>	Carbamoyl-phosphate synthetase (EC 6.3.5.5), glutamine (light) subunit	178, 1120, 1376
<i>carB</i>	<i>pyrA, cap, (arg + ura)</i>	Carbamoyl-phosphate synthetase (EC 6.3.5.5), ammonia (heavy) subunit	178, 1278, 1376
<i>pyrB</i>		Aspartate carbamoyltransferase (EC 2.1.3.2), catalytic subunit	1248, 1781, 1822
<i>pyrC</i>		Dihydro-ortotate (EC 3.5.2.3)	193, 262, 1759
<i>pyrD</i>		Dihydro-orotate oxidase (EC 1.3.3.1)	1759
<i>pyrE</i>		Orotate phosphoribosyltransferase (EC 2.4.2.10)	35, 1282
<i>pyrF</i>		Orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	1651
<i>pyrG</i>		CTP synthetase (EC 6.3.4.2)	1737
<i>pyrH</i>	<i>pyrR</i>	UMP kinase	240, 756
<i>pyrI</i>		Aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit	391
<i>pyrL</i>		<i>pyrBI</i> operon leader peptide	918
3. 2'-Deoxyribonucleotides			
<i>dcd</i>	<i>paxA</i>	2'-Deoxycytidine 5'-triphosphate deaminase (EC 3.5.4.-)	1709
<i>dut</i>	<i>sof, dnaS</i>	Deoxyuridinetriphosphatase (EC 3.6.1.23)	230, 654, 1709
<i>mutT</i>		(Deoxy)nucleoside triphosphatase prefers dGTP, causes AT-GC transversions	13, 1008, 1428
<i>nrdA</i>	<i>dnaF</i>	Ribonucleoside diphosphate reductase (EC 1.17.4.1) subunit B1	2, 1559, 1570
<i>nrdB</i>	<i>ftsB</i>	Ribonucleoside-diphosphate reductase (EC 1.17.4.1) subunit B2	1559, 1570
<i>thyA</i>		Thymidylate synthetase (EC 2.1.1.45)	1080
<i>tmk</i>		Thymidylate kinase (EC 2.7.4.9)	131
4. Salvage and interconversions			
<i>add</i>		Adenosine deaminase (EC 3.5.4.4)	237
<i>amn</i>		AMP nucleosidase (EC 3.2.2.4)	913
<i>apaH</i>		Diadenosine tetraphosphatase (EC 3.6.1.4)	454, 747
<i>apt</i>		Adenine phosphoribosyltransferase (EC 2.4.2.7)	920
<i>cdd</i>		Cytidine/deoxycytidine deaminase (EC 3.5.4.5)	1794
<i>codA</i>		Cytosine deaminase (EC 3.5.4.1)	332
<i>cpdB</i>		2':3'-Cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)	961
<i>deoA</i>	<i>tpp, TP</i>	Thymidine phosphorylase (EC 2.4.2.4)	1704
<i>deoB</i>	<i>drm, thyR</i>	Phosphopentomutase (EC 5.4.2.7)	467
<i>deoC</i>	<i>dra, thyR</i>	2-Deoxyribose-5-phosphate aldolase (EC 4.1.2.4)	1663
<i>deoD</i>	<i>pup</i>	Purine-nucleoside phosphorylase (EC 2.4.2.1)	467
<i>deoR</i>	<i>nucR</i>	Regulator for <i>deo</i> operon, <i>tsx</i> , and <i>nupG</i>	32, 329, 1106
<i>gpt</i>	<i>glyD, gpp, gcu</i>	Guanine-hypoxanthine phosphoribosyltransferase (EC 2.4.2.22)	653, 920, 921
<i>gsk</i>		Inosine-guanosine kinase (2.7.1.73)	669
<i>hpt</i>		Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	653, 920, 921
<i>optA</i>		Regulator for <i>dgt</i>	1306
<i>spoT</i>		Guanosine 3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (EC 3.1.7.1); synthesis and degradation of ppGpp	1270, 1414, 1782
<i>tdk</i>		Thymidine kinase (EC 2.7.1.21)	131
<i>upp</i>	<i>uraP</i>	Uracil phosphoribosyltransferase (EC 2.4.2.9)	36, 1314
C. Sugars and sugar nucleotides			
<i>cpsB</i>		Mannose-1-phosphate guanyltransferase (GDP-mannose pyrophorylase) (EC 2.7.7.22)	164, 552, 1637
<i>cpsG</i>		Phosphomannomutase (EC 5.4.2.8)	1027
<i>galE</i>	<i>galD</i>	UDP-galactose 4-epimerase (5.1.3.2)	97, 832, 1691
<i>galT</i>	<i>galB</i>	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	463, 1691
<i>mall</i>		Repressor of <i>mal</i> genes	1324, 1325
<i>manA</i>	<i>pmi</i>	Mannose-6-phosphate isomerase (EC 5.3.1.8)	1542

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>nagA</i>		<i>N</i> -Acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	1267, 1268
<i>nagB</i>	<i>glmD</i>	Glucosamine-6-phosphate deaminase (EC 5.3.1.10)	29, 1267, 1268
<i>nagR</i>	<i>nagC</i>	Repressor for the <i>nag</i> regulon	1266, 1268
<i>rfbA</i>	<i>som</i>	TDP-glucose pyrophosphorylase	1149
<i>rfbB</i>		TDP-glucose oxidoreductase	1149
<i>rfbD</i>		TDP-rhamnose synthetase	1149
<i>ushA</i>		UDP-sugar hydrolase (5'-nucleotidase)	207
D. Cofactors, prosthetic groups, electron carriers			
1. Biotin			
<i>bioA</i>		7,8-Diaminopelargonic acid synthetase (EC 2.6.1.62)	1203
<i>bioB</i>		Biotin synthetase	1203
<i>bioC</i>		Biotin biosynthesis; reaction prior to pimeloyl-CoA	1203
<i>bioD</i>		Dethiobiotin synthetase (EC 6.3.3.3)	1203
<i>bioF</i>		7-Keto-8-aminopelargonic acid synthetase (EC 2.3.1.47)	1203
<i>bioH</i>	<i>bioB</i>	Biotin biosynthesis; reaction prior to pimeloyl-CoA	1195
<i>birA</i>	<i>bioR, dhbB</i>	Biotin-(acetyl-CoA carboxylase) holoenzyme synthetase; biotin operon repressor (EC 6.3.4.15)	206
<i>bisC</i>		Biotin sulfoxide reductase	1256
2. Folic acid			
<i>folA</i>	<i>tmrA</i>	Dihydrofolate reductase (EC 1.5.1.3); trimethoprim resistance	54, 213, 486
<i>folC</i>		Dihydrofolate:folylpolyglutamate synthetase (EC 6.3.2.17); dihydrofolate synthetase (EC 6.3.2.12)	148, 802, 809
<i>folD</i>		5,10-Methylene-tetrahydrofolate dehydrogenase (EC 1.5.1.5); 5,10-methylene-tetrahydrofolate cyclohydrolase (EC 3.5.4.9)	334
<i>folE</i>		GTP cyclohydrolase I (EC 3.5.4.16)	1304
<i>folK</i>		7,8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase (EC 2.7.6.3)	1591, 1592
<i>folP</i>		7,8-Dihydropteroate synthase (EC 2.5.1.15)	325, 1591
<i>pabA</i>		<i>p</i> -Aminobenzoate synthetase, CoII	561
<i>pabB</i>		<i>p</i> -Aminobenzoate synthetase, CoII	561, 1703, 1800
<i>pabC</i>		Aminodeoxychorismate lyase	560, 561, 1800
3. Lipoate			
<i>lipA</i>	<i>lip</i>	Enzyme of lipoate biosynthesis, acts on octanoic acid	1321
<i>lipB</i>	<i>lip</i>	Enzyme of lipoate biosynthesis	1321
4. Molybdopterin			
<i>moaA</i>	<i>chlA, bisA, narA</i>	Molybdopterin biosynthesis	82, 644, 1312
<i>moaD</i>	<i>chlM</i>	Molybdopterin biosynthesis	644, 1312
<i>mob</i>	<i>chlB</i>	Molybdopterin-guanine dinucleotide biosynthesis	644, 745, 1312
<i>moeA</i>	<i>chlE, bisB</i>	Molybdopterin biosynthesis	644, 1165, 1312
<i>moeB</i>	<i>chlN</i>	Molybdopterin biosynthesis	644, 1165, 1312
5. Pantothenate			
<i>coaA</i>	<i>panK, rts</i>	Pantothenate kinase (EC 2.7.1.33)	1508, 1667
<i>panB</i>	<i>ts-9</i>	Ketopentoate hydroxymethyltransferase (EC 4.1.2.12)	310
<i>panC</i>		Pantothenate synthetase (EC 6.3.2.1)	310
<i>panD</i>		Aspartate 1-decarboxylase (EC 4.1.1.11)	310
6. Pyridoxine			
<i>pdxA</i>		Pyridoxine biosynthesis	1344
<i>pdxB</i>		Erythronate-4-phosphate dehydrogenase, placement of 5, 5', and 6' carbons into pyridine ring of pyridoxine (EC 1.1.1.-)	868, 1440
<i>pdxH</i>		Pyridoxinephosphate oxidase	869
<i>pdxJ</i>		Pyridoxine biosynthesis	867, 1590

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
7. Pyridine nucleotides			
<i>nadA</i>	<i>nicA</i>	Quinolinate synthetase, A protein	470, 1458
<i>nadB</i>	<i>nicB</i>	Quinolinate synthetase, B protein (EC 1.4.3.16)	470, 1458
<i>nadC</i>	<i>nic</i>	Quinolinate phosphoribosyltransferase (EC 2.4.2.19)	1638
<i>pncA</i>	<i>nam</i>	Nicotinamide deamidase (EC 3.5.1.19)	1221
<i>pncB</i>		Nicotinate phosphoribosyltransferase (EC 2.4.2.1)	1779
8. Thiamin			
<i>thiA</i>		Thiamin thiazole requirement	796
<i>thiB</i>		Thiamin phosphate pyrophosphorylase (EC 2.5.1.3)	796
<i>thiC</i>		Thiamin biosynthesis, pyrimidine moiety	1668
<i>thiD</i>		Phosphomethylpyrimidine kinase activity	705
<i>thiE</i>		Thiamin biosynthesis, thiazole moiety	1668
<i>thiF</i>		Thiamin biosynthesis, thiazole moiety	1668
<i>thiG</i>		Thiamin biosynthesis, thiazole moiety	1668
<i>thiH</i>		Thiamin biosynthesis, thiazole moiety	1668
<i>thiJ</i>		Thiamin biosynthesis	
<i>thiK</i>		Thiamin kinase (EC 2.7.1.89)	706
<i>thiL</i>		Thiamin monophosphate kinase (EC 2.7.4.16)	706
9. Riboflavin			
<i>ribA</i>		GTP cyclohydrolase II (EC 3.5.4.25)	1304
<i>ribB</i>	<i>htrP</i>	3,4-Dihydroxy-2-butanone-4-phosphate synthase	1338
<i>ribC</i>		Riboflavin synthase (EC 2.5.1.9)	1264
10. Thioredoxin, glutaredoxin, and glutathione			
<i>ggt</i>		γ-Glutamyltranspeptidase (EC 2.3.2.2)	1574
<i>gor</i>		Glutathione oxidoreductase (EC 1.6.4.2)	370, 446, 852
<i>gshA</i>		γ-Glutamate-cysteine ligase (EC 6.3.2.2)	165
<i>gshB</i>		Glutathione synthetase (EC 6.3.2.3)	348, 790, 1599
<i>trxA</i>	<i>fipA, tsnC</i>	Thioredoxin	539, 843, 993
11. Menaquinone and ubiquinones			
<i>ispA</i>		Geranyltranstransferase (farnesylidiphosphate synthase) (EC 2.5.1.10)	116, 490
<i>menA</i>		1,4-Dihydroxy-2-naphthoate → dimethylmenaquinone	116
<i>menB</i>		1,4-Dihydroxy-2-naphthoate synthase	116, 1471
<i>menC</i>		Conversion of chorismate to 2-o-succinylbenzoate, step 2	116, 1060, 1469a
<i>menD</i>		Conversion of chorismate to 2-o-succinylbenzoate, step 1	1060, 1214a, 1273
<i>menE</i>		o-Succinylbenzoate-CoA synthase	116
<i>ubiA</i>		4-Hydroxybenzoate → 3-octaprenyl-4-hydroxybenzoate	116, 1157, 1489
<i>ubiB</i>		2-Octaprenylphenol → 2-octaprenyl-6-methoxyphenol	116
<i>ubiC</i>		Chorismate lyase	116, 1157, 1489
<i>ubiD</i>		3-Octaprenyl-4-hydroxy-benzoate → 2-octaprenylphenol	116, 909
<i>ubiE</i>		2-Octaprenyl-6-methoxy-1,4-benzoquinone → 2-octaprenyl-3-methy-6-methoxy-1,4-benzoquinone	116
<i>ubiF</i>		2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone → 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone	116, 286
<i>ubiG</i>		2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone → ubiquinone 8	116, 528
<i>ubiH</i>		2-Octaprenyl-6-methoxyphenol → 2-octaprenyl-6-methoxy-1,4-benzoquinone	116
<i>ubiX</i>		Putative polyproprenyl p-hydroxybenzoate carboxylase	1167
12. Heme and porphyrins			
<i>cysG</i>		Uroporphyrinogen III methylase; siroheme biosynthesis (EC 2.1.1.-)	1238, 1716, 1717
<i>hemB</i>	<i>ncf</i>	5-Aminolevulinate dehydratase (EC 4.2.1.24) activity	415, 933, 1191
<i>hemC</i>	<i>popE</i>	Porphobilinogen deaminase (hydroxymethylbilane synthase) (EC 4.3.1.8)	751, 872, 1086
<i>hemD</i>		Uroporphyrinogen III synthase (EC 4.2.1.75)	30

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>hemE</i>	<i>hemC</i>	Uroporphyrinogen decarboxylase (EC 4.1.1.37)	1416
<i>hemF</i>	<i>popB, sec</i>	Coproporphyrinogen III oxidase (EC 1.3.3.3)	306
<i>hemG</i>		Protoporphyrinogen oxidase activity	1415
<i>hemH</i>	<i>visA?</i> , <i>popA</i> , <i>hemG</i>	Ferrochelatase (EC 4.99.1.1)	1095
<i>hemL</i>	<i>popC</i>	Glutamate-1-semialdehyde aminotransferase (-2,1-aminomutase) (EC 5.4.3.8)	566, 702, 703
<i>hemX</i>		Putative uroporphyrinogen III methylase (EC 2.1.1.-)	1417
<i>popD</i>		5-Aminolevulinate dehydratase (EC 4.2.1.24) activity	1513
E. Fatty acids and lipids			
<i>aas</i>		2-Acylglycerophosphoethanolamine acyltransferase, and acyl-acyl-carrier protein synthetase	672
<i>accA</i>		Acetyl-CoA carboxylase, carboxytransferase component, α sub-unit (EC 6.4.1.2)	937
<i>accB</i>	<i>fabE</i>	Acetyl-CoA carboxylase, BCCP ^a subunit (EC 6.4.1.2)	936
<i>accC</i>	<i>fabG</i>	Acetyl-CoA carboxylase, biotin carboxylase subunit (EC 6.3.4.14)	831, 1315
<i>accD</i>	<i>dedB, usg</i>	Acetyl-CoA carboxylase, carboxytransferase component, β sub-unit (EC 6.4.1.2)	937, 938
<i>acpP</i>		Acyl carrier protein	1315
<i>acpS</i>		CoA:apo-[acyl-carrier-protein] pantetheinephosphotransferase (EC 2.7.8.7) = holo-[acyl-carrier-protein] synthase	1292
<i>cdh</i>		CDP-diglyceride hydrolase (EC 3.6.1.26)	692
<i>cdsA</i>		CDP-diglyceride synthetase (CTP:phosphatidate cytidyltransferase) (EC 2.7.7.41)	693
<i>cdsS</i>		Stability of CDP-diglyceride synthetase activity	499
<i>cfa</i>	<i>cdfA</i>	Cyclopropane fatty acid synthase (EC 2.1.1.79)	1706a
<i>cls</i>		Cardiolipin synthase activity (EC 2.7.8.-)	649, 1481
<i>dgkA</i>		Diglyceride kinase (EC 2.7.1.107)	1386
<i>dgkR</i>		Level of diglyceride kinase	1307
<i>fabA</i>		β -Hydroxydecanoyl thioester dehydrase (EC 4.2.1.60)	309, 1469
<i>fabB</i>	<i>fabC</i>	3-Oxoacyl-[acyl-carrier-protein] synthase I (EC 2.3.1.41)	793, 1490, 1645
<i>fabD</i>		Malonyl-CoA-[acyl-carrier-protein] transacylase (EC 2.3.1.39)	1002, 1680
<i>fabF</i>	<i>cvc, vtrB</i>	3-Oxoacyl-[acyl-carrier-protein] synthase II (EC 2.3.1.41)	731, 1490
<i>fabH</i>		3-Oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41)	1644
<i>glpK</i>		Glycerol kinase (EC 2.7.1.30)	1250, 1731
<i>lpxA</i>		UDP-N-acetylglucosamine acetyltransferase (EC 2.4.1.-)	313, 496
<i>lpxB</i>	<i>pgsB</i>	Tetraacyldisaccharide-1-phosphate synthetase; early step in lipid A biosynthesis	313
<i>pgpA</i>		Phosphatidylglycerophosphate phosphatase, membrane bound (EC 3.1.3.27)	493, 690
<i>pgpB</i>		Phosphatidylglycerophosphate phosphatase, membrane bound (EC 3.1.3.27)	493
<i>pgsA</i>		Phosphatidylglycerophosphate synthetase (EC 2.7.8.5) = CDP-1,2-diacyl-sn-glycero-3-phosphate phosphatidyl transferase	1162, 1163
<i>pldA</i>		Detergent-resistant phospholipase A activity (EC 3.1.1.32)	1139
<i>pldB</i>		Lysophospholipase L ₂ (EC 3.1.1.5), membrane protein	778, 822
<i>pldC</i>		Lysophospholipase L ₁ (EC 3.1.1.5)	778
<i>plsB</i>		Glycerolphosphate acyltransferase activity (EC 2.3.1.15)	297, 1753
<i>plsC</i>		1-Acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	283
<i>plsX</i>		Glycerolphosphate auxotrophy in <i>plsB</i> background	882
<i>psd</i>		Phosphatidylserine decarboxylase (EC 4.1.1.65)	934, 935
<i>pssA</i>		Phosphatidylserine synthetase (EC 2.7.8.8)	356
<i>pssR</i>		Regulator of <i>pssA</i>	1511
<i>sbm</i>		Methylmalonyl-CoA mutase (MCM) (EC 5.4.9.2)	1374
F. Polyamines			
<i>speA</i>		Arginine decarboxylase (EC 4.1.1.19)	143, 1101, 1783
<i>speB</i>		Agmatinase (EC 3.5.3.11)	1580, 1581, 1783
<i>speC</i>		Ornithine decarboxylase isozyme (EC 4.1.1.17)	143, 1218
<i>speD</i>		S-Adenosylmethionine decarboxylase (EC 4.1.1.50)	1583, 1783
<i>speE</i>		Spermidine synthase = putrescine aminopropyltransferase (EC 2.5.1.16)	1783
<i>speF</i>		Ornithine decarboxylase isozyme, inducible (EC 4.1.1.17)	785

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
III. Macromolecule metabolism			
A. Synthesis and modification			
1. Ribosomal and “stable” RNAs			889, 1524
<i>rrfS</i>		Stable 4.5S RNA	195, 1239, 1274
<i>rrfA</i>		5S rRNA	422, 1199, 1742
<i>rrfB</i>		5S rRNA	422, 1199, 1742
<i>rrfC</i>		5S rRNA	422, 1199, 1742
<i>rrfD</i>		5S rRNA	422, 1199, 1742
<i>rrfE</i>		5S rRNA	422, 1199, 1742
<i>rrfG</i>		5S rRNA	422, 1199, 1742
<i>rrfH</i>		5S rRNA	53
<i>rrlA</i>		23S rRNA	185, 1093, 1604
<i>rrlB</i>		23S rRNA	185, 1093, 1604
<i>rrlC</i>		23S rRNA	185, 1093, 1604
<i>rrlD</i>		23S rRNA	185, 1093, 1604
<i>rrlE</i>		23S rRNA	185, 1093, 1604
<i>rrlG</i>		23S rRNA	185, 1093, 1604
<i>rrlH</i>		23S rRNA	185, 1093, 1604
<i>rrsA</i>		16S rRNA	316, 884, 1014
<i>rrsB</i>		16S rRNA	316, 884, 1014
<i>rrsC</i>		16S rRNA	316, 558, 884
<i>rrsD</i>		16S rRNA	316, 558, 884
<i>rrsE</i>		16S rRNA	316, 558, 884
<i>rrsG</i>		16S rRNA	316, 558, 884
<i>rrsH</i>		16S rRNA	316, 558, 884
<i>rrvD</i>	<i>rrfD</i>	Second copy of 5S rRNA in <i>rrnD</i> operon	410
<i>ssr</i>		Stable 6S RNA	673
<i>ssrA</i>		10Sa RNA, nonribosomal	1181
2. Ribosomal proteins and their modification			
<i>ksgC</i>		Kasugamycin resistance; affects ribosomal protein S2	1803
<i>prmA</i>	<i>prm-1</i>	Methylation of 50S ribosomal subunit protein L11	288
<i>prmB</i>	<i>prm-2</i>	Methylation of 50S ribosomal subunit protein L3	288
<i>rimE</i>		Modification of ribosomal proteins	858
<i>rimK</i>		Ribosomal protein S6 modification protein	773
<i>rimG</i>	<i>ramB</i>	Modification of 30S ribosomal subunit protein S4	1828
<i>rimI</i>		Modification of 30S ribosomal subunit protein S18; acetylation of N-terminal alanine (EC 2.3.1.-)	1801
<i>rimJ</i>		Modification of 30S ribosomal subunit protein S5; acetylation of N-terminal alanine (EC 2.3.1.-)	1801
<i>rimL</i>		Modification of 30S ribosomal subunit protein L7; acetylation of N-terminal serine (EC 2.3.1.-)	1598
<i>rplA</i>	<i>rpy</i>	50S ribosomal subunit protein L1, regulates synthesis of L1 and L11	423, 1396
<i>rplB</i>		50S ribosomal subunit protein L2	423, 1361
<i>rplC</i>		50S ribosomal subunit protein L3	1569
<i>rplD</i>	<i>eryA</i>	50S ribosomal subunit protein L4, regulates synthesis of S10 ribosomal protein operon	1818, 1819
<i>rplE</i>		50S ribosomal subunit protein L5	984
<i>rplF</i>		50S ribosomal subunit protein L6	1199
<i>rplI</i>		50S ribosomal subunit protein L9	557
<i>rplJ</i>		50S ribosomal subunit protein L10	1816
<i>rplK</i>	<i>relC</i>	50S ribosomal subunit protein L11	424, 777
<i>rplL</i>		50S ribosomal subunit protein L7/L12	1246, 1816
<i>rplM</i>		50S ribosomal subunit protein L13	1199
<i>rplN</i>		50S ribosomal subunit protein L14	1199, 1276
<i>rplO</i>		50S ribosomal subunit protein L15	479
<i>rplP</i>		50S ribosomal subunit protein L16	479, 1361
<i>rplQ</i>		50S ribosomal subunit protein L17	1199
<i>rplR</i>		50S ribosomal subunit protein L18	422
<i>rplS</i>		50S ribosomal subunit protein L19	1748
<i>rplT</i>	<i>pdzA</i>	50S ribosomal subunit protein L20, and regulator	912, 1569
<i>rplU</i>		50S ribosomal subunit protein L21	1199
<i>rplV</i>	<i>eryB</i>	50S ribosomal subunit protein L22	57

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)	
<i>rplW</i>		50S ribosomal subunit protein L23	423	
<i>rplX</i>		50S ribosomal subunit protein L24	1199	
<i>rplY</i>		50S ribosomal subunit protein L25	477	
<i>rpmA</i>	<i>rpz</i>	50S ribosomal subunit protein L27	1772	
<i>rpmB</i>		50S ribosomal subunit protein L28	1199	
<i>rpmC</i>		50S ribosomal subunit protein L29	557, 1199	
<i>rpmD</i>		50S ribosomal subunit protein L30	1199	
<i>rpmE</i>		50S ribosomal subunit protein L31	557	
<i>rpmF</i>		50S ribosomal subunit protein L32	1600	
<i>rpmG</i>		50S ribosomal subunit protein L33	1199	
<i>rpmH</i>		50S ribosomal subunit protein L34	677	
<i>rpmI</i>		50S ribosomal subunit protein A (L35)	912	
<i>rpmJ</i>		50S ribosomal subunit protein X	1657	
<i>rpsA</i>	<i>rps, ssyF</i>	30S ribosomal subunit protein S1	883, 1280, 1348	
<i>rpsB</i>		30S ribosomal subunit protein S2	33	
<i>rpsC</i>		30S ribosomal subunit protein S3	174, 196, 397	
<i>rpsD</i>		30S ribosomal subunit protein S4	23, 397	
<i>rpsE</i>		30S ribosomal subunit protein S5	397, 557	
<i>rpsF</i>		30S ribosomal subunit protein S6	1541	
<i>rpsG</i>		30S ribosomal subunit protein S7	397, 1014	
<i>rpsH</i>		30S ribosomal subunit protein S8	1040, 1771	
<i>rpsI</i>		30S ribosomal subunit protein S9	1744	
<i>rpsJ</i>		30S ribosomal subunit protein S10	1033	
<i>rpsK</i>		30S ribosomal subunit protein S11	1744	
<i>rpsL</i>		30S ribosomal subunit protein S12	23, 126	
<i>rpsM</i>		30S ribosomal subunit protein S13	1579	
<i>rpsN</i>		30S ribosomal subunit protein S14	557	
<i>rpsO</i>	<i>secC</i>	30S ribosomal subunit protein S15	1014, 1276	
<i>rpsP</i>		30S ribosomal subunit protein S16	1748	
<i>rpsQ</i>	<i>nea</i>	30S ribosomal subunit protein S17	557, 1744	
<i>rpsR</i>		30S ribosomal subunit protein S18	1098	
<i>rpsS</i>		30S ribosomal subunit protein S19	1732	
<i>rpsT</i>	<i>supS20</i>	30S ribosomal subunit protein S20	299	
<i>rpsU</i>		30S ribosomal subunit protein S21	174	
<i>strM</i>		Control of ribosomal ambiguity	1406	
3. Ribosomes and their maturation and modification				
<i>fusB</i>		Pleiotropic effects on RNA synthesis, ribosomes, and ribosomal protein S6	1589	
<i>rimB</i>		Maturation of 50S ribosomal subunit	199	
<i>rimC</i>		Maturation of 50S ribosomal subunit	199	
<i>rimD</i>		Maturation of 50S ribosomal subunit	199	
<i>rimF</i>	<i>res</i>	Modification of ribosome	507	
<i>rimH</i>		Modification of ribosome	746	
<i>rit</i>		Affects thermolability of 50S ribosomal subunit	1192	
<i>rmf</i>		Ribosome modulation factor	1694	
4. tRNAs and their modification, aminoacyl-tRNA synthetases				
<i>aat</i>		Aminoacyl-tRNA-protein transferase (EC 2.3.2.6)	376	
<i>alaS</i>	<i>lovB, ala-act</i>	Alanine tRNA synthetase (EC 6.1.1.7)	666, 1088	
<i>alaT</i>		Alanine tRNA 1B (duplicate of <i>alaU, V</i>)	1225, 1595, 1597	
<i>alaU</i>		Alanine tRNA 1B (duplicate of <i>alaT, V</i>)	1225, 1595, 1597	
<i>alaV</i>		Alanine tRNA 1B (duplicate of <i>alaT, U</i>)	1225, 1595, 1597	
<i>alaW</i>		Alanine tRNA 2 (duplicate of <i>alaX</i>)	1225, 1595, 1597	
<i>alaX</i>		Alanine tRNA 2 (duplicate of <i>alaW</i>)	1225, 1595, 1597	
<i>argQ</i>		Arginine tRNA 2 (duplicate of <i>argV, Y, Z</i>)	1049	
<i>argS</i>		<i>lov</i>	Arginine tRNA synthetase (EC 6.1.1.19)	121, 442, 952
<i>argU</i>		Arginine tRNA 4	243, 247, 1427	
<i>argV</i>		Arginine tRNA 2 (duplicate of <i>argQ, Y, Z</i>)	1049	
<i>argW</i>		Arginine tRNA 5	1049	
<i>argX</i>		Arginine tRNA 3	1049	
<i>argY</i>	<i>argVβ</i>	Arginine tRNA 2 (duplicate of <i>argV, Q, Z</i>)	1049	
<i>argZ</i>		Arginine tRNA 2 (duplicate of <i>argV, Y, Q</i>)	1049	
<i>asnS</i>		Asparagine tRNA synthetase (EC 6.1.1.22)	49, 642, 1001	
<i>asnT</i>		Asparagine tRNA	829	

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>asnU</i>		Asparagine tRNA	829
<i>asnV</i>		Asparagine tRNA	829
<i>aspS</i>	<i>ts</i>	Aspartate tRNA synthetase (EC 6.1.1.12)	443, 642
<i>aspT</i>	<i>tasC</i>	Aspartate tRNA 1 (duplicate of <i>aspV, U</i>)	829
<i>aspU</i>		Aspartate tRNA 1 (duplicate of <i>aspT, V</i>)	829
<i>aspV</i>		Aspartate tRNA 1 (duplicate of <i>aspT, U</i>)	829
<i>cca</i>		tRNA nucleotidyl transferase (EC 2.7.7.25)	1825
<i>cysS</i>		Cysteine tRNA synthetase (EC 6.1.1.16)	444, 667, 1217
<i>cysT</i>		Cysteine tRNA	1217, 1495
<i>divE</i>		tRNA ^{Ser¹} , affects cell division	1421, 1594
<i>fmt</i>		10-Formyltetrahydrofolate:L-methionyl-tRNA ^{fMet} N-formyltransferase (EC 2.1.2.9)	576, 892
<i>glnR</i>		Affects level of glutaminyl-tRNA synthetase	259
<i>glnS</i>		Glutamine tRNA synthetase (EC 6.1.1.18)	439, 608, 735
<i>glnT</i>		Affects level of glutamine tRNA 1 and glutamine synthetase	
<i>glnU</i>	<i>glnUα, supB</i>	Glutamine tRNA 1 (duplicate of <i>glnW</i>), suppressor of ochre (UAA) and amber (UAG) mutations	439, 735, 1353
<i>glnV</i>	<i>glnVα, Su2, sull</i>	Glutamine tRNA 2 (duplicate of <i>glnX</i>), suppressor of amber (UAG) mutations	439, 735, 1353
<i>glnW</i>	<i>supE</i>	Glutamine tRNA 1 (duplicate of <i>glnU</i>), suppressor of ochre (UAA) and amber (UAG) mutations	439, 735, 1353
<i>glnX</i>	<i>glnUβ</i>	Glutamine tRNA 1 (duplicate of <i>glnV</i>), suppressor of amber (UAG) mutations	439, 735, 1353
<i>glnX</i>	<i>glnVβ</i>	Glutamine tRNA 2 (duplicate of <i>glnV</i>), suppressor of amber (UAG) mutations	439, 735, 1353
<i>gltE</i>		Glutamate tRNA synthetase activity	877, 1129
<i>gltM</i>		Level of glutamate tRNA synthetase activity	1129
<i>gltT</i>	<i>tgtB</i>	Glutamate tRNA 2 (duplicate of <i>gltU, V, W</i>)	829
<i>gltU</i>	<i>tgtC</i>	Glutamate tRNA 2 (duplicate of <i>gltT, V, W</i>)	829
<i>gltV</i>	<i>tgtE</i>	Glutamate tRNA 2 (duplicate of <i>gltT, U, W</i>)	829
<i>gltW</i>		Glutamate tRNA 2 (duplicate of <i>gltT, U, V</i>)	829
<i>gltX</i>		Catalytic subunit for glutamate tRNA synthetase (EC 6.1.1.17)	189, 550, 1172
<i>glyQ</i>		Glycine tRNA synthetase, α chain (EC 6.1.1.14)	1631, 1632
<i>glyS</i>		Glycine tRNA synthetase, β chain (EC 6.1.1.14)	320
<i>glyT</i>		Glycine tRNA 2, suppressor	1050
<i>glyU</i>	<i>supA36, sumA, sup15B</i>	Glycine tRNA 1, suppressor	1050
<i>glyV</i>	<i>suA36, sufD</i>	Glycine tRNA 1, suppressor	1050
<i>glyV</i>	<i>supT, sumB</i>	Glycine tRNA 3 (duplicate of <i>glyX, Y, W</i>)	1050
<i>glyW</i>	<i>glnVα, suA78, suA58, ins</i>	Glycine tRNA 3 (duplicate of <i>glyV, X, Y</i>)	1050
<i>glyX</i>	<i>suA58, suA78, ins</i>	Glycine tRNA 3 (duplicate of <i>glyV, W, Y</i>)	1050
<i>glyY</i>	<i>glyVβ</i>	Glycine tRNA 3 (duplicate of <i>glyX, Y, W</i>)	1050
<i>hemM</i>		Glutamate tRNA dehydrogenase	406, 701, 932
<i>hisR</i>	<i>hisT</i>	Histidine tRNA	640
<i>hisS</i>		Histidine tRNA synthetase (EC 6.1.1.21)	640
<i>hisT</i>	<i>leuK, asuC</i>	Pseudouridine synthase I (EC 4.2.1.70)	346, 771, 1649
<i>ileS</i>		Isoleucine tRNA synthetase (EC 6.1.1.5)	1172, 1754
<i>ileT</i>	<i>tilA</i>	Isoleucine tRNA 1 (duplicate of <i>ileU, V</i>)	829
<i>ileU</i>	<i>tilD</i>	Isoleucine tRNA 1 (duplicate of <i>ileT, V</i>)	829
<i>ileV</i>		Isoleucine tRNA 1 (duplicate of <i>ileT, U</i>)	829
<i>ileX</i>		Isoleucine tRNA 2	829
<i>ilvU</i>		Regulator for <i>ileS</i> and modifier of isoleucine tRNA 2 and valine tRNA 2	457
<i>leuP</i>	<i>leuVβ</i>	Leucine tRNA 1 (duplicate of <i>leuQ, T, V</i>)	829
<i>leuQ</i>	<i>leuVγ</i>	Leucine tRNA 1 (duplicate of <i>leuP, T, V</i>)	829
<i>leuR</i>		Level of leucine tRNA synthetase	1611
<i>leuS</i>		Leucine tRNA synthetase (EC 6.1.1.4)	1743, 1757
<i>leuT</i>		Leucine tRNA 1 (duplicate of <i>leuQ, P, V</i>)	829
<i>leuU</i>		Leucine tRNA 2	829
<i>leuV</i>	<i>leuVα</i>	Leucine tRNA 1 (duplicate of <i>leuQ, P, T</i>)	829
<i>leuW</i>		Leucine tRNA 3	829
<i>leuX</i>	<i>Su-6, supP</i>	Leucine tRNA 5, suppressor of amber (UAG) mutations	1168
<i>leuY</i>		Level of leucine tRNA synthetase	1102
<i>leuZ</i>		Leucine tRNA 4	829
<i>trs</i>		Level of a single leucine tRNA	1661
<i>lysS</i>	<i>herC, asuD</i>	Lysine tRNA synthetase, constitutive; suppressor of ColE1 mutation in primer RNA (EC 6.1.1.6)	320

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>lysT</i>	<i>lysTa, supG, supL, sua</i>	Lysine tRNA (duplicate of <i>lysW, V</i>), suppressor of ochre (UAA) and amber (UAG) mutations	197
<i>lysU</i>		Lysine tRNA synthetase, inducible; heat shock protein (EC 6.1.1.6)	274, 916, 1145
<i>lysV</i>	<i>supN</i>	Lysine tRNA (duplicate of <i>lysT, W</i>), suppressor of ochre (UAA) and amber (UAG) mutations	829
<i>lysW</i>	<i>lysTβ, suaβ</i>	Lysine tRNA (duplicate of <i>lysT, W</i>), suppressor of ochre (UAA) and amber (UAG) mutations	829
<i>metG</i>		Methionine tRNA synthetase (EC 6.1.1.10)	526, 1057, 1676
<i>metT</i>	<i>metTa</i>	Methionine tRNA (duplicate of <i>metU</i>)	1444
<i>metU</i>	<i>metTβ</i>	Methionine tRNA (duplicate of <i>metT</i>)	1444
<i>metX</i>	<i>metZβ</i>	Methionine tRNA ^{fMet₁} (duplicate of <i>metZ</i>)	577, 1214, 1676
<i>metV</i>		Methionine tRNA ^{fMet₂}	801
<i>metZ</i>		Methionine tRNA ^{fMet₁} (duplicate of <i>metX</i>)	577, 1214, 1676
<i>miaA</i>	<i>metZα, trpX</i>	2-Methylthio-N6-isopentyladenosine hypermodification (EC 2.7.7.-)	294
<i>nuvA</i>		Uridine thiolation factor A activity	958, 1614
<i>nuvC</i>		4-Thiouridine modification of tRNA; near-UV sensitivity and resistance	958, 1614
<i>pheS</i>	<i>phe-act</i>	Phenylalanine tRNA synthetase (EC 6.1.1.20), α subunit	508, 787, 1249
<i>pheT</i>		Phenylalanine tRNA synthetase (EC 6.1.1.20), β subunit	508, 787, 1249
<i>pheU</i>	<i>pheW, pheR</i>	Phenylalanine tRNA (duplicate of <i>pheV</i>)	1, 508, 1249
<i>pheV</i>	<i>pheC</i>	Phenylalanine tRNA (duplicate of <i>pheU, R, W</i>)	1, 1249, 1261
<i>phtM</i>		Leader, phenylalanine tRNA synthetase	1213, 1519
<i>proK</i>	<i>proV</i>	Proline tRNA 1	829
<i>proL</i>	<i>proW</i>	Proline tRNA 2	829
<i>proM</i>	<i>proU, osrA</i>	Proline tRNA 3	829
<i>proS</i>	<i>drpA</i>	Proline tRNA synthetase (EC 6.1.1.15)	320
<i>pth</i>	<i>rap</i>	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	500, 1130
<i>queA</i>		tRNA modification, queine biosynthesis	1330
<i>selA</i>	<i>fdhA</i>	Selenocysteine synthase, step 1: L-seryl-tRNA dehydrated (EC 4.2.1.-)	473, 1425
<i>selC</i>	<i>fdhC</i>	Selenocystyl tRNA, when utilized, inserts at UGA	92, 940, 1425
<i>selD</i>	<i>fdhB</i>	Selenocysteine tRNA synthetase, step 2, H ₂ Se added to acrylyl-tRNA (EC 4.2.1.-)	473, 1425
<i>serR</i>		Level of seryl-tRNA synthetase	320
<i>serS</i>		Serine tRNA synthetase (EC 6.1.1.11); also charges selenocystein tRNA with serine	319, 1429
<i>serT</i>	<i>divE</i>	Serine tRNA 1	641, 1168, 1354
<i>serU</i>	<i>supD, supH, sul, Su-1, ftsM</i>	Serine tRNA 2; suppressor of amber (UAG) mutations	891, 1354
<i>serV</i>		Serine tRNA 3	641, 1168, 1354
<i>serW</i>		Serine tRNA 5 (duplicate of <i>serX</i>)	641, 1168, 1354
<i>serX</i>		Serine tRNA 5 (duplicate of <i>serW</i>)	641, 1168, 1354
<i>tgt</i>		tRNA-guanine transglycosylase (EC 2.4.2.29)	483
<i>thrS</i>		Threonine tRNA synthetase (EC 6.1.1.3)	1099, 1358
<i>thrT</i>		Threonine tRNA 3	603, 1613
<i>thrU</i>		Threonine tRNA 4	603, 1613
<i>thrV</i>		Threonine tRNA 1	603, 1613
<i>thrW</i>		Threonine tRNA 2	603, 1613
<i>trmA</i>		tRNA methyltransferase; tRNA (uracil-5)-methyltransferase (EC 2.1.1.35)	581, 1175, 1244
<i>trmB</i>		tRNA methyltransferase; tRNA (guanine-7)-methyltransferase (EC 2.1.1.33)	1026
<i>trmC</i>		tRNA methyltransferase; 5-methylaminoethyl-2-thiouridine biosynthesis	129, 586
<i>trmD</i>		tRNA methyltransferase; tRNA (guanine-1)-methyltransferase (EC 2.1.1.31)	214, 652, 1748
<i>trmE</i>	<i>asuE?</i>	tRNA methyltransferase; 5-methylaminoethyl-2-thiouridine biosynthesis	433
<i>trmF</i>		tRNA methyltransferase; 5-methylaminoethyl-2-thiouridine biosynthesis	433
<i>trnA</i>	<i>glnU</i>	Level of several tRNAs	259
<i>trpS</i>		Tryptophan tRNA synthetase (EC 6.1.1.2)	1073, 1353
<i>trpT</i>	<i>su8, su9, supU, supV, su7</i>	Tryptophan tRNA, suppressor of ochre (UAA) and amber (UAG) mutations	639, 1356
<i>tyrS</i>		Tyrosine tRNA synthetase (EC 6.1.1.1)	100, 102, 461

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>tyrT</i>	<i>tyrTa</i> , <i>Su-3</i> , <i>su_c</i> , <i>Su-4</i> , <i>supF</i> , <i>supE</i> , <i>tyrV</i> , <i>sulII</i> , <i>sul₃</i>	Tyrosine tRNA 1, duplicate of <i>tyrV</i> , suppressor of ochre (UAA) and amber (UAG) mutations; second gene product = rtT RNA, possible modulator	158, 641, 1081
<i>tyrU</i>	<i>supM</i>	Tyrosine tRNA 2, suppressor of ochre (UAA) and amber (UAG) mutations	641
<i>tyrV</i>	<i>tyrTβ</i>	Tyrosine tRNA 1 (duplicate of <i>tyrT</i>), suppressor of ochre (UAA) and amber (UAG) mutations	641
<i>valS</i>	<i>val-act</i>	Valine tRNA synthetase (EC 6.1.1.9)	268, 440
<i>valT</i>		Valine tRNA 1 (duplicate of <i>valU, X, Y</i>)	1596
<i>valU</i>	<i>valUα</i>	Valine tRNA 1 (duplicate of <i>valT, X, Y</i>)	197, 1596
<i>valV</i>		Valine tRNA 2B	1596
<i>valW</i>		Valine tRNA 2A	1596
<i>valX</i>	<i>valUβ</i>	Valine tRNA 1 (duplicate of <i>valT, U, Y</i>)	1596
<i>valY</i>	<i>valUγ</i>	Valine tRNA 1 (duplicate of <i>valT, U, X</i>)	1596
5. RNA synthesis, modification, and DNA transcription			
<i>dbpA</i>		Putative ATP-dependent RNA helicase	695
<i>dead</i>		Putative ATP-dependent RNA helicase	1630
<i>firA</i>	<i>skp?</i>	Transcription factor	381, 382, 1615
<i>hepA</i>		Probable RNA helicase	924, 1810
<i>nusA</i>		Transcription termination; L factor	533, 955
<i>nusB</i>	<i>groNB</i>	Transcription termination; L factor	1033, 1578
<i>nusG</i>		Component in transcription antitermination	955, 1567
<i>opr</i>		Rate of degradation of aberrant subunit proteins of RNA polymerase	1465
<i>pnp</i>		Polynucleotide phosphorylase (EC 2.7.7.8)	1323, 1793
<i>ranA</i>		RNA metabolism	53
<i>rhlB</i>		Putative ATP-dependent RNA helicase	760
<i>rho</i>	<i>psu</i> , <i>nitA</i> , <i>rnsC</i> , <i>tsu</i> , <i>SuA</i> , <i>sun</i>	Transcription termination factor Rho; polarity suppressor	390, 516, 540
<i>ridA</i>		Transcription and translation; dependence on rifampin and kasugamycin	321
<i>rne</i>	<i>ams</i>	RNase E activity, RNA processing, alteration of mRNA stability	425, 1113, 1526
<i>rpoA</i>	<i>phs</i> <i>sez</i>	RNA polymerase (EC 2.7.7.6), α subunit	609, 715, 1340
<i>rpoB</i>	<i>nitB</i> , <i>rif</i> , <i>tabD</i> , <i>ron</i> , <i>groN</i> , <i>stv</i> , <i>stl</i>	RNA polymerase (EC 2.7.7.6), β subunit	874, 1466, 1776
<i>rpoC</i>	<i>tabD</i>	RNA polymerase (EC 2.7.7.6), β' subunit	722, 994, 1247
<i>rpoZ</i>	<i>spoS</i>	DNA-directed RNA polymerase ω subunit (EC 2.7.7.6)	519, 520, 694
<i>srmB</i>		ATP-dependent RNA helicase (EC 2.7.7.-)	1161
6. Basic proteins			
<i>hns</i>	<i>bglY</i> , <i>drdX</i> , <i>fimG</i> , <i>topS</i> , <i>pilG</i> , <i>cur</i>	Histone-like protein HLP-II (HU, BH2, HD, NS); pleiotropic regulator	1044, 1520, 1785
<i>hupA</i>		DNA-binding protein HU- α (HU-2)	404, 548, 825
<i>hupB</i>	<i>hopD</i>	Histone-like protein HU-1 (HU- β , NS1)	404, 405, 548
<i>tpr</i>		A protaminelike protein	158
7. DNA (replication, restriction/modification, recombination, and repair)			
<i>aidB</i>		Induced by alkylating agents	1687
<i>aidC</i>		Induced by alkylating agents	1689
<i>alkA</i>	<i>aidA</i>	3-Methyl-adenine DNA glycosylase II, inducible (EC 3.2.2.-)	757, 1687, 1688
<i>alkB</i>	<i>aidD</i>	DNA repair system specific for alkylated DNA	830, 1687, 1688
<i>cer</i>		Site-specific recombinase	287
<i>dam</i>		DNA adenine methylase (EC 2.1.1.72)	83, 119, 1174
<i>dcm</i>	<i>mec</i>	DNA cytosine methylase (EC 2.1.1.73)	943
<i>del</i>		Frequency of IS1-mediated deletion	1154
<i>dfp</i>	<i>dnaS</i> , <i>dut</i>	Flavoprotein affecting synthesis of DNA and pantothenate metabolism	1517
<i>dinF</i>		Induced by UV and mitomycin C; subject to <i>recA</i> and <i>lexA</i> regulation	1616
<i>dnaA</i>		DNA biosynthesis; initiation of chromosome replication; global transcription regulator	311, 535, 659

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>dnaB</i>	<i>groP, grpA</i>	Chromosome replication; chain elongation	21, 1696, 1697
<i>dnaC</i>	<i>dnaD</i>	Chromosome replication; initiation and chain elongation	1028, 1696, 1697
<i>dnaE</i>	<i>polC</i>	DNA polymerase III, α chain (EC 2.7.7.7)	1561, 1775
<i>dnaG</i>	<i>dnaP, parB</i>	DNA biosynthesis; DNA primase (EC 2.7.7.-)	572, 1531
<i>dnaI</i>		DNA biosynthesis	824, 1601
<i>dnaJ</i>	<i>groPAB, grpC, groPC</i>	DNA biosynthesis; heat shock protein	497, 876, 1477
<i>dnaK</i>	<i>groPAB, grpC, grpF, groPC, groPF</i>	DNA biosynthesis; heat shock protein	876, 1558, 1750
<i>dnaL</i>	<i>dnaK</i>	DNA biosynthesis	1464
<i>dnaN</i>		DNA polymerase III holoenzyme, β subunit (EC 2.7.7.7)	563, 1561, 1775
<i>dnaQ</i>	<i>mutD</i>	DNA polymerase III holoenzyme, ϵ subunit; mutant alleles have mutator activity (EC 2.7.7.7)	1560, 1561, 1775
<i>dnaT</i>		DNA biosynthesis; primosomal protein i	1031
<i>dnaX</i>	<i>dnaZ</i>	DNA polymerase III holoenzyme, τ and γ subunits; DNA elongation factor III	1560, 1648, 1775
<i>endA</i>		DNA-specific endonuclease I	947
<i>fis</i>		Site-specific DNA inversion stimulation factor; DNA-binding protein; a transactivator for transcription	534, 841, 1202
<i>fpg</i>		Formamidopyrimidine DNA glycosylase	150, 151, 559
<i>gidA</i>		Glucose-inhibited division; chromosome replication?	65
<i>gidB</i>		Glucose-inhibited division; chromosome replication?	65
<i>gyrA</i>	<i>nalA</i>	DNA gyrase (EC 5.99.1.3), subunit A, resistance or sensitivity to nalidixic acid, DNA cleavage with transient covalent bonding	19, 1193, 1320
<i>gyrB</i>	<i>acrB, cou, pcbA, himB, nalC, D</i>	DNA gyrase (EC 5.99.1.3) subunit B, resistance or sensitivity to coumermycin, DNA cleavage with transient covalent bonding, ATPase activity	19, 1193, 1320
<i>helD</i>		DNA helicase IV (EC 3.6.1.-)	1766
<i>het</i>	<i>cop</i>	Binding of DNA sequences in OriC region to outer membrane; structural gene for DNA-binding protein?	1762
<i>himA</i>	<i>hid</i>	Integration host factor (IHF), α subunit; site-specific recombination	161, 775, 893
<i>himD</i>	<i>hip</i>	Integration host factor (IHF), β subunit; site-specific recombination	161, 548, 893
<i>holA</i>		DNA polymerase III, δ subunit (EC 2.7.7.7)	223, 395, 1775
<i>holB</i>		DNA polymerase III, δ' subunit (EC 2.7.7.7)	395, 1775
<i>holC</i>		DNA polymerase III, χ subunit (EC 2.7.7.7)	1775
<i>holD</i>		DNA polymerase III, ψ subunit (EC 2.7.7.7)	1775
<i>holE</i>		DNA polymerase III, θ subunit (EC 2.7.7.7)	568, 1775
<i>hsdM</i>	<i>rm, hsm, hsp, hs</i>	Host modification; DNA methylase M (EC 2.1.1.72)	978, 1289
<i>hsdS</i>	<i>rm, hss, hsp, hs</i>	Specificity determinant for <i>hsdM</i> and <i>hsdR</i>	978, 1289
<i>iciA</i>		Inhibitor of replication replication	686
<i>lig</i>		DNA ligase (EC 6.5.1.2)	902
<i>mcrC</i>		Component of methylcytosine restriction system	386, 846, 1823
<i>mfd</i>		Mutation frequency decline; transcription-repair coupling factor	506, 1460
<i>mioC</i>		Initiation of chromosome replication	976
<i>mmrA</i>		Recovery in rich medium following UV irradiation	998, 1470
<i>mrr</i>		Restriction of methylated adenine	1698
<i>msp</i>		Sensitivity or resistance of male strains to male-specific phages R17 and f2	209
<i>mutA</i>		Mutator, transversion specific	1079
<i>mutC</i>		Mutator, transversion specific	1079
<i>mutH</i>	<i>prv, mutR</i>	Methyl-directed mismatch repair	70, 1428, 1736
<i>mutL</i>	<i>mut-25</i>	Methyl-directed mismatch repair	111, 1428, 1778
<i>mutS</i>	<i>fdv</i>	Methyl-directed mismatch repair	70, 275, 942
<i>mutY</i>	<i>micA</i>	Adenine glycosylase; G → C → T → A transversions (EC 3.2.2.-)	69
<i>ogt</i>		O6-Alkylguanine-DNA/cysteine-protein methyltransferase (EC 2.1.1.63)	1281, 1319
<i>parC</i>		Topoisomerase IV subunit A (EC 5.99.1.-)	791, 792
<i>parE</i>		Topoisomerase IV subunit B (EC 5.99.1.-)	791
<i>phr</i>		Photoreactivation; deoxyribodipyrimidine photolyase (EC 4.1.99.3)	1790
<i>polA</i>	<i>resA</i>	DNA polymerase I (EC 2.7.7.7)	465, 1220, 1270
<i>polB</i>		DNA polymerase II (EC 2.7.7.7)	245, 679
<i>priA</i>		Primosomal protein N' (= factor Y)	894, 1173, 1814
<i>priB</i>		Primosomal replication protein N	22, 1813
<i>priC</i>		Primosomal replication protein N"	1813

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>recA</i>	<i>lexB, tif, umuB, zab, rnmB, recH</i>	General recombination, DNA repair, and induction of phage λ (EC 3.4.99.37)	1114, 1118, 1809
<i>recB</i>	<i>rorA</i>	Recombination and DNA repair; exonuclease V (EC 3.1.11.5)	147, 1215
<i>recC</i>		Recombination and DNA repair; exonuclease V (EC 3.1.11.5)	147, 1215
<i>recD</i>		Recombination and DNA repair; exonuclease V (EC 3.1.11.5) α subunit	147, 1215
<i>recF</i>	<i>uvrF</i>	Recombination and DNA repair	564, 1409
<i>recG</i>		Probable ATP-dependent DNA helicase	767, 968, 971
<i>recJ</i>		Exonuclease specific for single-stranded DNA; recombination and DNA repair	970, 985, 986
<i>recN</i>	<i>radB</i>	Recombination and DNA repair	969, 1368
<i>recO</i>		Conjugational recombination and DNA repair	1104
<i>recQ</i>		ATP-dependent DNA helicase, conjugational recombination and DNA repair	1660
<i>recR</i>		<i>recB</i> - and <i>recC</i> -independent recombinational repair	1006
<i>rep</i>	<i>dasC?</i> , <i>mmrA?</i>	<i>rep</i> helicase, a single-stranded DNA-dependent ATPase (EC 3.6.1.-)	238, 980, 1763
<i>rra</i>		Reverses <i>recBC</i> , <i>sbcA</i> alleviation of Rgl restriction of glucosyl-free DNA containing hydroxymethyl- and methylcytosine	774
<i>rvuA</i>		Branch migration of Holliday structures; repair	1230, 1480, 1643
<i>rvuB</i>		Branch migration Holliday structures; repair	1230, 1480, 1643
<i>rvuC</i>		Holliday junction nuclease; resolution of structures; repair	293, 968, 1586
<i>sbcB</i>	<i>xonA</i>	Exonuclease I; suppressor of <i>recB</i> and <i>recC</i> mutations (EC 3.1.11.1)	24, 1251
<i>sbcC</i>		Suppression of <i>recB</i> and <i>recC</i> mutations; recombination functions	1148
<i>ssb</i>	<i>exrB, lexC</i>	Single-stranded DNA-binding protein	204
<i>tag</i>		3-Methyladenine DNA glycosylase I, constitutive (EC 3.2.2.-)	128, 757
<i>tdi</i>		Transduction, transformation, and rates of mutation	1530
<i>toc</i>	<i>gyrB?</i>	Suppressor of <i>topA</i>	399
<i>topA</i>	<i>supX</i>	DNA topoisomerase I, ω protein (EC 5.99.1.2)	1096, 1833
<i>topB</i>	<i>mutR</i>	DNA topoisomerase III (EC 5.99.1.2)	385
<i>tus</i>	<i>tau</i>	DNA-binding protein; inhibition of replication at Ter sites	553, 633, 810
<i>umuC</i>	<i>uvn</i>	Induction of mutations by UV; error-prone repair; forms complex with UmuD and UmuD'	80, 823, 1768
<i>umuD</i>	<i>uvn</i>	Induction of mutations; error-prone repair; processed to UmuD'; forms complex with UmuC	80, 823, 1768
<i>ung</i>		Uracil-DNA-glycosylase (EC 3.2.2.-)	469, 1675
<i>uup</i>		Precise excision of insertion element	663
<i>uvrA</i>	<i>dar</i>	Repair of UV damage to DNA; excision nuclease	269, 833, 1045
<i>uvrB</i>	<i>visB, dar-1, 6</i>	DNA repair; excision nuclease	1196, 1456, 1457
<i>uvrC</i>	<i>dar-4, 5</i>	Repair of UV damage to DNA; excision nuclease	948, 1197, 1459
<i>uvrD</i>	<i>mutU, pdeB, rad, recl, dda, dar-2, uvrE, uvr 502</i>	DNA-dependent ATPase I and helicase II (EC 3.6.1.-)	238, 1718
<i>vsr</i>		DNA patch repair protein	624, 943, 1505
<i>xerC</i>		Site-specific recombinase of λ integrase family, acts on <i>cer</i> sequence of ColE1 and probably effects chromosome segregation at cell division	139, 287

8. Proteins (translation and modification)

<i>dsbA</i>	<i>ppfA</i>	Required for disulfide bond formation	91, 768
<i>frr</i>		Ribosome-releasing factor	689, 1482
<i>fusA</i>	<i>far</i>	Protein chain elongation factor EF-G	1097
<i>glnD</i>		Uridylyltransferase acts on regulator of <i>glnA</i>	67
<i>glnE</i>		Adenylylating enzyme for glutamine synthetase (EC 2.7.7.42)	27
<i>greA</i>		Elongation factor: cleaves 3' nucleotide of paused mRNA	157, 1509, 1510
<i>hha</i>		Hemolysin expression-modulating protein	1158
<i>iap</i>		Alkaline phosphatase isozyme conversion, aminopeptidase	716, 1147
<i>infA</i>		Protein chain initiation factor IF-1	315
<i>infB</i>	<i>ssyG</i>	Protein chain initiation factor IF-2	861, 1105, 1393
<i>infC</i>		Protein chain initiation factor IF-3	1127
<i>map</i>		Methionine aminopeptidase (EC 3.4.11.18)	110
<i>pcm</i>	<i>fit</i>	L-Isoaspartate protein carboxylmethyltransferase type II (EC 2.1.1.77)	489

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>ppiA</i>		Peptidyl-prolyl <i>cis-trans</i> isomerase A (a rotamase) (EC 5.2.1.8)	607, 964
<i>ppiB</i>		Peptidyl-prolyl <i>cis-trans</i> isomerase B (a rotamase) (EC 5.2.1.8)	607, 964
<i>prfA</i>	<i>sueB</i> , <i>uar</i> , <i>asuA?</i> , <i>ups?</i>	Protein synthesis release factor 1	308
<i>prfB</i>	<i>supK</i>	Protein synthesis release factor 2	308, 1083
<i>selB</i>	<i>fdhA</i>	Selenocysteinyl-tRNA-specific translation factor	474, 1425
<i>tsf</i>		Protein chain elongation factor EF-Ts	33, 687
<i>tufA</i>		Protein chain elongation factor EF-Tu	810, 1097, 1255
<i>tufB</i>		Protein chain elongation factor EF-Tu	810, 1604
<i>ups</i>		Efficiency of nonsense suppressors	341
9. Polysaccharides (cytoplasmic)			
<i>glgA</i>		Glycogen synthase (EC 2.4.1.21)	1360
<i>glgB</i>		1,4- α -Glucan branching enzyme (EC 2.4.1.18)	1360
<i>glgC</i>		Glucose-1-phosphate adenyltransferase (EC 2.7.7.27)	637, 901, 1077
<i>glgP</i>		Glycogen phosphorylase (EC 2.4.1.1)	1431, 1432, 1808
<i>glgS</i>		Glycogen biosynthesis, <i>rpoS</i> dependent	621
B. Degradation of macromolecules			
1. RNA			
<i>rna</i>	<i>rnsA</i> , <i>rns</i>	RNase I (EC 3.1.27.6)	1056, 1826
<i>rnb</i>		RNase II (EC 3.1.13.1)	396, 799
<i>rnc</i>		RNase III (EC 3.1.26.3)	249, 1322, 1527
<i>rnd</i>		RNase D (EC 3.1.26.3)	1820, 1821
<i>rnhA</i>	<i>dasF</i> , <i>herA</i> , <i>sin</i> , <i>sdrA</i>	RNase H (EC 3.1.26.4)	312, 721
<i>rnhB</i>		RNase HII (EC 3.1.26.4)	720
<i>rnpA</i>		RNase P, protein component (EC 3.1.26.5)	377, 1526, 1573
<i>rnpB</i>		RNase P, RNA component	377, 1526, 1573
<i>rnt</i>		RNase T, degradation of tRNA	1211
<i>rph</i>		RNase PH	377
<i>srnA</i>		Degradation of stable RNA	1185
<i>stsA</i>		RNase activity	908
2. DNA			
<i>hsdR</i>	<i>rm</i> , <i>hsr</i> , <i>hsp</i> , <i>hs</i>	Host restriction; endonuclease R (EC 3.1.21.3)	978, 1289
<i>mcrA</i>	<i>rglA</i>	Restriction of DNA at 5-methylcytosine residues (EC 3.1.21.-); locus of e14 element	645, 646
<i>mcrB</i>	<i>rglB</i>	Restriction of DNA at 5-methylcytosine residues (EC 3.1.21.-)	386, 846, 1824
<i>nfo</i>		Endonuclease IV (EC 3.1.21.2)	919
<i>nth</i>		Endonuclease III; a DNA N-glycosylase and phosphoric monoester lyase, specific for apurinic and/or apyrimidinic sites (EC 3.1.25.2)	64
<i>xseA</i>		Exonuclease VII, large subunit (EC 3.1.11.6)	241
<i>xseB</i>		Exonuclease VII, small subunit (EC 3.1.11.6)	1665, 1666
<i>xthA</i>		Exonuclease III (EC 3.1.11.2)	1401, 1410
3. Proteins			
<i>clpA</i>		ATP-dependent <i>clpA</i> protease, ATP-binding, regulatory subunit (EC 3.4.21.-)	551, 788, 1042
<i>clpB</i>		Similar to ATP-dependent <i>clp</i> protease ATP-binding subunit, heat shock proteins F84.1 and F68.5	1042, 1523, 1764
<i>clpP</i>		ATP-dependent protease, proteolytic subunit, heat shock protein F21.5 (EC 3.4.21.-)	551, 1042
<i>dcp</i>		Dipeptidyl carboxypeptidase	375
<i>eco</i>	<i>eti</i>	Ecotin, a serine protease inhibitor	1052, 1053
<i>hlyA</i>		Pro-hemolysin	658, 800, 1532
<i>hlyC</i>		Acyl carrier protein for processing prohemolysin	79, 718, 1705
<i>htrA</i>	<i>degP</i>	A periplasmic endopeptidase and heat shock protein	957
<i>pepA</i>	<i>xerB</i>	Aminopeptidase A/I (EC 3.4.11.1)	1545
<i>pepD</i>	<i>pepH</i>	Peptidase D, a dipeptidase (EC 3.4.13.3)	472, 625

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>pepN</i>		Aminopeptidase N (EC 3.4.11.-)	84a
<i>pepP</i>		Aminopeptidase P II (EC 3.4.11.9)	1805
<i>pepQ</i>		Proline dipeptidase (EC 3.4.13.9)	772
<i>prc</i>	<i>tsp</i>	Carboxy-terminal protease for penicillin-binding protein 3 precursor	598
<i>prlC</i>		Oligopeptidase A	292
<i>ptr</i>		Protease III	87
<i>sohB</i>		<i>htrA</i> suppressor, a protease?	81
<i>sppA</i>		Protease IV, a signal peptide peptidase (EC 3.4.-.-)	688, 1575
<i>sulA</i>	<i>sfiA, suf</i>	Suppressor of <i>lon</i>	373
<i>tlp</i>		Protease II (EC 3.4.21.-)	772
IV. Cell structure			
A. Membrane components			
<i>envD</i>		Envelope protein	813
<i>hlpA</i>	<i>skp</i>	Outer membrane protein	651
<i>mdoG</i>	<i>mdoA</i>	Periplasmic membrane-derived oligosaccharide (MDO) synthesis	864
<i>mdoH</i>	<i>mdoA</i>	Membrane glycosyltransferase, membrane-derived oligosaccharide (MDO) synthesis	864
<i>mvrC</i>		Membrane protein	1103
<i>nlpA</i>	<i>skp</i>	Lipoprotein-28	1789
<i>nlpB</i>		Lipoprotein-34	166
<i>ompA</i>	<i>con, tolG, tut</i>	Outer membrane protein 3a (II*;G;d)	400, 818
<i>ompT</i>		Outer membrane protein 3b (a), a protease	86, 596
<i>phoE</i>	<i>ompE</i>	Outer membrane pore protein e (E, Ic, NmpAB), structural gene	98, 357, 738
<i>qmeA</i>	<i>gts</i>	Unspecified membrane defect	1747
<i>qmeC</i>		Unspecified membrane defect; tolerance to glycine; penicillin sensitivity	1747
<i>qmeD</i>		Unspecified membrane defect; tolerance to glycine; penicillin sensitivity	1747
<i>qmeE</i>		Unspecified membrane defect	1747
<i>rfaD</i>	<i>htrM</i>	ADP-L-glycero-D-mannoheptose-6-epimerase; permits growth at high temperature (EC 5.1.3.-)	1241, 1311, 1363
<i>rlpA</i>		A minor lipoprotein	1588
<i>rlpB</i>		A minor lipoprotein	1588
<i>sipB</i>		Suppressor of outer membrane mutant	1303
<i>sipC</i>		Suppressor of outer membrane mutant	1303
<i>sipD</i>		Suppressor of outer membrane mutant	1303
B. Murein sacculus			
<i>amiA</i>		<i>N</i> -Acetylmuramyl-L-alanine amidase activity	1627
<i>bolA</i>		Possible regulator of murein genes	16
<i>dacA</i>	<i>pfv</i>	D-Alanyl-D-alanine carboxypeptidase, fraction A; penicillin-binding protein 5 (EC 3.4.16.4)	103, 732, 1669
<i>dacB</i>		D-Alanyl-D-alanine carboxypeptidase, fraction B; penicillin-binding protein 4 (EC 3.4.16.4)	834, 1110, 1111
<i>dacC</i>		D-Alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6 (EC 3.4.16.4)	192
<i>dadX</i>	<i>msuA?</i>	Alanine racemase (EC 5.1.1.1); isozyme	569, 1751
<i>ddlA</i>		D-Alanine-D-alanine ligase A (EC 6.3.2.4)	15, 1815
<i>ddlB</i>		D-Alanine-D-alanine ligase B (EC 6.3.2.4)	1815
<i>ftsI</i>	<i>pbp, sep</i>	Penicillin-binding protein 3	103, 104
<i>hipA</i>		Frequency of persistence following inhibition of murein biosynthesis	130
<i>lpp</i>	<i>mlpA</i>	Murein lipoprotein	712, 1112
<i>mepA</i>		Murein DD-endopeptidase	797
<i>mlt</i>		Murein transglycosylase (EC 2.4.99.-)	436
<i>mraB</i>		D-Alanine requirement; cell wall peptidoglycan biosynthesis	1094
<i>mraY</i>		Phospho-N-acetylglucosaminyl-pentapeptide transferase? (EC 2.7.8.13)	699
<i>mrbA</i>		UDP-N-acetylglucosaminyl-3-enolpyruvate reductase activity	1094
<i>mrbB</i>		Cell wall peptidoglycan biosynthesis; mutation causes D-alanine auxotrophy	1094

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>mrbC</i>		Cell wall peptidylglycan biosynthesis	1094
<i>mrcA</i>	<i>ponA</i>	Peptidoglycan transglycosylase-transpeptidase; penicillin-binding protein 1A	191, 1807
<i>mrcB</i>	<i>pbpF, ponB</i>	Peptidoglycan transglycosylase-transpeptidase; penicillin-binding protein 1Bs	191, 1807
<i>mrdA</i>	<i>pbpA</i>	Cell shape; penicillin-binding protein 2	66
<i>mrdB</i>	<i>rodA</i>	Rod shape-determining protein; sensitivity to radiation and drugs	103, 698
<i>mreB</i>		Rod shape-determining protein	389
<i>mreC</i>		Rod shape-determining protein	1692
<i>mreD</i>		Rod shape-determining protein	1692
<i>murB</i>		UDP-N-acetylglucosamine reductase (EC 1.1.1.158)	115, 1299
<i>murC</i>		L-Alanine-adding enzyme (EC 6.3.2.8)	538, 1068
<i>murD</i>		UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9)	538, 1067, 1068
<i>murE</i>		<i>meso</i> -Diaminopimelate-adding enzyme (EC 6.3.2.13)	538, 1067, 1068
<i>murF</i>	<i>mra</i>	D-Alanine:D-alanine-adding enzyme (EC 6.3.2.15)	413, 538, 1068
<i>murG</i>		Transferase in peptidoglycan synthesis	538, 1068
<i>murH</i>		Peptidoglycan biosynthesis, late stage	322, 538
<i>murZ</i>		Murein biosynthesis	538
<i>pal</i>		Peptidoglycan-associated lipoprotein	248, 888
<i>ponA</i>	<i>excC</i>	Peptidoglycan transglycosylase-transpeptidase, PBP 1A	
<i>slt</i>		Soluble lytic murein transglycosylase (EC 3.2.1.-)	435
C. Surface polysaccharides and antigens			
<i>cpsA</i>	<i>non*</i>	Capsular polysaccharide biosynthesis, colanic acid	1637
<i>cpsC</i>		Capsular polysaccharide biosynthesis, colanic acid	1637
<i>cpsD</i>		Capsular polysaccharide biosynthesis, colanic acid	1637
<i>cpsE</i>		Capsular polysaccharide biosynthesis, colanic acid	1637
<i>cpsF</i>		Capsular polysaccharide biosynthesis, colanic acid	1637
<i>kdsA</i>		3-Deoxy-D-manno-octulosonic acid 8-phosphate synthase (EC 4.1.2.16)	1761
<i>kdsB</i>		CTP: CMP-3-deoxy-D-manno-octulosonate transferase (EC 2.7.7.38)	462
<i>kdtA</i>		3-Deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	277, 1363
<i>lpcA</i>	<i>tfrA</i>	Lipopolysaccharide core biosynthesis; resistance to phages T4, T7, and P1; deficiency in conjugation	606, 1593
<i>lpcB</i>	<i>pon</i>	Lipopolysaccharide core biosynthesis	606, 1593
<i>ops</i>		Level of exopolysaccharide production	1829
<i>rcaA</i>		Positive regulator for <i>ctr</i> capsule biosynthesis	552, 1553, 1554
<i>rcaB</i>		Positive response regulator for <i>ctr</i> capsule biosynthesis (sensor for <i>rcaC</i>)	525, 552, 1553
<i>rcaC</i>		Negative regulator for <i>ctr</i> capsule biosynthesis, probable sensor acting on <i>rcaB</i> (EC 2.7.1.-)	184, 552, 1553
<i>rfaB</i>		UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyl-transferase	1287, 1363
<i>rfaC</i>		Lipopolysaccharide core biosynthesis; proximal heptose	1363
<i>rfaF</i>		Lipopolysaccharide core biosynthesis	1363
<i>rfaG</i>		Lipopolysaccharide core biosynthesis; glucosyltransferase I	1226, 1227, 1363
<i>rfaH</i>	<i>sfrB, hlyT</i>	Transcriptional activator affecting biosynthesis of lipopolysaccharide core, F pilin, and hemolysin	1288, 1363
<i>rfaI</i>		UDP-D-galactose:(glucosyl)lipopolysaccharide- α -1,3-D-galactosyl-transferase	1287, 1363
<i>rfaJ</i>		UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase	1287, 1363
<i>rfaK</i>		Lipopolysaccharide core biosynthesis	816, 1363
<i>rfaL</i>		Lipopolysaccharide core biosynthesis	816, 1363
<i>rfaM</i>		Lipopolysaccharide core biosynthesis; glucosyltransferase II	1363
<i>rfaP</i>		Lipopolysaccharide core biosynthesis; phosphorylation of core heptose	1226, 1227, 1363
<i>rfaQ</i>		Lipopolysaccharide core biosynthesis	1227, 1363
<i>rfaY</i>		Lipopolysaccharide core biosynthesis	816, 1363
<i>rfaZ</i>		Lipopolysaccharide core biosynthesis	816, 1363
<i>rfe</i>		Synthesis of enterobacterial common antigen (ECA): UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase, O antigen (EC 2.4.1.-)	1062, 1186
<i>rffA</i>		Synthesis of enterobacterial common antigen (ECA): TDP-4-keto-6-deoxy-D-glucose:TDP-D-glucosamine transaminase	848, 1062, 1063

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>rffC</i>		Synthesis of enterobacterial common antigen (ECA):ECA chain elongation	848, 1062, 1063
<i>rffD</i>		Synthesis of enterobacterial common antigen (ECA):UDP-Man-NAc dehydrogenase	848, 1062, 1063
<i>rffE</i>		Synthesis of enterobacterial common antigen (ECA):UDP-GlcNAc-2-epimerase	848, 1062, 1063
<i>rffM</i>		Synthesis of enterobacterial common antigen (ECA):UDP-Man-NAcA:lipid I transferase	93, 848, 1062
<i>rffT</i>		Synthesis of enterobacterial common antigen (ECA):TDP-Fuc4NAc:lipid II transferase	848, 1062, 1063
D. Surface structures			
<i>crl</i>		DNA-binding protein affecting expression of cryptic <i>csgA</i> gene for surface fibers	61, 1189
<i>csgA</i>		Curlin subunit, coiled surface structures; cryptic	61, 1189
<i>fimA</i>	<i>pil, pilA, fimD</i>	Type 1 fimbrial (pilin)	1048, 1449
<i>fimB</i>	<i>pil</i>	Regulator for <i>fimA</i>	1048
<i>fimC</i>	<i>pil</i>	Putative chaperone for type 1 fimbriae	1610
<i>fimD</i>	<i>pil</i>	Cell surface localization of type 1 fimbriae	815
<i>fimE</i>		Regulator for <i>fimA</i>	146, 1048
<i>fimF</i>		Fimbrial morphology	844, 1390
<i>fimG</i>		Fimbrial morphology	844, 1390
<i>fimH</i>		Minor fimbrial subunit, adhesin, mannose specificity	844, 1610
<i>flgA</i>	<i>flaU</i>	Flagellar biosynthesis; assembly of basal-body periplasmic P ring	697, 999, 1184
<i>flgB</i>	<i>flaA</i>	Flagellar biosynthesis, cell-proximal portion of basal-body rod	697, 999
<i>flgC</i>	<i>flaW</i>	Flagellar biosynthesis, cell-proximal portion of basal-body rod	697, 999
<i>flgD</i>	<i>flaV</i>	Flagellar biosynthesis, initiation of hook assembly	697, 999
<i>flgE</i>	<i>flaK</i>	Flagellar biosynthesis, hook protein	697, 999
<i>flgF</i>	<i>flaX</i>	Flagellar biosynthesis, cell-proximal portion of basal-body rod	697, 999
<i>flgG</i>	<i>flaL</i>	Flagellar biosynthesis, cell-distal portion of basal-body rod	697, 999
<i>flgH</i>	<i>flaY</i>	Flagellar biosynthesis, basal-body outer membrane L (lipopolysaccharide layer) ring protein	697, 748, 999
<i>flgI</i>	<i>flaM</i>	Flagellar biosynthesis, basal-body periplasmic P ring protein	697, 748, 999
<i>flgJ</i>	<i>flaZ</i>	Flagellar biosynthesis	697, 999
<i>flgK</i>	<i>flaS</i>	Flagellar biosynthesis, hook-filament junction protein	697, 999
<i>flgL</i>	<i>flaT</i>	Flagellar biosynthesis; hook-filament junction protein	697, 999
<i>flgM</i>		Anti-FliA (anti-sigma) factor; also known as Rf1 protein; active only when hook assembly not complete	697, 999
<i>flhA</i>	<i>flaH</i>	Flagellar biosynthesis; export of flagellar proteins?	697, 860, 999
<i>flhB</i>	<i>flaG</i>	Flagellar biosynthesis	697, 999
<i>flhC</i>	<i>flaA</i>	Regulator of flagellar biosynthesis acting on class 2 operons; transcription initiation factor?	697, 999
<i>flhD</i>	<i>flbB</i>	Regulator of flagellar biosynthesis, acting on class 2 operons; transcription initiation factor?	697, 999
<i>flhE</i>		Flagellar biosynthesis	697, 999
<i>fliA</i>	<i>flaD</i>	Flagellar biosynthesis; regulation of late gene expression (class 3a and 3b operons); sigma factor	697, 794, 999
<i>fliB</i>		Flagellar biosynthesis; in <i>Salmonella</i> spp., methylation of lysine residues on the filament protein, flagellin	697, 794, 999
<i>fliC</i>	<i>H, hag, flaF</i>	Flagellin; flagellar biosynthesis, filament structural protein	60, 697, 999
<i>fliD</i>	<i>flbC rfs</i>	Flagellar biosynthesis; filament-capping protein; enables filament assembly	60, 697, 999
<i>fliE</i>	<i>flaN</i>	Flagellar biosynthesis; basal-body component, possibly at (MS-ring)-rod junction	697, 999, 1119
<i>fliF</i>	<i>flaBI</i>	Flagellar biosynthesis; basal-body MS (membrane and supramembrane)-ring and collar protein	697, 794, 999
<i>fliG</i>	<i>flaBII</i>	Flagellar biosynthesis, component of motor switching and energizing, enabling rotation and determining its direction	804, 999, 1357
<i>fliH</i>	<i>flaBIII</i>	Flagellar biosynthesis; export of flagellar proteins?	697, 794, 999
<i>fliI</i>	<i>flaC</i>	Flagellar biosynthesis; export of flagellar proteins?	697, 794, 999
<i>fliJ</i>	<i>flaO</i>	Flagellar biosynthesis	697, 794, 999
<i>fliK</i>	<i>flaE</i>	Flagellar biosynthesis, hook length control	697, 794, 999
<i>fliL</i>	<i>flaAI</i>	Flagellar biosynthesis	697, 999, 1011
<i>fliM</i>	<i>flaAII</i>	Flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction	804, 999, 1357

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>fliN</i>	<i>motD</i>	Flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction	804, 999, 1357
<i>fliO</i>	<i>fliB</i>	Flagellar biosynthesis	697, 794, 999
<i>fliP</i>	<i>fliR</i>	Flagellar biosynthesis	697, 794, 999
<i>fliQ</i>	<i>fliQ</i>	Flagellar biosynthesis	697, 794, 999
<i>fliR</i>	<i>fliP</i>	Flagellar biosynthesis	697, 794, 999
<i>fliS</i>		Flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)	697, 794, 999
<i>fliT</i>		Flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)	697, 794, 999
<i>flu</i>		Metastable gene affecting surface properties, pilation, and colonial morphology	383
<i>mor</i>		Regulator of switching between two sets of surface properties	1715

V. Cellular processes

A. Transport/binding proteins

<i>abpS</i>		Low-affinity transport, arginine and ornithine; periplasmic binding protein	231, 232
<i>araE</i>		Low-affinity L-arabinose transport system; L-arabinose proton symport	190, 1000
<i>araF</i>		L-Arabinose-binding protein	664, 1679
<i>araG</i>		High-affinity L-arabinose transport system	664
<i>araH</i>		High-affinity L-arabinose transport system; membrane protein	664
<i>argP</i>		Transport of arginine, ornithine, and lysine	234
<i>argT</i>		Probable lysine-, arginine-, and ornithine-binding protein	1167
<i>aroP</i>		General aromatic amino acid transport	661
<i>aroT</i>	<i>aroR, trpP</i>	Transport of aromatic amino acids, alanine, and glycine	1617
<i>bcp</i>		Bacterioferritin comigratory protein	45
<i>betT</i>		High-affinity choline transport	871
<i>bfr</i>		Bacterioferritin	47
<i>bioP</i>	<i>birB</i>	Biotin transport	127, 1257
<i>brnQ</i>		Transport system 1 for isoleucine, leucine, and valine	1792
<i>brnR</i>		Component of transport systems 1 and 2 for isoleucine, leucine, and valine	1792
<i>brnS</i>		Transport system for isoleucine, leucine, and valine	574
<i>brnT</i>		Low-affinity transport system for isoleucine	574
<i>btuB</i>	<i>bfe, cer, btuA</i>	Receptor for vitamin B ₁₂ , E colicins, and bacteriophage BF23	108, 840
<i>btuC</i>		Vitamin B ₁₂ transport	1343
<i>btuD</i>		Vitamin B ₁₂ transport, membrane-associated protein	1343
<i>btuR</i>		Regulator for <i>btuB</i>	992
<i>bymA</i>		Bypass of maltose permease at <i>malB</i>	655
<i>cadB</i>		Transport of lysine/cadaverine	1066, 1720
<i>calA</i>		Calcium transport	181
<i>calC</i>		Calcium transport	181
<i>calD</i>		Calcium transport	181
<i>cbt</i>		Dicarboxylate-binding protein	974
<i>codB</i>		Cytosine transport	332
<i>cog</i>		Regulator of <i>ompG</i>	1092
<i>corA</i>		Mg ²⁺ transport, system I	530, 1224
<i>corB</i>		Mg ²⁺ transport, system I	530, 1224
<i>crr</i>	<i>treD, tgs, gsr, iex</i>	Glucose phosphotransferase system enzyme III ^{glc}	371, 589, 1394
<i>cup</i>		Uptake of carbohydrates	1005
<i>cutE</i>		Copper homeostasis protein	1355
<i>cycA</i>	<i>dagA</i>	Resistance to D-cycloserine and D-serine; transport of D-alanine, D-serine, and glycine	301, 1346
<i>cysA</i>		Sulfate permease A protein; chromate resistance	1387, 1495
<i>cysU</i>	<i>cysT</i>	Sulfate permease T protein	1496
<i>cysW</i>	<i>cysT</i>	Sulfate permease W protein	1495
<i>dctA</i>		Uptake of C ₄ -dicarboxylic acids	973
<i>dctB</i>		Uptake of C ₄ -dicarboxylic acids	973
<i>dgoT</i>		Galactonate transport	298
<i>dgsA</i>		Enzyme IIA/IIB of phosphotransferase system	1351
<i>appA</i>		Dipeptide transport protein	4, 1190
<i>ecfA</i>	<i>metC?</i>	Energy coupling factor; pleiotropic effects on active transport coupling to metabolic energy; may be <i>metC</i>	660

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>entA</i>		2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28), enterochelin biosynthesis	962, 1650
<i>entB</i>	<i>entG</i>	2,3-Dihydro-2,3-dihydroxybenzoate synthetase (EC 3.3.2.1), enterochelin biosynthesis	1384, 1528
<i>entC</i>		Isochorismate synthetase (EC 5.4.99.6), enterochelin biosynthesis	763, 963, 1207
<i>entD</i>		Enterochelin synthetase, component D	59, 279, 1528
<i>entE</i>		Enterochelin synthetase, component E	1528, 1529
<i>entF</i>		Enterochelin synthetase, component F	1385, 1528
<i>exbB</i>		Uptake of enterochelin; resistance or sensitivity to colicins	176, 426
<i>exbC</i>		Uptake of enterochelin; resistance or sensitivity to colicins	1302
<i>exbD</i>		Uptake of enterochelin	426, 1279
<i>exuT</i>		Transport of hexuronates	1155
<i>fadL</i>	<i>ttr</i>	Transport of long-chain fatty acids; sensitivity to phage T2	133, 134, 1397
<i>fecA</i>		Citrate-dependent iron transport, outer membrane receptor	1533, 1673
<i>fecB</i>		Citrate-dependent iron transport, periplasmic protein	1533, 1673
<i>fecC</i>		Citrate-dependent iron(III) transport protein, cytosolic	1533, 1673
<i>fecD</i>		Citrate-dependent iron transport, membrane-bound protein	1533, 1673
<i>fecE</i>		Citrate-dependent iron(III) transport protein, membrane-bound protein	1533, 1673
<i>fecI</i>		Regulator for <i>fec</i> operon, membrane location	1673
<i>fecR</i>		Regulator for <i>fec</i> operon, periplasmic	1673
<i>feo</i>		Ferrous iron transport system	
<i>fepA</i>	<i>cbr, cbt, feuB</i>	Receptor for ferric enterobactin (enterochelin) and colicins B and D	58, 1132, 1208
<i>fepB</i>		Ferric enterobactin (enterochelin) uptake; periplasmic component	429, 1208
<i>fepC</i>		Ferric enterobactin (enterochelin) uptake; cytoplasmic membrane component	1208, 1474
<i>fepD</i>		Ferric enterobactin (enterochelin) uptake	1208, 1474
<i>fepE</i>		Ferric enterobactin (enterochelin) uptake	1208
<i>fepG</i>		Ferric enterobactin transport protein	1474
<i>fes</i>		Enterochelin esterase	182
<i>fhuA</i>	<i>T1, T5rec, tonA</i>	Outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and φ80	177, 222, 807
<i>fhuB</i>		Hydroxamate-dependent iron uptake, cytoplasmic membrane component	837, 838, 1446
<i>fhuC</i>		Hydroxamate-dependent iron uptake, cytoplasmic membrane component	837, 838, 1446
<i>fhuD</i>		Hydroxamate-dependent iron uptake, cytoplasmic membrane component	837–839
<i>fhuE</i>		Outer membrane receptor for ferric iron uptake	1422
<i>fhuF</i>		Ferric hydroxamate transport	597
<i>fii</i>		Ferric iron uptake, outer membrane protein	317
<i>fruA</i>	<i>ptsF</i>	Fructose phosphotransferase enzyme II (EC 2.7.1.69)	1194, 1294
<i>fruB</i>		Fructose phosphotransferase enzyme III	512
<i>fruF</i>	<i>fpr</i>	Phosphohistidinoprotein-hexose phosphotransferase, fructose specific	573, 1194
<i>fucP</i>		Fucose permease	250
<i>gabP</i>		Transport of γ-aminobutyrate	620, 1076
<i>galP</i>	<i>Pgal</i>	Galactose permease	1342
<i>gatA</i>		Galactitol-specific enzyme II of phosphotransferase system	903–905
<i>glnH</i>		Periplasmic glutamine-binding protein	1166
<i>glnP</i>		Glutamine high-affinity transport system; membrane component	1166
<i>glnQ</i>		Glutamine high-affinity transport system	1166
<i>glpF</i>		Facilitated diffusion of glycerol	1576, 1731
<i>glpT</i>		sn-Glycerol-3-phosphate permease	427, 881
<i>gltP</i>		Glutamate-aspartate symport protein	359, 1626
<i>gltR</i>		Regulator for <i>gltS</i>	1023
<i>gltS</i>	<i>gltC</i>	Glutamate transport	402, 765
<i>gntS</i>	<i>gntM, usgA</i>	Second system for transport and possible phosphorylation of gluconate	74, 280
<i>gntT</i>	<i>gntM, usgA</i>	High-affinity transport of gluconate	451, 1136
<i>hisJ</i>		Histidine-binding protein of high-affinity histidine transport system	55
<i>hisM</i>		Histidine transport, membrane protein M	842
<i>hisP</i>		Histidine transport, inner membrane receptor protein P	842, 1089
<i>kdgT</i>		2-Keto-3-deoxy-D-gluconate transport system	1015
<i>kdpA</i>	<i>kac</i>	High-affinity potassium transport system; probable K ⁺ -stimulated ATPase (EC 3.6.1.36)	1269

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>kdpB</i>	<i>kac</i>	High-affinity potassium transport system (EC 3.6.1.36)	1269
<i>kdpC</i>	<i>kac</i>	High-affinity potassium transport system (EC 3.6.1.36)	1269
<i>kdpE</i>		Regulator of <i>kdp</i> operon (effector)	1146, 1269, 1701
<i>kefB</i>	<i>trkB</i>	K ⁺ efflux; NEM ^a -activable K ⁺ /H ⁺ antiporter	431
<i>kefC</i>	<i>trkC</i>	K ⁺ efflux; NEM-activatable K ⁺ /H ⁺ antiporter	431, 1125
<i>kgtP</i>	<i>witA</i>	α-Ketoglutarate permease	1463
<i>lacY</i>	<i>y</i>	Galactoside permease (M protein)	190, 759, 1395
<i>lctP</i>		L-Lactate permease	393
<i>lepA</i>		GTP-binding membrane protein	1491
<i>livF</i>		Leucine transport protein	6
<i>livG</i>	<i>hrbBCD</i>	High-affinity branched-chain amino acid transport system	6
<i>livH</i>	<i>hrbBCD</i>	High-affinity branched-chain amino acid transport system; membrane component	6
<i>livJ</i>	<i>hrbBCD</i>	High-affinity branched-chain amino acid transport system; periplasmic binding protein for leucine, isoleucine, and valine	6
<i>livK</i>	<i>hrbBCD</i>	High-affinity branched-chain amino acid transport system; leucine-specific periplasmic binding protein	6
<i>livL</i>		High-affinity branched-chain amino acid transport	6
<i>livM</i>		High-affinity branched-chain amino acid transport	6
<i>lysP</i>	<i>cadR</i>	Lysine-specific permease; pleiotropic increase in lysine decarboxylase	1536
<i>lysX</i>		Lysine excretion	
<i>malE</i>	<i>malB</i>	Periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis	101, 1534
<i>malF</i>	<i>malB</i>	Transport of maltose; cytoplasmic membrane protein	342, 350
<i>malG</i>	<i>malB</i>	Transport of maltose and maltodextrins	342, 350
<i>malK</i>	<i>malB</i>	Transport of maltose	351, 1325, 1331
<i>malX</i>		Phosphotransferase enzyme II, maltose and glucose specific (EC 2.7.1.69)	1324
<i>manX</i>	<i>ptsL, ptsM, gptB, mpt, ptsX</i>	Mannose phosphotransferase system, protein II-A(III)	447, 448
<i>manY</i>	<i>ptsM, pel, ptsP, ptsX</i>	Mannose phosphotransferase system: Pel protein II-P; penetration of phage λ (EC 2.7.1.69)	447, 448
<i>manZ</i>	<i>ptsM, ptsX, gptB, mpt</i>	Mannose phosphotransferase system, enzyme IIB(IIM) (EC 2.7.1.69)	447, 448
<i>mdoA</i>		Membrane-derived oligosaccharides; membrane-localized component of glucosyl transferase system	515, 864
<i>mdoB</i>		Membrane-derived oligosaccharides; phosphoglycerol transferase I activity	515, 864
<i>melB</i>	<i>mel-4</i>	Melibiose utilization; thiomethylgalactoside permease II	1283, 1284
<i>metD</i>		High-affinity uptake of D- and L-methionine	760, 761
<i>mgID</i>		Regulator for methyl-galactoside transport	1345
<i>mgIR</i>	R-MG	<i>mgI</i> regulator	498
<i>mgt</i>		Mg ²⁺ transport, system II	498
<i>modA</i>		Molybdate uptake	619, 644
<i>modB</i>	<i>tslJ</i>	Molybdate uptake	644
<i>modC</i>	<i>chlD</i>	Molybdate uptake	619, 644, 1454
<i>modD</i>		Molybdate uptake	644
<i>molR</i>		Molybdate transport	644, 895
<i>mtLA</i>		Mannitol-specific enzyme II of phosphotransferase system (EC 2.7.1.69)	1277, 1566
<i>mtr</i>		Tryptophan-specific transport protein	612, 1412, 1413
<i>nagE</i>	<i>ptsN</i>	N-Acetylglucosamine-specific enzyme II of phosphotransferase system <i>nalD</i> (EC 2.7.1.69)	1267, 1268, 1686
<i>narK</i>		Transport of nitrate	369
<i>nhaA</i>	<i>ant, antA</i>	Na ⁺ /H ⁺ antiporter activity	1258, 1584, 1612
<i>nhaB</i>		Na ⁺ /H ⁺ antiporter	1258, 1612
<i>nhaR</i>	<i>antO, yaab</i>	Activator of <i>nhaA</i>	1309
<i>nikA</i>	<i>hydC</i>	Transport of Ni, essential for hydrogenases	1777
<i>nikB</i>	<i>hydD</i>	Transport of Ni, essential for hydrogenases	1777
<i>nupC</i>	<i>cru</i>	Transport of nucleosides except guanosine	1122
<i>nupG</i>		Transport of nucleosides	1121, 1739
<i>ompG</i>		Outer membrane porin protein	1092
<i>oppA</i>		Oligopeptide transport; periplasmic binding protein	41, 784, 786
<i>oppB</i>		Oligopeptide transport	42
<i>oppC</i>		Oligopeptide transport	42
<i>oppD</i>		Oligopeptide transport	42

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>oppE</i>		Oligopeptide transport	42
<i>oppF</i>		Oligopeptide transport, ATP hydrolysis	42
<i>panF</i>		Pantothenate permease	730, 1328
<i>pheP</i>		Phenylalanine-specific transport system	1253
<i>phnC</i>		Utilization of phosphorus-containing compounds, probable transport	1009, 1075, 1713
<i>phoU</i>	<i>phoT</i>	Regulator for high-affinity phosphate-specific transport system	1313, 1712
<i>pit</i>		Low-affinity P _i transport	434
<i>potA</i>		Spermidine/putrescine transport protein	494
<i>potB</i>		Spermidine/putrescine transport protein	494
<i>potA</i>		Spermidine/putrescine transport protein	494
<i>potB</i>		Spermidine/putrescine transport protein	494
<i>potC</i>		Spermidine/putrescine transport protein	494
<i>potD</i>		Spermidine/putrescine transport protein	494
<i>potE</i>		Putrescine transport protein	785
<i>proP</i>		Low-affinity transport system for glycine betaine and proline; proline permease II	229, 314
<i>proT</i>		Proline transport	1108, 1109
<i>proV</i>	<i>proU</i>	High-affinity transport system for glycine betaine and proline; glycine betaine-binding protein	229, 340, 1547
<i>proW</i>	<i>proU</i>	High-affinity transport system for glycine betaine and proline	229, 340, 1547
<i>pstA</i>	<i>phoT, phoR2b, R2^{pho}</i>	High-affinity phosphate-specific transport system	1313
<i>pstB</i>	<i>phoT</i>	High-affinity phosphate-specific transport system, cytoplasmic membrane protein?	1313
<i>pstC</i>	<i>phoW</i>	High-affinity phosphate-specific transport system, cytoplasmic membrane component	1313
<i>pstS</i>	<i>nmpA phoR2a, phoST R2pho</i>	High-affinity phosphate-specific transport system; periplasmic phosphate-binding protein	1010
<i>ptsG</i>	<i>car, cat, CR, gpt, tgl, umg, gptA</i>	Glucosephosphotransferase enzyme II (EC 2.7.1.69)	203, 1382, 1392
<i>ptsH</i>	<i>ctr, Hpr, HPr</i>	Phosphohistidinoprotein-hexose phosphotransferase (EC 2.7.1.69)	371, 1382
<i>ptsI</i>	<i>ctr</i>	Phosphotransferase system enzyme I (EC 2.7.3.9)	371, 593, 1382
<i>purP</i>		High-affinity adenine transport	
<i>putP</i>		Major proline permease	314, 594, 1328
<i>rbsA</i>	<i>prlB, rbsP, rbsT</i>	D-Ribose high-affinity transport system; membrane-associated protein	202
<i>rbsB</i>	<i>rbsP</i>	D-Ribose periplasmic binding protein	568
<i>rbsC</i>	<i>rbsP</i>	D-Ribose high-affinity transport system; membrane-associated protein	107
<i>rbsD</i>	<i>rbsP</i>	D-Ribose high-affinity transport system; membrane-associated protein	107
<i>rhaT</i>		Rhamnose transport	84
<i>rsgA</i>	<i>gen-165</i>	Ferritin-like protein	729
<i>sbp</i>		Periplasmic sulfate-binding protein	733
<i>shiA</i>		Shikimate and dehydroshikimate permease	1262
<i>srlA</i>	<i>gutA, sbl</i>	D-Glucitol (sorbitol)-specific enzyme II of phosphotransferase system (EC 2.7.1.69)	1787
<i>srlB</i>	<i>gutB</i>	D-Glucitol (sorbitol)-specific enzyme III of phosphotransferase system	589, 1787
<i>tdcC</i>		Anaerobically inducible L-threonine, L-serine permease	549, 1452, 1568
<i>tnaB</i>	<i>tnaP</i>	Low-affinity tryptophan permease	538, 1799
<i>tonB</i>	<i>exbA, T1rec</i>	Membrane protein; uptake of chelated iron and cyanocobalamin; sensitivity to phages T1 and φ80 and colicins	52, 108, 177
<i>treB</i>		Enzyme II of PEP:CHO phosphotransferase system, trehalose specific	155, 814
<i>trkA</i>		Transport of potassium	159
<i>trkD</i>		Transport of potassium	160
<i>trkE</i>		Transport of potassium	401
<i>trkG</i>		Potassium uptake	401
<i>trkH</i>		Potassium uptake	401
<i>trpP</i>		Low-affinity tryptophan-specific permease	417
<i>tsx</i>	<i>nupA, T6rec</i>	Nucleoside channel; receptor of phage T6 and colicin K	179, 524
<i>tyrP</i>		Tyrosine-specific transport system	1770
<i>tyrR</i>		Regulation of <i>aroF</i> , <i>aroG</i> , and <i>tyrA</i> and aromatic amino acid transport systems	1260
<i>ugpA</i>	<i>psiB, psiC</i>	sn-Glycerol 3-phosphate transport system	1205, 1564

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>ugpB</i>	<i>psiB, psiC</i>	<i>sn</i> -Glycerol 3-phosphate transport system; periplasmic binding protein	1205
<i>ugpC</i>		<i>sn</i> -Glycerol 3-phosphate transport system	1205
<i>ugpE</i>		<i>sn</i> -Glycerol 3-phosphate transport system, membrane protein	1205
<i>uhpA</i>		Response regulator, positive activator of <i>uhpT</i> transcription (sensor for <i>uhpB</i>)	717
<i>uhpB</i>		Regulator of <i>uhp</i> , sensor for histidine protein kinase (EC 2.7.1.-)	717
<i>uhpC</i>		Regulator	717
<i>uhpR</i>		Regulation of hexose phosphate transport; outer membrane receptor for glucose 6-phosphate?	762, 1473
<i>uhpT</i>		Hexose phosphate transport protein	31
<i>xylE</i>		Xylose-proton symport	190, 347
<i>xylF</i>	<i>xylT</i>	Xylose binding protein transport system	7, 620
<i>xylU</i>		D-Xylose uptake protein	620, 857
B. Cell division			
<i>dicA</i>		Regulator of <i>dicB</i>	105
<i>dicB</i>		Inhibition of cell division	215
<i>dicC</i>		Regulator of <i>dicB</i>	105
<i>dicF</i>		RNA of 65 nucleotides, cell division inhibitor	456, 1609
<i>envA</i>		Cell envelope and cell separation; UDP-3-O-acetyl-N-acetylgalcosamine deacetylase	1359
<i>envB</i>	<i>mon, rodY</i>	Cell shape and sensitivity to antibiotics	50, 981, 1740
<i>envC</i>		Cell division; chain formation	813
<i>fcsA</i>		Cell division; septation	847
<i>fic</i>		Filamentation in presence of cyclic AMP in mutant	828
<i>ftsA</i>	<i>divA</i>	Cell division	1681
<i>ftsE</i>		Cell division	527, 531, 532
<i>ftsH</i>		Cell division; insertion of penicillin-binding protein 3 into membrane?	103, 1180
<i>ftsQ</i>		Cell division	1681
<i>ftsW</i>		Cell division; membrane protein involved in shape determination	698
<i>ftsX</i>		Cell division	527, 531, 532
<i>ftsY</i>		Cell division	527, 531, 532
<i>ftsZ</i>	<i>sfiB, sulB</i>	GTPase involved in cell division	323, 531, 1318
<i>mbrA</i>		Coupling of cell division and DNA replication	1639, 1640
<i>mbrB</i>		Link between growth rate and partitioning chromosomes	1639, 1640
<i>mbrC</i>		Partitioning chromosomes	1639, 1640
<i>minB</i>		Formation of minute cells containing no DNA; complex locus, position of division septum	1117
<i>minC</i>		Cell division inhibitor	354, 355
<i>minD</i>		Cell division inhibitor, a membrane ATPase, activates <i>minC</i>	353–355
<i>minE</i>		Cell division topological specificity factor	354, 355
<i>mukB</i>		Cell division protein involved in chromosome partitioning	647, 648, 1159
<i>mukC</i>		Cell division and chromosome partitioning	648
<i>mukD</i>		Cell division and chromosome partitioning	648
<i>pcsA</i>		Cell division; chromosome segregation	847
<i>sdiA</i>		Regulator of transcription of <i>ftsQAZ</i> gene cluster	1711
<i>sefA</i>		Septum formation	1169
<i>sfiC</i>		Cell division inhibition; locus of element e14	734, 1003, 1004
<i>tig</i>		Trigger factor; a molecular chaperone involved in cell division	582
<i>weeA</i>		Cell elongation	360, 361
C. Chemotaxis and mobility			
<i>cheA</i>		Sensor for <i>cheY</i> and <i>cheB</i> chemotactic response; histidine protein kinase (EC 2.7.1.-)	514, 1054, 1543
<i>cheB</i>		Response regulator for chemotaxis (<i>cheA</i> sensor); protein methyl-esterase (EC 3.1.1.61) demethylates receptors	514, 995, 1054
<i>cheR</i>	<i>cheX</i>	Response regulator for chemotaxis; protein glutamate methyltransferase activity (EC 2.1.1.80), methylates receptors	1388
<i>cheW</i>		Positive regulator of CheA protein activity	514, 965, 1054
<i>cheY</i>		Response regulator for chemotactic response (<i>cheA</i> sensor); switch regulator, placing it in counterclockwise state	989, 1357, 1408
<i>cheZ</i>		Chemotactic response; CheY protein phosphatase; antagonist of CheY as switch regulator	1548

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>mglA</i>	<i>mglP</i>	Methyl-galactoside transport and galactose taxis, cytoplasmic membrane protein	656
<i>mglB</i>	<i>mglP</i>	Galactose-binding protein; receptor for galactose taxis	656, 1442
<i>mglC</i>		Methyl-galactoside transport and galactose taxis	656
<i>motA</i>		Proton conductor component of motor; no effect on switching	137, 138, 1551
<i>motB</i>		Enables flagellar motor rotation, linking torque machinery to cell wall; no effect on switching	137, 138, 1551
<i>tap</i>		Methyl-accepting chemotaxis protein IV, peptide receptor	1017
<i>tar</i>	<i>cheM</i>	Ethyl-accepting chemotaxis protein II, chemoreceptor for aspartate	503, 896
<i>trg</i>		Methyl-accepting chemotaxis protein III, ribose receptor	208, 1222, 1784
<i>tsr</i>	<i>cheD</i>	Methyl-accepting chemotaxis protein I, serine receptor	510, 965
D. Protein secretion			
<i>excD</i>		Export of periplasmic proteins	887
<i>expA</i>		Expression of a group of export proteins	336
<i>hlyB</i>		Secretion protein for hemolysin	521, 755, 836
<i>hlyD</i>		Secretion protein for hemolysin	521, 836, 1532
<i>lepB</i>	<i>lep</i>	Leader peptidase (signal peptidase I)	132, 1021
<i>lspA</i>		Prolipoprotein signal peptidase (SPaseII) (EC 3.4.99.35)	1124
<i>secA</i>	<i>prlD, azi, pea</i>	Protein secretion	180, 1485, 1565
<i>secB</i>		Protein export; molecular chaperone	357, 850, 1750
<i>secD</i>		Protein secretion	1038, 1565
<i>secE</i>	<i>prlG</i>	Inner membrane protein, protein secretion (with <i>secY</i>)	198, 1164, 1565
<i>secF</i>		Membrane protein, protein secretion function	1038, 1565
<i>secY</i>	<i>prlA</i>	Membrane protein, protein secretion (with <i>secE</i>)	198, 1164, 1577
<i>ssaD</i>		Suppression of <i>secA</i> mutation	501, 1188, 1478
<i>ssaE</i>		Suppression of <i>secA</i> mutation	1188, 1478
<i>ssaG</i>		Suppression of <i>secA</i> mutation	1188, 1478
<i>ssaH</i>		Suppression of <i>secA</i> mutation	1186, 1478
<i>ssyA</i>		Suppressor of <i>secY</i> mutation	1478
<i>ssyB</i>		Suppressor of <i>secY</i> mutation	1479
<i>ssyD</i>		Suppressor of <i>secY</i> mutation	1479
E. Osmotic adaptation			
<i>betA</i>		Choline dehydrogenase (EC 1.1.99.1), a flavoprotein	871
<i>betB</i>		NAD ⁺ -dependent betaine aldehyde dehydrogenase (EC 1.2.1.8)	452, 871
<i>betI</i>		Probably repressor of <i>bet</i> genes	871
<i>envM</i>		Osmotically remedial envelope defect	120, 1654
<i>envN</i>		Osmotically remedial envelope defect	418
<i>envP</i>		Osmotically remedial envelope defect	418
<i>envQ</i>		Osmotically remedial envelope defect	418
<i>envT</i>		Osmotically remedial envelope defect	448
<i>envY</i>		Envelope protein; thermoregulation of porin biosynthesis	990
<i>micF</i>	<i>stc</i>	Regulatory antisense RNA affecting <i>ompF</i> expression	34
<i>ompC</i>	<i>par, meoA</i>	Outer membrane protein 1b (Ib;c)	366, 1339, 1721
<i>ompF</i>	<i>cmlB, coa, tolF, cry</i>	Outer membrane protein 1a (Ia;b;F)	475, 555, 1461
<i>osmB</i>		Osmotically inducible lipoprotein	622
<i>osmC</i>		Osmotically inducible protein	584
<i>osmY</i>		Hyperosmotically inducible periplasmic protein	1801
<i>otsA</i>	<i>pexA?</i>	Trehalose phosphate synthase (EC 2.4.1.15)	622, 758, 871
<i>otsB</i>		Trehalose phosphate synthase (EC 2.4.1.15)	622, 758, 871
<i>otsP</i>	<i>treE</i>	Trehalose-6-phosphate phosphatase (EC 3.1.3.12)	814
<i>otsR</i>		Regulation of <i>ots</i>	814
<i>proX</i>	<i>proU</i>	Periplasmic glycine betaine-binding protein	229, 340, 1547
<i>treA</i>		Trehalase, periplasmic (EC 3.2.1.28)	583, 622
VI. Other functions			
A. Cryptic genes			
<i>arbT</i>		Phosphorylation and transport of arbutin; cryptic	1228
<i>argM</i>		A second acetylornithine transaminase; cryptic gene (EC 2.6.1.11)	1341
<i>ascB</i>	<i>sac</i>	6-Phospho-β-glucosidase (EC 3.2.1.86); cryptic	590, 1228

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>ascF</i>	<i>sac</i>	Phosphotransferase enzyme II (<i>asc</i>), cryptic, transports specific β -glucosides (EC 2.7.1.69)	590, 1228
<i>ascG</i>	<i>sac</i>	<i>asc</i> operon repressor	590, 1228
<i>bglA</i>	<i>bglD</i>	Phospho- β -glucosidase A (EC 3.2.1.86)	1439
<i>bglB</i>	<i>bglA</i>	Phospho- β -glucosidase B (EC 3.2.1.86)	1439
<i>bglF</i>	<i>bglB, bglC</i>	β -Glucoside transport, PEP ^a -dependent enzyme II (EC 2.7.1.69), part of cryptic operon	172, 1438
<i>bglG</i>	<i>bglC, bglS</i>	Positive regulation of <i>bgl</i> operon	1437
<i>bglT</i>	<i>bglE</i>	Regulator for phospho- β -glucosidase A biosynthesis	1290, 1291
<i>celA</i>		PEP-dependent phosphotransferase transport system for cellobiose, arbutin, and salicin; enzyme IV	1229, 1329
<i>celB</i>		PEP-dependent phosphotransferase transport system for cellobiose, arbutin, and salicin; enzyme II (EC 2.7.1.69); part of cryptic operon	1229, 1329
<i>celC</i>		PEP-dependent phosphotransferase transport system for cellobiose, arbutin, and salicin; enzyme III (EC 2.7.1.69); part of cryptic operon	589, 1229, 1329
<i>celD</i>		Negative regulator of <i>cel</i> operon	1229
<i>celF</i>		Phospho- β -glucosidase (EC 3.2.1.86)	1229
<i>citA</i>		Cryptic gene of citrate transport system	587
<i>citB</i>		Cryptic gene of citrate transport system	587
<i>ebgA</i>		β -D-Galactosidase, α subunit; cryptic gene (EC 3.2.1.23)	588, 930
<i>ebgB</i>		Possible homolog of <i>lacY</i>	588
<i>ebgC</i>		β -D-Galactosidase, β subunit; cryptic gene (EC 3.2.1.23)	588, 930
<i>ebgR</i>		Regulator of <i>ebg</i> operon	991
<i>ilvF</i>		Acetolactate synthase activity (valine insensitive) (EC 4.1.3.18), probably a fifth isozyme	20
<i>ilvG</i>		Acetolactate synthase II (EC 4.1.3.18), valine insensitive, large subunit, silent in K-12	676
<i>ilvM</i>		Acetolactate synthase II (EC 4.1.3.18), valine insensitive, small subunit, silent in K-12	676, 1728
<i>ilvJ</i>		Acetolactate synthase IV (EC 4.1.3.18), valine insensitive, silent in K-12, a fourth isozyme	1350
<i>narV</i>		Cryptic nitrate reductase II (EC 1.7.99.4), γ subunit	145
<i>narW</i>		Cryptic nitrate reductase II, δ subunit, assembly function	145
<i>narY</i>		Cryptic nitrate reductase II (EC 1.7.99.4), β subunit	145
<i>narZ</i>		Cryptic nitrate reductase II (EC 1.7.99.4), α subunit	145
<i>phnE</i>		Utilization of phosphorus-containing compounds, gene cryptic in K-12, probably transport	1009, 1075, 1713
<i>pqq</i>		Redox cofactor, functions as cofactor of apoglucose dehydrogenase; cryptic in wild type	127

B. Phage-related functions and prophages

<i>bfm</i>		Phage BF23 multiplication	1486
<i>e14</i>		Cryptic, excisable chromosomal element; contains <i>lit</i> , <i>mcrA</i> , <i>pin</i> , and <i>sfiC</i>	636
<i>esp</i>		Site for efficient packaging of phage T1	403
<i>fipB</i>		Morphogenesis of phage F1	982
<i>fipC</i>		Morphogenesis of phage F1	982
<i>gprA</i>		Replication of certain lambdoid phages	1178, 1405
<i>gprB</i>		Replication of certain lambdoid phages	1178, 1405
<i>grpD</i>		Initiation of phage lambda DNA replication; host DNA synthesis	1178, 1405
<i>grpE</i>		Phage λ replication; host DNA synthesis; heat shock protein	497, 876, 1558
<i>hflB</i>		Probable protease specific for phage λ cII repressor	89
<i>hflC</i>	<i>hflA</i>	Protease specific for phage λ cII repressor	88, 254
<i>hflK</i>	<i>hflA</i>	Protease specific for phage λ cII repressor	88, 254
<i>hfq</i>		Host factor I for bacteriophage Q β replication	764
<i>int</i>		Prophage DLP12 integrase	954
<i>lamB</i>	<i>malB</i>	Phage λ receptor protein; maltose high-affinity uptake system	482, 988
<i>lit</i>		Phage T4 late gene expression; locus of e14 element	636, 776
<i>mopA</i>	<i>groE, hdh, tabB, groEL</i>	Molecular chaperone affecting head assembly of phages T4 and λ	201, 523
<i>mopB</i>	<i>groE, hdh, tabB, groES</i>	Molecular chaperone affecting head assembly of phages T4 and λ	880
<i>mul</i>		Mutability of UV-irradiated phage λ	1693
<i>nmpC</i>		Outer membrane porin protein; locus of qsr prophage	143

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TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>ogr</i>		Regulator of late transcription in phage P2; part of cryptic P2 prophage	900, 1499
<i>OriJ</i>		Origin function in rac prophage	
<i>phxB</i>		Adsorption of ϕ X174	1123
<i>pin</i>		Inversion of adjacent DNA; locus of e14 element	859
<i>qin</i>	<i>kim</i>	Cryptic lambdoid phage	941
<i>qsr'</i>		Defective prophage qsr'	954
<i>rac</i>	<i>sbcA</i>	Defective prophage rac; contains <i>recE</i> and <i>oriJ</i>	941
<i>rap</i>		Growth of phage λ	1242
<i>recE</i>	<i>rac</i>	A function of the Rac prophage: recombination and DNA repair; exonuclease VIII (EC 3.1.11.-)	266
<i>tabC</i>		Development of phage T4, related to Rho?	225, 1587
<i>tnm</i>		Transposition of Tn9 and other transposons; development of phage Mu	704, 972
C. Colicin-related functions			
<i>cet</i>	<i>ref, refII</i>	Tolerance to colicin E2	407
<i>cirA</i>	<i>feuA</i>	Iron-regulated colicin I receptor; porin; requires <i>tonB</i> gene product	108, 565
<i>cma</i>		Colicin M	600
<i>creD</i>	<i>cet, refII</i>	Inner membrane protein involved in colicin E2-mediated killing	407
<i>cvpA</i>		Required for colicin V production	455
<i>tolA</i>	<i>cim, tol-2, excC, lky</i>	Tolerance to group A colicins and single-stranded filamentous DNA phage; leakage of periplasmic proteins	112, 914
<i>tolB</i>	<i>lky, tol-3</i>	Tolerance to colicins E2, E3, A, and K; leakage of periplasmic proteins	915
<i>tolC</i>	<i>colE1-i, mtcB, refI, tol-8</i>	Specific tolerance to colicin E1; expression of outer membrane proteins	399, 648, 1705
<i>tolD</i>		Tolerance to colicins E2 and E3; ampicillin resistance	445
<i>tolE</i>		Tolerance to colicins E2 and E3; ampicillin resistance	445
<i>tolI</i>		Tolerance to colicins Ia and Ib	219
<i>tolJ</i>		Resistance to colicins L, A, and S4; partial resistance to colicins E and K	343
<i>tolM</i>	<i>cmt</i>	Mutant phenotype: high-level tolerance to colicin M	600, 601
<i>tolQ</i>	<i>fii, tolP?</i>	Tolerance to group A colicins and single-stranded filamentous DNA phage	176, 426
<i>tolR</i>	<i>fii</i>	Tolerance to group A colicins and single-stranded filamentous DNA phage	426
<i>tolZ</i>		Tolerance to colicins E2, E3, D, 1a, and 1b; generation of chemical proton gradient	1039
D. Plasmid-related functions			
<i>mafA</i>		Maintenance of F-like plasmids	1695
<i>mafB</i>		Maintenance of F-like plasmids	1695
<i>mprA</i>		Regulator of plasmid <i>mcrB</i> operon (microcin B17)	364, 365
<i>pcnB</i>		Plasmid copy number control	1034
E. Drug/analog sensitivity			
<i>abs</i>		Sensitivity and permeability to antibiotics and dyes	271
<i>acrA</i>	<i>lir, Mb, mbl, mtcA</i>	Sensitivity to acriflavine, phenethyl alcohol, sodium dodecyl sulfate	284, 627, 1140
<i>acrC</i>		Sensitivity to acriflavine	1141
<i>ampC</i>	<i>ampA</i>	β -Lactamase; penicillin resistance (EC 3.5.2.6)	480
<i>ampD</i>		Regulates <i>ampC</i>	953
<i>ampE</i>		Regulates <i>ampC</i>	953
<i>azaA</i>		Resistance or sensitivity to azaserine	1756
<i>azaB</i>		Resistance or sensitivity to azaserine	1756
<i>can</i>		Canavanine resistance	233
<i>cmlA</i>		Resistance or sensitivity to chloramphenicol	99
<i>dvl</i>		Sensitivity to sodium dodecyl sulfate and toluidine blue plus light	1699
<i>eryD</i>	<i>mac</i>	Erythromycin growth dependence	1749
<i>inm</i>		Susceptibility to mutagenesis by nitrosoguanidine	1383
<i>ksgA</i>		<i>S</i> -Adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase (EC 2.1.1.-); kasugamycin resistance	1672

Continued on following page

TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>ksgB</i>		Second-step (high-level) resistance to kasugamycin	476
<i>ksgD</i>		Kasugamycin resistance	476
<i>lev</i>		Resistance to levallorphan	327
<i>linB</i>		High-level resistance to lincomycin	683
<i>lytA</i>		Tolerance to β -lactams; autolysis defective?	602, 1484
<i>marA</i>		Multiple antibiotic resistance; tetracycline efflux system	585
<i>mng</i>		Resistance or sensitivity to manganese	1492
<i>mvrA</i>		Resistance to methyl viologen	1641
<i>nalB</i>		Resistance or sensitivity to nalidixic acid	595
<i>nalD</i>		Penetration of nalidixic acid through outer membrane	670
<i>neaB</i>		Resistance to neamine	367
<i>nek</i>	<i>amk</i>	Resistance to neomycin, kanamycin, and other aminoglycoside antibiotics	680
<i>nfnA</i>		Sensitivity to nitrofurantoin	1418, 1462
<i>nfnB</i>		Sensitivity to nitrofurantoin	1418, 1462
<i>nfsA</i>		Nitrofuran reductase I activity	1046
<i>nfsB</i>		Nitrofuran reductase I activity	1046
<i>sbmA</i>		Sensitivity to microcin B17	885
<i>semA</i>		Sensitivity to microcin E492	1301
<i>sloB</i>		Low growth rate; tolerance to amidopenicillin and nalidixic acid	981
<i>strC</i>	<i>strB</i>	Low-level streptomycin resistance	1347
<i>tlnA</i>	<i>tlnI</i>	Resistance or sensitivity to thiolutin	1497
F. Radiation sensitivity			
<i>ior</i>		Radiation sensitivity, particularly gamma rays; recombination ability decreased	450
<i>radA</i>		Sensitivity to gamma and UV radiation and methyl methane-sulfonate	388
<i>radC</i>		Sensitivity to radiation	459, 460
<i>ras</i>		Sensitivity to UV and X rays	1702
<i>rer</i>		Resistance to UV and gamma rays	1525
G. DNA sites^b			
<i>att186</i>		Integration site for prophage 186	
<i>att253</i>		Integration site for prophage 253	
<i>atte14</i>		Integration site for element e14	
<i>attHK139</i>		Integration site for phage HK139	
<i>attHK22</i>	<i>attB-htt</i>	Integration site for phage HK022	
<i>attλ</i>	<i>att82</i>	Integration site for prophages λ, 82, and 434	
<i>attP1, P7</i>	<i>att434</i>		
<i>attP22</i>	<i>loxB</i>	Integration site for phages P1 and P7	
<i>attP2H</i>	<i>ata</i>	Integration site for phage P22	
<i>attP2II</i>		Phage P2 integration site H	
<i>attP4</i>		Phage P2 integration site II	
<i>attPA-2</i>		Integration site for phage P4	
<i>attφ80</i>		Integration site for phage PA-2	
<i>Dif</i>		Integration site for prophage φ80	
<i>OriC</i>	<i>poh?</i>	A recombination site in terminus region; resolves sister chromosomes	
<i>TerA</i>	<i>tre</i>	Origin of replication of chromosome	
<i>TerB</i>		Terminus; chromosomal DNA replication inhibition; site of Tus-mediated inhibition of DnaB helicase	
<i>TerC</i>		Terminus; chromosomal DNA replication termination; site of Tus-mediated inhibition of DnaB helicase	
<i>TerD</i>		Terminus; chromosomal DNA replication inhibition; site of Tus-mediated inhibition of DnaB helicase	
<i>TerE</i>		Terminus; chromosomal DNA replication inhibition; site of Tus-mediated inhibition of DnaB helicase	
H. Adaptations to atypical conditions			
<i>crg</i>		Cold-resistant growth	795
<i>cspA</i>		Cold shock protein 7.4, transcriptional activator of <i>hns</i>	543

Continued on following page

TABLE 2—Continued

Gene	Synonym	Gene product and description	Reference(s)
<i>cstA</i>		Carbon starvation protein	1445
<i>dps</i>		Global regulator, starvation conditions	28
<i>gef</i>		Polypeptide destructive to membrane potential	364, 365
<i>htgA</i>		Protein required for high-temperature growth	352
<i>htpG</i>		Heat shock protein C 62.5	617, 1512
<i>htpX</i>		Heat shock protein	835
<i>htrB</i>		Protein required for growth at high temperature	779–781
<i>htrC</i>		Pleiotrophic effects on growth at high temperatures, radiation sensitivity, proteolysis	781, 1310
<i>htrD</i>		High temperature growth factor; probable regulator, cysteine transport	362
<i>pspA</i>		Shock protein, associated with inner membrane	186, 187
<i>pspB</i>		Shock protein B	186, 187
<i>pspC</i>		Shock protein activates <i>psp</i> operon expression	186, 187
<i>pspD</i>		Shock protein D	187
<i>pspE</i>		Shock protein E	186, 187
<i>rdgA</i>		Dependence of growth on <i>recA</i> gene product	487
<i>rdgB</i>		Dependence of growth and viability on <i>recA</i> function	487
<i>relF</i>		Polypeptide destructive to membrane potential	364, 365
<i>uspA</i>		Universal stress protein, regulator?	1176

^a BCCP, biotin carboxyl carrier protein; CoA, coenzyme A; DCCD, *N,N'*-dicyclohexylcarbodiimide; NEM, *N*-ethylmaleimide; PEP, phosphoenol-pyruvate.

^b DNA sites listed for completeness. No gene product is made.

defined, enzymes are by far the largest category, with transport proteins and regulatory proteins following. Among the genes presently known, genes that encode RNA molecules constitute only 7% of the whole.

How much will these relative proportions change as we approach complete knowledge of the genes and gene products of *E. coli*? As a guess, in the future one might expect to find genes for functions that are more difficult to dissect at the molecular level, such as genes for components of the cell structure and genes for the components of complex interrelated regulatory networks that govern cellular processes.

GENOME CONTENTS

Density of Information in the Genome

One gene, one enzyme, one catalyzed reaction? The density of biochemical information in terms of reactions catalyzed per kilobase of genetic material is highly variable in the bacterial genome because genes do not always have a one-to-one relationship with a biochemical reaction. By common usage, we hold to the principle that one gene encodes one polypeptide chain (or one cistron encodes one polypeptide). In the case of simple enzymes composed of one polypeptide, often one reaction is catalyzed per gene, but the composition and catalytic capabilities of enzymes in terms of polypeptide chains varies greatly. For enzymes made from multiple subunits (and often more than one chain of each subunit polypeptide), as many as four genes are needed to describe the enzyme and the reaction it catalyzes (e.g., the *sdhA*, *sdhB*, *sdhC*, and *sdhD* genes for succinic dehydrogenase) (211, 1152). At the other end of the spectrum there are polyfunctional polypeptides, where one gene encodes a polypeptide that has as many as four catalytic activities. The two-subunit fatty acid oxidation complex encoded by *fadA* and *fadB* catalyzes five reactions. The polypeptide of the *fadB* gene catalyzes four of the five. These are entirely separate reactions of some biochemical variety as reflected in the range of the EC numbers: 1.1.1.35, 5.1.2.3, 5.3.3.8, and 4.2.1.17 (1795, 1797). Clearly, the effi-

ciency of biochemical information per kilobase of DNA or kilodalton of protein, if one can think of it that way, depends on the makeup of the catalytic proteins and varies over a wide range from the efficiency of very small RNase molecules encoded by single genes and highly efficient single polypeptides with multiple catalytic domains such as the *fadB*-encoded polypeptide to the other extreme, very large polypeptides with a single catalytic activity such as the *lacZ* β-galactosidase and huge multienzyme complexes such as pyruvate dehydrogenase requiring three genes, three enzyme components, and as many as 24 polypeptide chains per enzyme.

Density of code use in the genome. As more of the genome is sequenced and long stretches of continuous sequence are produced, including many instances of contiguous genes, it is not uncommon to find the promoter for one coding sequence placed within the C-terminal coding sequence of the upstream gene. Examples are legion. Adjacent genes such as *trpA-trpB*, *ilvA-ilvD*, *pdxA-ksgA*, *selA-selB*, *alkB-ada*, *mreC-mreD*, and the group *ddl-ftsQ-ftsA-ftsZ* all have short overlaps of part of the stop codon of the upstream gene and the first part of the initial methionine codon of the downstream gene, and the promoters for downstream genes are found in the coding region of the upstream gene. Other genes, such as *miaA* and *miaD*, overlap by several nucle-

TABLE 3. Distribution of cellular functions of *E. coli* gene products^a

Function category	% of gene products in category
I. Intermediary metabolism	22
II. Biosynthesis of small molecules	19
III. Macromolecule metabolism	24
IV. Cell structure	8
V. Cellular processes	18
VI. Other functions	9

^a Excludes 20 DNA sites with no gene product and 12 genes of independent genetic elements such as prophages.

otides (294), and still others, such as the EF-Tu gene, overlap even more. The promoters for transcription of the EF-Tu gene lie hundreds of base pairs into the coding region of the upstream *fus* gene (1817). The *thdF* gene involved in thiophene oxidation overlaps several hundred bases with regulatory and structural sequences of the *tnaA* gene on the opposite strand (14).

There are only a few examples of extensively overlapping coding regions. Two open reading frames in the *cysE* locus, *cysX* and *cysE*, are coded on opposite strands and overlap (1605). Coding sequences are used more than once in the *mcrB*, *trpR*, and *dnaX* genes. The *mcrB* gene of a restriction system produces two or possibly three proteins, one of 51 to 53 kDa and one or two additional polypeptides of about 34 kDa (386, 846). The N-terminal sequences of the large protein and one small protein differ, but their C-terminal sequences are the same; therefore the gene has at least two initiation sites and produces at least two polypeptides (1824). The C-terminal portion of the *trpR* gene is translated in both the 0 and the +1 frames. The two proteins produced have identical N-terminal sequences, but a translational frame-shift produces different C-terminal sequences (113). The *dnaX* gene encodes two subunits of DNA polymerase III, the gamma and tau subunits. The gamma subunit is produced by translation in a frameshift mode relative to the tau translation (1646, 1647). These few genes are densely packed with information, actually doubling up their use of coding sequences. Although the *trpR* gene seems unremarkable in composition, the *mcrB* and *dnaX* genes are not typical *E. coli* genes. The G+C content of the *mcrB* gene is low (40.3%), and that of the *dnaX* gene is high (57.7%) (1379). It seems possible that these exceptional genes were acquired by *E. coli* from foreign sources.

There is a wide range in the density of genomic information. In contrast to these examples of close-packed coding information, other parts of the genome seem to be less densely packed. Within the long section of the genome sequenced by Blattner and colleagues were sections dubbed "gray holes" that had no recognized open reading frames and no known function and were apparently unexpressed DNA (331). Yura et al., who have sequenced another long section of the genome, postulate many short open reading frames in intragenic sequences (1810). If these short open reading frames are not expressed, some of these intergenic regions could also be gray holes.

Unexpressed DNA and cryptic genes. It has been known for some time that not all of the genes in the *E. coli* genome are expressible. Some of the DNA of the genome seems to be silent, carried along from generation to generation without expression. There are cryptic operons with recognizable genes that are unable to be expressed because they lack functional promoters or harbor several mutations or an insert of genetic material that prevents normal expression. Under severe selection, the faults can be reversed and cryptic operons can become active (430, 590, 1229). These unexpressed operons, in a manner of speaking, represent a class of zero density of code usage. Why are these nonexpressed genes carried in the genome? They carry functions that are nonessential for the cell under normal circumstances, but under particular conditions that are unfavorable to the wild type, the genes can be recalled to function by rare mutations. The ability to mutate a cryptic operon to full function could be a critical survival advantage for a population of bacteria (939), making it worth harboring dormant elements in the genome until a time of need.

Optional genetic elements. Some of the genetic elements in

TABLE 4. Classification of *E. coli* gene products and gene descriptions

Gene description	No. of genes
Enzymes, leader peptides, enzyme activity	748
Phenotypes.....	314
Transport, binding proteins	221
Regulators.....	164
Components of cell structure	113
RNA	104
Protein factors	36
DNA sites, no gene product	20
Total	1,720

the *E. coli* genome derive from external sources, for instance phages and plasmids, and are adventitious (not a fundamental part of the *E. coli* genome). Since some *E. coli* strains do not have prophages or plasmids, evidently the prophages are not essential to the viability of the cell, but they may be an important part of the dynamics of gene exchange and gene enrichment in populations of *E. coli*. A possible benefit from harboring prophages could be the gain of an occasional function. Some prophage genes function from their prophage locations in the *E. coli* K-12 cell, or they may be silent but require only one or two mutations to gain function. For instance, the *mcrA* methyltransferase gene resides in prophage e14 (645), as do the *pin* invertase and the *lit* membrane protein (776). These genes are expressed in *E. coli* and provide seemingly useful functions. The *rac* prophage contributes a second origin of replication for the chromosome, *oriJ*, useful if *oriC* is not functioning. Also derived from *rac* are an exonuclease gene, *recE*, and a potassium transport gene, *trkG*, which does not even seem to belong to the lambda genome yet provides a function to the *E. coli* host (1434). A lambdoid phage, *qsr'*, contributes the *nmpC* gene, and phage PA-2 contributes the *lc* gene; these are very similar membrane protein genes (143). Another potassium transport gene, *trkK*, resides in a lambda prophage. Therefore not all of a prophage genome is silent or of no value to the bacterial genome. Some phage functions seem to be useful.

Redundancy of Genes and Gene Products

For many cellular functions of *E. coli* there are two genes, as if the genetic program of *E. coli* calls for backup systems. Redundancy or repetition might seem an example of reduced density of genetic information and an unnecessary dilution of genetic information, but in at least some cases we understand that the seemingly redundant information is regulated differently and is used for different purposes in the cell.

What sort of genes are redundant? There are many examples. For instance, there are multiple genes for most tRNAs. There are of course genes that produce similar tRNAs that carry different anticodons for a given amino acid, but there are also exact duplicate genes for some tRNAs. There are also groups and pairs of genes that code for very similar proteins. There are very similar transport proteins, DNA-binding proteins, and sensor-regulator pairs of proteins, but perhaps the simplest to list are the redundant enzymes, such as, for instance, the three fumarase isozymes. There are many pairs and groups of genes for enzymes that carry out the same or closely similar reactions. The GeneFunction data base is sorted by EC number to identify multiple genes identified with a single reaction. Among these are examples

of redundant functions. Also, the literature was consulted to find cases in which two enzymes are known but only one has been associated with a gene. The result is shown in Table 5. There are 125 gene products that group into 58 pairs or clusters whose members have identical or very similar properties. In all but two of the pairs and groups the enzymatic reactions appear to be identical. In the exceptions, there are slight differences in a pair of enzymes (one may use NAD, and the other may use NADP), but the two enzymes of a pair carry out essentially the same biochemical reaction.

For some of these redundant genes and enzymes, we know that the regulation of the genes and gene products can be different, as for the isozymes encoded by the *aroF*, *aroG*, and *aroH* genes. All three enzymes are 3-deoxy-D-arabino-heptulosonate-7-phosphate synthases, but each is sensitive to different end product metabolites that exert a feedback inhibition type of control of enzyme activity (1259). The *aroF* enzyme is sensitive to tyrosine (1722), the *aroG* enzyme is sensitive to phenylalanine (344, 345), and the *aroH* enzyme is sensitive to tryptophan (1317). The same kinds of differential sensitivities affect the synthesis and activities of aspartokinase I-homoserine dehydrogenase I, aspartokinase II-homoserine dehydrogenase II, and aspartokinase III. The activity of each enzyme is inhibited by a different one or more amino acids, and the expression of the genes is repressed by different amino acids (281). Such subtleties of control mechanisms provide a rationale of regulatory fine tuning to account for what otherwise might seem to be supernumerary copies of some genes.

Another example of filling separate needs are the genes for glycerol-3-phosphate dehydrogenase. One enzyme is made and used under aerobic conditions (encoded by *glpD*) (71), and the other enzyme is part of a membrane-bound complex that is made and used under anaerobic conditions (by *glpA*, *glpB*, and *glpC*) (282). The advantages to the cell can easily be imagined in these cases. However, there are many other cases of doubled genes for which we have no explanation at the moment. Why does *E. coli* maintain more than one gene and gene product for so many functions?

In fact, to broaden the inquiry to more than enzymes, sequence similarities have been sought on a systematic basis among all *E. coli* protein gene products (862), by using the FASTA sequence comparison program, with the result that more than 30% of the *E. coli* protein sequences entered in the SwissProt data base version 23 have at least 20% and often much higher amino acid identity with one or more partner sequences and that these partner proteins almost always have a similar or related function. Further analysis of these sequence relationships may shed light on evolutionary processes as well as on the place of redundancy in *E. coli* cell physiology.

Most of the members of pairs or groups of redundant genes and enzymes listed in Table 5 are similar to one another in nucleotide and amino acid sequence. Perhaps these genes of similar sequence are the result of a process of duplication of genes followed by some divergence of sequence but little change in function. The duplications could have taken place within an ancestor *E. coli* genome or in an ancestral enteric bacterium prior to differentiation of species, as seems to be the case for the *tufA-tufB* gene pairs in *E. coli* and *S. typhimurium* (1472).

In contrast to the instances of sequence similarity, there are a few cases of redundancy in function but dissimilarity in the sequences of the genes and their gene products. These cases could be examples either of convergent evolution or of

lateral transfer of genetic material from another source. With respect to lateral transfer, there are telltale characteristics that help identify genes acquired by *E. coli* from a foreign source. One characteristic is G+C content, especially in the third position of codons; another is codon usage.

The G+C content of sequenced *E. coli* genes has been tabulated (1379). A small fraction of the whole have extreme values of G+C content, below 43% G+C or above 58% G+C. Some of the genes of extreme composition are prophage genes, a few cryptic genes, the Rhs elements that resemble transposons, and the *phn* operon (phosphonate utilization); these are all plausible candidates for having been acquired from a foreign source. Some of the redundant genes listed in Table 5 are also atypical in G+C content, suggesting an external source. Genes with a high G+C content are *argF* (58.7%), *gabD* (58.3%), and *alkA* (55.6%). Genes with a low G+C content are *tdcA* (42.2%) and *glpA* (45.6%).

The sequences of the *argI* and *argF* genes, coding for two ornithine transcarbamylases, have been analyzed further (1674). When the three codon positions were examined separately, the G+C content of the third positions of the codons was found to be unusually high for *E. coli* (78%), giving strong support for the proposition that this extra gene was acquired from another source, perhaps from another enteric organism. (A similar situation exists for the *phoN* gene of *S. typhimurium*, which has a higher A+T content than most *S. typhimurium* genes [571].)

Codon usage also identifies groups of genes. Medigue et al. (1058) have shown that in addition to the previously recognized two categories of codon usage that reflect low and high rates of gene expression, there is a third category. Genes that fall into this third category may be genes of foreign origin. In this category are genes of external elements such as prophages and plasmids and also genes that one can easily imagine to have been acquired by *E. coli* from outside sources, such as genes that encode surface elements of the cell and are often found in the genomes of mobile elements (1058). The following members of redundant gene pairs (Table 5) have codon usage patterns that fall into this third class: *alkA*, *tdcA*, *aroL*, *pgpA*, and *ilvM*. These genes code respectively for a second 3-methyladenine DNA glycosylase, a second threonine dehydratase, shikimate kinase II, a second phosphatidylglycerophosphate phosphatase, and one of the several acetolactate synthase isozymes. These redundant genes seem likely to have been acquired from a foreign source, particularly the *alkA* and *tdcA* genes, which are aberrant both in G+C composition and in codon usage class.

Chromosomal locations of physiologically related genes. Many years ago, the observation was made that many groups of genes whose gene products were physiologically related were positioned on the genetic map in clusters that had a tendency to lie approximately 90° or 180° apart (1831). As more data on *E. coli* genes were amassed, reexamination of the question showed that only the genes encoding the enzymes of glucose catabolism seemed to occupy positions at four equidistant loci on the circular map, a juxtaposition not likely to have arisen by chance (1832). Now that even more information is available, the map positions of the genes that were grouped in the various categories of cellular function (Table 2) were examined for any tendency to be positioned nonrandomly on the map of the genome. None of the genes within the functional groupings used in Table 2 showed any such tendency, except possibly the genes of glucose catabolism. When one looks at the placement of genes for enzymes of glycolysis, the pentose shunt, the

TABLE 5. Redundancy in the *E. coli* genome

EC no.	Gene name	Enzyme name	Reference
1.1.1.3	<i>metL</i>	Homoserine dehydrogenase II	1811
	<i>thrA</i>	Homoserine dehydrogenase I	1231
1.1.99.5	<i>glpA</i>	Glycerol-3-phosphate dehydrogenase	282
	<i>glpD</i>	Glycerol-3-phosphate dehydrogenase	71
1.2.1.2	<i>fdnG</i>	Formate dehydrogenase-N	118
	<i>fdhF</i>	Formate dehydrogenase-H	72
1.2.1.12	<i>gapA</i>	Glyceraldehyde 3-phosphate dehydrogenase	175
	<i>gapB</i>	Glyceraldehyde 3-phosphate dehydrogenase	18
1.2.1.16	<i>gabD</i>	Succinate-semialdehyde dehydrogenase(NADP)	95
1.2.1.24	<i>sad</i>	Succinate-semialdehyde dehydrogenase(NAD)	1024
1.6.6.9	<i>tor</i> — ^a	Inducible trimethylamine N oxide reductase Constitutive trimethylamine N oxide reductase	1494
1.7.99.4	<i>narG</i>	Nitrate reductase alpha subunit	144
	<i>narZ</i>	Nitrate reductase alpha subunit	145
1.7.99.4	<i>narH</i>	Nitrate reductase beta subunit	144
	<i>narY</i>	Nitrate reductase beta subunit	145
1.7.99.4	<i>narI</i>	Nitrate reductase gamma subunit	144
	<i>narV</i>	Nitrate reductase gamma subunit	145
1.8.1.4	<i>lpd</i>	Lipoamide dehydratase	1540
	— ^a	Lipoamide dehydratase	1335
1.10.3.-	<i>cydA</i>	Cytochrome oxidase subunit I	303
	<i>appB</i>	Cytochrome oxidase subunit I	337
	<i>cyaA</i>	Cytochrome oxidase subunit	256
1.10.3.-	<i>cydB</i>	Cytochrome oxidase subunit II	303
	<i>appC</i>	Cytochrome oxidase subunit II	337
	<i>cyoB</i>	Cytochrome oxidase subunit	256
1.11.1.6	<i>katE</i>	Catalase HP I	1690
	<i>katG</i>	Catalase HP II	1635
1.15.1.1	<i>sodA</i>	Superoxide dismutase (Mn)	123
	<i>sodB</i>	Superoxide dismutase (Fe)	220
1.18.99.1	<i>hydA</i>	Hydrogen lyase, beta subunit	1298
	<i>hybC</i>	Hydrogen lyase, beta subunit	1298
	<i>hycE</i>	Hydrogen lyase, beta subunit	1298
2.1.1.13	<i>metE</i>	Homocysteine transmethylase, vitamin B ₁₂ dependent	996
2.1.1.14	<i>methH</i>	Homocysteine transmethylase	1187
2.1.1.63	<i>ada</i>	6-Methylguanine-DNA methyltransferase	1047
	<i>ogt</i>	6-Methylguanine-DNA methyltransferase	1025
2.1.3.3	<i>argF</i>	Ornithine carbamoyl transferase	1674
	<i>argI</i>	Ornithine carbamoyl transferase	114
2.3.1.41	<i>fabB</i>	3-Oxoacyl-[acyl carrier protein]synthase	793
	<i>fabF</i>	3-Oxoacyl-[acyl carrier protein]synthase	731
	<i>fabH</i>	3-Oxoacyl-[acyl carrier protein]synthase	1644
2.4.1.1	<i>malP</i>	α-Glucan phosphorylase	1808
	<i>glgP</i>	α-Glucan phosphorylase	263
2.4.2.1	<i>xapA</i>	Purine-nucleoside phosphorylase II	124
	<i>deoD</i>	Purine-nucleoside phosphorylase I	629
2.4.99.-	— ^a	Murein lytic transglycosylase (<islt-35< i="">)</islt-35<>	436
	<i>slt</i>	Murein lytic transglycosylase (<islt-70< i="">)</islt-70<>	435
2.5.1.6	<i>metK</i>	S-Adenosylmethionine synthetase	1420
	— ^a	S-Adenosylmethionine synthetase	1419
2.7.1.11	<i>pfkA</i>	6-Phosphofructokinase	618
	<i>pfkB</i>	6-Phosphofructokinase	324
2.7.1.40	<i>pykA</i>	Pyruvate kinase	1059
	<i>pykF</i>	Pyruvate kinase	1183
2.7.1.71	<i>aroK</i>	Shikimate kinase I	977
	<i>aroL</i>	Shikimate kinase II	1085
2.7.2.4	<i>lysC</i>	Aspartate kinase III	226
	<i>metL</i>	Aspartate kinase II	1811
	<i>thrA</i>	Aspartate kinase I	789
3.1.1.5	<i>pldC</i>	Lysophospholipase L ₁	778
	<i>pldB</i>	Lysophospholipase L ₂	822
3.1.3.27	<i>pgpA</i>	Phosphatidylglycerophosphate phosphatase	690
	<i>pgpB</i>	Phosphatidylglycerophosphate phosphatase	691
	— ^a	Phosphatidylglycerophosphate phosphatase	493

Continued

TABLE 5—Continued

EC no.	Gene name	Enzyme name	Reference
3.1.4.-	<i>glpQ</i>	Glycerophosphodiester phosphodiesterase	1628
	<i>ugpQ</i>	Glycerophosphodiester phosphodiesterase	
3.1.26.4	<i>rnhA</i>	RNAse HI	56
	<i>rnhB</i>	RNAse HII	720
3.2.1.23	<i>ebgA</i>	β-Galactosidase, evolved	588
	<i>lacZ</i>	β-Galactosidase	614
3.2.1.86	<i>ascB</i>	6-Phospho-β-glucosidase	590
	<i>celF</i>	6-Phospho-β-glucosidase	1229
	<i>bglB</i>	6-Phospho-β-glucosidase	1439
3.2.2.21	<i>alkA</i>	3-Methyladenine DNA glycosylase I	757
3.2.2.20	<i>tag</i>	3-Methyladenine DNA glycosylase II	1035
3.4.16.4	<i>dacA</i>	Penicillin-binding protein 5	1669
	<i>dacC</i>	Penicillin-binding protein 6	191
3.4.21.-	<i>clpA</i>	ATP-dependent protease, ATP-binding subunit	551
	<i>clpB</i>	ATP-dependent protease, ATP-binding subunit	1764
3.5.1.1	<i>ansA</i>	Asparaginase I	743
	<i>ansB</i>	Asparaginase II	154
3.6.1.-	<i>held</i>	DNA helicase IV	1766
	<i>rep</i>	DNA helicase	980
	<i>uvrD</i>	DNA helicase II	238
3.6.1.34	<i>atpA</i>	H ⁺ -transporting ATP synthase, alpha subunit	1411
	<i>atpD</i>	H ⁺ -transporting ATP synthase, beta subunit	1411
4.1.1.15	<i>gadA</i>	Glutamate decarboxylase	1500
	<i>gadB</i>	Glutamate decarboxylase	1500
4.1.1.17	<i>speC</i>	Ornithine decarboxylase, constitutive	785
	<i>speF</i>	Ornithine decarboxylase, inducible	171
4.1.2.13	<i>fba</i>	Fructose-bisphosphate aldolase class II	17
	— ^a	Fructose-bisphosphate aldolase class I	1235
4.1.2.15	<i>aroF</i>	DAHPase ^b	1722
	<i>aroG</i>	DAHPase ^b	1317
	<i>aroH</i>	DAHPase ^b	678
4.1.3.18	<i>ilvBN</i>	Acetolacetate synthase I	484
	<i>ilvHI</i>	Acetolacetate synthase III	1522
	<i>ilvGM</i>	Acetolacetate synthase II	886
	<i>ilvJ</i>	Possible acetolacetate synthase IV	1350
	<i>ilvF</i>	Possible acetolactate synthase V	20
4.2.1.13	<i>sdaA</i>	Serine dehydratase	1563
	<i>sdaB</i>	Serine dehydratase	1562
4.2.1.16	<i>tdcAB</i>	Threonine dehydratase	339
	<i>ilvA</i>	Threonine dehydratase	1585
4.2.1.51	<i>pheA</i>	Prephenate dehydratase	1152
	<i>tyrA</i>	Prephenate dehydratase	1030
4.2.1.2	<i>fumA</i>	Fumarate hydratase	109
	<i>fumB</i>	Fumarate hydratase	1769
	<i>fumC</i>	Fumarate hydratase	1656
4.2.99.8	<i>cysK</i>	Cysteine synthase A	923
	<i>cysM</i>	Cysteine synthase B	1495
5.1.1.1	<i>alr</i>	Alanine racemase	1708
	<i>dadX</i>	Alanine racemase	1751
5.2.1.8	<i>ppiA</i>	Peptidylprolyl-cis-trans-isomerase	289
	<i>ppiB</i>	Peptidylprolyl-cis-trans-isomerase	
5.4.99.5	<i>pheA</i>	Chorismate mutase	1152
	<i>tyrA</i>	Chorismate mutase	1030
5.99.1.3	<i>parC</i>	DNA topoisomerase IV, subunit A	791
	<i>gyrA</i>	DNA gyrase, subunit A	19
	<i>parE</i>	DNA topoisomerase IV, subunit B	791
	<i>gyrB</i>	DNA gyrase, subunit B	19
6.1.1.6	<i>lysS</i>	Constitutive lysine-tRNA synthetase	917
	<i>lysU</i>	Inducible lysine-tRNA synthetase	274
6.3.1.1	<i>asnA</i>	Asparagine synthetase A	1144
	<i>asnB</i>	Asparagine synthetase B	1453
6.3.2.4	<i>ddlA</i>	D-Alanine:D-alanine ligase	1815
	<i>ddlB</i>	D-Alanine:D-alanine ligase	413

^a Gene has not been identified.^b DAHP, 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase.

Entner-Doudoroff pathway, and the tricarboxylic acid cycle, a picture still emerges of four clusters of genes at around 16, 41, 66, and 91 map units, but in addition there are genes that group around 25, 88, and 93 map units, as well as a few singlets at other positions. With data from nearly all of the genes for the pertinent enzymes now available, the picture of the arrangement of the glucose-catabolizing genes no longer conforms to a simple picture of four equidistant gene clusters. If the map positions have any meaning at all, the clustering is more complex than that. It may be that in fact the map locations are random.

EPILOG

Inevitably there are errors of fact and of omission in this compilation of data, but one hopes that they are not so extensive as to interfere with the utility of the tables and bibliography. Corrections and suggestions for improvements will be most welcome. I would be pleased to incorporate both new information and corrections into the data base.

As the sequencing projects on *E. coli* DNA proceed and characterization of all the gene products and their functions is concluded, biologists will be able to answer a good many questions about how a simple cell works. How many functions and, specifically, what kinds of functions are sufficient to genetically determine a free-living cell that is able to derive energy and synthesize its own substance from a simple, defined medium? We will also be in a better position to answer other questions. For instance, how much of the information in the *E. coli* genome is represented more than once? Are redundant genes present as backup devices to fill in if one is lost or damaged, or are the seemingly duplicate gene products different from each other in some important way such as location in the cell or specificity of regulation, so that each gene is active and the gene products are utilized for different purposes under different circumstances? Ultimately, we will be in a position to understand the workings of all the interconnected regulatory circuits that manage the expression of all the genes of *E. coli* in an orchestrated way that allows the cell to respond appropriately to changing conditions. Even after all structural genes of *E. coli* are identified and characterized, unraveling the subtleties of interconnected regulation mechanisms will be a demanding enterprise.

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