

Escherichia coli Gene Products: Physiological Functions and Common Ancestries

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INTRODUCTION

Knowledge about *Escherichia coli* genes, their gene products, and their roles in cell physiology has reached a point that invites a look at the horizon. We can look at what we know today and see it in a context of some kind of totality of knowledge about *E. coli* genes and their gene products that will be reached in time. Assembled here is a table of *E. coli* K-12 genes whose gene products are known, organized by principal physiological function, with literature references through most of 1994. We have summarized the distribution of gene products among physiological and functional categories. Also assembled is information on the amino acid sequence relatedness of *E. coli* proteins and classification of the functional relatedness of sequence-related pairs. These results are interpreted in the context of evolution, with the objective of understanding more about how genes evolve and ultimately of identifying the relatively small numbers of unique ancestral sequences that probably have generated the families of sequences we observe in *E. coli* today. We also present a compilation of multiple enzymes present in *E. coli* that carry out the same biochemical reaction. Some multiple enzymes are related by sequence and thus are likely to have descended from a common ancestor, but others have no apparent sequence relationship and may have derived from different ancestral sequences independently by convergent evolution, or they may have been acquired from another source by lateral transmission. We discuss the capacity for these multiple enzymes to serve as a rich resource that contributes significantly to the adaptive capability of *E. coli*.

FUNCTIONAL CATEGORIES

Table 1 presents a scheme of categories of cellular functions. Any such classification is arbitrary in that there are many ways to organize the complex function of a cell, and it is artificial in that it seems to create hard boundaries between functional categories when of course cellular functions and processes are complexly intertwined. Also, some categories refer to metabolic pathways, others such as "transport" refer to processes, and still others such as "membranes" refer to cellular structure, categories that are not comparable in kind or mutually exclusive. Thus, one gene product can belong to more than one category. Nevertheless, this classification scheme allows a gross assignment of a major cellular role to each gene and gene product. This allows us to view as a whole the activities and division of labor of the genes and gene products of *E. coli* that have been characterized to date.

TABLE 1 Categories of cellular functions.

Physiological function	Numbers of genes
Small-molecule metabolism	
Degradation	
Carbon compounds	96
Amino acids and amines	24
Fatty acids	12
Phosphorus compounds	20
Energy metabolism	
Glycolysis	17
Pyruvate dehydrogenase	4
Tricarboxylic acid cycle	16
Pentose phosphate pathway	
Oxidative branch	3
Nonoxidative branch	5
Entner-Doudoroff pathway	3
Respiration	
Aerobic	30
Anaerobic	61
Electron transport	13
Fermentation	25
ATP-proton motive force interconversion	9
Central intermediary metabolism	
General	46
Gluconeogenesis	5
Sugar-nucleotide biosynthesis, conversions	7
Amino sugars	5
Sulfur metabolism	13
Amino acid biosynthesis	
Glutamate family	
Glutamate	2
Glutamine	5
Arginine	10
Proline	3
Aspartate family	
Aspartate	2
Asparagine	3
Lysine	10
Threonine	5
Methionine	8
Serine family	
Glycine	2
Serine	3
Cysteine	4
Aromatic amino acid family	
Common stem	9
Phenylalanine	3
Tyrosine	3
Tryptophan	9
Histidine	9
Pyruvate family	
Alanine	2
Branched-chain family	
Valine and isoleucine	17
Leucine	7
Polyamine biosynthesis	7
Purines, pyrimidines, nucleosides, nucleotides	
Purine ribonucleotide biosynthesis	21
Pyrimidine ribonucleotide biosynthesis	9
2'-Deoxyribonucleotide metabolism	10
Salvage of nucleosides and nucleotides	19
Miscellaneous	8
Biosynthesis of cofactors, prosthetic groups, and carriers	
Biotin	8
Folic acid	9
Lipoate	2
Molybdopterin	9
Pantothenate	4
Pyridoxine	4
Pyridine nucleotide	7
Thiamine	10
Riboflavin	5
Thioredoxin, glutaredoxin, and glutathione	5

TABLE 1 *Continued*

Physiological function	Numbers of genes
Menaquinone and ubiquinone	16
Heme and porphyrin	13
Enterochelin	6
Fatty acid biosynthesis	26
Broad regulatory functions	51
Macromolecules	
Synthesis and modification of macromolecules	
Ribosomal and “stable” RNAs	25
Ribosomal protein synthesis and modification	57
Ribosome maturation and modification	15
tRNAs	80
Aminoacyl tRNA synthetases and their modification	49
Nucleoproteins	7
DNA replication, modification, recombination	91
Protein translation and modification	27
RNA synthesis, modification, transcription	28
Polysaccharides (cytoplasmic)	6
Phospholipids	12
Degradation of macromolecules	
RNA	13
DNA	22
Proteins and peptides	30
Polysaccharides	3
Cell envelope	
Membranes, lipoproteins, porins	31
Surface polysaccharides, lipopolysaccharides	44
Surface structures	55
Murein sacculus and peptidoglycan	37
Processes	
Transport/binding proteins	
Amino acids and amines	57
Cations	62
Anions	15
Carbohydrates, organic alcohols, and acids	92
Nucleosides, purines, and pyrimidines	7
Other 1	17
Chaperones	7
Cell division	37
Chemotaxis and mobility	12
Protein and peptide secretion	30
Osmotic adaptation	16
Detoxification	10
Cell killing	6
Other	
Phage-related functions and prophages	25
Colicin-related functions	12
Plasmid-related functions	7
Drug/analog sensitivity	46
Radiation sensitivity	5
Adaptations and atypical conditions	11

Table 2 lists 1,827 characterized gene products of *E. coli* K-12. Since not all known *E. coli* genes have characterized gene products, the list of genes that have been sequenced and mapped (see chapter 109) is longer than the list of genes for which the function of the gene product is known. We followed certain rules in choosing genes and gene products for listing. Most open reading frames with hypothetically translated gene products were excluded, except for a few with strong sequence similarities to other well-characterized gene products whose functions are known. These are noted as “putative” or “possible” functions in the table. Genes were excluded whose presence was simply deduced from the phenotype of a mutant, when the effect of the mutation was not described in enough detail to allow assignment of the gene product to a physiological category. However, genes were included whose effect has been characterized as to the physiological role in the cell even though the nature of the actual gene product (enzyme, regulator, permease, etc.) is not yet clear. Such genes were

included in the list, assigned a physiological category, but classified as having only a phenotype known rather than having the type of gene product specified. All of the genes in the compilation by Barbara Bachmann in the first edition of this work (88) have been retained, even though some genes are known only by phenotype (228 of them). One hesitates to delete information of any kind, but it is possible that “old” genes that were known only by mutant phenotype and have not been subjects of study for, say, 20 years should be removed from any subsequent listing of gene products of *E. coli*.

TABLE 2 *E. coli* genes grouped by function of gene product.

Category and gene	Gene product description ^a	Reference(s)
I. SMALL-MOLECULE METABOLISM		
A. Degradation		
1. Carbon compounds		
<i>araA</i>	L-Arabinose isomerase	1097, 1177
<i>araB</i>	L-Ribulokinase	1097, 1177
<i>araC</i>	Activator and repressor protein for <i>ara</i> genes	1096, 1177, 1297
<i>araD</i>	L-Ribulosephosphate 4-epimerase	1097
<i>ascB</i>	6-Phospho-β-glucosidase; cryptic	696, 1507
<i>ascG</i>	<i>ascBF</i> operon repressor	696, 1507
<i>bglA</i>	Phospho-β-glucosidase A; cryptic	696, 1507, 1769
<i>bglB</i>	Phospho-β-glucosidase B; cryptic	696, 1507, 1769
<i>bglG</i>	Positive regulation of <i>bgl</i> operon	696, 1767
<i>bglT</i>	Regulator for phospho-β-glucosidase A biosynthesis	1581, 1582
<i>celD</i>	Negative regulator of <i>cel</i> operon	1508
<i>celF</i>	Phospho-β-glucosidase; cryptic	1508
<i>cynR</i>	<i>cyn</i> operon positive regulator	52, 1071, 1935
<i>dgd</i>	D-Galactose dehydrogenase	1171
<i>dgoA</i>	2-Oxo-3-deoxygalactonate 6-phosphate aldolase	356
<i>dgoD</i>	Galactonate dehydratase	356
<i>dgoK</i>	2-Oxo-3-deoxygalactonate kinase	356
<i>dgoR</i>	Regulator of <i>dgo</i> operon	356
<i>ebgA</i>	Evolved β-D-galactosidase, alpha subunit; cryptic gene	499, 694, 1132
<i>ebgB</i>	Possible homolog of <i>lacY</i>	694
<i>ebgC</i>	Evolved β-D-galactosidase, beta subunit; cryptic gene	694, 1132
<i>ebgR</i>	Regulator of <i>ebg</i> operon	1196
<i>exuR</i>	Negative regulator of <i>exu</i> regulon, <i>exuT</i> , <i>uxaAC</i> , and <i>uxuB</i>	173
<i>fucA</i>	L-Fuculose-1-phosphate aldolase	298, 299, 2273
<i>fucI</i>	L-Fucose isomerase	298, 299
<i>fucK</i>	L-Fuculokinase	298, 299
<i>fucO</i>	L-1,2-Propanediol oxidoreductase	299, 353
<i>fucR</i>	Positive regulator of the <i>fuc</i> operon	299, 1192
<i>galE</i>	UDP-galactose 4-epimerase	111, 1019, 2085
<i>galK</i>	Galactokinase	2085
<i>galR</i>	Repressor of <i>galETK</i> operon	1219, 1997, 2129
<i>galS</i>	<i>mgl</i> repressor, a lactose operon inducer	1219, 1997, 2129
<i>galT</i>	Galactose-1-phosphate uridylyltransferase	535, 2085
<i>galU</i>	Glucose-1-phosphate uridylyltransferase	2135
<i>garA</i>	Glucarate utilization	1663
<i>garB</i>	Glucarate utilization	1663
<i>gatD</i>	Galactitol-1-phosphate dehydrogenase	435, 1108
<i>gatR</i>	Regulator, galactitol metabolism	1108
<i>gcd</i>	Glucose dehydrogenase	333, 2212, 2216
<i>glk</i>	Glucokinase	381
<i>gntV</i>	Gluconokinase, thermosensitive	336, 857
<i>gurB</i>	Utilization of methyl-β-D-glucuronide; <i>crp</i> ?	1910
<i>gurC</i>	Utilization of methyl-β-D-glucuronide	1910
<i>gurD</i>	Utilization of methyl-β-D-glucuronide	1910
<i>gutD</i>	Glucitol (sorbitol)-6-phosphate dehydrogenase	2215
<i>gutM</i>	Glucitol operon activator	2215
<i>gutR</i>	Regulator for <i>gut</i> (<i>srl</i>), glucitol operon	2215
<i>kdgK</i>	Ketodeoxygluconokinase	1576
<i>kdgR</i>	Regulator of <i>kdgK</i> , <i>kdgT</i> , and <i>eda</i>	1576
<i>lacA</i>	Thiogalactoside acetyltransferase	56
<i>lacI</i>	Repressor of the <i>lac</i> operon	977, 1012, 1718
<i>lacZ</i>	β-D-galactosidase	607
<i>mac</i>	Maltose acetyltransferase, broad specificity	210
<i>malI</i>	Repressor of <i>malX</i> and <i>malY</i> genes	1629, 1630
<i>malM</i>	Periplasmic protein of <i>mal</i> regulon	636, 1692
<i>malP</i>	Maltodextrin phosphorylase	826

Category and gene	Gene product description ^a	Reference(s)
<i>malT</i>	Positive regulator of <i>mal</i> regulon	1765
<i>malY</i>	Enzyme that may degrade or block biosynthesis of endogenous <i>mal</i> inducer	1629
<i>malZ</i>	Maltodextrin glucosidase	1765
<i>manA</i>	Mannose-6-phosphate isomerase	1901
<i>manC</i>	D-Mannose isomerase regulation; utilization of D-lyxose	1901
<i>melA</i>	α -Galactosidase	1147, 1379, 1574
<i>melR</i>	Regulator of melibiose operon	2124
<i>milD</i>	Mannitol-1-phosphate dehydrogenase	1980
<i>milR</i>	Repressor for <i>mil</i>	536
<i>nlp</i>	Regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu	313, 408
<i>pac</i>	Penicillin acylase, detaches phenylacetate residue	119, 1301
<i>pga</i>	Penicillin G acylase; precursor polypeptide processed to two nonidentical subunits	310, 1448
<i>pgm</i>	Phosphoglucomutase	914, 1191, 1577
<i>poxA</i>	Regulator for <i>poxB</i>	2057
<i>poxB</i>	Pyruvate oxidase	654, 2104
<i>prp</i>	Propionate metabolism	1876
<i>pta</i>	Phosphotransacetylase activity	681, 1587, 2113
<i>rbsK</i>	Ribokinase	49, 785
<i>rbsR</i>	Regulator for <i>rbs</i> operon	1187
<i>rhaA</i>	L-Rhamnose isomerase	90, 1341, 1902
<i>rhaB</i>	Rhamnulokinase	90, 1341
<i>rhaD</i>	Rhamnulose-phosphate aldolase	90, 1341
<i>rhaR</i>	Positive regulator for <i>rhaRS</i> operon	488, 1995, 1996
<i>rhaS</i>	Positive regulator for <i>rhaBAD</i> operon	488, 1995
<i>sfsA</i>	Probable regulator for maltose metabolism	964
<i>treC</i>	Amylotrehalase	189, 1919
<i>treE</i>	Trehalose-6-P phosphatase, catabolic	997, 1919
<i>treF</i>	Cytoplasmic trehalase	94
<i>uidA</i>	β -D-Glucuronidase	171, 889
<i>uidR</i>	Regulator for <i>uid</i>	171
<i>uxaA</i>	Altronate hydrolase	1564
<i>uxaB</i>	Altronate oxidoreductase	172
<i>uxaC</i>	Uronate isomerase	1431
<i>uxuA</i>	Mannonate hydrolase	173
<i>uxuB</i>	Mannonate oxidoreductase	173
<i>uxuR</i>	Regulator of <i>uxuBA</i> operon	173
<i>xylA</i>	D-Xylose isomerase	110, 1688
<i>xylB</i>	Xylulokinase	191, 1688
<i>xylR</i>	Regulator for <i>xyl</i>	1688, 1861
<i>xylR</i>	Putative regulator of <i>xyl</i> operon	1554, 1688, 1861
2. Amino acids and amines		
<i>adi</i>	Biodegradative arginine decarboxylase	1905
<i>ansA</i>	Cytoplasmic L-asparaginase I, isozyme	814, 898, 1879
<i>ansB</i>	Periplasmic L-asparaginase II; secreted isozyme	188, 894, 2128
<i>asu</i>	Asparagine utilization, as sole nitrogen source	304
<i>cadA</i>	Lysine decarboxylase	1293, 2119
<i>cadC</i>	Transcriptional activator of <i>cad</i> operon	1400, 2119
<i>dadA</i>	D-Amino acid dehydrogenase subunit	1180, 1462, 2158
<i>dadB</i>	D-Amino acid dehydrogenase subunit	563, 585, 1462
<i>dadQ</i>	Regulator of <i>dad</i> regulon	563
<i>dadX</i>	Alanine racemase; isozyme	670, 1180, 2157
<i>dsdA</i>	D-Serine deaminase	1233–1235
<i>dsdC</i>	Activator for <i>dsdA</i>	1493
<i>maoA</i>	Tyramine oxidase	1376, 2220
<i>poaR</i>	Regulation of proline oxidase production	347
<i>putA</i>	Proline dehydrogenase	232, 2183
<i>sdaA</i>	L-Serine deaminase	1233, 1923, 1925
<i>sdaB</i>	L-Serine deaminase, L-SD2	1811, 1924
<i>tdcA</i>	Transcriptional activator of <i>tdc</i> operon	589, 1787
<i>tdcB</i>	Threonine dehydratase, catabolic	648, 772, 2199
<i>tdcR</i>	Threonine dehydratase operon activator protein	1786
<i>tdh</i>	Threonine dehydrogenase	71, 366, 509
<i>tnaA</i>	Tryptophanase	637, 1998
<i>tnaL</i>	Tryptophanase leader peptide	642
3. Fatty acids		
<i>atoA</i>	Acetyl-CoA:acetoacetyl-CoA transferase beta-subunit	892, 1516
<i>atoB</i>	Acetyl-CoA acetyltransferase	892, 1516
<i>atoC</i>	Positive regulator of <i>ato</i>	891, 892, 1516

Category and gene	Gene product description ^a	Reference(s)
<i>atoD</i>	Acetyl-CoA:acetoacetyl-CoA transferase alpha-subunit?	892, 1516
<i>fadA</i>	Thiolase I	2227
<i>fadB</i>	3-Hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-epimerase; <i>delta</i> (3)- <i>cis</i> - <i>delta</i> (2)- <i>trans</i> -enoyl-CoA isomerase; enoyl-CoA-hydratase	2226, 2229
<i>fadD</i>	Acyl-CoA synthetase	
<i>fadE</i>	Electron transport flavoprotein (ETF) of beta-oxidation	323, 1478
<i>fadH</i>	2,4-Dienoyl-CoA reductase	2244
<i>fadR</i>	Negative regulator for <i>fad</i> regulon, and positive activator of <i>fabA</i>	164, 451, 743
<i>fatA</i>	Utilization of <i>trans</i> -unsaturated fatty acids	445
<i>sbm</i>	Methylmalonyl-CoA mutase (MCM)	1696
4. Phosphorus compounds		
<i>phnF</i>	Putative regulator, <i>phn</i> operon	1305, 1306, 2111
<i>phnG</i>	Probably carbon-P lyase subunit	1305, 1306, 2112
<i>phnH</i>	Probably carbon-P lyase subunit	1305, 1306, 2112
<i>phnI</i>	Probably carbon-P lyase subunit	1305, 1306, 2112
<i>phnJ</i>	Probably carbon-P lyase subunit	1305, 1306, 2112
<i>phnK</i>	Probably carbon-P lyase subunit	1305, 1306, 2112
<i>phnL</i>	Probably carbon-P lyase subunit	1305, 1306, 2112
<i>phnM</i>	Probably carbon-P lyase subunit	1304–1306
<i>phnN</i>	Probably accessory to carbon-P lyase	1304–1306
<i>phnO</i>	Putative regulator, <i>phn</i> operon	1304–1306
<i>phnP</i>	Probably accessory to carbon-P lyase	1305, 1306, 2112
<i>phoA</i>	Alkaline phosphatase	440, 853, 1577
<i>phoH</i>	PhoB-dependent, ATP-binding <i>pho</i> regulon component; induced by P starvation	987, 1303
<i>pldA</i>	Outer membrane phospholipase A	226, 1386
<i>pldB</i>	Lysophospholipase L(2)	946, 1007
<i>pldC</i>	Lysophospholipase L(1)	946
<i>ppk</i>	Polyphosphate kinase	15, 16, 371
<i>ppx</i>	Exopolyphosphatase	16, 371, 1637
<i>psiE</i>	<i>phoB</i> -dependent <i>pho</i> regulon component; induced by P starvation	1303, 2111
<i>psiF</i>	Induced by phosphate starvation	1303, 2111
B. Energy metabolism		
1. Glycolysis		
<i>eno</i>	Enolase	849, 850, 1880
<i>fbp</i>	Fructose-bisphosphate aldolase, class II	23, 97, 1526
<i>fruK</i>	Fructose-1-phosphate kinase	1467
<i>fruL</i>	<i>fruR</i> leader peptide	884
<i>fruR</i>	Repressor of <i>fru</i> operon and others	609, 883, 1616
<i>fruS</i>	Regulator of <i>fruA</i> and <i>fruF</i>	187
<i>gapA</i>	Glyceraldehyde-3-phosphate dehydrogenase A	289, 759, 849
<i>gapB</i>	Glyceraldehyde 3-phosphate dehydrogenase B	24, 464
<i>gpmA</i>	Phosphoglyceromutase	389
<i>gpmB</i>	Phosphoglyceromutase	389
<i>pfkA</i>	6-Phosphofructokinase I	446, 1047, 1803
<i>pfkB</i>	6-Phosphofructokinase II; suppressor of <i>pfkA</i>	85, 680
<i>pgi</i>	Glucosephosphate isomerase	573
<i>pgk</i>	Phosphoglycerate kinase	1402
<i>pykA</i>	Pyruvate kinase II, glucose stimulated	1280, 2047
<i>pykF</i>	Pyruvate kinase I (formerly F), fructose stimulated	1449, 1873
<i>tpiA</i>	Triosephosphate isomerase	165, 1559
2. Pyruvate dehydrogenase		
<i>aceE</i>	Pyruvate dehydrogenase (decarboxylase component)	656, 657, 1527
<i>aceF</i>	Pyruvate dehydrogenase (dihydrolipoyltransacetylase component)	397, 1780, 1781
<i>lpdA</i>	Lipoamide dehydrogenase (NADH); component of 2-oxodehydrogenase and pyruvate complex, L-protein of glycine cleavage complex	35, 1898
<i>pdhR</i>	Transcriptional regulator for pyruvate dehydrogenase complex	722, 1598
3. Tricarboxylic acid cycle		
<i>acnA</i>	Aconitate hydratase A	674, 1587, 1588
<i>acnB</i>	Aconitate hydratase B	674
<i>fumA</i>	Fumarase A = fumarate hydratase class I; aerobic isozyme	2030, 2186, 2247
<i>fumB</i>	Fumarase B = fumarate hydratase class I; anaerobic isozyme	124, 676, 2186
<i>fumC</i>	Fumarase C = fumarate hydratase class II; isozyme	1159, 2121, 2185
<i>glfA</i>	Citrate synthase	50, 457, 1225
<i>icdC</i>	Isocitrate dehydrogenase, specific for NADP ⁺ , chromosomal e14 hybrid	756, 816, 817
<i>icdE</i>	Isocitrate dehydrogenase, specific for NADP ⁺ , chromosomal fragment	263, 816, 817
<i>mdh</i>	Malate dehydrogenase	2078
<i>sdhA</i>	Succinate dehydrogenase, flavoprotein subunit	211, 2181

Category and gene	Gene product description ^a	Reference(s)
<i>sdhB</i>	Succinate dehydrogenase, iron sulfur protein	348, 401, 1319
<i>sdhC</i>	Succinate dehydrogenase, cytochrome <i>b</i> ₅₅₆	993, 1319, 1370
<i>sdhD</i>	Succinate dehydrogenase, hydrophobic subunit	1319, 2181
<i>sucA</i>	2-Oxoglutarate dehydrogenase (decarboxylase component)	744
<i>sucB</i>	2-Oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase component)	744, 1483
<i>sucC</i>	Succinyl-CoA synthetase, beta subunit	1220, 2177
<i>sucD</i>	Succinyl-CoA synthetase, alpha subunit	1220, 2177
5. Pentose phosphate pathway		
a. Oxidative branch		
<i>gnd</i>	Gluconate-6-phosphate dehydrogenase, decarboxylating	271, 1694, 2070
<i>pgl</i>	6-Phosphogluconolactonase	1051
<i>zwf</i>	Glucose-6-phosphate dehydrogenase	1694, 1695
b. Nonoxidative branch		
<i>rpiA</i>	Ribosephosphate isomerase, constitutive	794, 1851
<i>talA</i>	Transaldolase A	94
<i>talB</i>	Transaldolase B	94, 2248
<i>tktA</i>	Transketolase	913, 1877
<i>tktB</i>	Transketolase isozyme	833
6. Entner-Doudoroff pathway		
<i>eda</i>	2-Keto-3-deoxygluconate 6-phosphate aldolase; 2-keto-4-hydroxyglutarate aldolase	487, 1514, 2076
<i>edd</i>	6-Phosphogluconate dehydratase	487, 496
<i>gntR</i>	Regulator of <i>edd</i> ; transport and phosphorylation of gluconate	87, 336
7. Respiration		
a. Aerobic		
<i>cyoA</i>	Cytochrome <i>o</i> ubiquinol oxidase subunit II	1325, 1390, 2054
<i>cyoB</i>	Cytochrome <i>o</i> ubiquinol oxidase subunit I	302, 1205, 1326
<i>cyoC</i>	Cytochrome <i>o</i> ubiquinol oxidase subunit III	302, 1205, 1326
<i>cyoD</i>	Cytochrome <i>o</i> ubiquinol oxidase subunit IV	302, 303, 1326
<i>cyoE</i>	Heme O biosynthesis, protoheme IX farnesyltransferase	302, 303, 1326
<i>lld</i>	D-Lactate dehydrogenase, FAD protein, NADH independent	923, 1702, 2017
<i>glpD</i>	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (aerobic)	84, 864, 1784
<i>hyaA</i>	Hydrogenase-1 small subunit	1299, 1591, 1754
<i>hyaB</i>	Hydrogenase-1 large subunit	1299, 1591, 1754
<i>hyaC</i>	Possible membrane-spanning protein of <i>hya</i> operon	1299, 1300, 1591
<i>hyaD</i>	Processing of HyaA and HyaB proteins	1299, 1300, 1591
<i>hyaE</i>	Processing of HyaA and HyaB proteins	1299, 1300, 1591
<i>hyaF</i>	Nickel incorporation into hydrogenase-1 proteins	1299, 1300, 1591
<i>lctD</i>	L-Lactate dehydrogenase, FMN protein	459, 862
<i>lctR</i>	Putative <i>lct</i> repressor	459
<i>ndh</i>	Respiratory NADH dehydrogenase	571, 843, 888
<i>nuoA</i>	NADH dehydrogenase I chain A	260
<i>nuoB</i>	NADH dehydrogenase I chain B	260
<i>nuoC</i>	NADH dehydrogenase I chain C	260
<i>nuoD</i>	NADH dehydrogenase I chain D	260
<i>nuoE</i>	NADH dehydrogenase I chain E	260
<i>nuoF</i>	NADH dehydrogenase I chain F	260, 1590, 2130
<i>nuoG</i>	NADH dehydrogenase I chain G	260, 1590, 2130
<i>nuoH</i>	NADH dehydrogenase I chain H	260, 1590, 2130
<i>nuoI</i>	NADH dehydrogenase I chain I	260, 1590, 2130
<i>nuoJ</i>	NADH dehydrogenase I chain J	260, 1590, 2130
<i>nuoK</i>	NADH dehydrogenase I chain K	260, 1590, 2130
<i>nuoL</i>	NADH dehydrogenase I chain L	260, 1590, 2130
<i>nuoM</i>	NADH dehydrogenase I chain M	260, 1590, 2130
<i>nuoN</i>	NADH dehydrogenase I chain N	260, 1590, 2130
<i>dmsA</i>	Anaerobic dimethyl sulfoxide reductase subunit A	1727, 1728, 2009
b. Anaerobic		
<i>dmsC</i>	Anaerobic dimethyl sulfoxide reductase subunit C	1727, 1728
<i>dniR</i>	Regulator for nitrite reductase (cytochrome <i>c</i> ₅₅₂) expression	928
<i>fdhD</i>	Affects formate dehydrogenase-N	1904
<i>fdhE</i>	Affects formate dehydrogenase-N	1762, 1904
<i>fdhF</i>	Selenopolypeptide subunit of formate dehydrogenase H (part of formate hydrogen-lyase complex [FHL complex])	292, 1690, 2277
<i>fdnG</i>	Formate dehydrogenase-N, nitrate inducible, major subunit	136, 1133, 1653
<i>fdnH</i>	Formate dehydrogenase-N, nitrate inducible, iron-sulfur subunit	136, 507, 1133
<i>fdnI</i>	Formate dehydrogenase-N, nitrate inducible, cytochrome <i>B</i> ₅₅₆ (Fdn) subunit	136, 507, 1133
<i>fdoG</i>	Formate dehydrogenase-O, major subunit	1554, 1752
<i>fdoH</i>	Formate dehydrogenase-O, iron-sulfur subunit	1554, 1752

Category and gene	Gene product description ^a	Reference(s)
<i>fdoI</i>	Formate dehydrogenase, cytochrome <i>b</i> ₅₅₆ (Fdo) subunit	1554, 1752
<i>frdA</i>	Fumarate reductase, anaerobic, flavoprotein subunit	211, 349, 1289
<i>frdB</i>	Fumarate reductase, anaerobic, iron-sulfur protein subunit	349, 1229, 2145
<i>frdC</i>	Fumarate reductase, anaerobic, membrane anchor polypeptide	349, 1289
<i>frdD</i>	Fumarate reductase, anaerobic, membrane anchor polypeptide	349, 1289
<i>glpA</i>	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), large subunit	338, 1080, 1775
<i>glpB</i>	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit	338, 1080, 1775
<i>glpC</i>	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic), K-small subunit	338, 1080, 1775
<i>glpE</i>	Protein of <i>glp</i> regulon	864
<i>glpG</i>	Protein of <i>glp</i> regulon	1785
<i>glpR</i>	Repressor of the <i>glp</i> operon	864, 1080, 2268
<i>hybA</i>	Putative small subunit of hydrogenase-2, probable iron-sulfur protein	183, 1298, 1591
<i>hybB</i>	Putative cytochrome component of hydrogenase-2	1298, 1591
<i>hybC</i>	Probable large subunit, hydrogenase-2	1298, 1591
<i>hybD</i>	Probable processing element for hydrogenase-2	1298, 1591
<i>hybE</i>	Member of <i>hyb</i> operon	1298
<i>hybF</i>	May modulate levels of hydrogenase-2	1298
<i>hybG</i>	May effect maturation of large subunit of hydrogenase-2	1298, 1591
<i>hydL</i>	Probable member of <i>hyb</i> operon; pleiotropic effects	1911
<i>hydN</i>	Probably involved in electron transport from formate to hydrogen	
<i>hypA</i>	Pleiotropic effects on three hydrogenase isozymes	1148, 1203, 1591
<i>hypC</i>	Pleiotropic effects on three hydrogenase isozymes	1148, 1203
<i>hypD</i>	Pleiotropic effects on three hydrogenase isozymes	1148, 1203
<i>hypE</i>	Plays structural role in synthesis of hydrogenase	1203
<i>narG</i>	Nitrate reductase, alpha subunit	175, 478, 552
<i>narH</i>	Nitrate reductase, beta subunit	175, 478, 552
<i>narI</i>	Cytochrome <i>b</i> (NR), nitrate reductase, gamma subunit	175, 478, 1206
<i>narJ</i>	Nitrate reductase, delta subunit, assembly function	175, 478
<i>narL</i>	Pleiotropic regulation of anaerobic respiration	489, 1425, 1487
<i>narP</i>	Nitrate/nitrite response regulator	1602
<i>narQ</i>	Sensor for nitrate reductase system, protein histidine kinase	305
<i>narV</i>	Cryptic nitrate reductase II, gamma subunit	176
<i>narW</i>	Cryptic nitrate reductase II, delta subunit, assembly function	176, 177
<i>narX</i>	Nitrate sensor, histidine protein kinase acts on <i>narL</i>	305, 342, 1953
<i>narY</i>	Cryptic nitrate reductase II, beta subunit	176
<i>narZ</i>	Cryptic nitrate reductase II, alpha subunit	176
<i>nirB</i>	Nitrite reductase [NAD(P)H] subunit	706
<i>nirC</i>	Nitrite reductase activity	706
<i>nirD</i>	Nitrite reductase [NAD(P)H] subunit	706
<i>nrfA</i>	Formate-dependent nitrite reductase; tetra-heme cytochrome <i>c</i> ₅₅₂	179, 818
<i>nrfB</i>	Formate-dependent nitrite reductase; a penta-heme cytochrome <i>c</i>	818
<i>nrfC</i>	Formate-dependent nitrite reductase; Fe-S centers	818
<i>nrfD</i>	Formate-dependent nitrate reductase complex; transmembrane protein	818, 1487
<i>nrfE</i>	Formate-dependent nitrite reductase; assembly function?	818, 1487
<i>nrfF</i>	Part of formate-dependent nitrite reductase complex	818, 1487
<i>nrfG</i>	Part of formate-dependent nitrite reductase complex	818, 1487
<i>torA</i>	Trimethylamine <i>N</i> -oxide reductase subunit	1288, 1840, 1841
<i>torC</i>	Trimethylamine <i>N</i> -oxide reductase, cytochrome subunit	848, 1288
<i>torR</i>	Regulator for <i>torA</i>	1513
c. Electron transport		
<i>ackA</i>	Acetate kinase	1256, 1849, 2113
<i>appB</i>	Probable third cytochrome oxidase, subunit II	404
<i>appC</i>	Probable third cytochrome oxidase, subunit I	404
<i>cybB</i>	Cytochrome <i>b</i> ₅₆₁	476, 1325, 1413
<i>cybC</i>	Cytochrome <i>b</i> ₅₆₂	1135, 1413, 2013
<i>cydA</i>	Cytochrome <i>d</i> terminal oxidase, polypeptide subunit I	362, 524, 717
<i>cydB</i>	Cytochrome <i>d</i> terminal oxidase, polypeptide subunit II	362, 524, 717
<i>fdx</i>	[2FE-2S] ferredoxin, electron carrier protein	1790, 1948
<i>fldA</i>	Flavodoxin	1022, 1471
<i>fpr</i>	Ferredoxin-NADP reductase	147, 148
<i>fre</i>	Ferrisiderophore reductase; flavin reductase (NADPH:flavin oxidoreductase)	363, 600, 1882
<i>hmpA</i>	Hemoprotein; ferrisiderophore reductase activity	58, 540, 2064
<i>qor</i>	Quinone oxidoreductase	179
8. Fermentation		
<i>acd</i>	Acetaldehyde-CoA dehydrogenase	326
<i>act</i>	Pyruvate formate-lyase-activating enzyme	1751
<i>adhC</i>	Alcohol dehydrogenase class III; formaldehyde dehydrogenase, glutathione dependent	378
<i>adhE</i>	Alcohol dehydrogenase; CoA-linked acetaldehyde dehydrogenase; pyruvate	681, 975, 1699

Category and gene	Gene product description ^a	Reference(s)
	formate-lyase deactivase	
<i>adhR</i>	Regulator for <i>acd</i> and <i>adhE</i>	328
<i>ald</i>	Aldehyde dehydrogenase, NAD linked	753
<i>aldH</i>	Aldehyde dehydrogenase, prefers NADP over NAD	729
<i>fhlA</i>	Formate hydrogen-lyase transcriptional activator for <i>fdhF</i> , <i>hyc</i> , and <i>hyp</i> operons	867, 1261, 1690
<i>fhlB</i>	Regulator for formate hydrogen lyase (FHL complex)	1261, 1690
<i>hycA</i>	Transcriptional repression of <i>hyc</i> and <i>hyp</i> operons	1591, 1750
<i>hycB</i>	Probable small subunit of hydrogenase-3, iron-sulfur protein (part of formate hydrogen lyase (FHL complex))	183, 1591, 1750
<i>hycC</i>	Membrane-spanning protein of hydrogenase-3 (part of FHL complex)	183, 1591, 1750
<i>hycD</i>	Membrane-spanning protein of hydrogenase-3 (part of FHL complex)	183, 1591, 1750
<i>hycE</i>	Large subunit of hydrogenase-3 (part of FHL complex)	1591, 1689, 1750
<i>hycF</i>	Probable iron-sulfur protein of hydrogenase-3 (part of FHL complex)	183, 1591, 1750
<i>hycG</i>	Hydrogenase activity	183, 1591, 1750
<i>hycH</i>	Processing of large subunit (HycE) of hydrogenase-3 (part of FHL complex)	1591, 1750
<i>hydG</i>	Two-component regulation of hydrogenase-3 activity (with HydH)	179, 1148, 1911
<i>hydH</i>	Two-component regulation of hydrogenase-3 activity (sensor kinase of HydG)	1148, 1911
<i>hypB</i>	Guanine-nucleotide-binding protein, functions as nickel donor for large subunit of hydrogenase-3	1148, 1203, 1218
<i>ldhA</i>	D-Lactate dehydrogenase, NAD dependent	325, 1255, 1974
<i>pfl</i>	Pyruvate formate-lyase	1005, 1753
<i>ppc</i>	Phosphoenolpyruvate carboxylase	285, 1978, 1979
<i>tda</i>	L-Tartrate dehydratase	1623
<i>tdb</i>	L-Tartrate dehydratase	1623
9. ATP-proton motive force		
<i>atpA</i>	Membrane-bound ATP synthase, F ₁ sector, alpha-subunit	895, 915, 1128
<i>atpB</i>	Membrane-bound ATP synthase, F ₀ sector, subunit a	239, 895, 2075
<i>atpC</i>	Membrane-bound ATP synthase, F ₁ sector, epsilon-subunit	239, 1078, 1291
<i>atpD</i>	Membrane-bound ATP synthase, F ₁ sector, beta-subunit	239, 895, 1098
<i>atpE</i>	Membrane-bound ATP synthase, F ₀ sector, subunit c	239, 2075, 2267
<i>atpF</i>	Membrane-bound ATP synthase, F ₀ sector, subunit b	239, 1273, 2075
<i>atpG</i>	Membrane-bound ATP synthase, F ₁ sector, gamma-subunit	239, 813, 895
<i>atpH</i>	Membrane-bound ATP synthase, F ₁ sector, delta-subunit	239, 504, 895
<i>atpI</i>	Membrane-bound ATP synthase, dispensable protein	239, 895, 1766
C. Central intermediary metabolism		
1. General		
<i>aceA</i>	Isocitrate lyase	4, 1006, 1697
<i>aceB</i>	Malate synthase A	256a, 2055
<i>aceK</i>	Isocitrate dehydrogenase kinase/phosphatase	319, 358, 359
<i>agp</i>	Periplasmic glucose-1-phosphatase	405, 1577
<i>appA</i>	Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase	404, 1473
<i>appY</i>	Regulatory protein affecting <i>appA</i> and other genes	81
<i>aspA</i>	Aspartate ammonia-lyase (aspartase)	522, 1373, 2185
<i>cpsG</i>	Phosphomannomutase	1242
<i>cxm</i>	Methylglyoxal biosynthesis	982
<i>cynS</i>	Cyanate aminohydrolase, cyanase	52, 679, 1162
<i>cynT</i>	Carbonic anhydrase	52, 679, 1071
<i>dprA</i>	Dihydropteridine reductase	668, 2065
<i>gabC</i>	Regulator for <i>gabPDT</i>	109, 1307, 1410
<i>gabD</i>	Succinate-semialdehyde dehydrogenase, NADP-dependent activity	109, 1410
<i>gabT</i>	4-Aminobutyrate aminotransferase activity	109, 1307, 1410
<i>gadA</i>	Glutamate decarboxylase isozyme	1232, 1856
<i>gadB</i>	Glutamate decarboxylase isozyme	1232, 1856
<i>gadR</i>	Regulator for <i>gadS</i>	1201, 1856
<i>galM</i>	Galactose-1-epimerase (mutarotase)	198, 1251
<i>gcl</i>	Glyoxylate carboligase	283
<i>gcvA</i>	Positive regulator of <i>gcv</i>	2169, 2170
<i>gcvH</i>	H protein of glycine cleavage complex, carrier of aminomethyl moiety	1458, 1894, 1895
<i>gcvP</i>	Glycine decarboxylase, P protein of glycine cleavage system	1458, 1894
<i>gcvT</i>	T protein (tetrahydrofolate dependent) of glycine cleavage system	1458, 1894
<i>glc</i>	Malate synthase G	2055
<i>gldA</i>	Glycerol dehydrogenase, NAD dependent	899, 2016
<i>glpK</i>	Glycerol kinase	140, 439, 2281
<i>glpQ</i>	Glycerophosphodiester phosphodiesterase, periplasmic	1080, 2002
<i>gltB</i>	Glutamate synthase, large subunit	605, 733, 1231
<i>gltD</i>	Glutamate synthase, small subunit	274, 605, 733
<i>gltF</i>	Regulator of <i>gltBDF</i> operon, induction of Ntr enzymes	275
<i>hdhA</i>	NAD-dependent 7 α -hydroxysteroid dehydrogenase, dehydroxylation of bile	2241

Category and gene	Gene product description ^a	Reference(s)
	acids	
<i>iclR</i>	Repressor of <i>aceBA</i> operon	359, 1401, 1936
<i>kba</i>	Ketose-bisphosphate aldolase, active on D-tagatose-1,6-diphosphate	1526
<i>kbl</i>	2-Amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)	1357, 1358
<i>lrp</i>	Regulator for leucine (or <i>lrp</i>) regulon and high-affinity branched-chain amino acid transport system	516, 1152, 2109
<i>metF</i>	5,10-Methylenetetrahydrofolate reductase	1721
<i>metK</i>	Methionine adenosyltransferase (AdoMet synthetase); methyl and propylamine donor, corepressor of <i>met</i> genes	174, 1746, 1747
<i>metX</i>	Methionine adenosyltransferase 2 (AdoMet synthase)	1459, 1747
<i>pntA</i>	Pyridine nucleotide transhydrogenase, alpha subunit	9, 34, 2004
<i>pntB</i>	Pyridine nucleotide transhydrogenase, beta subunit	9, 10, 2004
<i>ppa</i>	Inorganic pyrophosphatase	1064, 1065
<i>pqq</i>	Redox cofactor, functions as cofactor of apoglucose dehydrogenase; cryptic in K-12	155
<i>prrA</i>	γ -Aminobutyraldehyde (pyrroline) dehydrogenase activity	1340, 1584
<i>sad</i>	Succinate-semialdehyde dehydrogenase, NAD dependent	1240
<i>ugpQ</i>	Glycerophosphodiester phosphodiesterase, cytosolic	2002
2. Gluconeogenesis		
<i>fbp</i>	Fructose-bisphosphatase	86, 699
<i>maeA</i>	NAD-linked malate dehydrogenase	354, 1216
<i>maeB</i>	NADP-linked malate dehydrogenase	230, 871
<i>pckA</i>	Phosphoenolpyruvate carboxykinase	285, 286, 1036
<i>ppsA</i>	Phosphoenolpyruvate synthase	286, 1515
3. Sugar-nucleotides		
<i>cpsB</i>	Mannose-1-phosphate guanyltransferase	199, 652, 2010
<i>glmU</i>	<i>N</i> -Acetylglucosamine-1-phosphate uridyltransferase	1296, 2098
<i>rfbA</i>	TDP-glucose pyrophosphorylase	1399, 1902, 2233
<i>rfbB</i>	DTDP-glucose-4,6 dehydratase	1399, 1902, 2233
<i>rfbC</i>	DTDP-4-dehydrorhamnose-3,5 epimerase	1902, 2233
<i>rfbD</i>	DTDP-4-dehydrorhamnose reductase	1003, 1399, 1902
<i>ushA</i>	UDP-sugar hydrolase (5'-nucleotidase)	250
4. Amino sugars		
<i>glmS</i>	L-Glutamine:D-fructose-6-phosphate aminotransferase	89, 543, 2029
<i>nagA</i>	<i>N</i> -Acetylglucosamine-6-phosphate deacetylase	1551, 1552, 2079
<i>nagB</i>	Glucosamine-6-phosphate deaminase	38, 1551, 1552
<i>nagC</i>	Repressor of <i>nag</i> operon	1550, 1552, 1553
<i>nagD</i>	<i>N</i> -Acetylglucosamine metabolism	1551
5. Sulfur metabolism		
<i>aslA</i>	Arylsulfatase	395
<i>aslB</i>	Putative arylsulfatase regulatory protein	395
<i>atsA</i>	Putative arylsulfatase	395
<i>cysC</i>	Adenosine 5'-phosphosulfate kinase	1130, 1131
<i>cysD</i>	ATP:sulfurylase (ATP:sulfate adenyltransferase), subunit 2	1129-1131
<i>cysH</i>	Phosphoadenylylsulfate reductase	1040, 1475
<i>cysI</i>	Sulfite reductase, alpha subunit	314, 1475, 1836
<i>cysJ</i>	Sulfite reductase flavoprotein, beta subunit	314, 1474, 1836
<i>cysN</i>	ATP-sulfurylase (ATP:sulfate adenyltransferase) subunit 1, probably a GTPase	1129-1131
<i>cysQ</i>	Affects pool of 3'-phosphoadenosine-5'-phosphosulfate in pathway of sulfite synthesis	1405, 2116
<i>sseA</i>	Putative thiosulfate sulfur transferase	94
<i>thdA</i>	Sulfone and sulfoxide oxidase activity	20, 917
D. Amino acid biosynthesis		
1. Glutamate family		
<i>gdhA</i>	NADP-specific glutamate dehydrogenase	733, 1725, 2069
<i>gltH</i>	Glutamate requirement	1238
<i>glnA</i>	Glutamine synthetase	36, 1633, 1833
<i>glnB</i>	Regulatory protein P-II for glutamine synthetase	79, 725
<i>glnD</i>	Uridyltransferase acts on regulator of <i>glnA</i>	79
<i>glnG</i>	Response regulator for <i>gln</i> (sensor <i>glnL</i>) (nitrogen regulator I [NRI])	1415, 1822, 2127
<i>glnL</i>	Histidine protein kinase sensor for <i>glnG</i> regulator (nitrogen regulator II [NRII])	79, 1415, 1633
<i>argA</i>	Amino acid acetyltransferase; <i>N</i> -acetylglutamate synthase	233, 1105, 1249
<i>argB</i>	Acetylglutamate kinase	208, 1510, 2077
<i>argC</i>	<i>N</i> -Acetyl- γ -glutamylphosphate reductase	208, 1510, 2077

Category and gene	Gene product description ^a	Reference(s)
<i>argD</i>	Acetylornithine δ -aminotransferase	152, 153, 730
<i>argE</i>	Acetylornithine deacetylase	207, 1287
<i>argF</i>	Ornithine carbamyltransferase 2	331, 792, 1102
<i>argG</i>	Argininosuccinate synthetase	646, 2061
<i>argH</i>	Argininosuccinate lyase	208
<i>argI</i>	Ornithine carbamoyltransferase 1	1050, 1322, 2251
<i>argR</i>	Repressor of <i>arg</i> regulon; <i>cer</i> -mediated site specific recombination	1274, 1907, 1989
<i>proA</i>	γ -Glutamylphosphate reductase	724, 1791
<i>proB</i>	γ -Glutamate kinase	724, 1791
<i>proC</i>	Pyrroline-5-carboxylate reductase	442, 724
2. Aspartate family		
<i>aspC</i>	Aspartate aminotransferase	1052, 2230, 2231
<i>asnA</i>	Asparagine synthetase A	764
<i>asnB</i>	Asparagine synthetase B	814, 1788
<i>asnC</i>	Regulator for <i>asnA</i> , <i>asnC</i> , and <i>gidA</i>	1013
<i>asd</i>	Aspartate-semialdehyde dehydrogenase	950
<i>dapA</i>	Dihydrodipicolinate synthase	1062, 1817
<i>dapB</i>	Dihydrodipicolinate reductase	205, 1962
<i>dapC</i>	Tetrahydrodipicolinate succinylase	248
<i>dapD</i>	Tetrahydrodipicolinate <i>N</i> -succinyltransferase	248, 1179, 1645
<i>dapE</i>	<i>N</i> -Succinyl-diaminopimelate deacylase	204, 2190
<i>dapF</i>	Diaminopimelate epimerase	755, 1069, 2172
<i>lysA</i>	Diaminopimelate decarboxylase	300, 1918
<i>lysC</i>	Aspartokinase III, lysine sensitive	273
<i>lysR</i>	Positive regulator for <i>lys</i>	739
<i>ilvR</i>	Positive regulator for <i>thr</i> and <i>ilv</i> operons	902
<i>thrA</i>	Aspartokinase I-homoserine dehydrogenase I	918, 1808, 2074
<i>thrB</i>	Homoserine kinase	251, 361, 1509
<i>thrC</i>	Threonine synthase	526, 1512
<i>thrL</i>	<i>thr</i> operon leader peptide	394, 595
<i>metA</i>	Homoserine transsuccinylase	479, 1312, 1683
<i>metB</i>	Cystathionine gamma-synthase	781, 1246, 1693
<i>metC</i>	Cystathionine beta-lyase	781, 1246, 1693
<i>metE</i>	Tetrahydropteroyltriglutamate methyltransferase	316
<i>metH</i>	B ₁₂ -dependent homocysteine- <i>N</i> ⁵ -methyltetrahydrofolate transmethylase, repressor of <i>metE</i> and <i>metF</i>	99, 179
<i>metJ</i>	Repressor of all <i>met</i> genes but <i>metF</i>	1538
<i>metL</i>	Aspartokinase II and homoserine dehydrogenase II	1511
<i>metR</i>	Regulator for <i>metE</i> and <i>metH</i>	1264
3. Serine family		
<i>glyA</i>	Serine hydroxymethyltransferase	61, 1831, 1917
<i>sbaA</i>	Regulation of serine and branched-chain amino acid metabolism	392
<i>serA</i>	D-3-Phosphoglycerate dehydrogenase	1771, 1776
<i>serB</i>	3-Phosphoserine phosphatase	2036
<i>serC</i>	3-Phosphoserine aminotransferase	481, 1067
<i>cysB</i>	Positive regulator for cysteine regulon	1224, 1338
<i>cysE</i>	Serine acetyltransferase	1037, 1224, 2152
<i>cysK</i>	Cysteine synthase A, <i>O</i> -acetylserine sulfhydrylase A	257, 1480
<i>cysM</i>	Cysteine synthase B, <i>O</i> -acetylserine sulfhydrylase B	1480, 1842, 1843
4. Aromatic amino acid family		
<i>aroA</i>	5-Enolpyruvylshikimate-3-phosphate synthetase	51, 1485, 1834
<i>aroB</i>	Dehydroquinate synthase	995
<i>aroC</i>	Chorismate synthase	287, 2148
<i>aroD</i>	5-Dehydroquinate dehydratase	291, 995, 996
<i>aroE</i>	Dehydroshikimate reductase	62
<i>aroF</i>	Phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP synthetase, tyrosine repressible)	1622
<i>aroG</i>	Phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP synthetase, phenylalanine repressible)	412, 1899
<i>aroH</i>	Phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP synthetase, tryptophan repressible)	809, 1621, 1622
<i>aroI</i>	Member of <i>aro</i> operon	630
<i>aroK</i>	Shikimate kinase I	1179
<i>aroL</i>	Shikimate kinase II	425, 728
<i>aroM</i>	Regulated by <i>aroR</i>	425
<i>pheA</i>	Chorismate mutase-P-prephenate dehydratase	603, 604, 1403
<i>pheL</i>	Leader peptide of chorismate mutase-P-prephenate dehydratase	601, 604, 1488
<i>tyrA</i>	Chorismate mutase T and prephenate dehydrogenase	1248, 2027, 2028
<i>tyrB</i>	Tyrosine aminotransferase, tyrosine repressible	614, 1806, 2224

Category and gene	Gene product description ^a	Reference(s)
<i>trpA</i>	Tryptophan synthase, A protein	242, 1446, 1710
<i>trpB</i>	Tryptophan synthase, B protein	242, 483, 1710
<i>trpC</i>	<i>N</i> -(5-Phosphoribosyl)anthranilate isomerase and indole-3-glycerolphosphate synthetase	2166
<i>trpD</i>	Glutamine amidotransferase and phosphoribosylanthranilate transferase	790, 1826
<i>trpE</i>	Anthranilate synthase	749, 1826
<i>trpL</i>	<i>trp</i> operon leader peptide	1073, 1668
<i>trpR</i>	Regulator for <i>trp</i> operon and <i>aroH</i> ; <i>trp</i> aporepressor	72, 1044, 2228
<i>wrbA</i>	<i>trp</i> repressor-binding protein; affects association of <i>trp</i> repressor and operator	2228
5. Histidine		
<i>hisA</i>	<i>N</i> -(5'-phospho-L-ribosyl-formimino)-5-amino- 1-(5'-phosphoribosyl)-4-imidazolecarboxamide isomerase	266
<i>hisB</i>	Imidazole glycerol phosphate dehydratase and histidinol phosphate phosphatase	266, 307
<i>hisC</i>	Histidinol phosphate aminotransferase	266
<i>hisD</i>	L-Histidinal:NAD ⁺ oxidoreductase; L-histidinol:NAD ⁺ oxidoreductase	266, 306, 916
<i>hisF</i>	Imidazole glycerol phosphate synthase subunit in heterodimer with HisH = imidazole glycerol phosphate synthase holoenzyme	596, 998, 1650
<i>hisG</i>	ATP phosphoribosyltransferase	266
<i>hisH</i>	Glutamine amidotransferase subunit of heterodimer with HisF = imidazole glycerol phosphate synthase holoenzyme	266, 998, 1650
<i>hisIE</i>	Phosphoribosyl-AMP cyclohydrolase; phosphoribosyl-ATP pyrophosphatase	266, 306
<i>hisL</i>	<i>his</i> operon leader peptide	282
6. Pyruvate family		
<i>alr</i>	Alanine racemase; isozyme	2106, 2153
<i>avtA</i>	Alanine- α -ketoisovalerate transaminase, transaminase C	2108
7. Branched-chain family		
<i>azl</i>	Regulation of <i>ilv</i> and <i>leu</i> genes; azaleucine resistance	1549
<i>ileR</i>	Negative regulator for <i>thr</i> and <i>ilv</i> operons	2134
<i>ilvA</i>	Threonine deaminase	497, 542, 1951
<i>ilvB</i>	Acetolactate synthase I, valine sensitive, large subunit	568, 2132, 2141
<i>ilvC</i>	Ketol-acid reductoisomerase	2139
<i>ilvD</i>	Dihydroxyacid dehydratase	548, 804
<i>ilvE</i>	Branched-chain amino acid aminotransferase	846, 934
<i>ilvF</i>	Acetolactate synthase (valine insensitive) activity, probably fifth isozyme, silent in K-12	26
<i>ilvG</i>	Acetolactate synthase II, valine insensitive, large subunit, silent in K-12	804
<i>ilvH</i>	Acetolactate synthase III, valine sensitive, small subunit	1640, 1641, 2132
<i>ilvI</i>	Acetolactate synthase III, valine sensitive, large subunit	1640, 1883, 2132
<i>ilvJ</i>	Acetolactate synthase IV, valine insensitive	878, 1664
<i>ilvL</i>	<i>IlvGEDA</i> operon leader peptide	1085
<i>ilvM</i>	Acetolactate synthase II, valine insensitive, small subunit	804, 2132
<i>ilvN</i>	Acetolactate synthase I, valine sensitive, small subunit	568, 2132, 2141
<i>ilvY</i>	Positive regulator for <i>ilvC</i>	2139, 2140
<i>ivbL</i>	<i>ilvB</i> operon leader peptide	569, 2141
<i>leuA</i>	2-Isopropylmalate synthase	615, 1864
<i>leuB</i>	3-Isopropylmalate dehydrogenase	1049
<i>leuC</i>	Isopropylmalate isomerase subunit	579
<i>leuD</i>	Isopropylmalate isomerase subunit	579
<i>leuJ</i>	Regulator for <i>leu</i> and <i>ilv</i> operons	1432
<i>leuL</i>	<i>leu</i> operon leader peptide	108, 969
<i>leuO</i>	Probable activator protein for <i>leuABCD</i> operon	739
E. Polyamine biosynthesis		
<i>pat</i>	Putrescine aminotransferase activity	1584
<i>speA</i>	Biosynthetic arginine decarboxylase	725, 1339
<i>speB</i>	Agmatinase	1946, 1947, 2206
<i>speC</i>	Ornithine decarboxylase isozyme	1496, 2189
<i>speD</i>	<i>S</i> -Adenosylmethionine decarboxylase	1949, 2206
<i>speE</i>	Spermidine synthase = putrescine aminopropyltransferase	1949, 2206
<i>speF</i>	Ornithine decarboxylase isozyme, inducible	954
F. Purines, pyrimidines, nucleosides, and nucleotides		
1. Purine ribonucleotide biosynthesis		
<i>adk</i>	Adenylate kinase activity; pleiotropic effects on glycerol-3-phosphate acyltransferase activity	623, 1631, 1686
<i>gmk</i>	Guanylate kinase	616
<i>guaA</i>	GMP synthetase	1992

Category and gene	Gene product description ^a	Reference(s)
<i>guaB</i>	IMP dehydrogenase	57
<i>guaC</i>	GMP reductase	57
<i>ndk</i>	Nucleoside diphosphate kinase	698
<i>prs</i>	Phosphoribosylpyrophosphate synthetase	206, 793
<i>purA</i>	Adenylosuccinate synthetase	460, 1163, 1860
<i>purB</i>	Adenylosuccinate lyase	726
<i>purC</i>	Phosphoribosylaminoimidazole-succinocarboxamide synthetase = SAICAR synthetase	1990
<i>purD</i>	Phosphoribosylglycinamide synthetase = GAR synthetase	11, 1818
<i>purE</i>	Phosphoribosylaminoimidazole carboxylase = AIR carboxylase, catalytic subunit	1311, 1991, 2118
<i>purF</i>	Amidophosphoribosyltransferase = PRPP amidotransferase	1282, 1729
<i>purH</i>	Phosphoribosylaminoimidazolecarboxamide formyltransferase = AICAR formyltransferase; IMP cyclohydrolase	11, 547
<i>purK</i>	Phosphoribosylaminoimidazole carboxylase = AIR carboxylase, CO ₂ -fixing subunit	1311, 1991, 2118
<i>purL</i>	Phosphoribosylformyl glycinamide synthetase = FGAM synthetase	1758
<i>purM</i>	Phosphoribosylaminoimidazole synthetase = AIR synthetase	1857
<i>purN</i>	5'-Phosphoribosyl glycinamide (GAR) transformylase 1	844, 845
<i>purR</i>	Repressor for <i>pur</i> regulon, <i>glyA</i> , <i>glnB</i> , <i>prsA</i> , <i>speA</i>	312, 1782, 1897
<i>purT</i>	5'-Phosphoribosylglycinamide (GAR) transferase 2	1243
<i>purU</i>	Provides formate for <i>purT</i> -dependent FGAR synthesis	1384
2. Pyrimidine ribonucleotide biosynthesis		
<i>carA</i>	Carbamoyl-phosphate synthetase, glutamine (small) subunit	216, 1365, 1698
<i>carB</i>	Carbamoyl-phosphate synthase large subunit	216, 1365, 1698
<i>pyrB</i>	Aspartate carbamoyltransferase, catalytic subunit	1533, 2204, 2208
<i>pyrC</i>	Dihydro-orotase	231, 311, 2167
<i>pyrD</i>	Dihydro-orotate oxidase	2167
<i>pyrE</i>	Orotate phosphoribosyltransferase	47, 1573
<i>pyrF</i>	Orotidine-5'-phosphate decarboxylase	2026
<i>pyrI</i>	Aspartate carbamoyltransferase, regulatory subunit	2265, 2266
<i>pyrL</i>	<i>pyrBI</i> operon leader peptide	1119
3. 2-Deoxyribonucleotide metabolism		
<i>dcd</i>	2'-Deoxycytidine 5'-triphosphate deaminase	2107, 2133
<i>dut</i>	Deoxyuridine triphosphatase	277, 776, 2107
<i>grx</i>	Glutaredoxin, redox coenzyme for glutathione-dependent ribonucleotide reductase	782, 1706, 1732
<i>mutT</i>	(Deoxy)nucleoside triphosphatase, prefers dGTP, causes AT-GC transversions	17, 145, 1756
<i>nrdA</i>	Ribonucleoside diphosphate reductase, subunit B1	334, 1428, 1933
<i>nrdB</i>	Ribonucleoside-diphosphate reductase subunit B2	1428, 1920, 1933
<i>nrdD</i>	Anaerobic ribonucleoside-triphosphate reductase	147, 707, 1934
<i>thyA</i>	Thymidylate synthetase	1314
<i>tmk</i>	Thymidylate kinase	160
<i>trxB</i>	Thioredoxin reductase	1053, 1328, 1589
4. Salvage of nucleosides and nucleotides		
<i>add</i>	Adenosine deaminase	284
<i>amn</i>	AMP nucleosidase	1114
<i>apaH</i>	Diadenosine tetraphosphatase	525, 904, 1659
<i>apt</i>	Adenine phosphoribosyltransferase	1121–1123, 748a
<i>cdd</i>	Cytidine/deoxycytidine deaminase	2223
<i>codA</i>	Cytosine deaminase	396
<i>cpdB</i>	2':3'-cyclic nucleotide 2'-phosphodiesterase	1164
<i>deoA</i>	Thymidine phosphorylase	541, 2102, 2133
<i>deoB</i>	Phosphopentomutase	255, 541
<i>deoC</i>	2-Deoxyribose-5-phosphate aldolase	2046
<i>deoD</i>	Purine-nucleoside phosphorylase	541
<i>deoR</i>	Regulator for <i>deo</i> operon, <i>tsx</i> , <i>nupG</i>	44, 393, 1348
<i>gpt</i>	Guanine-hypoxanthine phosphoribosyltransferase	775, 1122, 1123
<i>gsk</i>	Inosine-guanosine kinase	795
<i>hpt</i>	Hypoxanthine phosphoribosyltransferase	775, 1122, 1123
<i>optA</i>	Regulator for <i>dgt</i>	1601
<i>tdk</i>	Thymidine kinase	160
<i>udp</i>	Uridine phosphorylase	221, 1316
<i>upp</i>	Uracil phosphoribosyltransferase	48, 1619
5. Miscellaneous nucleoside/nucleotide reactions		
<i>dgt</i>	Deoxyguanosine triphosphate triphosphohydrolase	1600, 1601, 2203

Category and gene	Gene product description ^a	Reference(s)
<i>lepA</i>	GTP-binding membrane protein	1237
<i>mvp</i>	Putative ATPase	399
<i>pyrG</i>	CTP synthetase	2144
<i>pyrH</i>	UMP kinase	288, 919, 2219
<i>udk</i>	Uridine/cytidine kinase	2045
<i>xapA</i>	Xanthosine phosphorylase	143, 144
<i>xapR</i>	Regulator for <i>xapA</i>	256
G. Biosynthesis of cofactors, prosthetic groups, and carriers		
1. Biotin		
<i>bioA</i>	7,8-Diaminopelargonic acid synthetase	829, 1477
<i>bioB</i>	Biotin synthetase	829, 1477, 1737
<i>bioC</i>	Biotin biosynthesis; reaction prior to pimeloyl-CoA	829, 1477
<i>bioD</i>	Dethiobiotin synthetase	27, 829, 1477
<i>bioF</i>	7-Keto-8-aminopelargonic acid synthetase	829, 1477
<i>bioH</i>	Biotin biosynthesis; reaction prior to pimeloyl CoA	829, 1468
<i>birA</i>	Biotin-(acetyl-CoA carboxylase) holoenzyme synthetase; biotin operon repressor	2, 368, 1331
<i>bisC</i>	Biotin sulfoxide reductase	1542
2. Folic acid		
<i>folA</i>	Dihydrofolate reductase; trimethoprim resistance	523, 570, 805
<i>folC</i>	Dihydrofolate:folylpolyglutamate synthetase; dihydrofolate synthetase	182, 974, 989
<i>folD</i>	5,10-Methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase	400
<i>folE</i>	GTP cyclohydrolase I	1599, 1764, 1770
<i>folK</i>	7,8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase	1959, 1960
<i>folP</i>	7,8-Dihydropteroate synthase	390, 1959
<i>pabA</i>	<i>p</i> -Aminobenzoate synthetase, component II	661
<i>pabB</i>	<i>p</i> -Aminobenzoate synthetase, component I	661, 2100, 2235
<i>pabC</i>	Aminodeoxychorismate lyase	660, 661, 2235
3. Lipoate		
<i>lipA</i>	Protein of lipoate biosynthesis	721, 1626
<i>lipB</i>	Protein of lipoate biosynthesis	1626
4. Molybdopterin		
<i>moaA</i>	Molybdopterin biosynthesis, protein A	1612, 1657, 1809
<i>moaB</i>	Molybdopterin biosynthesis, protein B	1657
<i>moaC</i>	Molybdopterin biosynthesis, protein C	1657
<i>moaD</i>	Molybdopterin biosynthesis	765, 1612, 1657
<i>moaE</i>	Molybdopterin-converting factor, subunit 2	1657
<i>mob</i>	Molybdopterin → molybdopterin-guanine dinucleotide	903, 1612, 1657
<i>moeA</i>	Molybdopterin biosynthesis	765, 1424, 1657
<i>moeB</i>	Molybdopterin biosynthesis	765, 1424, 1657
<i>mog</i>	Required for the efficient incorporation of molybdate in molybdoproteins	765, 1657
5. Pantothenate		
<i>coaA</i>	Pantothenate kinase	1866, 1867, 2050
<i>panB</i>	Ketopantoate hydroxymethyltransferase	370, 906
<i>panC</i>	Pantothenate synthetase	370
<i>panD</i>	Aspartate 1-decarboxylase	370
6. Pyridoxine		
<i>pdxA</i>	Pyridoxine biosynthesis	1659
<i>pdxB</i>	Erythronate-4-phosphate dehydrogenase	1067, 1771
<i>pdxH</i>	Pyridoxinephosphate oxidase	1068
<i>pdxJ</i>	Pyridoxine biosynthesis	1066, 1958
7. Pyridine nucleotide		
<i>nadA</i>	Quinolate synthetase, A protein	546, 1794
<i>nadB</i>	Quinolate synthetase, B protein	546, 1794
<i>nadC</i>	Quinolate phosphoribosyltransferase	2011
<i>nadE</i>	NAD synthetase, prefers NH ₃ over glutamine	2165
<i>nadR</i>	Probable <i>nadAB</i> transcriptional regulator	554
<i>pncA</i>	Nicotinamide deamidase	1499
<i>pncB</i>	Nicotinate phosphoribosyltransferase	2200
8. Thiamine		
<i>thiA</i>	Thiamine thiazole requirement	965, 2051
<i>thiB</i>	Thiamine phosphate pyrophosphorylase	965, 2051
<i>thiC</i>	Thiamine biosynthesis, pyrimidine moiety	2051

Category and gene	Gene product description ^a	Reference(s)
<i>thiD</i>	Phosphomethylpyrimidine kinase activity	841, 2051
<i>thiE</i>	Thiamine biosynthesis, thiazole moiety	2051
<i>thiF</i>	Thiamine biosynthesis, thiazole moiety	179, 2051
<i>thiG</i>	Thiamine biosynthesis, thiazole moiety	2051
<i>thiH</i>	Thiamine biosynthesis, thiazole moiety	2051
<i>thiK</i>	Thiamine kinase	842
<i>thiL</i>	Thiamine monophosphate kinase	842
9. Riboflavin		
<i>ribA</i>	GTP cyclohydrolase II	1092, 1599, 1646
<i>ribB</i>	3,4-Dihydroxy-2-butanone-4-phosphate synthase	1647
<i>ribC</i>	Riboflavin synthase, alpha chain	2088
<i>ribD</i>	Deaminase in pathway of riboflavin synthesis	253
<i>ribE</i>	Riboflavin synthase, beta chain	2088
10. Thioredoxin, glutaredoxin, and glutathione		
<i>ggt</i>	γ -Glutamyltranspeptidase	1939
<i>gor</i>	Glutathione oxidoreductase	439, 513, 1048
<i>gshA</i>	γ -Glutamate-cysteine ligase	202
<i>gshB</i>	Glutathione synthetase	415, 957, 1968
<i>trxA</i>	Thioredoxin	1035, 1198, 1706
11. Menaquinone and ubiquinone		
<i>ispA</i>	Geranyltranstransferase (farnesyl diphosphate synthase)	132, 576, 1819
<i>ispB</i>	Octaprenyl diphosphate synthase	76
<i>menA</i>	1,4-Dihydroxy-2-naphthoate \rightarrow dimethylmenaquinone	132, 1815, 1828
<i>menB</i>	Dihydroxynaphthoic acid synthetase	132
<i>menC</i>	<i>o</i> -Succinylbenzoyl-CoA synthase	132, 1281, 1814
<i>menD</i>	Menaquinone biosynthesis	1281, 1491, 1562
<i>menE</i>	<i>o</i> -Succinylbenzoate-CoA synthase	132
<i>ubiA</i>	<i>p</i> -Hydroxybenzoate:octaprenyltransferase	1290, 1835, 2193
<i>ubiB</i>	2-Octaprenylphenol \rightarrow 2-octaprenyl-6-methoxyphenol	132
<i>ubiC</i>	Chorismate lyase	132, 1409, 1835
<i>ubiD</i>	3-Octaprenyl-4-hydroxy-benzoate \rightarrow 2-octaprenylphenol	132, 1110
<i>ubiE</i>	2-Octaprenyl-6-methoxy-1,4-benzoquinone \rightarrow 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	132
<i>ubiF</i>	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone \rightarrow 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone	132, 343
<i>ubiG</i>	2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone \rightarrow ubiquinone 8	132, 629, 2194
<i>ubiH</i>	2-Octaprenyl-6-methoxyphenol \rightarrow 2-octaprenyl-6-methoxy-1,4-benzoquinone	132, 1387
<i>ubiX</i>	Putative polyprenyl <i>p</i> -hydroxybenzoate carboxylase	1427
12. Heme and porphyrin		
<i>cysG</i>	Uroporphyrinogen III methylase; siroheme biosynthesis	1517, 2115, 2116
<i>hemA</i>	Enzyme in alternate path of synthesis of 5-aminolevulinic acid	837, 1134, 2067
<i>hemB</i>	5-Aminolevulinic acid dehydratase = porphobilinogen synthase	1331, 1464, 1872
<i>hemC</i>	Porphobilinogen deaminase = hydroxymethylbilane synthase	691, 1072, 1321
<i>hemD</i>	Uroporphyrinogen III synthase	40
<i>hemE</i>	Uroporphyrinogen decarboxylase	1743
<i>hemF</i>	Coproporphyrinogen III oxidase	365, 2012
<i>hemG</i>	Protoporphyrinogen oxidase activity	1742
<i>hemL</i>	Glutamate-1-semialdehyde aminotransferase	667, 838, 839
<i>hemM</i>	An enzyme in the main pathway of synthesis of 5-aminolevulinic acid, possibly glutamyl-tRNA dehydrogenase	837
<i>hemX</i>	Putative uroporphyrinogen III methylase	395, 1744
<i>popD</i>	5-Aminolevulinic acid dehydratase activity	1872
<i>visA</i>	Ferrochetalase: final enzyme of heme biosynthesis	574, 1334
13. Cobalamin (incomplete in K-12)		
<i>btuR</i>	Cob(I)alamin adenosyltransferase	517
14. Enterochelin		
<i>entA</i>	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase, enterochelin biosynthesis	1165, 1481, 2025
<i>entB</i>	2,3-Dihydro-2,3-dihydroxybenzoate synthetase, enterochelin biosynthesis	1703, 1888
<i>entC</i>	Isochorismate synthetase, enterochelin biosynthesis	927, 1166, 1481
<i>entD</i>	Enterochelin synthetase, component D	68, 335, 1888
<i>entE</i>	ATP-dependent activation of 2,3-dihydroxybenzoate	1888, 1889
<i>entF</i>	ATP-dependent serine-activating enzyme	1535, 1704, 1888

Category and gene	Gene product description ^a	Reference(s)
H. Fatty acid biosynthesis		
<i>aas</i>	2-Acylglycerophospho-ethanolamine acyl transferase; acyl-acyl carrier protein synthetase	800, 876
<i>accA</i>	Acetyl-CoA carboxylase, carboxytransferase component, alpha subunit	1140, 1141
<i>accB</i>	Acetyl-CoA carboxylase, BCCP subunit; carrier of biotin	1139, 1938
<i>accC</i>	Acetyl-CoA carboxylase, biotin carboxylase subunit	1018, 1212
<i>accD</i>	Acetyl-CoA carboxylase, carboxytransferase component, beta subunit	1140–1142
<i>acpP</i>	Acyl carrier protein	779, 780, 1620
<i>acpS</i>	CoA:apo-[acyl-carrier-protein] pantetheinophosphotransferase = holo-[acyl-carrier-protein] synthase	1556, 1583
<i>acs</i>	Acetyl-CoA synthetase	179, 2194
<i>cdh</i>	CDP-diglyceride hydrolase	827
<i>cdsA</i>	CDP-diglyceride synthetase (CTP:phosphatidate cytidyltransferase)	828
<i>cdsS</i>	Stability of CDP-diglyceride synthetase activity	591
<i>cfa</i>	Cyclopropane fatty acyl synthase	2105
<i>dgkA</i>	Diglyceride kinase	1705
<i>dgkR</i>	Level of diglyceride kinase	1604, 2101
<i>eutB</i>	Ethanolamine-ammonia lyase heavy subunit	911, 912, 1441
<i>eutC</i>	Ethanolamine-ammonia lyase light subunit	911, 912, 1441
<i>fabA</i>	β-Hydroxydecanoyl thioester dehydrase	327, 369, 1812
<i>fabB</i>	3-Oxoacyl-[acyl-carrier-protein] synthase I	960, 1837, 2021
<i>fabD</i>	Malonyl-CoA-[acyl-carrier-protein] transacylase	1213, 2071
<i>fabF</i>	3-Oxoacyl-[acyl-carrier-protein] synthase II	877, 1837
<i>fabG</i>	3-Oxoacyl-[acyl-carrier-protein] reductase	1018, 1620
<i>fabH</i>	3-Oxoacyl-[acyl-carrier-protein] synthase III; acetyl-CoA [acyl-carrier protein] transacylase	2020
<i>fabI</i>	Enoyl-ACP reductase (NADH)	137, 138
<i>hlyC</i>	Acyl carrier protein for processing prohemolysin	856, 2103
<i>tesA</i>	Acyl-CoA thioesterase I; also functions as protease I	308, 309, 821
<i>tesB</i>	Acyl-CoA thioesterase II	1383
II. BROAD REGULATORY FUNCTIONS		
<i>anr</i>	Activator of <i>ntrL</i> gene	986
<i>arcA</i>	Negative response regulator of genes in aerobic pathways (sensors for <i>arcB</i> and <i>cpxA</i>)	863, 865, 1839
<i>arcB</i>	Aerobic respiration sensor response protein; histidine protein kinase/phosphatase (sensor for <i>arcA</i>)	861, 866, 869
<i>barA</i>	Sensor regulator, probably activates OmpR by phosphorylation	1381
<i>cpxA</i>	Probable inner membrane sensor protein (histidine protein kinase), acting on <i>arcA</i> , energy coupling factor, F-pilin formation	2123
<i>creB</i>	Catabolic regulation response regulator	1039, 1170, 1500
<i>creC</i>	Catabolite repression sensor autophosphorylates and phosphorylates PhoB; alternative sensor for <i>pho</i> regulon	1305, 2111, 2113
<i>crp</i>	Cyclic AMP receptor protein	103, 750, 1714
<i>csrA</i>	Carbon storage regulator; affects glycogen synthesis, gluconeogenesis, cell size and surface properties	1679, 1680
<i>cstA</i>	Carbon starvation protein	1778
<i>cyaA</i>	Adenylate cyclase	1530
<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>	104, 1520, 1862
<i>ecfA</i>	Energy-coupling factor; pleiotropic effects on active transport coupling to metabolic energy	783
<i>envZ</i>	Protein histidine kinase/phosphatase sensor for <i>ompR</i> , modulates expression of <i>ompF</i> and <i>ompC</i>	553, 2120
<i>era</i>	GTP-binding protein	297, 1111, 1154
<i>fexB</i>	<i>fexA</i> (<i>arcA</i>) phenotype affected	1112
<i>fnr</i>	Regulatory gene for oxidoreductases and others	867, 1289, 1874
<i>fmH</i>	Regulation of superoxide response regulon	530, 662
<i>fur</i>	Ferric iron uptake; negative regulator	715, 2126
<i>gppA</i>	Guanosine pentaphosphatase; exopolyphosphatase	121, 967, 1637
<i>kdpD</i>	Regulator (sensor) for high-affinity potassium transport system	1394, 1395, 2097
<i>kdpE</i>	Regulator of <i>kdp</i> operon (transcriptional effector)	1395, 1557, 2097
<i>lctZ</i>	Pleiotropic effects on components of respiratory chain	364
<i>lexA</i>	Regulator for SOS(<i>lexA</i>) regulon	1151
<i>lon</i>	DNA-binding, ATP-dependent protease La; heat shock K protein	441
<i>lytB</i>	Control of stringent response; involved in penicillin tolerance	682
<i>ntrL</i>	Nitrogen-regulatory protein	33
<i>ompR</i>	Response regulator (sensor, <i>envZ</i>) affecting <i>ompC</i> and <i>ompF</i> ; outer membrane protein synthesis	832, 1709, 2120
<i>oxyR</i>	Activator, hydrogen peroxide-inducible genes	186, 1971, 1972
<i>phoB</i>	Positive response regulator for <i>pho</i> regulon, autophosphorylates and phosphorylates, sensor for <i>phoR</i>	1221, 1304

Category and gene	Gene product description ^a	Reference(s)
<i>phoP</i>	Sensor for <i>phoQ</i>	671, 951
<i>phoQ</i>	Response regulator (sensor for <i>phoP</i>)	951
<i>phoR</i>	Positive and negative sensor protein for <i>pho</i> regulon	1221, 2111, 2213
<i>phoU</i>	Negative regulator for <i>pho</i> regulon and putative enzyme in phosphate metabolism	1304, 1618
<i>pus</i>	Effect of suppressors on <i>relB</i> mutations	448
<i>relA</i>	Regulation of RNA synthesis; stringent factor; (p)ppGpp synthetase I	1308, 1773, 2205
<i>relB</i>	Negative regulator of translation	1349
<i>relX</i>	Control of synthesis of ppGpp	1497
<i>rpoD</i>	RNA polymerase, σ^{70} subunit; regulation of proteins induced at high temperatures	593, 1046, 2096
<i>rpoE</i>	RNA polymerase, σ^E factor; heat shock and oxidative stress	1184
<i>rpoH</i>	RNA polymerase, σ^{32} subunit; regulation of proteins induced at high temperatures	890, 1378, 2035
<i>rpoN</i>	RNA polymerase, σ^{54} or σ^{60} subunit; nitrogen and fermentation regulation	909, 1632
<i>rpoS</i>	RNA polymerase, sigma S (σ^{38}) subunit; synthesis of many growth phase-related proteins	1075, 1408, 1855
<i>soxR</i>	Redox-sensing activator of <i>soxS</i>	41, 754, 2196
<i>soxS</i>	Regulation of superoxide response regulon	530, 2196
<i>spf</i>	Spot 42 RNA, inhibition of DNA synthesis	747, 1558, 1642
<i>spoT</i>	(p)ppGpp synthetase II; also guanosine-3',5'-bispyrophosphate 3'-pyrophosphohydrolase	748, 1309, 1807
<i>sspA</i>	Stringent starvation protein A	577, 2161, 2162
<i>sspB</i>	Stringent starvation protein B	2162
<i>shuA</i>	Induction of heat shock genes	1994
<i>uspT</i>	Histidine protein kinase (sensor) for universal stress protein	1438

III. MACROMOLECULE METABOLISM

A. Synthesis and modification of macromolecules

1. rRNA and "stable" RNAs

<i>ffs</i>	4.5S RNA	234, 1519, 1563
<i>rrfA</i>	5S rRNA	490, 1472, 2149
<i>rrfB</i>	5S rRNA	490, 1472, 2149
<i>rrfC</i>	5S rRNA	490, 1472, 2149
<i>rrfD</i>	5S rRNA	490, 1472, 2149
<i>rrfE</i>	5S rRNA	490, 1472, 2149
<i>rrfG</i>	5S rRNA	490, 1472, 2149
<i>rrfH</i>	5S rRNA	490, 1472, 2149
<i>rrlA</i>	23S rRNA	1, 95, 1332
<i>rrlB</i>	23S rRNA	1, 95, 1332
<i>rrlC</i>	23S rRNA	1, 95, 1332
<i>rrlD</i>	23S rRNA	1, 95, 1332
<i>rrlE</i>	23S rRNA	1, 95, 1332
<i>rrlG</i>	23S rRNA	1, 95, 1332
<i>rrlH</i>	23S rRNA	1, 95, 1332
<i>rrsA</i>	16S rRNA	379, 1083, 1736
<i>rrsB</i>	16S rRNA	379, 1083, 1736
<i>rrsC</i>	16S rRNA	379, 1083, 1736
<i>rrsD</i>	16S rRNA	379, 1083, 1736
<i>rrsE</i>	16S rRNA	379, 1083, 1736
<i>rrsG</i>	16S rRNA	379, 1083, 1736
<i>rrsH</i>	16S rRNA	379, 1083, 1736
<i>rrvD</i>	5S rRNA	480
<i>ssr</i>	6S RNA	801, 1090
<i>ssrA</i>	10Sa RNA, nonribosomal	991, 1447

2. Ribosomal protein synthesis and modification

<i>prmA</i>	Methylation of 50S ribosomal subunit protein L11	345
<i>prmB</i>	Methylation of 50S ribosomal subunit protein L3	345
<i>rplA</i>	50S ribosomal subunit protein L1, regulates synthesis of L1 and L11	491, 1719
<i>rplB</i>	50S ribosomal subunit protein L2	491, 1682
<i>rplC</i>	50S ribosomal subunit protein L3	1932
<i>rplD</i>	50S ribosomal subunit protein L4, regulates expression of S10 operon	2258–2260
<i>rplE</i>	50S ribosomal subunit protein L5	1188
<i>rplF</i>	50S ribosomal subunit protein L6	1472
<i>rplI</i>	50S ribosomal subunit protein L9	658
<i>rplJ</i>	50S ribosomal subunit protein L10	1687, 2257
<i>rplK</i>	50S ribosomal subunit protein L11	492, 945, 1687
<i>rplL</i>	50S ribosomal subunit protein L7/L12	1531, 2257
<i>rplM</i>	50S ribosomal subunit protein L13	1472
<i>rplN</i>	50S ribosomal subunit protein L14	1472, 1565

Category and gene	Gene product description ^a	Reference(s)
<i>rplO</i>	50S ribosomal subunit protein L15	560
<i>rplP</i>	50S ribosomal subunit protein L16	560, 1682
<i>rplQ</i>	50S ribosomal subunit protein L17	1472
<i>rplR</i>	50S ribosomal subunit protein L18	490
<i>rplS</i>	50S ribosomal subunit protein L19	2155
<i>rplT</i>	50S ribosomal subunit protein L20, and regulator	1113, 1932
<i>rplU</i>	50S ribosomal subunit protein L21	897, 1472
<i>rplV</i>	50S ribosomal subunit protein L22	65
<i>rplW</i>	50S ribosomal subunit protein L23	491
<i>rplX</i>	50S ribosomal subunit protein L24	1472
<i>rplY</i>	50S ribosomal subunit protein L25	557
<i>rpmA</i>	50S ribosomal subunit protein L27	897, 2188
<i>rpmB</i>	50S ribosomal subunit protein L28	1472
<i>rpmC</i>	50S ribosomal subunit protein L29	658, 1472
<i>rpmD</i>	50S ribosomal subunit protein L30	1472
<i>rpmE</i>	50S ribosomal subunit protein L31	658
<i>rpmF</i>	50S ribosomal subunit protein L32	1969
<i>rpmG</i>	50S ribosomal subunit protein L33	1472
<i>rpmH</i>	50S ribosomal subunit protein L34	807
<i>rpmI</i>	50S ribosomal subunit protein A	1113
<i>rpmJ</i>	50S ribosomal subunit protein X	2034
<i>rpsA</i>	30S ribosomal subunit protein S1	212, 1082, 1568
<i>rpsB</i>	30S ribosomal subunit protein S2	45
<i>rpsC</i>	30S ribosomal subunit protein S3	212, 235, 463
<i>rpsD</i>	30S ribosomal subunit protein S4	30, 1227, 2138
<i>rpsE</i>	30S ribosomal subunit protein S5	463, 658
<i>rpsF</i>	30S ribosomal subunit protein S6	941, 1900
<i>rpsG</i>	30S ribosomal subunit protein S7, initiates assembly	463, 901, 1227
<i>rpsH</i>	30S ribosomal subunit protein S8, and regulator	1227, 1260, 2195
<i>rpsI</i>	30S ribosomal subunit protein S9	2151
<i>rpsJ</i>	30S ribosomal subunit protein S10	1253
<i>rpsK</i>	30S ribosomal subunit protein S11	1900, 2151
<i>rpsL</i>	30S ribosomal subunit protein S12	30, 150, 1993
<i>rpsM</i>	30S ribosomal subunit protein S13	1945
<i>rpsN</i>	30S ribosomal subunit protein S14	658
<i>rpsO</i>	30S ribosomal subunit protein S15	1227, 1565
<i>rpsP</i>	30S ribosomal subunit protein S16	2138, 2155
<i>rpsQ</i>	30S ribosomal subunit protein S17	658, 2138
<i>rpsR</i>	30S ribosomal subunit protein S18	1336, 1900
<i>rpsS</i>	30S ribosomal subunit protein S19	2137
<i>rpsT</i>	30S ribosomal subunit protein S20	357, 1712, 2138
<i>rpsU</i>	30S ribosomal subunit protein S21	212
<i>rpsV</i>	30S ribosomal subunit protein S22	94, 1216
3. Ribosome maturation and modification		
<i>fusB</i>	Pleiotropic effects on RNA synthesis, ribosomes, and ribosomal protein S6	1956
<i>rimB</i>	Maturation of 50S ribosomal subunit	240
<i>rimC</i>	Maturation of 50S ribosomal subunit	240
<i>rimD</i>	Maturation of 50S ribosomal subunit	240
<i>rimE</i>	Modification of ribosomal proteins	1055
<i>rimF</i>	Modification of ribosome	598
<i>rimG</i>	Modification of 30S ribosomal subunit protein S4	2275
<i>rimH</i>	Modification of ribosome	598
<i>rimI</i>	Modification of 30S ribosomal subunit protein S18; acetylation of N-terminal alanine	2239
<i>rimJ</i>	Modification of 30S ribosomal subunit protein S5; acetylation of N-terminal alanine	990, 2239
<i>rimK</i>	Ribosomal protein S6 modification protein	941
<i>rimL</i>	Modification of 30S ribosomal subunit protein L7; acetylation of N-terminal serine	1967
<i>rit</i>	Affects thermolability of 50S ribosomal subunit	1465
<i>rmf</i>	Ribosome modulation factor	2090
<i>strM</i>	Modifies ribosome structure	1731
4. tRNAs		
<i>alaT</i>	Alanine tRNA 1B (duplicate of <i>alaUV</i>)	1503, 1964, 1966
<i>alaU</i>	Alanine tRNA 1B (duplicate of <i>alaTV</i>)	1503, 1964, 1966
<i>alaV</i>	Alanine tRNA 1B (duplicate of <i>alaTU</i>)	1503, 1964, 1966
<i>alaW</i>	Alanine tRNA 2 (duplicate of <i>alaX</i>)	1503, 1964, 1966
<i>alaX</i>	Alanine tRNA 2 (duplicate of <i>alaW</i>)	1503, 1964, 1966
<i>argQ</i>	Arginine tRNA 2 (duplicate of <i>argVYZ</i>)	1271
<i>argU</i>	Arginine tRNA 4	294, 1724, 1755

Category and gene	Gene product description ^a	Reference(s)
<i>argV</i>	Arginine tRNA 2 (duplicate of <i>argQYZ</i>)	1271
<i>argW</i>	Arginine tRNA 5	1271
<i>argX</i>	Arginine tRNA 3	1271
<i>argY</i>	Arginine tRNA 2 (duplicate of <i>argVQZ</i>)	1271
<i>argZ</i>	Arginine tRNA 2 (duplicate of <i>argVYQ</i>)	1271
<i>asnT</i>	Asparagine tRNA	1016, 1138
<i>asnU</i>	Asparagine tRNA	1016, 1138
<i>asnV</i>	Asparagine tRNA	1016, 1138
<i>aspT</i>	Aspartate tRNA 1 (duplicate of <i>aspVU</i>)	1016
<i>aspU</i>	Aspartate tRNA 1 (duplicate of <i>aspTV</i>)	1016
<i>aspV</i>	Aspartate tRNA 1 (duplicate of <i>aspTU</i>)	1016
<i>divE</i>	tRNA ^{Ser1} , affects cell division	1748, 1963
<i>glnU</i>	Glutamine tRNA 1 (duplicate of <i>glnW</i>)	505, 882, 1670
<i>glnV</i>	Glutamine tRNA 2 (duplicate of <i>glnX</i>)	505, 882, 1670
<i>glnW</i>	Glutamine tRNA 1 (duplicate of <i>glnU</i>)	505, 882, 1670
<i>glnX</i>	Glutamine tRNA 2 (duplicate of <i>glnV</i>)	505, 882, 1670
<i>gltT</i>	Glutamate tRNA 2 (duplicate of <i>gltUVW</i>)	1016
<i>gltU</i>	Glutamate tRNA 2 (duplicate of <i>gltTVW</i>)	1016
<i>gltV</i>	Glutamate tRNA 2 (duplicate of <i>gltTUV</i>)	1016
<i>gltW</i>	Glutamate tRNA 2 (duplicate of <i>gltTUV</i>)	1016
<i>glyT</i>	Glycine tRNA 2	1272
<i>glyU</i>	Glycine tRNA 1	1272
<i>glyV</i>	Glycine tRNA 3 (duplicate of <i>glyXYW</i>)	1272
<i>glyW</i>	Glycine tRNA 3 (duplicate of <i>glyVXY</i>)	1272
<i>glyX</i>	Glycine tRNA 3 (duplicate of <i>glyVWY</i>)	1272
<i>glyY</i>	Glycine tRNA 3 (duplicate of <i>glyXYW</i>)	1272
<i>hisR</i>	Histidine tRNA	761
<i>ileT</i>	Isoleucine tRNA 1 (duplicate of <i>ileUV</i>)	1016
<i>ileU</i>	Isoleucine tRNA 1 (duplicate of <i>ileTV</i>)	1016
<i>ileV</i>	Isoleucine tRNA 1 (duplicate of <i>ileTU</i>)	1016
<i>ileX</i>	Isoleucine tRNA 2	1016
<i>leuP</i>	Leucine tRNA 1 (duplicate of <i>leuQTV</i>)	73, 1016
<i>leuQ</i>	Leucine tRNA 1 (duplicate of <i>leuPTV</i>)	73, 1016
<i>leuT</i>	Leucine tRNA 1 (duplicate of <i>leuQPV</i>)	73, 1016
<i>leuU</i>	Leucine tRNA 2	73, 1016
<i>leuV</i>	Leucine tRNA 1 (duplicate of <i>leuOPT</i>)	73, 1016
<i>leuW</i>	Leucine tRNA 3	73, 1016
<i>leuX</i>	Leucine tRNA 5	73, 1429
<i>leuZ</i>	Leucine tRNA 4	73, 1016
<i>lrs</i>	Level of leucine tRNA	2040
<i>lysT</i>	Lysine tRNA (duplicate of <i>lysWV</i>)	236, 1271, 1966
<i>lysV</i>	Lysine tRNA (duplicate of <i>lysTW</i>)	1016, 1271, 1966
<i>lysW</i>	Lysine tRNA (duplicate of <i>lysTV</i>)	1016, 1271, 1966
<i>metT</i>	Methionine tRNA (duplicate of <i>metU</i>)	1777
<i>metU</i>	Methionine tRNA (duplicate of <i>metT</i>)	1777
<i>metV</i>	Methionine tRNA-fMet2	416, 2063
<i>metW</i>	Methionine tRNA fMet1 (duplicate of <i>metZ</i>)	678, 1489, 2063
<i>metY</i>	Methionine tRNA(fMet2)	973
<i>metZ</i>	Methionine tRNA-fMet1 (duplicate of <i>metW</i>)	678, 1489, 2063
<i>pheR</i>	Phenylalanine tRNA (replicate of <i>pheUVW</i>)	3, 602, 603
<i>pheU</i>	Phenylalanine tRNA (replicate of <i>pheVWR</i>)	3, 603, 1534
<i>pheV</i>	Phenylalanine tRNA (replicate of <i>pheURW</i>)	3, 1488, 1534
<i>pheW</i>	Phenylalanine tRNA (replicate of <i>pheUVR</i>)	3, 602, 2168
<i>proK</i>	Proline tRNA 1	1016
<i>proL</i>	Proline tRNA 2	1016
<i>proM</i>	Proline tRNA 3	1016
<i>selC</i>	Selenocystyl tRNA inserts at UGA	106, 1143, 1752
<i>serT</i>	Serine tRNA 1	762, 1429, 1672
<i>serU</i>	Serine tRNA 2	190, 762, 1089
<i>serV</i>	Serine tRNA 3	762, 1429, 1672
<i>serW</i>	Serine tRNA 5 (duplicate of <i>serX</i>)	762, 1429, 1672
<i>serX</i>	Serine tRNA 5 (duplicate of <i>serW</i>)	762, 1429, 1672
<i>thrT</i>	Threonine tRNA 3	238, 714, 1985
<i>thrU</i>	Threonine tRNA 4	760, 1490, 1674
<i>tyrT</i>	Tyrosine tRNA 1 (duplicate of <i>tyrV</i>)	194, 762, 1315
<i>tyrU</i>	Tyrosine tRNA 2	762
<i>tyrV</i>	Tyrosine tRNA 1 (duplicate of <i>tyrT</i>)	762
<i>valT</i>	Valine tRNA 1 (duplicate of <i>valUXY</i>)	1965
<i>valU</i>	Valine tRNA 1 (duplicate of <i>valTXY</i>)	236, 1965
<i>valV</i>	Valine tRNA 2B	1965
<i>valW</i>	Valine tRNA 2A	1965
<i>valX</i>	Valine tRNA 1 (duplicate of <i>valTUY</i>)	1965

Category and gene	Gene product description ^a	Reference(s)
<i>valY</i>	Valine tRNA 1 (duplicate of <i>valTUX</i>)	1965
5. Aminoacyl tRNA synthetases and their modification		
<i>aat</i>	Leucyl, phenylalanyl-tRNA-protein transferase	1832
<i>alaS</i>	Alanyl-tRNA synthetase	245, 538, 1323
<i>argS</i>	Arginine tRNA synthetase	139, 510, 1153
<i>asnS</i>	Asparagine tRNA synthetase	763, 1211
<i>aspS</i>	Aspartate tRNA synthetase	511, 575, 763
<i>cca</i>	tRNA nucleotidyltransferase	708, 2271
<i>cysS</i>	Cysteine tRNA synthetase	885, 1015, 1494
<i>fmt</i>	10-Formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase	677, 1091, 1286
<i>glnS</i>	Glutamine tRNA synthetase	720, 882, 1670
<i>gltE</i>	Glutamate tRNA synthetase; possible regulatory subunit	1077, 1374, 1944
<i>gltM</i>	Level of glutamate tRNA synthetase activity	1374
<i>gltX</i>	Glutamate tRNA synthetase, catalytic subunit	223, 1433, 1944
<i>glyQ</i>	Glycine tRNA synthetase, alpha subunit	2006, 2007
<i>glyS</i>	Glycine tRNA synthetase, beta subunit	383, 971, 2007
<i>hisS</i>	Histidine tRNA synthetase	761
<i>hisT</i>	Pseudouridine synthase I	413, 935, 2023
<i>ileS</i>	Isoleucine tRNA synthetase	1433, 2160
<i>ilvU</i>	Regulator for <i>ileS</i> and modifier of isoleucine tRNA 2 and valine tRNA 2	529
<i>leuR</i>	Level of leucine tRNA synthetase	1983
<i>leuS</i>	Leucine tRNA synthetase	2150, 2164
<i>leuY</i>	Level of leucine tRNA synthetase	1983
<i>lysS</i>	Lysine tRNA synthetase, constitutive; suppressor of ColE1 mutation in primer RNA	962, 1118, 1393
<i>lysU</i>	Lysine tRNA synthetase, inducible; heat shock protein	329, 716, 1392
<i>metG</i>	Methionine tRNA synthetase	626, 1279, 2063
<i>miaA</i>	Δ^2 -isopentenylpyrophosphate tRNA-adenosine transferase	352
<i>nuvA</i>	Uridine thiolation factor A activity	1161, 1986
<i>nuvC</i>	4-Thiouridine modification of tRNA; near-UV sensitivity and resistance	1161, 1986
<i>pheM</i>	Phenylalanine tRNA synthetase leader peptide	1488, 1881
<i>pheS</i>	Phenylalanine tRNA synthetase, alpha subunit	603, 956, 1534
<i>pheT</i>	Phenylalanine tRNA synthetase, beta subunit	603, 956, 1534
<i>proS</i>	Proline tRNA synthetase	383
<i>prnC</i>	tRNA(Lys)-specific anticodon nuclease	1124, 1340
<i>pth</i>	Peptidyl-tRNA hydrolase	592, 1375
<i>queA</i>	Synthesis of queuine in tRNA; probably S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1638,1852
<i>selA</i>	Selenocysteine synthase: L-seryl-tRNA dehydrated	550, 1752
<i>selD</i>	Selenophosphate synthase, H ₂ Se added to acrylyl-tRNA	985, 1104, 1752
<i>serR</i>	Level of seryl-tRNA synthetase	383
<i>serS</i>	Serine tRNA synthetase; also charges selenocysteine tRNA with serine	74, 382, 1757
<i>tgt</i>	tRNA-guanine transglycosylase	567, 2031
<i>thrS</i>	Threonine tRNA synthetase	238, 1337, 1677
<i>trmA</i>	tRNA methyltransferase; tRNA (uracil-5-)methyltransferase	683, 1436, 1529
<i>trmB</i>	tRNA methyltransferase; tRNA (guanine-7-)methyltransferase	1241
<i>trmC</i>	tRNA methyltransferase; 5-methylaminoethyl-2-thiouridine biosynthesis	157, 692
<i>trmD</i>	tRNA methyltransferase; tRNA (guanine-7-)methyltransferase	258, 774, 2155
<i>trmE</i>	tRNA methyltransferase; 5-methylaminoethyl-2-thiouridine biosynthesis	157, 692
<i>trmF</i>	tRNA methyltransferase; 5-methylaminoethyl-2-thiouridine biosynthesis	157, 692
<i>trpS</i>	Tryptophan tRNA synthetase	1302, 1490, 1669
<i>tyrS</i>	Tyrosine tRNA synthetase	116, 117, 539
<i>valS</i>	Valine tRNA synthetase	317, 506
6. Nucleoproteins		
<i>hns</i>	Histone-like protein HLP-II (HU, BH2, HD, NS); pleiotropic regulator	1265, 2033, 2211
<i>hnsA</i>	DNA-binding protein H-NS	520, 1560
<i>hnsB</i>	DNA-binding protein H-NS	520, 1560, 2238
<i>hupA</i>	DNA-binding protein HU-alpha (HU-2)	473, 647, 1011
<i>hupB</i>	DNA-binding protein HU-beta, NS1 (HU-1)	473, 474, 647
<i>stpA</i>	H-NS-like protein	2261
<i>tpr</i>	A protamine-like protein	194
7. DNA replication, restriction/modification, and recombination		
<i>ada</i>	O ⁶ -Methylguanine-DNA methyltransferase; transcription activator/repressor	14, 1207, 1726
<i>aidB</i>	Induced by alkylating agents	2081, 2084
<i>alkA</i>	3-Methyladenine DNA glycosylase II, inducible	920, 1385, 2081
<i>alkB</i>	DNA repair system specific for alkylated DNA	1017, 2081, 2082
<i>cer</i>	Site-specific recombinase	344
<i>dam</i>	DNA adenine methylase	990, 1435, 1654
<i>dcm</i>	DNA cytosine methylase	643, 1146, 2225

Category and gene	Gene product description ^a	Reference(s)
<i>dfp</i>	Flavoprotein affecting synthesis of DNA and pantothenate metabolism	1875
<i>dinG</i>	Probably ATP-dependent helicase	1021, 1127
<i>dksA</i>	<i>dnaK</i> suppressor protein	940
<i>dnaA</i>	DNA biosynthesis; initiation of chromosome replication; can be transcription regulator	80, 559, 2174
<i>dnaB</i>	Chromosome replication; chain elongation; part of primosome	29, 2092, 2093
<i>dnaC</i>	Chromosome replication; initiation and chain elongation	29, 1245, 2092
<i>dnaE</i>	DNA polymerase III, alpha subunit	664, 1922, 2191
<i>dnaG</i>	DNA biosynthesis; DNA primase	672, 1891
<i>dnaI</i>	DNA biosynthesis	1010, 1970
<i>dnaN</i>	DNA polymerase III, beta subunit	664, 1922, 2191
<i>dnaQ</i>	DNA polymerase III, epsilon subunit	1921, 1922, 2191
<i>dnaR</i>	Thermosensitive initiation of chromosome replication	1723
<i>dnaT</i>	DNA biosynthesis; primosomal protein i	29, 1250
<i>dnaX</i>	DNA polymerase III, tau and gamma subunits; DNA elongation factor III	1921, 2022, 2191
<i>fis</i>	Site-specific DNA inversion stimulation factor; DNA-binding protein; a <i>trans</i> activator for transcription	1414, 1476, 2249
<i>fpg</i>	Formamidopyrimidine DNA glycosylase	184, 185, 659
<i>gidA</i>	Glucose-inhibited division; chromosome replication?	77, 1445
<i>gidB</i>	Glucose-inhibited division; chromosome replication?	77, 1445
<i>gyrA</i>	DNA gyrase, subunit A, type II topoisomerase, DNA cleavage with transient covalent bonding	475, 1466, 1625
<i>gyrB</i>	DNA gyrase subunit B, type II topoisomerase, DNA cleavage with transient covalent bonding, ATPase activity	25, 432, 466
<i>helD</i>	DNA helicase IV	1033, 1292, 2182
<i>het</i>	Binding of DNA sequences in <i>oriC</i> region to outer membrane; DNA-binding protein?	2176
<i>himA</i>	Integration host factor (IHF), alpha subunit; site-specific recombination	197, 943, 1093
<i>himD</i>	Integration host factor (IHF), beta subunit; site-specific recombination	197, 564, 1093
<i>holA</i>	DNA polymerase III, delta subunit	268, 461, 2191
<i>holB</i>	DNA polymerase III, delta prime subunit	267, 270, 461
<i>holC</i>	DNA polymerase III, chi subunit	2191
<i>holD</i>	DNA polymerase III, psi subunit	269, 2191
<i>holE</i>	DNA polymerase III, theta subunit	664, 1853, 2191
<i>hsdM</i>	Host modification; DNA methylase M	1181, 1580
<i>hsdS</i>	Specificity determinant for <i>hsdM</i> and <i>hsdR</i>	1181, 1580
<i>iciA</i>	Replication initiation inhibitor, binds to 13-mers at <i>oriC</i>	819, 1987
<i>lig</i>	DNA ligase	1103
<i>mfd</i>	Mutation frequency decline; transcription-repair coupling factor	597, 1797
<i>mioC</i>	Initiation of chromosome replication	1178
<i>mmrA</i>	Postreplication repair	1208, 1813
<i>mrr</i>	Restriction of methylated adenine	1615, 2094
<i>mutA</i>	Mutator, transversion specific	1313
<i>mutC</i>	Mutator, transversion specific	1313
<i>mutH</i>	Methyl-directed mismatch repair	83, 1756, 2143
<i>mutL</i>	Enzyme in methyl-directed mismatch repair	127, 666, 2198
<i>mutS</i>	Methyl-directed mismatch repair	83, 330, 1145
<i>mutY</i>	Adenine glycosylase; G·C → T·A transversions	82, 2018
<i>ogt</i>	O ⁶ -Alkylguanine-DNA/cysteine-protein methyltransferase	1207, 1569, 1624
<i>parC</i>	DNA topoisomerase IV subunit A	958, 1523, 1524
<i>parE</i>	DNA topoisomerase IV subunit B	868, 958, 1524
<i>phrA</i>	Photoreactivation	468, 988, 2218
<i>phrB</i>	Deoxyribodipyrimidine photolyase (photoreactivation)	468, 2131
<i>pinO</i>	Calcium-binding protein required for initiation of chromosome replication	687, 688
<i>polA</i>	DNA polymerase I, 3' → 5' polymerase, 5' → 3' and 3' → 5' exonuclease	264, 1024, 1498
<i>polB</i>	DNA polymerase II	293, 811
<i>priA</i>	Primosomal protein N' (= factor Y)(putative helicase)	29, 1434, 2255
<i>priB</i>	Primosomal replication protein N	28, 29, 2254
<i>priC</i>	Primosomal replication protein N''	29, 2254
<i>recA</i>	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprotease	1033, 1617, 1850
<i>recF</i>	ssDNA and dsDNA binding, ATP binding	321, 1033, 2037
<i>recG</i>	DNA helicase, resolution of Holliday junctions, branch migration	1033, 1172, 2147
<i>recN</i>	Protein in recombination and DNA repair	1033, 1173, 1691
<i>recO</i>	Protein interaction with RecR and possibly RecF proteins	1033, 1713, 1734
<i>recQ</i>	ATP-dependent DNA helicase	1033, 2038, 2039
<i>recT</i>	Recombinase, DNA renaturation	322, 697, 1033
<i>rep</i>	<i>rep</i> helicase, ssDNA-dependent ATPase	42, 2178, 2179
<i>rob</i>	Right origin-binding protein	1848
<i>rra</i>	Reverses <i>recBC</i> , <i>sbcA</i> alleviation of Mcr (formerly Rgl) restriction of glucosyl-free DNA containing hydroxymethyl- and methylcytosine	942
<i>rus</i>	Suppressor of <i>ruv</i> mutants; with <i>recG</i> processes Holliday junctions	1226

Category and gene	Gene product description ^a	Reference(s)
<i>ruvA</i>	Branch migration of Holliday structures; repair	872, 1058, 2019
<i>ruvB</i>	Branch migration of Holliday structures; repair helicase	1362, 1823, 2019
<i>ruvC</i>	Holliday junction nuclease; resolution of structures; repair	129, 873, 1952
<i>seqA</i>	Negative modulator of initiation of replication	1190
<i>ssb</i>	ssDNA-binding protein	247, 1033
<i>tag</i>	3-Methyladenine DNA glycosylase I, constitutive	156, 920
<i>tdi</i>	Transduction, transformation, and rates of mutation	1890
<i>toc</i>	Suppressor of <i>topA</i>	466
<i>topA</i>	DNA topoisomerase type I, omega protein	475, 751, 2280
<i>topB</i>	DNA topoisomerase III	449, 751
<i>tus</i>	DNA-binding protein; inhibition of replication at Ter sites	653, 752, 994
<i>umuC</i>	SOS mutagenesis; error-prone repair; forms complex with UmuD and UmuD'	1008, 1865, 2184
<i>umuD</i>	SOS mutagenesis; error-prone repair; processed to UmuD'; forms complex with UmuC	92, 562, 1008
<i>ung</i>	Uracil-DNA glycosylase	545, 2062
<i>uup</i>	Precise excision of insertion element	787
<i>uvrA</i>	Repair of UV damage to DNA; excision nuclease subunit A	320, 1020, 1267
<i>uvrD</i>	DNA-dependent ATPase I and helicase II	1292, 1342, 2117
<i>xerC</i>	Site-specific recombinase, acts on <i>cer</i> sequence of ColE1, effects chromosome segregation at cell division	169, 769, 1274
<i>xerD</i>	Site-specific recombinase	170, 769, 1274
8. Protein translation and modification		
<i>def</i>	Peptide deformylase	1266, 1285
<i>dsbA</i>	Protein disulfide isomerase I	905, 2202, 2253
<i>frr</i>	Ribosome-releasing factor	824, 1825
<i>fusA</i>	Protein chain elongation factor EF-G	791, 901, 1335
<i>glnE</i>	Adenylylating enzyme for glutamine synthetase	36
<i>greA</i>	Transcription elongation factor: cleaves 3' nucleotide of paused mRNA	192, 193, 1868
<i>hha</i>	Hemolysin expression-modulating protein	1411
<i>iap</i>	Alkaline phosphatase isozyme conversion, aminopeptidase	853, 1396
<i>infA</i>	Protein chain initiation factor IF-1	376, 377
<i>infB</i>	Protein chain initiation factor IF-2	1059, 1347, 1715
<i>infC</i>	Protein chain initiation factor IF-3	1371
<i>map</i>	Methionine aminopeptidase	126
<i>pcm</i>	L-Isoaspartate protein carboxylmethyltransferase type II	640
<i>pmbA</i>	Maturation of antibiotic MccB17	1665
<i>pms</i>	Sulfoxide reductase for peptide methionine	1609
<i>ppiA</i>	Peptidyl-prolyl <i>cis-trans</i> isomerase A (a rotamase)	346, 719, 1168
<i>ppiB</i>	Peptidyl-prolyl <i>cis-trans</i> isomerase B (a rotamase)	346, 719, 1168
<i>prfA</i>	Peptide chain release factor RF-1	367, 604
<i>prfB</i>	Peptide chain release factor RF-2	367, 1318
<i>prfC</i>	Peptide chain release factor RF-3	663, 1317
<i>prfH</i>	Probable peptide chain release factor	1522
<i>selB</i>	Selenocysteinyl-tRNA-specific translation factor	551, 1653, 1752
<i>slyD</i>	Probable rotamase, peptidyl-prolyl <i>cis-trans</i> isomerase	1685, 2201
<i>tsf</i>	Protein chain elongation factor EF-Ts	45, 820
<i>tufA</i>	Protein chain elongation factor EF-Tu (duplicate of <i>tufB</i>)	994, 1335, 1541
<i>tufB</i>	Protein chain elongation factor EF-Tu (duplicate of <i>tufA</i>)	820, 994, 1973
<i>ups</i>	Efficiency of nonsense suppressors	409
9. RNA synthesis, RNA modification, and DNA transcription		
<i>baeR</i>	Transcriptional regulatory protein	1380
<i>baeS</i>	Sensor protein	1380
<i>basR</i>	Transcriptional regulatory protein	1380
<i>basS</i>	Sensor protein for <i>basR</i>	1380
<i>dbpA</i>	ATP-dependent RNA helicase	578, 831
<i>deaD</i>	Putative ATP-dependent RNA helicase	2005, 2219
<i>evgA</i>	Putative positive transcription regulator	2043
<i>evgS</i>	Putative sensor for EvgA	2043
<i>greB</i>	Transcription elongation factor and transcript cleavage	193
<i>hepA</i>	Probable RNA helicase	1127, 2248
<i>msrA</i>	Methionine sulfoxide reductase	1608
<i>nusA</i>	Transcription termination; L factor	635, 1158
<i>nusB</i>	Transcription termination; L factor	1252, 1423, 1976
<i>nusG</i>	Component in transcription antitermination	1158, 1930
<i>opr</i>	Rate of degradation of aberrant subunit proteins of RNA polymerase	1804
<i>pcnB</i>	Poly(A) polymerase I	931, 2207
<i>pnp</i>	Polynucleotide phosphorylase	1628, 2222
<i>ranA</i>	RNA metabolism	63
<i>rhlB</i>	Putative ATP-dependent RNA helicase	933, 1450

Category and gene	Gene product description ^a	Reference(s)
<i>rhIE</i>	Putative ATP-dependent RNA helicase	1450
<i>rho</i>	Transcription termination factor Rho; polarity suppressor	612, 613, 1795
<i>rpoA</i>	RNA polymerase, alpha subunit	723, 851, 1651
<i>rpoB</i>	RNA polymerase, beta subunit	1074, 1805, 2192
<i>rpoC</i>	RNA polymerase, beta prime subunit	860, 1199, 1532
<i>rpoZ</i>	RNA polymerase, omega subunit	617, 618, 830
<i>spoU</i>	Putative rRNA methylase	1022
<i>srmB</i>	ATP-dependent RNA helicase	1416, 1450
<i>tabC</i>	Possible rho factor	272
10. Polysaccharides (cytoplasmic)		
<i>glgA</i>	Glycogen synthase	556, 583, 584
<i>glgB</i>	1,4- α -Glucan branching enzyme	1681
<i>glgC</i>	Glucose-1-phosphate adenylyltransferase	627, 758, 1310
<i>glgP</i>	Glycogen phosphorylase	1759, 1760, 2246
<i>glgS</i>	Glycogen biosynthesis, <i>rpoS</i> dependent	737
<i>glgX</i>	Probably part of glycogen operon	1681
11. Phospholipids		
<i>cls</i>	Cardiolipin synthase, a major membrane phospholipid	771, 1418, 1824
<i>gpsA</i>	<i>sn</i> -Glycerol-3-phosphate dehydrogenase [NAD(P) ⁺]	484
<i>lgt</i>	Phosphatidylglycerol-prolipoprotein diacylglyceryltransferase; a major membrane phospholipid	1735
<i>pgpA</i>	Nonessential phosphatidylglycerophosphate phosphatase, membrane bound	580, 826
<i>pgpB</i>	Nonessential phosphatidylglycerophosphate phosphatase, membrane bound	580, 825
<i>pgsA</i>	Phosphatidylglycerophosphate synthetase = CDP-1,2-diacyl- <i>sn</i> -glycero-3-phosphate phosphatidyltransferase	1417, 2042
<i>plsB</i>	Glycerolphosphate acyltransferase activity	355, 2159
<i>plsC</i>	1-Acyl- <i>sn</i> -glycerol-3-phosphate acyltransferase	339
<i>plsX</i>	Glycerolphosphate auxotrophy in <i>plsB</i> background	1081
<i>psd</i>	Phosphatidylserine decarboxylase; phospholipid synthesis	1136, 1137, 1821
<i>pssA</i>	Phosphatidylserine synthase; phospholipid synthesis	423, 1821
<i>pssR</i>	Regulator of <i>pssA</i>	1870
B. Degradation of macromolecules		
1. RNA		
<i>rna</i>	RNase I, cleaves phosphodiester bond between any two nucleotides	1278, 2272
<i>rnb</i>	RNase II, mRNA degradation	462, 970, 2274
<i>rnc</i>	RNase III, dsRNA	297, 1627, 1887
<i>rnd</i>	RNase D, processes tRNA precursor	970, 2263, 2264
<i>rne</i>	RNase E, enzyme complex for RNA processing, mRNA turnover, maturation of 5S RNA	493, 1886
<i>rnhA</i>	RNase HI, degrades RNA of DNA-RNA hybrids, participates in DNA replication	372, 859, 1444
<i>rnhB</i>	RNase HII, degrades RNA of DNA-RNA hybrids	858
<i>rnpA</i>	RNase P, protein component; processes tRNA, 4.5S RNA	708, 992, 1937
<i>rnpB</i>	RNase P, RNA component; processes tRNA, 4.5S RNA	444, 1886, 1937
<i>rnt</i>	RNase T, degrades tRNA	806, 970, 1486
<i>rph</i>	RNase PH	444, 970
<i>srnA</i>	Degradation of stable RNA	1453
<i>stsA</i>	RNase activity	1109
2. DNA		
<i>endA</i>	DNA-specific endonuclease I	1149, 1880
<i>hsdR</i>	Host restriction; endonuclease R	1181, 1580
<i>mcrA</i>	Restriction of DNA at 5-methylcytosine residues; at locus of e14 element	766, 767, 1615
<i>mcrB</i>	Component of McrBC 5-methylcytosine restriction system	1041, 1614, 2270
<i>mcrC</i>	Component of McrBC 5-methylcytosine restriction system	450, 1041, 2269
<i>nfo</i>	Endonuclease IV	709, 1120, 1957
<i>nth</i>	Endonuclease III; specific for apurinic and/or apyrimidinic sites	75
<i>recB</i>	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease, chi sequence recognition	321, 1033, 1492
<i>recC</i>	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease, chi sequence recognition	321, 1033, 1492
<i>recD</i>	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease, chi sequence recognition	321, 1033, 1492
<i>recE</i>	Exonuclease VIII, dsDNA exonuclease, 5' \rightarrow 3' specific	315, 321, 1033
<i>recJ</i>	ssDNA exonuclease, 5' \rightarrow 3' specific	321, 1033, 1189
<i>sbcB</i>	Exonuclease I, 3' \rightarrow 5' specific; deoxyribosephosphodiesterase	32, 225, 1536
<i>sbcC</i>	ATP-dependent dsDNA exonuclease	453, 1088, 1397
<i>sbcD</i>	ATP-dependent dsDNA exonuclease	453, 631, 1088
<i>uvrB</i>	DNA repair; excision nuclease subunit B	1470, 1792, 1793

Category and gene	Gene product description ^a	Reference(s)
<i>uvrC</i>	Repair of UV damage to DNA; excision nuclease subunit C	1150, 1796, 2059
<i>vsr</i>	DNA mismatch endonuclease, patch repair protein	398, 740, 1863
<i>xseA</i>	Exonuclease VII, large subunit	290
<i>xseB</i>	Exonuclease VII, small subunit	2048, 2049
<i>xthA</i>	Exonuclease III	1722, 1738, 1957
3. Proteins, peptides, and glycopeptides		
<i>alpA</i>	Transcriptional regulator of <i>slpA</i> gene; a prophage P4-like protein	991, 2008
<i>clpA</i>	ATP-binding subunit of serine protease, alternate subunit determines specificity	650, 651
<i>clpB</i>	Probable alternate ATP-binding subunit of serine protease, determines specificity; heat shock proteins F84.1 and F68.5	1504, 1884, 2180
<i>clpP</i>	ATP-dependent proteolytic subunit of <i>clpA-clpP</i> serine protease, heat shock protein F21.5	1262, 1263, 2180
<i>clpX</i>	ATP-binding subunit of <i>clpP</i> serine protease, alternate subunit determines specificity	649
<i>dcp</i>	Dipeptidyl carboxypeptidase	443
<i>eco</i>	Ecotin, a serine protease inhibitor	1275, 1276
<i>hflC</i>	Protease specific for phage lambda cII repressor	102, 301
<i>hflK</i>	Protease specific for phage lambda cII repressor	102, 301
<i>hflX</i>	GTP-binding subunit of protease specific for phage lambda cII repressor	1422
<i>hlyA</i>	Hemolysin	972, 1194, 1892
<i>htrA</i>	Periplasmic serine protease Do and heat shock protein	1160, 1801
<i>pepA</i>	Aminopeptidase A/I	1906
<i>pepD</i>	Peptidase D, a dipeptidase where amino-terminal residue is histidine	549, 741, 742
<i>pepE</i>	Peptidase E, a dipeptidase where amino-terminal residue is aspartate	179, 350
<i>pepN</i>	Aminopeptidase N	98, 1269
<i>pepP</i>	Aminopeptidase P II	2242
<i>pepQ</i>	Proline dipeptidase	395, 939
<i>pepT</i>	Putative peptidase T	1183
<i>prc</i>	Carboxy-terminal protease for penicillin-binding protein 3	705
<i>prlC</i>	Oligopeptidase A	351
<i>ptrA</i>	Protease III	101
<i>ptrB</i>	Protease II	939
<i>slpA</i>	Regulator of expression of Alp protease; integrase of P4-like prophage	991
<i>sms</i>	Probable ATP-dependent protease	1404
<i>snoB</i>	Affects degradability of <i>Rhizobium</i> NifA in <i>E. coli</i>	802
<i>snoC</i>	Increases rate of degradation by <i>lon</i> pathway of <i>Rhizobium</i> NifA in <i>E. coli</i>	802
<i>sohA</i>	Putative protease	93
<i>sohB</i>	Putative protease	93
<i>sppA</i>	Protease IV, a signal peptide peptidase	822, 1940
4. Polysaccharides		
<i>amyA</i>	Cytoplasmic alpha-amylase	1605, 1606
<i>malQ</i>	4- α -glucanotransferase (amylomaltase)	1594
<i>malS</i>	α -Amylase	565, 1765
C. Cell envelope		
1. Membranes, lipoproteins, and porins		
<i>acrA</i>	Lipoprotein mutants sensitive to drugs	340, 1204, 1389
<i>acrE</i>	Transmembrane protein; mutants sensitive to drugs	1204
<i>cog</i>	Regulator of <i>ompG</i>	1327
<i>envN</i>	Envelope protein; osmotically remedial envelope defect	486
<i>envP</i>	Envelope protein; osmotically remedial envelope defect	486
<i>envQ</i>	Envelope protein; osmotically remedial envelope defect	486
<i>envT</i>	Envelope protein; osmotically remedial envelope defect	486
<i>envY</i>	Envelope protein; thermoregulation of porin biosynthesis	1195
<i>fhuA</i>	Outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and ϕ 80	983, 984, 1009
<i>hlpA</i>	Outer membrane protein	773
<i>micF</i>	Regulatory antisense RNA affecting <i>ompF</i> expression	46
<i>nlpA</i>	Lipoprotein-28	2217
<i>nlpB</i>	Lipoprotein-34	203
<i>nlpD</i>	Lipoprotein	823
<i>ompA</i>	Outer membrane protein 3a (II*; G; d)	467, 1004, 1658
<i>ompC</i>	Outer membrane protein 1b (Ib; c)	433, 1649, 2120
<i>ompF</i>	Outer membrane protein 1a (Ia; b; F)	655, 1649, 1798
<i>ompG</i>	Outer membrane porin protein	1327
<i>ompP</i>	Outer membrane protease; receptor for phage OX2	959
<i>ompT</i>	Outer membrane protein 3b (a), a protease	100, 703, 959

Category and gene	Gene product description ^a	Reference(s)
<i>phoE</i>	Outer membrane pore protein E (E; Ic; NmpAB), structural gene	112, 424, 886
<i>qmeA</i>	Unspecified membrane defect	2154
<i>qmeC</i>	Unspecified membrane defect; tolerance to glycine; penicillin sensitivity	2154
<i>qmeD</i>	Unspecified membrane defect; tolerance to glycine; penicillin sensitivity	2154
<i>qmeE</i>	Unspecified membrane defect	2154
<i>rlpA</i>	A minor lipoprotein	1954
<i>rlpB</i>	A minor lipoprotein	1954
<i>sipB</i>	Suppressor of outer membrane mutant	1597
<i>sipC</i>	Suppressor of outer membrane mutant	1597
<i>sipD</i>	Suppressor of outer membrane mutant	1597
<i>smpA</i>	Membrane protein	1406
2. Surface polysaccharides, lipopolysaccharides, and antigens		
<i>cpsA</i>	Capsular polysaccharide biosynthesis, colanic acid	2010
<i>cpsC</i>	Capsular polysaccharide biosynthesis, colanic acid	2010
<i>cpsD</i>	Capsular polysaccharide biosynthesis, colanic acid	2010
<i>cpsE</i>	Capsular polysaccharide biosynthesis, colanic acid	2010
<i>cpsF</i>	Capsular polysaccharide biosynthesis, colanic acid	2010
<i>envA</i>	UDP-3-O-acyl N-acetylglucosamine deacetylase; lipid A biosynthesis; splits layers of septum during cell division	456, 1678
<i>firA</i>	UDP-3-O-(R-3-hydroxymyristoyl)-glucosamine N-acyltransferase; third step of endotoxin synthesis	2175
<i>kdsB</i>	CTP: CMP-3-deoxy-D-manno-octulosonate transferase	534
<i>kdtA</i>	3-Deoxy-D-manno-octulosonic acid transferase (KDO transferase)	125, 332, 1684
<i>kdtB</i>	Putative enzyme of lipopolysaccharide synthesis	1684
<i>lpcA</i>	Lipopolysaccharide core biosynthesis; resistance to phages T4, T7, and P1; deficiency in conjugation	718, 1961
<i>lpcB</i>	Lipopolysaccharide core biosynthesis	718, 1961
<i>lpxA</i>	UDP-N-acetylglucosamine acetyltransferase; lipid A biosynthesis	373, 586, 1603
<i>lpxB</i>	Lipid A disaccharide synthetase; lipid A biosynthesis	373, 1603
<i>nanA</i>	N-Acetylneuraminatase lyase (aldolase)	12, 13
<i>ops</i>	Level of exopolysaccharide production	2276
<i>rcsA</i>	Positive regulator for <i>ctr</i> capsule biosynthesis	652, 1915, 1916
<i>rcsB</i>	Positive response regulator for <i>ctr</i> capsule biosynthesis, (sensor, <i>rcsC</i>)	625, 652, 1915
<i>rcsC</i>	Negative regulator for <i>ctr</i> capsule biosynthesis, probable histidine kinase sensor acting on <i>rcsB</i>	222, 652, 1915
<i>rcsF</i>	Regulator in solanic acid synthesis; interacts with RcsB	624
<i>rfaB</i>	UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase	1505, 1578, 1684
<i>rfaC</i>	Lipopolysaccharide core biosynthesis; heptosyltransferase I	295, 1684
<i>rfaD</i>	ADP-L-glycero-D-mannoheptose-6-epimerase; permits growth at high temperature	949, 1521, 1610
<i>rfaF</i>	Lipopolysaccharide core biosynthesis	1684
<i>rfaG</i>	Lipopolysaccharide core biosynthesis; glucosyltransferase I	1505, 1506, 1684
<i>rfaH</i>	Transcriptional activator affecting biosynthesis of lipopolysaccharide core, F pilin, and hemolysin	91, 1579, 1684
<i>rfaI</i>	UDP-D-galactose:(glucosyl)lipopolysaccharide- α -1,3-D-galactosyltransferase	1505, 1578, 1684
<i>rfaJ</i>	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase	1505, 1578, 1684
<i>rfaK</i>	Lipopolysaccharide core biosynthesis; probably hexose transferase	1001, 1002, 1506
<i>rfaL</i>	Lipopolysaccharide core biosynthesis; O-antigen ligase	1001, 1002, 1684
<i>rfaM</i>	Lipopolysaccharide core biosynthesis; glucosyltransferase II	1684
<i>rfaP</i>	Lipopolysaccharide core biosynthesis; phosphorylation of core heptose; attaches phosphate-containing substrate to lipopolysaccharide core	1505, 1506
<i>rfaQ</i>	Lipopolysaccharide core biosynthesis	1001, 1506, 1684
<i>rfaS</i>	Lipopolysaccharide core biosynthesis	1001, 1003, 1578
<i>rfaY</i>	Lipopolysaccharide core biosynthesis	1002, 1684
<i>rfaZ</i>	Lipopolysaccharide core biosynthesis	1001, 1002, 1684
<i>rfbX</i>	Hydrophobic protein involved in assembly of O antigen	1902, 2233
<i>rfe</i>	Synthesis of enterobacterial common antigen (ECA): UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase	1455, 1648, 1902
<i>rffA</i>	Synthesis of enterobacterial common antigen (ECA): TDP-4-keto-6-deoxy-D-glucose:TDP-D-glucosamine transaminase	1043, 1283, 1284
<i>rffC</i>	Synthesis of enterobacterial common antigen (ECA): ECA chain elongation	1043, 1283, 1284
<i>rffD</i>	Synthesis of enterobacterial common antigen (ECA): UDP-ManNAc dehydrogenase (UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase)	1043, 1283, 1284
<i>rffE</i>	Synthesis of enterobacterial common antigen (ECA): UDP-GlcNAc-2-epimerase	1043, 1283, 1284
<i>rffM</i>	Synthesis of enterobacterial common antigen (ECA): UDP-ManNAc:lipid I transferase	107, 1283, 1284
<i>rffT</i>	Synthesis of enterobacterial common antigen (ECA): TDP-Fuc4NAc:lipid II transferase	1043, 1283, 1284

Category and gene	Gene product description ^a	Reference(s)
3. Surface structures		
<i>crl</i>	DNA-binding protein affecting expression of cryptic <i>csgA</i> gene for surface fibers	70, 1461
<i>csgA</i>	Curlin subunit, coiled surface structures; cryptic	70, 1461
<i>dsbB</i>	Reoxidizes DsbA protein following formation of disulfide bond in P-ring of flagella	105, 1328
<i>dsbC</i>	Protein disulfide isomerase II	1330, 1820
<i>ecpD</i>	Probable pilin chaperone similar to PapD	1611
<i>fimA</i>	Major type 1 subunit fimbrin (pilin)	180, 999, 1469
<i>fimB</i>	Regulator for <i>fimA</i>	1270, 1495, 1783
<i>fimC</i>	Periplasmic chaperone, required for type 1 fimbriae	907, 1982
<i>fimD</i>	Outer membrane protein; export and assembly of type 1 fimbriae	1000
<i>fimE</i>	Regulator for <i>fimA</i>	181, 1270, 1495
<i>fimF</i>	Fimbrial morphology	1038, 1708
<i>fimG</i>	Fimbrial morphology	1038, 1708
<i>fimH</i>	Minor fimbrial subunit, D-mannose-specific adhesin	907, 1038, 1982
<i>fimZ</i>	Fimbrial Z protein; probable signal transducer	1372
<i>flgA</i>	Flagellar biosynthesis; assembly of basal-body periplasmic P-ring	834, 1209, 1453
<i>flgB</i>	Flagellar biosynthesis, cell-proximal portion of basal-body rod	834, 1209
<i>flgC</i>	Flagellar biosynthesis, cell-proximal portion of basal-body rod	834, 1209
<i>flgD</i>	Flagellar biosynthesis, initiation of hook assembly	834, 1209
<i>flgE</i>	Flagellar biosynthesis, hook protein	834, 1209
<i>flgF</i>	Flagellar biosynthesis, cell-proximal portion of basal-body rod	834, 1209
<i>flgG</i>	Flagellar biosynthesis, cell-distal portion of basal-body rod	834, 1209
<i>flgH</i>	Flagellar biosynthesis, basal-body outer membrane L (lipopolysaccharide layer)-ring protein	834, 908, 1209
<i>flgJ</i>	Flagellar biosynthesis	834, 1209
<i>flgK</i>	Flagellar biosynthesis, hook-filament junction protein	834, 1209
<i>flgL</i>	Flagellar biosynthesis; hook-filament junction protein	834, 1209
<i>flgM</i>	Anti-FliA (anti-sigma) factor; also known as RflB protein; active only when hook assembly not completed	834, 1209
<i>flhA</i>	Flagellar biosynthesis; export of flagellar proteins?	834, 1057, 1209
<i>flhB</i>	Flagellar biosynthesis	834, 1209
<i>flhC</i>	Regulator of flagellar biosynthesis acting on class 2 operons; transcription initiation factor?	834, 1209
<i>flhD</i>	Regulator of flagellar biosynthesis, acting on class 2 operons; transcriptional initiation factor?	834, 1209
<i>flhE</i>	Flagellar biosynthesis	834, 1209
<i>fliA</i>	Flagellar biosynthesis; regulation of late gene expression (class 3a and 3b operons); sigma factor	834, 961, 1209
<i>fliB</i>	Flagellar biosynthesis; in <i>Salmonella</i> spp., methylation of lysine residues on the filament protein, flagellin	834, 961, 1209
<i>fliC</i>	Flagellar biosynthesis; flagellin, filament structural protein	69, 834, 1209
<i>fliD</i>	Flagellar biosynthesis; filament capping protein; enables filament assembly	69, 834, 1209
<i>fliE</i>	Flagellar biosynthesis; basal-body component, possibly at (MS-ring)-rod junction	834, 1209, 1364
<i>fliF</i>	Flagellar biosynthesis; basal-body MS (membrane and supramembrane)-ring and collar protein	834, 961, 1209
<i>fliG</i>	Flagellar biosynthesis, component of motor switching and energizing, enabling rotation and determining its direction	976, 1209, 1675
<i>fliH</i>	Flagellar biosynthesis; export of flagellar proteins?	834, 961, 1209
<i>fliI</i>	Flagellar biosynthesis; export of flagellar proteins?	834, 961, 1209
<i>fliJ</i>	Flagellar biosynthesis	834, 961, 1209
<i>fliK</i>	Flagellar biosynthesis, hook length control	834, 961, 1209
<i>fliL</i>	Flagellar biosynthesis	834, 1209, 1223
<i>fliM</i>	Flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction	976, 1209, 1676
<i>fliN</i>	Flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction	976, 1209, 1676
<i>fliO</i>	Flagellar biosynthesis	961, 1209, 1222
<i>fliP</i>	Flagellar biosynthesis	961, 1209, 1222
<i>fliQ</i>	Flagellar biosynthesis	961, 1209, 1222
<i>fliR</i>	Flagellar biosynthesis	961, 1209, 1222
<i>fliS</i>	Flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)	834, 961, 1209
<i>fliT</i>	Flagellar biosynthesis; repressor of class 3a and 3b operons (RflA activity)	834, 961, 1209
<i>fliU</i>	Involved in secretion of flagellin and motility	455
<i>fliV</i>	Involved in secretion of flagellin and motility	455
<i>flu</i>	Metastable gene affecting surface properties, piliation, and colonial morphology	447
<i>mor</i>	Regulator of switching between two sets of surface properties	2114

Category and gene	Gene product description ^a	Reference(s)
4. Murein sacculus and peptidoglycan		
<i>amiA</i>	<i>N</i> -Acetylmuramoyl-1-alanine amidase I, septum separation	2000, 2056
<i>amiB</i>	<i>N</i> -Acetylmuramoyl-1-alanine amidase II; a murein hydrolase	2024
<i>bolA</i>	Possible regulator of murein genes	22
<i>dacA</i>	D-Alanyl-D-alanine carboxypeptidase, fraction A; penicillin-binding protein 5	118, 879, 2053
<i>dacB</i>	D-Alanyl-D-alanine carboxypeptidase, fraction B; penicillin-binding protein 4	1023, 1352, 1353
<i>dacC</i>	D-Alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6	229
<i>ddlA</i>	D-Alanine-D-alanine ligase A	21, 2256
<i>ddlB</i>	D-Alanine-D-alanine ligase B	2256
<i>hipA</i>	Frequency of persistence to inhibition of murein or DNA biosynthesis, DNA-binding regulator	158, 159
<i>hipB</i>	Frequency of persistence to inhibition of murein or DNA biosynthesis; regulatory protein interacts with HipA	158
<i>lpp</i>	Murein lipoprotein	847, 1355
<i>mepA</i>	Murein DD-endopeptidase	968
<i>mlt</i>	Membrane-bound lytic murein transglycosylase	503, 2041
<i>mraA</i>	D-Alanine carboxypeptidase	1333
<i>mraB</i>	D-Alanine requirement; cell wall peptidoglycan biosynthesis	1333
<i>mraY</i>	Phospho- <i>N</i> -acetylmuramoyl-pentapeptide transferase?	836
<i>mrba</i>	UDP- <i>N</i> -acetylglucosaminyl-3-enolpyruvate reductase activity	1333
<i>mrbb</i>	Cell wall peptidylglycan biosynthesis; mutation causes D-alanine auxotrophy	1333
<i>mrbc</i>	Cell wall peptidylglycan biosynthesis	1333
<i>mrcA</i>	Peptidoglycan synthetase; cell wall biosynthesis; penicillin-binding protein 1A	228, 2245
<i>mrcB</i>	Peptidoglycan synthetase; cell wall biosynthesis; penicillin-binding protein 1B	228, 2245
<i>mrda</i>	Cell shape; peptidoglycan synthetase; penicillin-binding protein 2	78, 852, 1955
<i>mrdB</i>	Rod shape-determining protein; sensitivity to radiation and drugs	118, 835, 1258
<i>mreB</i>	Rod shape-determining protein	454
<i>mreC</i>	Rod shape-determining protein	2087
<i>mreD</i>	Rod shape-determining protein	2087
<i>murB</i>	UDP- <i>N</i> -acetylenolpyruvoylglucosamine reductase	130, 1592
<i>murC</i>	L-Alanine-adding enzyme, UDP- <i>N</i> -acetyl-muramate-alanine ligase	638, 1295
<i>murD</i>	UDP- <i>N</i> -acetylmuramoylalanine-D-glutamate ligase	638, 1294, 1295
<i>murE</i>	<i>meso</i> -Diaminopimelate-adding enzyme	638, 1294, 1295
<i>murF</i>	D-Alanine:D-alanine-adding enzyme	482, 638, 1295
<i>murG</i>	Transferase in peptidoglycan synthesis	638, 1295
<i>murH</i>	Peptidoglycan biosynthesis, late stage	384, 638
<i>murI</i>	Glutamate racemase, required for biosynthesis of D-glutamate and peptidoglycan	470, 1593, 2243
<i>murZ</i>	First step in murein biosynthesis; UDP- <i>N</i> -glucosamine 1-carboxyvinyltransferase	638, 1244
<i>pal</i>	Peptidoglycan-associated lipoprotein	296, 1087
<i>slt</i>	Soluble lytic murein transglycosylase	502, 503, 2041

IV. CELL PROCESSES

A. Transport/binding proteins

1. Amino acids and amines

<i>abpS</i>	Low-affinity transport, arginine and ornithine; periplasmic binding protein	278, 279
<i>argP</i>	Transport of arginine, ornithine, and lysine	281
<i>argT</i>	Lysine-, arginine-, ornithine-binding protein	1427
<i>aroP</i>	General aromatic amino acid transport	784
<i>aroT</i>	Transport of aromatic amino acids, alanine and glycine	1988
<i>artI</i>	Arginine periplasmic transport system protein	2173
<i>artJ</i>	Arginine-binding protein	2173
<i>artM</i>	Arginine periplasmic transport system protein	2173
<i>artP</i>	Arginine periplasmic transport system protein	2173
<i>artQ</i>	Arginine periplasmic transport system protein	2173
<i>brnQ</i>	Transport system 1 for isoleucine, leucine, and valine	2221
<i>brnR</i>	Component of transport systems 1 and 2 for isoleucine, leucine, and valine	2221
<i>brnS</i>	Transport system for isoleucine, leucine, and valine	675
<i>brnT</i>	Low-affinity transport system for isoleucine	675
<i>cadB</i>	Transport of lysine/cadaverine	1293, 2119
<i>cycA</i>	Transport of D-alanine, D-serine, and glycine	360, 362, 1661
<i>glnH</i>	Periplasmic glutamine-binding protein	1426
<i>glnP</i>	Glutamine high-affinity transport system; membrane component	1426
<i>glnQ</i>	Glutamine high-affinity transport system	1426
<i>gltP</i>	Glutamate-aspartate symport protein	427, 1999
<i>gltR</i>	Regulator for <i>gltS</i>	1239

Category and gene	Gene product description ^a	Reference(s)
<i>gltS</i>	Glutamate transport	471, 932
<i>hisJ</i>	Histidine-binding protein of high-affinity histidine transport system	64
<i>hisM</i>	Histidine transport, membrane protein M	1034
<i>hisP</i>	Histidine transport, inner membrane receptor protein P	1034, 1324
<i>livF</i>	Leucine transport protein	7
<i>livG</i>	High-affinity branched-chain amino acid transport system	7
<i>livH</i>	High-affinity branched-chain amino acid transport system; membrane component	7
<i>livJ</i>	High-affinity amino acid transport system; periplasmic binding protein	7
<i>livK</i>	High-affinity leucine-specific transport system; periplasmic binding protein	7
<i>livL</i>	High-affinity branched-chain amino acid transport	7
<i>livM</i>	High-affinity branched-chain amino acid transport	7
<i>lysP</i>	Lysine-specific permease; pleiotropic increase in lysine decarboxylase	1400, 1896
<i>lysX</i>	Lysine excretion	893
<i>metD</i>	High-affinity uptake of D- and L-methionine	924, 925
<i>mtr</i>	Tryptophan-specific transport protein	727, 1739, 1741
<i>nagE</i>	Phosphotransferase system enzyme II, specific for <i>N</i> -acetylglucosamine	1528, 1671, 2080
<i>pheP</i>	Phenylalanine-specific transport system	1539, 1540
<i>potA</i>	Spermidine/putrescine transport protein	581, 953
<i>potB</i>	Spermidine/putrescine transport protein	581
<i>potC</i>	Spermidine/putrescine transport protein	581
<i>potD</i>	Spermidine/putrescine transport protein	581, 953
<i>potE</i>	Putrescine transport protein	954
<i>potF</i>	Periplasmic putrescine-binding protein	1546
<i>potG</i>	Putrescine transport protein	1546
<i>potH</i>	Putrescine transport protein	1546
<i>potI</i>	Putrescine transport protein	1546
<i>proP</i>	Low-affinity transport system; proline permease II	276, 375
<i>proT</i>	Proline transport	1350, 1351
<i>proV</i>	High-affinity transport system; glycine betaine-binding protein	276, 407, 1908
<i>proW</i>	High-affinity transport system for glycine betaine and proline	276, 407, 1908
<i>sdaC</i>	Probable serine transporter	1810
<i>tdcC</i>	Anaerobically inducible L-threonine, L-serine permease	648, 1787, 1931
<i>tnaB</i>	Low-affinity tryptophan permease	1740, 2232
<i>tyrP</i>	Tyrosine-specific transport system	2187
<i>tyrR</i>	Regulation of <i>aroF</i> , <i>aroG</i> , and <i>tyrA</i> and aromatic amino acid transport systems	66, 374, 1547
<i>bfr</i>	Bacterioferritin	59, 60
2. Cations		
<i>calA</i>	Calcium transport	219
<i>calC</i>	Calcium transport	219
<i>calD</i>	Calcium transport	219
<i>chaA</i>	Sodium-calcium/proton antiporter	870, 1456, 1484
<i>cirA</i>	Iron-regulated colicin I receptor; porin; requires <i>tonB</i> gene product	123, 665
<i>corA</i>	Mg ²⁺ transport, system I	632, 1502, 1858
<i>corB</i>	Mg ²⁺ transport, system I	632, 1502, 1858
<i>cutE</i>	Copper homeostasis protein	1673
<i>exbB</i>	Uptake of enterochelin; <i>tonB</i> -dependent uptake of B colicins	213, 215, 937
<i>exbC</i>	Uptake of enterochelin; sensitivity or resistance to colicins	1596
<i>exbD</i>	Uptake of enterochelin; <i>tonB</i> -dependent uptake of B colicins	215, 494, 1567
<i>fecA</i>	Citrate-dependent iron transport, outer membrane receptor	1029, 1893, 2060
<i>fecB</i>	Citrate-dependent iron transport, periplasmic protein	1029, 1893, 2060
<i>fecC</i>	Citrate-dependent iron(III) transport protein, cytosolic	1029, 1893, 2060
<i>fecD</i>	Citrate-dependent iron transport, membrane-bound protein	1029, 1893, 2060
<i>fecE</i>	Citrate-dependent iron(III) transport protein, membrane bound	1029, 1893, 2060
<i>fecI</i>	Regulator for <i>fec</i> operon, membrane location	2060
<i>fecR</i>	Regulator for <i>fec</i> operon, periplasmic	2060
<i>feoA</i>	Ferrous iron transport protein A	936
<i>feoB</i>	Ferrous iron transport protein B	936
<i>fepA</i>	Receptor for ferric enterobactin (enterochelin) and colicins B and D	1167, 1377, 2171
<i>fepB</i>	Ferric enterobactin (enterochelin) uptake; periplasmic component	498, 1482
<i>fepC</i>	Ferric enterobactin (enterochelin) uptake; cytoplasmic membrane component	1482, 1816
<i>fepD</i>	Ferric enterobactin (enterochelin) uptake	1482, 1816
<i>fepE</i>	Ferric enterobactin (enterochelin) uptake	1482
<i>fepG</i>	Ferric enterobactin transport protein	1816
<i>fes</i>	Enterochelin esterase	220, 2171
<i>fhuB</i>	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	1028, 1030, 1779
<i>fhuC</i>	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	1028, 1030, 1779
<i>fhuD</i>	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	1028, 1030, 1031
<i>fhuE</i>	Outer membrane receptor for ferric iron uptake	1749
<i>fhuF</i>	Ferric hydroxamate transport	704

Category and gene	Gene product description ^a	Reference(s)
<i>fiu</i>	Ferric iron uptake, outer membrane protein	380
<i>ftn</i>	Ferritin	808
<i>kch</i>	Putative potassium channel protein	1320
<i>kdpA</i>	High-affinity potassium transport system; probable K ⁺ -stimulated ATPase	39, 1557
<i>kdpB</i>	High-affinity potassium transport system	39, 1557
<i>kdpC</i>	High-affinity potassium transport system	39, 1557
<i>kdpF</i>	Inner membrane protein in potassium transport	39
<i>kefB</i>	K ⁺ efflux; NEM-activable K ⁺ /H ⁺ antiporter	500
<i>kefC</i>	K ⁺ efflux; NEM-activable K ⁺ /H ⁺ antiporter	500, 1369
<i>kup</i>	Low-affinity potassium transport system	196, 1761
<i>mgt</i>	Mg ²⁺ transport, system II	590
<i>molR</i>	Regulation of <i>mod</i> locus governing molybdate transport	765, 1094
<i>nhaA</i>	Na ⁺ /H antiporter, pH dependent	1544, 1545, 1950
<i>nhaB</i>	Na ⁺ /H ⁺ antiporter, pH independent	1544, 1545, 1984
<i>nhaR</i>	Activator of <i>nhaA</i>	1484, 1607
<i>nikA</i>	Periplasmic binding protein for nickel	1398, 2197
<i>nikB</i>	Transport of nickel, membrane protein	1398, 2197
<i>nikC</i>	Transport of nickel, membrane protein	1398
<i>nikD</i>	Transport of nickel, ATP-binding protein	1398
<i>nikE</i>	Transport of nickel, ATP-binding protein	1398
<i>panF</i>	Sodium/pantothenate symporter	875, 1635
<i>putP</i>	Major sodium/proline symporter	375, 701, 1635
<i>rsgA</i>	Ferritin-like protein	808, 874
<i>tonB</i>	Energy transducer; uptake of iron and cyanocobalamin; sensitivity to phages, colicins	214, 887, 1847
<i>trkA</i>	Transport of potassium	195, 469, 1763
<i>trkD</i>	Kup protein, transport of potassium, cesium	196, 1761
<i>trkE</i>	Transport of potassium	469
<i>trkG</i>	Potassium uptake	469
<i>trkH</i>	Potassium uptake	469
<i>trpP</i>	Low-affinity tryptophan-specific permease	485
3. Carbohydrates, organic acids, and alcohols		
<i>alu</i>	5-Aminolevulinic acid uptake	2066
<i>araE</i>	Low-affinity L-arabinose transport system; L-arabinose proton symport	227, 736, 1210
<i>araF</i>	L-arabinose-binding protein	789, 2068
<i>araG</i>	High-affinity L-arabinose transport system	789
<i>araH</i>	High-affinity L-arabinose transport system; membrane protein	789
<i>arbT</i>	Phosphorylation and transport of arbutin; cryptic	1507
<i>ascF</i>	Phosphotransferase enzyme II (<i>asc</i>), cryptic, transports specific β-glucosides	696
<i>bglF</i>	β-Glucoside transport, PEP-dependent enzyme II, part of cryptic operon	209, 1768, 1769
<i>bymA</i>	Bypass of maltose permease at <i>malB</i>	777
<i>cbt</i>	Dicarboxylate-binding protein	1176
<i>celA</i>	PEP-dependent phosphotransferase enzyme IV for cellobiose, arbutin, and salicin	1508, 1636
<i>celB</i>	PEP-dependent phosphotransferase enzyme II for cellobiose, arbutin, and salicin	1508, 1636
<i>celC</i>	PEP-dependent phosphotransferase enzyme III for cellobiose, arbutin, and salicin	695, 1636
<i>citA</i>	Cryptic gene of citrate transport system	693
<i>citB</i>	Cryptic gene of citrate transport system	693
<i>cmtA</i>	PEP-dependent phosphotransferase enzyme IIBC for mannitol	1878
<i>cmtB</i>	PEP-dependent phosphotransferase enzyme IIA for mannitol	1878
<i>crr</i>	Glucose phosphotransferase enzyme III ^{Glc}	438, 695, 1716
<i>cup</i>	Uptake of carbohydrates	1217
<i>dctA</i>	Uptake of C ₄ -dicarboxylic acids	1175
<i>dctB</i>	Uptake of C ₄ -dicarboxylic acids	1175
<i>dcuA</i>	Anaerobic dicarboxylic acid uptake	1845, 1846
<i>dcuB</i>	Anaerobic dicarboxylate transport	1845, 1846
<i>dgoT</i>	Galactonate transport	356
<i>dgsA</i>	Enzyme IIA/IIB of phosphotransferase system	1666
<i>exuT</i>	Transport of hexuronates	1407
<i>fadL</i>	Transport of long-chain fatty acids; sensitivity to phage T2	162, 163, 1720
<i>fruA</i>	Fructose phosphotransferase enzyme II	1467, 1585
<i>fruB</i>	Fructose phosphotransferase enzyme III	608
<i>fruF</i>	Phosphohistidinoprotein-hexose phosphotransferase, fructose specific	608, 673, 1467
<i>frvA</i>	Fructose-like phosphotransferase enzyme IIA; cryptic	1634
<i>frvB</i>	Fructose-like phosphotransferase enzyme IIBC; cryptic	1634
<i>frvR</i>	Putative <i>frv</i> operon regulatory protein	1634
<i>fucP</i>	Fucose permease	298, 299
<i>gabP</i>	Transport of γ-aminobutyrate	1410
<i>galP</i>	Galactose permease	1655

Category and gene	Gene product description ^a	Reference(s)
<i>gatA</i>	Galactitol-specific enzyme IIA of phosphotransferase system	1106–1108
<i>gatB</i>	Galactitol-specific enzyme IIB of phosphotransferase system	435, 1108
<i>gatC</i>	Galactitol-specific enzyme IIC of phosphotransferase system	1106, 1108
<i>glpF</i>	Facilitated diffusion of glycerol	1942, 2136
<i>glpT</i>	<i>sn</i> -Glycerol-3-phosphate permease	495, 1080
<i>glvB</i>	Arbutin-like phosphotransferase enzyme type IIB	1634
<i>glvC</i>	Arbutin-like phosphotransferase enzyme type IIC	1634
<i>glvG</i>	Probable 6-phospho- β -glucosidase	1634
<i>gntS</i>	Second system for transport and possible phosphorylation of gluconate	87, 336
<i>gntT</i>	High-affinity transport of gluconate	519, 1382
<i>gutA</i>	D-Glucitol (sorbitol)-specific enzyme II of phosphotransferase system	2214
<i>gutB</i>	D-Glucitol (sorbitol)-specific enzyme II of phosphotransferase system	695, 2214
<i>kdgT</i>	2-Keto-3-deoxy-D-gluconate transport system	1228
<i>kgtP</i>	α -Ketoglutarate permease	1802
<i>lacY</i>	Galactoside permease (M protein)	149, 227, 922
<i>lamB</i>	Phage lambda receptor protein; maltose high-affinity uptake system	566, 1193
<i>lctP</i>	L-Lactate permease	458, 459
<i>malE</i>	Periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis	410, 417, 788
<i>malF</i>	Maltose transport; cytoplasmic membrane protein	403, 410, 417
<i>malG</i>	Active transport of maltose and maltodextrins	403, 410, 417
<i>malK</i>	Maltose permeation	418, 1630, 1639
<i>malX</i>	Phosphotransferase enzyme II, maltose and glucose specific	1629
<i>manX</i>	Mannose phosphotransferase system, protein II-A (III)	514, 515, 1913
<i>manY</i>	Mannose phosphotransferase system: Pel protein II-P; penetration of phage lambda	514, 515, 1913
<i>manZ</i>	Mannose phosphotransferase system, enzyme IIB (IIM)	514, 515, 1913
<i>melB</i>	Melibiose permease II	1575, 1667, 2252
<i>mglA</i>	Methylgalactoside transport and galactose taxis, cytoplasmic membrane protein	778
<i>mglB</i>	Galactose-binding protein; receptor for galactose taxis	778, 1772
<i>mglC</i>	Methylgalactoside transport and galactose taxis	778
<i>mglD</i>	Regulator for methylgalactoside transport	1660
<i>mglR</i>	<i>mgl</i> regulator	590
<i>mtlA</i>	Mannitol-specific enzyme II of phosphotransferase system	1566, 1878, 1928
<i>ptsG</i>	Glucosephosphotransferase enzyme II	246, 1700, 1711
<i>ptsH</i>	Phosphohistidinoprotein-hexose phosphotransferase, HPr	246, 438, 1700
<i>ptsI</i>	PEP-protein phosphotransferase system enzyme I	438, 700, 1700
<i>rbsA</i>	D-Ribose high-affinity transport system; membrane-associated protein	244
<i>rbsB</i>	D-Ribose periplasmic binding protein	154, 669
<i>rbsC</i>	D-Ribose high-affinity transport system; membrane-associated protein	122
<i>rbsD</i>	D-Ribose high-affinity transport system; membrane-associated protein	122
<i>rhaT</i>	Rhamnose transport	96, 1975
<i>shiA</i>	Shikimate and dehydroshikimate permease	1548
<i>treB</i>	PEP:CHO phosphotransferase system enzyme II, trehalose specific	997, 1919
<i>ugpA</i>	<i>sn</i> -Glycerol 3-phosphate transport system, integral membrane protein	241, 1479, 1926
<i>ugpB</i>	<i>sn</i> -Glycerol 3-phosphate transport system; periplasmic binding protein	241, 1479
<i>ugpC</i>	<i>sn</i> -Glycerol 3-phosphate transport system, permease	241, 1479
<i>ugpE</i>	<i>sn</i> -Glycerol 3-phosphate transport system, integral membrane protein	241, 1479
<i>uhpA</i>	Response regulator, positive activator of <i>uhpT</i> transcription (sensor, <i>uhpB</i>)	855
<i>uhpB</i>	Regulator of <i>uhpT</i> , sensor for histidine protein kinase	854, 855
<i>uhpC</i>	Regulator of <i>uhpT</i>	854, 855
<i>uhpR</i>	Regulation of hexose phosphate transport; receptor for glucose 6-phosphate	462, 926
<i>uhpT</i>	Hexose phosphate transport protein	43
<i>xylE</i>	Xylose-proton symport	227, 414
<i>xylF</i>	Xylose binding protein transport system	8, 736, 1861
<i>xylG</i>	Putative xylose transport, ATP-binding protein	1554, 1861
<i>xylH</i>	Putative xylose transport, membrane component	1861
<i>xylU</i>	D-Xylose uptake protein	736, 1054
4. Nucleosides, purines, and pyrimidines		
<i>codB</i>	Cytosine transport	396
<i>nupC</i>	Transport of nucleosides, except guanosine	1367
<i>nupG</i>	Transport of nucleosides	1366, 2146
<i>pnuC</i>	Membrane protein required for NMN transport	554
<i>purP</i>	High-affinity adenine transport	254
<i>tsx</i>	Nucleoside channel; receptor of phage T6 and colicin K	217, 575, 622
<i>uraA</i>	Uracil transport, ABC transporter	94
5. Anions		
<i>cysA</i>	Sulfate permease A protein; chromate resistance	1706, 1842
<i>cysP</i>	Thiosulfate-binding protein	799

Category and gene	Gene product description ^a	Reference(s)
<i>cysT</i>	Sulfate, thiosulfate transport system	1842
<i>cysW</i>	Sulfate permease W protein	1842
<i>cysZ</i>	Required for sulfate transport	224
<i>modA</i>	Molybdate uptake	735, 765, 1657
<i>modB</i>	Molybdate uptake	765, 1657, 1789
<i>modC</i>	Molybdate uptake	900, 1657, 1789
<i>narK</i>	Transport of nitrate	436
<i>pit</i>	Low-affinity phosphate transport	501
<i>pstA</i>	High-affinity phosphate-specific transport system	1618
<i>pstB</i>	High-affinity phosphate-specific transport system, cytoplasmic membrane protein?	1618
<i>pstC</i>	High-affinity phosphate-specific transport system, cytoplasmic membrane component	1618
<i>pstS</i>	High-affinity phosphate-specific transport system; periplasmic phosphate-binding protein	1221
<i>sbp</i>	Periplasmic sulfate-binding protein	880
6. Other		
<i>abc</i>	ABC transporter	34
<i>abs</i>	Sensitivity and permeability to antibiotics and dyes	324
<i>betT</i>	High-affinity choline transport	53, 1070
<i>bioP</i>	Biotin transport	262, 1543
<i>btuB</i>	Receptor for transport of vitamin B ₁₂ , E colicins, and bacteriophage BF23	123, 1032, 1197
<i>btuC</i>	Vitamin B ₁₂ transport	1656
<i>btuD</i>	Vitamin B ₁₂ transport, membrane-associated protein	1656
<i>btuE</i>	Vitamin B ₁₂ transport	1656
<i>cydC</i>	Putative transport component of cytochrome <i>d</i> terminal oxidase	115, 757, 1561
<i>cydD</i>	Putative transport component of cytochrome <i>d</i> terminal oxidase, Zn sensitive	115, 757, 1561
<i>htrE</i>	Probable porin protein similar to PapC	1611
<i>mdl</i>	ATP-binding transport protein	34
<i>modD</i>	Molybdate uptake	735, 765, 1789
<i>msbA</i>	Probable ATP-binding transport protein; multicopy suppressor of <i>htrB</i>	34, 948
<i>phnC</i>	Binding protein-dependent alkylphosphonate transporter, permease component	1305, 1306, 2112
<i>phnD</i>	Binding protein-dependent alkylphosphonate transporter, periplasmic component	1305, 1306, 2112
<i>phnE</i>	Binding protein-dependent alkylphosphonate transporter, integral membrane component, cryptic in K-12	1305, 1306, 2112
B. Chaperones		
<i>cbpA</i>	Curved DNA-binding protein; functions closely related to DnaJ	2032
<i>dnaJ</i>	Chaperone with DnaK; heat shock protein	588, 1076, 1774
<i>dnaK</i>	Chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins	319, 1076, 1774
<i>hscA</i>	Member of Hsp70 protein family	966
<i>htpG</i>	Chaperone Hsp90, heat shock protein C62.5	732, 1871
<i>mopA</i>	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein	243, 620, 1644
<i>mopB</i>	Chaperone affecting head assembly of phages T4 and lambda	1079
C. Cell division		
<i>cafA</i>	Bundles of cytoplasmic filaments	1457
<i>cfcA</i>	Frequency of cell division	1419
<i>dicA</i>	Regulator of <i>dicB</i>	120
<i>dicB</i>	Inhibition of cell division	120, 261, 1361
<i>dicC</i>	Regulator of <i>dicB</i>	120
<i>fcsA</i>	Cell division; septation	1042
<i>fic</i>	Induced in stationary phase, recognized by <i>rpoS</i> , affects cell division	1014, 2044
<i>ftsA</i>	Cell division protein, complexes with FtsZ	385, 456
<i>ftsE</i>	Cell division membrane protein	628, 633
<i>ftsH</i>	Inner membrane protein essential for cell division, putative ATPase, chaperone	18, 746, 2003
<i>ftsI</i>	Septum formation; penicillin-binding protein 3; peptidoglycan synthetase	118, 119, 639
<i>ftsJ</i>	Cell division protein	1448, 2003
<i>ftsL</i>	Cell division protein; ingrowth of wall at septum	456, 689
<i>ftsN</i>	Essential cell division protein	388
<i>ftsQ</i>	Cell division protein; ingrowth of wall at septum	385, 2073
<i>ftsW</i>	Cell division; membrane protein involved in shape determination	835
<i>ftsX</i>	Cell division membrane protein	628, 633, 634
<i>ftsY</i>	Cell division membrane protein	628, 633, 634
<i>ftsZ</i>	Cell division; forms circumferential ring; GTP-binding protein and GTPase	1202, 1356, 2086
<i>mbrA</i>	Coupling of cell division and DNA replication	2014, 2015
<i>mbrB</i>	Link between growth rate and partitioning chromosomes	2014, 2015
<i>mbrC</i>	Partitioning chromosomes	2014, 2015

Category and gene	Gene product description ^a	Reference(s)
<i>minB</i>	Formation of minute cells containing no DNA; complex locus, position of division septum	1360
<i>minC</i>	Cell division inhibitor, inhibits <i>ftsZ</i> ring formation	146, 421, 422
<i>minD</i>	Cell division inhibitor, a membrane ATPase, activates <i>minC</i>	420–422
<i>minE</i>	Cell division topological specificity factor, reverses <i>min</i> inhibition	421, 422, 456
<i>mukB</i>	Cell division protein involved in chromosome partitioning	768, 770, 1412
<i>mukC</i>	Cell division and chromosome partitioning	770
<i>mukD</i>	Cell division and chromosome partitioning	770
<i>pcsA</i>	Cell division; chromosome segregation	1042
<i>sdiA</i>	Regulator of transcription of <i>ftsQAZ</i> gene cluster	2110
<i>sefA</i>	Septum formation	1430
<i>sfiC</i>	Cell division inhibition; at locus of element e14	881, 1214, 1215
<i>sulA</i>	Suppressor of <i>lon</i> ; inhibits cell division and <i>ftsZ</i> ring formation	146, 441
<i>tig</i>	Trigger factor; a molecular chaperone involved in cell division	684
<i>tolC</i>	Outer membrane channel; specific tolerance to colicin E1; segregation of daughter chromosomes	133, 456, 770
<i>weeA</i>	Cell elongation	428, 429
D. Chemotaxis and mobility		
<i>cheA</i>	Chemotaxis protein	610, 1346, 1941
<i>cheB</i>	Response regulator for chemotaxis (<i>cheA</i> sensor); protein methyltransferase	200, 1200, 1903
<i>cheR</i>	Response regulator for chemotaxis; protein glutamate methyltransferase	1707
<i>cheW</i>	Positive regulator of CheA protein activity	610, 1169, 1277
<i>cheY</i>	Chemotaxis protein transmits chemoreceptor signals to flagellar motors	201, 537, 1346
<i>cheZ</i>	Chemotactic response; CheY protein phosphatase; antagonist of CheY as switch regulator	178, 803, 1909
<i>motA</i>	Proton conductor component of motor; no effect on switching	166, 167, 1912
<i>motB</i>	Enables flagellar motor rotation, linking torque machinery to cell wall; no effect on switching	166, 168, 1912
<i>tap</i>	Methyl-accepting chemotaxis protein IV, peptide receptor	1230
<i>tar</i>	Methyl-accepting chemotaxis protein II, chemoreceptor for aspartate	594, 1095
<i>trg</i>	Methyl-accepting chemotaxis protein III, ribose receptor	252, 2209, 2210
<i>tsr</i>	Methyl-accepting chemotaxis protein I, serine receptor	606, 1169
E. Protein and peptide secretion		
<i>dppA</i>	Dipeptide transport protein	5, 1463
<i>excD</i>	Export of periplasmic proteins	1086
<i>expA</i>	Expression of a group of export proteins	402
<i>ffh</i>	Protein transport	1537
<i>hlyB</i>	ABC protein translocator, exports hemolysin	619, 1025, 1027
<i>hlyD</i>	With HlyB, protein translocator for hemolysin	1026, 1892, 2262
<i>lepB</i>	Leader peptidase (signal peptidase I)	151, 161, 1236
<i>lspA</i>	Prolipoprotein signal peptidase (SPaseII)	1368
<i>msyB</i>	Acidic protein suppresses mutants lacking function of protein export	2031
<i>oppA</i>	Oligopeptide transport; periplasmic binding protein	54, 952, 955
<i>oppB</i>	Oligopeptide transport	55, 1501
<i>oppC</i>	Oligopeptide transport	55
<i>oppD</i>	Oligopeptide transport	55
<i>oppE</i>	Oligopeptide transport	55
<i>oppF</i>	Oligopeptide transport, ATP hydrolysis	55
<i>prlF</i>	Protein export	979, 1859
<i>sapF</i>	Peptide transport, ABC family of transporters	94
<i>secA</i>	Protein secretion, ATP hydrolysis	218, 318, 1829
<i>secB</i>	Protein export; molecular chaperone	341, 713, 1045
<i>secD</i>	Protein secretion; membrane protein	1257, 1555, 1927
<i>secE</i>	Inner membrane protein, protein secretion (with <i>secY</i>)	237, 1420, 1927
<i>secF</i>	Membrane protein, protein secretion function	1257, 1717, 1927
<i>secG</i>	Protein export; membrane protein	1421
<i>secY</i>	Membrane protein, protein secretion (with <i>secE</i>)	237, 1420, 1943
<i>ssaE</i>	Suppression of <i>secA</i> mutation	1460
<i>ssaG</i>	Suppression of <i>secA</i> mutation	1460
<i>ssaH</i>	Suppression of <i>secA</i> mutation	1460
<i>ssyA</i>	Suppression of <i>secY</i> mutation	1460
<i>ssyB</i>	Suppression of <i>secY</i> mutation	1460
<i>ssyD</i>	Suppression of <i>secY</i> mutation	1460
F. Osmotic adaptation		
<i>betA</i>	Choline dehydrogenase, a flavoprotein	53, 1070
<i>betB</i>	NAD ⁺ -dependent betaine aldehyde dehydrogenase	53, 521, 1070
<i>betI</i>	Probably repressor of <i>bet</i> genes	53, 1070
<i>mdoA</i>	Membrane-derived oligosaccharides; component of glucosyltransferase	611, 1063

Category and gene	Gene product description ^a	Reference(s)
	system	
<i>mdoB</i>	Membrane-derived oligosaccharides; phosphoglycerol transferase I activity	611, 1063
<i>mdoG</i>	Periplasmic membrane-derived oligosaccharide synthesis	1063
<i>mdoH</i>	Membrane glycosyltransferase, membrane-derived oligosaccharide synthesis	1063
<i>osmB</i>	Osmotically inducible lipoprotein	738
<i>osmC</i>	Osmotically inducible protein	686
<i>osmY</i>	Hyperosmotically inducible periplasmic protein	2236
<i>otsA</i>	Trehalose-6-phosphate synthase	738, 921, 1919
<i>otsB</i>	Trehalose-6-phosphate phosphatase, biosynthetic	738, 921, 1919
<i>otsR</i>	Regulation of <i>ots</i>	997
<i>proX</i>	High-affinity transport system for glycine betaine and proline	276, 407, 1908
<i>treA</i>	Trehalase, periplasmic	685, 738, 1919
<i>treR</i>	Repressor of <i>treABC</i>	94
G. Detoxification		
<i>ahpC</i>	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	1914
<i>ahpF</i>	Alkyl hydroperoxide reductase, F52a subunit; detoxification of hydroperoxides	1914
<i>katC</i>	Regulation of catalase activity	2083
<i>katE</i>	Catalase hydroperoxidase HPII(III)	6, 416, 2083
<i>katG</i>	Catalase-peroxidase hydroperoxidase HPI(I)	6, 1182, 1359
<i>sodA</i>	Superoxide dismutase, manganese	141, 786, 1586
<i>sodB</i>	Superoxide dismutase, iron	142, 530, 1586
<i>thdC</i>	Detoxification of furans and thiophenes	20, 917
<i>thdD</i>	Detoxification of furans and thiophenes	20, 917
<i>thdF</i>	GTP-binding protein in thiophene and furan oxidation	19, 249
H. Cell killing		
<i>cma</i>	Colicin M	711
<i>gef</i>	Polypeptide destructive to membrane potential	1570–1572
<i>gefL</i>	Leader peptide of Gef	1572
<i>kicA</i>	Killing protein	533
<i>kicB</i>	Suppressor of killing protein	533
<i>relF</i>	Polypeptide destructive to membrane potential	430, 621, 1570
V. OTHER		
A. Phage-related functions and prophage		
<i>bfm</i>	Phage BF23 multiplication	1830
<i>dicF</i>	RNA of 65 nucleotides, cell division inhibitor of Kim prophage	528, 1981
<i>esp</i>	Site for efficient packaging of phage T1	472
<i>fipB</i>	Morphogenesis of phage F1	1186
<i>fipC</i>	Morphogenesis of phage F1	1186
<i>gprA</i>	Replication of certain lambdoid phages	1443, 1730
<i>gprB</i>	Replication of certain lambdoid phages	1443, 1730
<i>grpE</i>	Phage lambda replication; host DNA synthesis; heat shock protein; protein repair	588, 1076, 1774
<i>hfq</i>	Host factor I for bacteriophage Q β replication, a growth-related protein	929, 930
<i>lit</i>	Phage T4 late gene expression; at locus of e14 element	756, 944
<i>msp</i>	Sensitivity or resistance of male strains to male-specific phages R17 and f2	255
<i>mul</i>	Mutability of UV-irradiated phage lambda	2089
<i>nfrA</i>	Bacteriophage N4 receptor, outer membrane protein	978, 980, 981
<i>nfrB</i>	Bacteriophage N4 receptor, outer membrane protein	978, 980, 981
<i>nfrC</i>	Bacteriophage N4 adsorption protein, cytoplasmic	978
<i>nfrD</i>	Bacteriophage N4 adsorption protein	978, 980
<i>nmpC</i>	Outer membrane porin protein; locus of <i>qsr</i> prophage	174
<i>ogr</i>	Regulator of late transcription in phage P2; part of cryptic P2 prophage	1100, 1854
<i>phxB</i>	Adsorption of ϕ X174	1733
<i>pin</i>	Inversion of adjacent DNA; at locus of e14 element	1056
<i>qin</i>	Cryptic lambdoid phage	1144
<i>qsr</i>	Defective prophage <i>qsr'</i>	1157
<i>racC</i>	Defective prophage <i>rac</i> ; contains <i>recE</i> and <i>oriJ</i>	1144
<i>rap</i>	Growth of phage lambda	1525
<i>tnm</i>	Transposition of Tn9 and other transposons; development of phage Mu	840, 1174
B. Colicin-related functions		
<i>cet</i>	Tolerance to colicin E2	477
<i>cvpA</i>	Required for colicin V production	527
<i>tolA</i>	Membrane-spanning protein, required for outer membrane integrity	128, 1115, 1117
<i>tolB</i>	Tolerance to colicins E2, E3, A, and K; leakage of periplasmic proteins	1116, 2125
<i>tolD</i>	Tolerance to colicins E2 and E3; ampicillin resistance	512
<i>tolE</i>	Tolerance to colicins E2 and E3; ampicillin resistance	512

Category and gene	Gene product description ^a	Reference(s)
<i>tolI</i>	Tolerance to colicins Ia and Ib	265
<i>tolJ</i>	Resistance to colicins L, A, and S4; partial resistance to colicins E and K	411
<i>tolM</i>	Mutant phenotype: high-level tolerance to colicin M	710
<i>tolQ</i>	Inner membrane protein, membrane spanning, maintains integrity of cell envelope; tolerance to group A colicins	213, 938, 2072
<i>tolR</i>	Inner membrane protein, maintains integrity of cell envelope; tolerance to group A colicins	494, 938, 1363
<i>tolZ</i>	Tolerance to colicins E2, E3, D, 1a, and 1b; generation of chemical proton gradient	1259, 2125
C. Plasmid-related functions		
<i>chpAI</i>	Suppressor of growth inhibitor ChpAK	1254
<i>chpAK</i>	Growth inhibitor	1254
<i>chpBI</i>	Suppressor of growth inhibitor ChpBK	1254
<i>chpBK</i>	Growth inhibitor	1254
<i>mafA</i>	Maintenance of F-like plasmids	2091
<i>mafB</i>	Maintenance of F-like plasmids	2091
<i>mprA</i>	Regulator of plasmid <i>mcrB</i> operon (microcin B17 synthesis)	430, 431
D. Drug/analog sensitivity		
<i>acrB</i>	Sensitivity to acriflavine	1204
<i>acrC</i>	Sensitivity to acriflavine	1388
<i>ampC</i>	β -lactamase; penicillin resistance	561
<i>ampD</i>	Regulates <i>ampC</i>	1155
<i>ampE</i>	Regulates <i>ampC</i>	1155
<i>ampG</i>	Regulates β -lactamase synthesis	1156
<i>azaA</i>	Resistance or sensitivity to azaserine	2163
<i>azaB</i>	Resistance or sensitivity to azaserine	2163
<i>bacA</i>	Bacitracin resistance; possibly phosphorylates undecaprenol	259
<i>bcr</i>	Bicyclomycin resistance protein; transmembrane protein	131
<i>can</i>	Canavanine resistance	280
<i>cmlA</i>	Resistance or sensitivity to chloramphenicol	113
<i>dvl</i>	Sensitivity to sodium dodecyl sulfate and toluidine blue plus light	2095
<i>emrA</i>	Multidrug resistance efflux pump	582, 1126
<i>emrB</i>	Multidrug resistance efflux pump	582, 1126
<i>emrE</i>	Membrane protein, methyl viologen resistance	1343
<i>eryD</i>	Erythromycin growth dependence	2156
<i>inn</i>	Susceptibility to mutagenesis by nitrosoguanidine	1701
<i>ksgA</i>	S-Adenosylmethionine-6- <i>N'</i> , <i>N'</i> -adenosyl (rRNA) dimethyltransferase; kasugamycin resistance	2058
<i>ksgB</i>	Second-step (high-level) resistance to kasugamycin	555
<i>ksgC</i>	Kasugamycin resistance; affects ribosomal protein S2	2240
<i>ksgD</i>	Kasugamycin resistance	555
<i>lev</i>	Resistance to levallorphan	391
<i>linB</i>	High-level resistance to lincomycin	815
<i>lytA</i>	Tolerance to β -lactams; autolysis defective?	712, 1827
<i>marA</i>	Multiple antibiotic resistance; transcriptional activator of defense systems	67, 690
<i>marB</i>	Multiple antibiotic resistance protein	67, 337, 587
<i>marR</i>	Multiple antibiotic resistance protein; repressor of <i>mar</i> operon	67, 337
<i>mng</i>	Resistance or sensitivity to manganese	1838
<i>nalB</i>	Resistance or sensitivity to nalidixic acid	702, 796, 797
<i>nalD</i>	Penetration of nalidixic acid through outer membrane	798
<i>neaB</i>	Resistance to neamine	434
<i>nek</i>	Resistance to neomycin, kanamycin, and other aminoglycoside antibiotics	812
<i>nfnA</i>	Sensitivity to nitrofurantoin	1745, 1799
<i>nfnB</i>	Sensitivity to nitrofurantoin	1745, 1799
<i>nfsA</i>	Nitrofuran reductase I activity	1268, 1345
<i>nfsB</i>	Nitrofuran reductase I activity	1268, 1345
<i>nov</i>	Sensitivity to novobiocin	1613
<i>psu</i>	Pleiotropic suppressor; resistance to oxolinic acid	508
<i>sbmA</i>	Sensitivity to microcin B17, possibly envelope protein	1084, 2237
<i>semA</i>	Sensitivity to microcin E492	1595
<i>sloB</i>	Low growth rate; tolerance to amidinopenicillin and nalidixic acid	1185
<i>strC</i>	Low-level streptomycin resistance	1662
<i>tehA</i>	Tellurite resistance	1977
<i>tehB</i>	Tellurite resistance	1977
<i>tlnA</i>	Resistance or sensitivity to thiolutin	1844
E. Radiation sensitivity		
<i>ior</i>	Radiation sensitivity, particularly gamma rays; recombination ability decreased	518

Category and gene	Gene product description ^a	Reference(s)
<i>radA</i>	Sensitivity to gamma and UV radiation and methyl methanesulfonate	452
<i>radC</i>	Sensitivity to radiation	531, 532
<i>ras</i>	Sensitivity to UV and X rays	2099
<i>rer</i>	Resistance to UV and gamma radiation	1885
F. Adaptations and atypical conditions		
<i>crg</i>	Cold-resistant growth	963
<i>cspA</i>	Cold shock protein 7.4, transcriptional activator of <i>hns</i>	641, 910, 1099
<i>cspB</i>	Cold shock protein; may affect transcription	910, 1099
<i>dps</i>	Global regulator, starvation conditions	37
<i>htgA</i>	Positive regulator for σ^{32} heat shock promoters, permitting growth at high temperature	419, 1329
<i>ibpA</i>	16-kDa heat shock protein A; belongs to the small heat shock (HSP20) family	31, 249
<i>ibpB</i>	16-kDa heat shock protein B; belongs to the small heat shock (HSP20) family	31, 249
<i>mscL</i>	Mechanosensitive channel	1929
<i>rdgA</i>	Dependence of growth upon <i>recA</i> gene product	572
<i>rdgB</i>	Dependence of growth and viability upon <i>recA</i> function	572
<i>uspA</i>	Universal stress protein; broad regulatory function?	1438–1440

^aAbbreviations: ABC, ATP-binding cassette; BCCP, biotin carboxyl carrier protein; CoA, coenzyme A; dsDNA, ssDNA, double-stranded DNA and single-stranded DNA; FAD, flavin adenine dinucleotide; FGAR, *N*-formylglycinamide ribonucleotide-5'-phosphate; FMN, flavin mononucleotide; NEM, *N*-ethylmaleimide; NMN, nicotinamide mononucleotide; PEP, phosphoenolpyruvate.

References of genes that were listed in an earlier compilation of gene products (1652) are updated in Table 2 when possible. The choice of references in Table 2 has some arbitrary features. In the previous compilation of gene products of *E. coli* (1652), early papers on a gene product were cited as well as more recent references. In Table 2 in this chapter, the accent is on more recent work on each gene product. Citations were limited arbitrarily to three per entry. It was not possible in any reasonable time frame to become well enough informed to cite the most meritorious work for each entry; instead, citation to some of the more recent papers on each entry is used. Earlier literature should be accessible by tracing back citations. Genes and gene products that have not received attention in recent years still carry their original citations. The citations in Table 2 are intended to help the reader enter the literature, not to make any judgment on the priority or scientific value of any paper cited or omitted.

Table 2 shows only one assignment to a category of function for each gene product, even though some gene products play multiple roles in the cell. For instance, in metabolism, the acetyl kinase enzyme functions in aerobic catabolism of acetate as a carbon source, but it also is an important enzyme of anaerobic fermentation. A protein kinase or an adenylation enzyme can be classified either as an enzyme that modifies proteins or as a regulator. Likewise, a porin can be classified either as a transport entity or as a part of a membrane component of the cell structure. A phosphotransferase enzyme can be classified either as a transport entity or as an enzyme of phosphorus metabolism. In each such case, multiple assignments of functional categories have been made and all are provided in the electronic version of the table. However, in the printed version of Table 2 here, one physiological category has been chosen for each gene product and the entries are ordered by that one category of cellular function. The electronic version of the data will be useful to reveal other functions and also will permit views of many other aspects of the data. To this end, the tabulation of the data in electronic format is sortable for instance alphabetically by gene, alphabetically by gene type, numerically by EC number, and so forth. The data is in a database for PC computers called GenProtEc, available by anonymous ftp from mbl.edu as /pub/ecoli.zip or by mail on an MS-DOS disk from M. Riley on request.

Besides providing a list of the presently known gene products of *E. coli* and entries to the literature for each gene product, Table 2 contains information on how many currently known gene products carry out each kind of functions. Some of this information is shown in Table 1 and is summarized in Tables 3 and 4. The number of gene products assigned to each physiological category is shown in Table 1. These are grouped and summarized in Table 3. Small-molecule metabolism involves 435 genes or 22.9% of the presently known whole. Large-molecule metabolism involves an even larger fraction: 643 genes or 33.9% of the whole. Of the 370 genes assigned to cell processes, transport involves 253 genes, by far the largest component.

Transport functions alone make up 13.3% of the whole. Some of the miscellaneous group are genes concerned with phages and plasmids; others, such as the many heat shock proteins or drug resistance factors, are poorly characterized gene products that will be better delineated with further study.

The number of *E. coli* gene products that fall in each major category of type of gene product is shown in Table 4. In this view, gene products are classified as either an enzyme, a regulator, a transporter, a protein factor, a membrane component, or an RNA molecule. Assignment of the type of gene product could be made for only 1,616 of the 1,897 genes. The rest are too vaguely defined at present to know what the gene product is. Of the 1,616 gene products, enzymes of metabolism constitute the major fraction. The enzymes and proteins of transport functions and regulatory function constitute two other large categories. The number of gene products in the category of structural elements of the cell is relatively small compared with metabolic functions. This is caused partly by the fact that many membrane components have roles in cellular processes such as transport or cell division and thus were not listed primarily as structural elements and partly by the fact that the enzymes of synthesis of macromolecular components of the cell structure such as peptidoglycans or phospholipids are not classified as structural elements but rather as metabolic functions. Also, we recognize that we still have much to learn about the genetic basis of the structure of the cell and the process of assembly of structural components.

TABLE 3 Distribution of *E. coli* gene products among physiological categories

Category	No. of genes
Small molecules	
Degradation and energy metabolism	316
Central intermediary metabolism	78
Broad regulatory functions	51
Biosynthesis	
Amino acids, polyamines	122
Purines, pyrimidines, nucleosides, and nucleotides	60
Cofactors and prosthetic groups	98
Fatty acids	26
Macromolecules	
Synthesis and modification	406
Degradation	69
Cell envelope	168
Cell processes	
Transport	253
Other, e.g., cell division, chemotaxis, mobility, osmotic adaptation, detoxification, and cell killing	118
Miscellaneous	107
Total	894

TABLE 4 Distribution types of gene products among classifiable *E. coli* genes^a

Type of gene product	No. of genes
Enzymes, leader sequences	
Transport	256
Regulators	217
RNA	107
Structural components	122
Factors	62
Carriers	8
Total 1	616

^aNot including 279 genes known only by mutant phenotype.

As the remainder of the *E. coli* genes are sequenced and function is assigned to the gene products, the proportions of cellular roles will probably change. More functions of cell structure and its assembly probably will be added. Possibly, more global regulatory mechanisms will surface. There is room for

many more aspects of the life process in the unsequenced portion of the *E. coli* genome. Even in the parts already sequenced, the Blattner group has found many non-open reading frames, that is, sequences that do not constitute transcribable genes as we presently understand them. These sequences have no known shape or function and have been dubbed grey holes (395). After we have unlocked all their secrets, the distribution of functions of all *E. coli* gene products may change from what we are seeing today.

RELATIONSHIPS AMONG GENES, ENZYMES, AND REACTIONS

In its time, the historic one gene-one enzyme hypothesis illuminated the relationship of genes to cellular function (114). Later, the word “cistron” was introduced to define the genetic element coding for a gene product that is not subdividable by the *trans* complementation test (134). The cistron emphasized the basic genetic element as the coding entity for a polypeptide chain rather than the genetic unit underlying a functional entity such as an enzyme. Today, with many genes, enzymes, and reactions characterized in *E. coli*, we appreciate the many types of relationships that exist in reality between genes and enzymes and the reactions they catalyze.

In many cases, one gene encodes one polypeptide, which catalyzes one biochemical reaction. However, these relationships are not always one to one to one. Figure 1 diagrams some of the other types of relationships found for reactions, enzymes, and genes in *E. coli*. In the case of isozymes such as fumarase, more than one gene and polypeptide are capable of carrying out one reaction. In a different kind of case, a single polypeptide carries out more than one reaction. Illustrating this is the FadB polypeptide, which catalyzes four separate reactions. Another kind of case is TrpD. The N-terminal part of the TrpD polypeptide associates with the TrpE polypeptide to catalyze one reaction, and the C-terminal part of TrpD catalyzes another reaction. One gene can make two polypeptides when, as in the case of the *speD* gene, the initial gene product is further processed into two nonidentical subunits. Sometimes there is confusion about the relationships of enzymes, reactions, and EC numbers. (An EC number, designated by the Enzyme Commission of the International Union of Biochemistry and Molecular Biology, represents a biochemical reaction and thus is associated with each component of a multimeric enzyme [1518].) Therefore, in the case of a multisubunit enzyme, like succinate dehydrogenase, more than one gene and one polypeptide are required to carry out the one reaction described by one EC number, in this case 1.3.99.1. Finally, levels of organization can be more complex than multimeric enzymes. Multienzyme complexes like pyruvate dehydrogenase contain more than one multimeric enzyme that work together in catalyzing a concerted set of reactions.

Because of the variable relationships between polypeptides and reactions, there are many possible relationships of genes to metabolic reactions. Analysis of mutant phenotypes and genetic complementation tests can be complicated by the variety of possible gene-enzyme-reaction relationships.

MULTIPLE ENZYMES

As is the case for isozymes, some metabolic reactions are carried out in *E. coli* by more than one enzyme. Table 5 lists examples of “multiple” proteins that catalyze the same reaction or very similar reactions. Only enzymes of metabolism of small molecules are shown. Multiple genes and enzymes also exist for metabolism of large molecules such as DNA polymerases, sigma factors, and nucleases, but these are not included in Table 5.

Why does *E. coli* contain more than one enzyme for so many reactions? Are they redundant? Do the multiple enzymes serve in the cell as backup systems in case of loss of one enzyme for a vital function? In fact, one may ask how we were able to isolate mutants lacking one enzyme if another enzyme for that reaction existed in the cell. One answer is that quite a few mutants are leaky and that leakiness in many cases is known now to be a consequence of multiple enzymes. Another answer is that the conditions under which many of the pairs of genes are expressed can differ and also the conditions under which the

two enzymes are catalytically active can differ. A list of ways that multiple enzymes for the same reaction differ from each other is given in Table 6.

This phenomenon of enzyme repetition and specialization must have the effect of extending the metabolic capabilities of *E. coli*. With genes producing a given enzyme under more than one set of conditions and with multiple enzymes being active under different conditions, the bacteria are able to address successfully a wide range of environmental conditions that require enzymes with appropriate properties to become available. For instance, the *speA* gene produces the biosynthetic arginine decarboxylase; gene expression is induced by growth in minimal media and is repressed by putrescine and spermidine. The enzyme is located in the periplasm and is inhibited by cyclic AMP (1339). The *adi* gene, on the other hand, produces the degradative arginine decarboxylase, and gene expression is induced under acid conditions and anaerobiosis. The degradative enzyme is located in the cytoplasm (1905). Another example involves the *sodA* and *sodB* genes. The *sodA* gene is induced by oxidative stress under aerobic conditions to produce a manganese-activated superoxide dismutase, whereas the *sodB* gene is expressed under both aerobic and anaerobic conditions, constitutively producing an iron-activated superoxide dismutase (786).

In terms of evolution, one can ask if multiple enzymes descended from common ancestors. If so, one might expect to see residual similarities in amino acid sequence. Comparison of sequences of the 75 pairs of isozymes for which the sequence is known for both proteins showed that 44 of 75 pairs are related by sequence, some very closely related, some less so. The other 31 pairs were not demonstrably related by sequence (Table 7). Therefore, somewhat over half of the pairs of the currently known multiple enzymes involved in small-molecule metabolism seem to be related by a common ancestor. The other half either do not share ancestry or have diverged to a point that the relationship is no longer detectable. It is possible that the pairs that are not related by sequence are examples of convergent evolution, that is, descendants of separate ancestral sequences evolving to the same function; alternatively, the gene for one of a pair of isozymes might have been acquired in the past by lateral transfer from another organism.

PROTEIN SEQUENCE RELATIONSHIPS AS A TOOL TO STUDY THE ORIGIN OF *E. COLI* GENES

In the context of evolution, we believe that many of the genes of present-day *E. coli* originated by a process of duplication of ancestral genes followed by divergence, then by further duplication of these genes, followed by more divergence, and so on (1125, 1454). The very early genes and their proteins are visualized as having broad specificity of action, which then narrowed successively in the descendants formed by duplication and divergence (896, 2234). If all descendants of all ancestral sequences still retain detectable vestiges of sequence similarity, we could expect to be able to identify all ancestral relationships and build a set of trees of evolutionary descent of all organisms that extend back to a set of unique ancestral sequences that were parents of all the genes and gene products extant today.

By examining the relationships among protein sequences within one organism, one is identifying pairs of proteins which display significant level of similarity. This is generally interpreted as a demonstration that these proteins are products of paralogous genes, i.e., homologous genes that descended from a common ancestor by duplication and divergence, according to the definitions proposed by Fitch (544), who opposed paralogy (homology in which divergence occurs after gene duplication in the same species) and orthology (divergence of homologous genes through speciation). Moreover, groups of proteins whose sequences are related could also be detected, meaning it is possible to identify present-day genes descending from shared ancestral genes (familial relationships within a genome).

We have engaged in such a study, identifying pairs and groups of *E. coli* proteins whose sequence similarities could indicate shared ancestry. Indeed, a higher percentage of all its protein sequences are available for *E. coli* than for any other organism, providing the opportunity to test for compatibility of the sequence relationships among *E. coli* proteins with accepted ideas of mechanisms of molecular evolution. *E. coli* is also the organism for which the greatest proportion of chromosomal genes

sequenced to date correspond to genes previously well characterized in terms of function of gene product and regulation. No other organism provides a better opportunity to determine how many ancestral relationships can be detected and how important the mechanism of duplication and divergence has been during the evolution of a genome and its encoded proteins than the massively sequenced *E. coli* genome does.

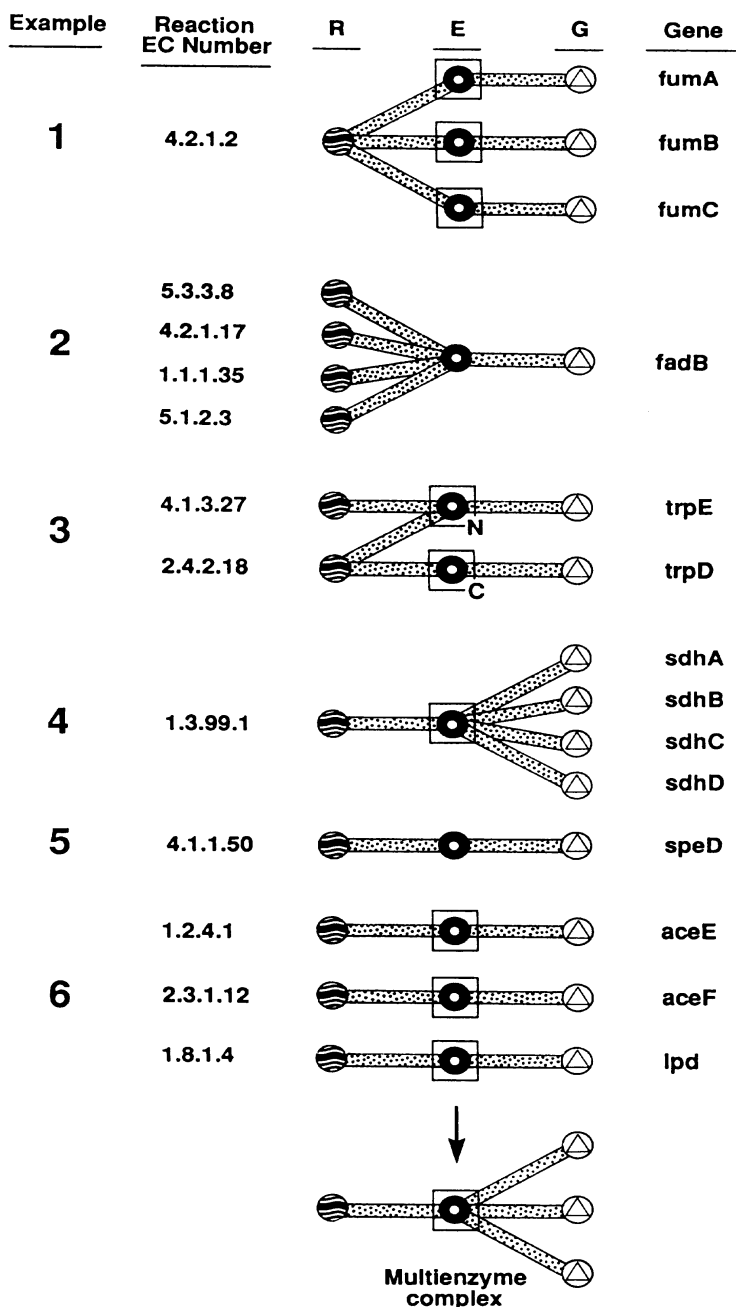


FIGURE 1 Types of gene-enzyme-reaction relationships in *E. coli*. Nodes labelled R, E, and G represent the number of unique reactions, enzymes, and genes, respectively, present in *E. coli* K-12 for each example. A boxed node for an enzyme signifies a dimer.

TABLE 6 Ways in which multiple enzymes differ from each other

Conditions of enzyme synthesis
Constitutive/inducible
Conditions of induction
Identity of inducer
Physical conditions: anaerobic/aerobic, pH
Physical properties of enzyme
Substrate specificity
Sensitivity of enzyme to inhibitors/activators
Heat stability
Subunit organization
Chemistry of enzyme
Substrate specificity
Mechanism of reaction
Cofactor requirement
Cell location
Cytoplasmic
Periplasmic
Membrane

TABLE 7 Sequence relationships between pairs of multiple enzymes

Relationship	No. of pairs
Sequences unrelated (>250 PAM)	31
Sequences related (<250 PAM)	44
Sequence not known for both	14
Total pairs	89

Our main goal being to identify descendants of past whole-gene duplications, we undertook to detect any significant similarity extending along either the whole sequence or at least long stretches of each amino acid sequence. We call this kind of similarity “extended sequence similarity,” as opposed to “local similarity,” i.e., similarity localized to domains or motifs. To do that, we analyzed all the *E. coli* K-12 chromosomal sequences longer than 100 residues present in the SwissProt database by using two different algorithms designed for extended sequence homology searches. In one study, we first used the well-known FASTA program (1518) and retained any pair displaying alignment of segments at least 100 amino acids long and with at least 20% identity. Then, from the obtained FASTA alignments, we excluded those of questionable biological significance by imposing a high threshold on the number of gaps (corresponding to a NAS [Normalized Alignment Score] of at least 180, calculated according to the method of Doolittle et al. [465]). In a subsequent study, the ALLALLDB program (Darwin package available at the CRBG server at the ETH, Zurich, Switzerland) was used to detect any match corresponding to an alignment of at least 100 amino acid residues and separated no more than 250 PAM (percent accepted mutations) units (644). These two approaches gave us very similar results (1060, 1061), which can be summarized as follows.

The 1,862 protein sequences derived from the sequences of *E. coli* chromosomal genes present in SwissProt database (version 28) (1,339 known genes and 523 open reading frames) were compared in all pairwise combinations. This operation gave us 2,329 matches separated by no more than 250 PAM units. The distribution of the PAM values was found to be Gaussian only when confined to the matches displaying identity values greater than 20% (Fig. 2). The large majority of the excess pairs with identity values less than 20% but PAM values less than 250 corresponded to the more distantly related members of large families (as defined below).

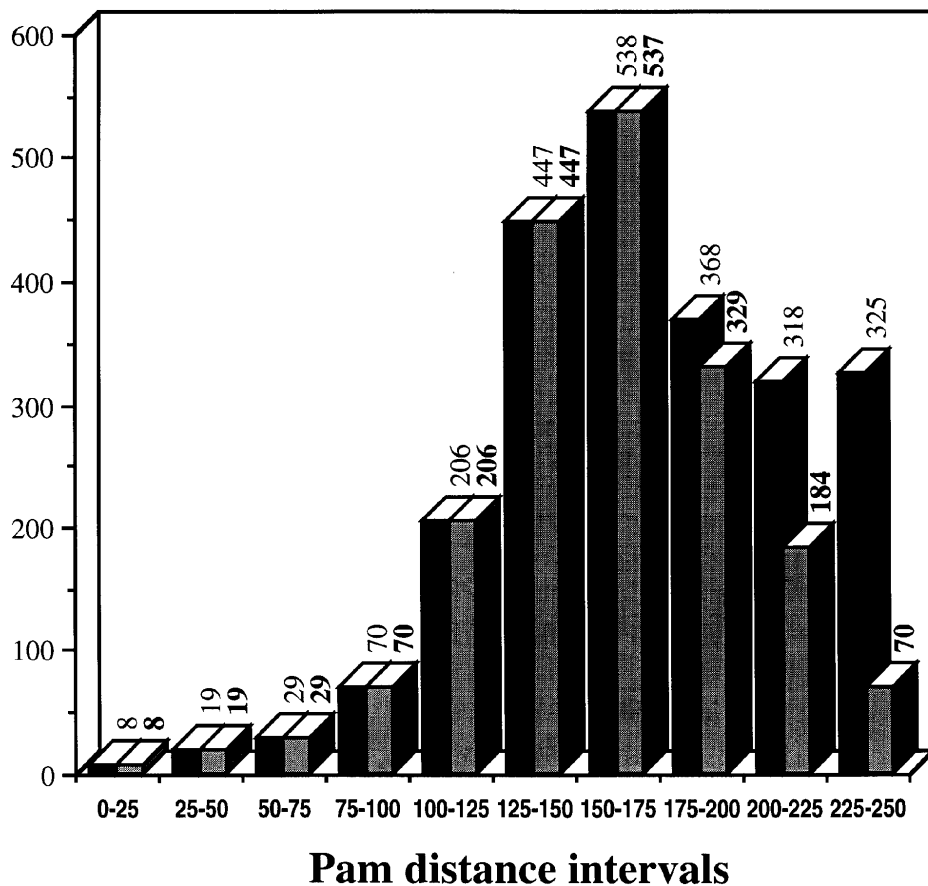


FIGURE 2 Distribution of PAM values among 2,329 pairs of protein sequences. In black is shown the number of pairs for all 2,329 matches. In grey is shown the number of pairs that have amino acid identity values greater than 20%.

The 2,329 pairs corresponded to a large set of 971 sequences (52.15% of the total) displaying similarities to at least one other sequence of this set. An alphabetical list of these 971 proteins (using the SwissProt mnemonics) that have at least one paralogous partner is given in Table 8; 786 of these sequences code for proteins the function of which is known, amounting to 58.7% of all known and sequenced genes. The rest correspond to 185 open reading frames (34.58% of all open reading frames). Thus, a significant number of the genes already sequenced—more than half—appear to be coding for paralogous proteins, and this proportion is even higher when considering only the genes known to have

a functional gene product. Interestingly, when we used only the latter, i.e., genes known to be functional, for the ALLALLDB search, we lost only 44 of them, corresponding to those found to match exclusively with an open reading frame. The high proportion, over half of sequences in alignments, is without doubt a minimum figure, since our arbitrary cutoff criteria exclude some well-known examples of proteins believed to share evolutionary ancestry but corresponding to an alignment of less than 100 amino acids. Indeed, there seem to be biologically significant relationships at even lower levels of similarity, comparable to those we detected between far remote members of the same large family. However, such putative supplementary paralogous genes will be added only when we obtain better phylogenetic arguments (see below).

TABLE 8 List of the 971 sequences displaying similarities to at least one other *E. coli* K-12 chromosomal sequence

3MG2	ASG2	CPXA	DHSA	FECD	GABP	HISP	LIPA
6PGD	ASLA	CREB	DHSB	FECE	GABT	HISX	LIVF
A	ASLB	CREC	DLDH	FECI	GALE	HMPA	LIVG
AAS	ASNB	CRED	DMSA	FENR	GALR	HNS	LIVH
AAT	ASNC	CRP	DMSB	FEPA	GALS	HOLB	LIVJ
ABC	ASPA	CSTA	DNAA	FEPB	GALU	HSLU	LIVK
ACCC	ATP6	CUTE	DNAB	FEPC	GCL	HTRA	LIVM
ACKA	ATKA	CVPA	DNAC	FEPD	GCSP	HTRB	LON
ACON	ATKB	CYBH	DNAJ	FEPE	GCST	HTRE	LPXA
ACRA	ATPA	CYDA	DNAK	FEPG	GCVA	HTRH	LRP
ACRB	ATPB	CYDB	DNLJ	FES	GENA	HYCB	LVSP
ACUA	ATPF	CYDD	DP3X	FHLA	GENF	HYCC	LYSR
ADA	BAER	CYNR	DPO1	FHUA	GLDA	HYDA	MALE
ADHE	BAES	CYOE	DPO2	FHUB	GLGB	HYDG	MALF
ADI	BARA	CYPB	DPPA	FHUC	GLGC	HYDH	MALG
AGAL	BASR	CYPH	EBGR	FHUD	GLGX	HYDN	MALI
AGP	BASS	CYSA	ECPD	FHUE	GLMS	HYPD	MALK
AK1H	BCCP	CYSB	EDD	FIMB	GLNE	HYPE	MALT
AK2H	BCR	CYSD	EFG	FIMC	GLNH	IBPA	MALY
AK3	BETT	CYSE	EFTA	FIMD	GLNP	IBPB	MALZ
ALD	BGA2	CYSH	EFTB	FIME	GLNQ	ICIA	MARA
ALKH	BGAL	CYSI	EFTS	FIMF	GLPA	IDH	MARR
ALR1	BGLB	CYSJ	EMRA	FIMG	GLPD	IF2	MBHL
ALR2	BGLR	CYSK	EMRB	FIMZ	GLPF	ILVB	MCP1
AMPM	BIOA	CYSM	END3	FIRA	GLPG	ILVC	MCP2
AMPP	BIOB	CYSN	ENTA	FKBX	GLPK	ILVD	MCP3
AMY1	BIOC	CYSP	ENTC	FLGL	GLPR	ILVE	MCP4
AMY2	BIOF	CYSQ	ENTE	FLIA	GLPT	ILVG	MDL
APPB	BISC	CYST	ENTF	FLIC	GLPX	ILVI	MDOH
APPC	BTUB	CYSW	ENVC	FLID	GLTB	ILVY	MDRA
APPY	BTUC	CYTR	ENVD	FLIG	GLTP	IMP	MELB
ARAC	BTUD	DACA	ENVM	FLIR	GLTS	INAA	MELR
ARAD	BTUR	DACC	ENVY	FM1A	GLYA	IPYR	MENB
ARAE	CADB	DAMX	ENVZ	FMT	GPPA	ISPA	MEND
ARAF	CADC	DAPA	ERA	FNR	GREA	K1PF	METB
ARAG	CARA	DAPB	EVGA	FOLC	GREB	K6P2	METC
ARAH	CARB	DAPD	EVGS	FRDA	GRPE	KBL	METE
ARAJ	CCA	DAPE	EX5A	FRDB	GSA	KDPD	METH
ARCA	CDSA	DBPA	EX5B	FRE	GSH2	KDPE	METK
ARCB	CELD	DCDA	EX5C	FRUR	GSHR	KDSB	METR
ARGA	CELF	DCEA	EX7L	FTSA	GUAA	KDTA	METX
ARGB	CFA	DCEB	EXBB	FTSE	GUAC	KEFC	MFD
ARGD	CH60	DCLY	EXBD	FTSN	GUTD	KGTP	MGLA
ARGE	CHAA	DCOR	FABA	FTSW	GUTR	KGUA	MGLC
ARGT	CHEA	DCOS	FABG	FTSY	GYRA	KIRI	MIOC
ARLY	CHEB	DCP	FABH	FUCA	GYRB	KPRS	MIND
AROA	CHEY	DDLA	FADB	FUCK	HDHA	KPY1	MOAA
AROF	CHEZ	DDLB	FADR	FUCO	HELD	KPY2	MOAB
AROG	CIRA	DEAD	FDHD	FUCP	HEM1	KUP	MODB
AROH	CISY	DEDA	FDHF	FUCR	HEMX	LACI	MODC
AROP	CLPA	DEDD	FDNG	FUMA	HEPA	LACY	MOEB
ARTI	CLPB	DEOC	FDNH	FUMB	HFLC	LAMB	MPRA
ARTJ	CLPX	DEOD	FDNI	FUMC	HFLK	LCFA	MRAY
ARTM	CMTA	DEOR	FDOG	FUR	HFLX	LEPA	MREB
ARTP	CN16	DGAL	FDOH	G3P1	HIS4	LEU1	MRED

TABLE 8 Continued

ARTQ	COAA	DHAB	FDOI	G3P2	HIS6	LEU2	MRP
ASCB	CODB	DHAL	FECA	G6PD	HIS7	LEU3	MSBA
ASCG	CPSB	DHAS	FECB	G6PI	HIS8	LEUO	MSBB
ASG1	CPSG	DHNA	FECC	GABD	HISM	LEXA	MTLD
MTR	PABC	PT2B	ROB	TDH	YAAG	YFIB	YIFG
MUKB	PAL	PT2D	RODA	TESB	YAAJ	YFJA	YIFI
MURC	PANF	PT2F	RP32	THD1	YAAL	YGGA	YIFK
MURD	PARC	PT2G	RP70	THD2	YAAM	YGGB	YIGK
MURE	PARE	PT2M	RPOS	THDF	YAAP	YGGC	YIGM
MURF	PBP2	PT2N	RS1	THGA	YAAS	YGIE	YIGN
MURZ	PBP3	PT2P	RS4	THIF	YAAU	YGIF	YIGO
MUTL	PBPA	PT2X	RUVA	THIH	YABE	YHAA	YIGT
MUTS	PBPB	PT3G	RUVB	TKT	YABG	YHAE	YIHG
MUTY	PCNB	PT3M	SBCC	TNAA	YABI	YHBD	YIHI
NADB	PDXB	PTR	SBM	TNAB	YABJ	YHBE	YIHK
NAGA	PEPQ	PUR1	SDHD	TOLA	YABK	YHBF	YIHL
NAGB	PFL	PUR2	SDHL	TOLR	YABM	YHBG	YIHN
NAGR	PFLA	PUR3	SDHM	TONB	YADB	YHBI	YIHO
NARG	PFS	PUR5	SECA	TOP1	YADD	YHDE	YIHP
NARH	PHEA	PURA	SECD	TOP3	YAEA	YHDF	YIHQ
NARI	PHEP	PURR	SECF	TRKA	YAEC	YHDG	YIHU
NARJ	PHNC	PUTP	SECY	TRKD	YAED	YHDH	YIHV
NARK	PHNE	PYRB	SELA	TRKG	YAEF	YHDK	YIHW
NARL	PHNF	PYRE	SELB	TRKH	YAFB	YHFD	YIHX
NARP	PHNJ	RARD	SERA	TRPB	YAFD	YHGA	YIHY
NARQ	PHNK	RBSA	SLT	TRPE	YAFG	YHHI	YIIA
NARV	PHNL	RBSB	SLYD	TRPG	YAJF	YHIA	YIIG
NARW	PHNN	RBSC	SMBA	TRXB	YBBA	YHID	YIII
NARX	PHOB	RBSK	SMS	TTDA	YBDA	YIBC	YIJJ
NARY	PHOE	TBSR	SODF	TTDB	YBEF	YIBF	YIJK
NARZ	PHOP	RCSB	SODM	TTK	YBFB	YIBH	YIIT
NFRB	PHOQ	RCSC	SOHB	TYRA	YBFD	YICC	YIIX
NHAA	PHOR	RECA	SOXS	TYRB	YBIB	YICE	YIJE
NHAB	PHOU	RECE	SPEA	TYRP	YCAC	YICF	YIJG
NHAR	PHRA	RECG	SPOT	TYRR	YCAD	YICI	YIJH
NIRB	PHSG	RECN	SPPA	UBIA	YCAE	YICJ	YIJJ
NIRC	PHSM	RECQ	SRMB	UBIG	YCEE	YICK	YIJL
NLPA	PLSB	RELA	SRP5	UBIH	YCEF	YICL	YIJM
NMPC	PLSC	REP	SSPA	UDHA	YCHE	YICM	YIJO
NOHA	PNP	RF1	STPA	UDP	YCIB	YICO	YIJP
NOHB	PNTA	RF2	SUBI	UGPA	YCIE	YICP	YJBB
NPL	PNTB	RFAD	SUCD	UGPB	YCIF	YICQ	YJBI
NRFC	POTA	RFAH	SUHB	UGPC	YDBC	YIDA	YJBK
NRFE	POTB	RFAI	SURA	UGPE	YDCC	YIDE	YJBN
NTRB	POTC	RFAJ	SYA	UHPA	YDDA	YIDF	YJCC
NTRC	POTD	RFAL	SYC	UHPB	YDDC	YIDJ	YJCD
NUOM	POTE	RFAP	SYD	UHPC	YDDD	YIDK	YJCE
NUPC	POTF	RFAQ	SYE	UHPT	YDEA	YIDL	YJCF
NUPG	POTG	RFE	SYFA	UIDP	YDEB	YIDM	YJCG
NUSA	POTH	RFFE	SYGA	UMUC	YDED	YIDN	YJCP
NUSG	POTI	RFFM	SYGB	UMUD	YDEE	YIDO	YJCQ
ODO2	POXB	RFFT	SYI	UPP	YDEK	YIDP	YJCR
ODP1	PPA	RHAA	SYK1	URK	YEBB	YIDT	YJCT
ODP2	PPB	RHAB	SYK2	USG	YECB	YIDU	YJCU
OGT	PPSA	RHAR	SYK3	USHA	YEDA	YIDW	YJCV
OMPC	PPX	RHAS	SYL	USPA	YEFA	YIDY	YJCW
OMPF	PRC	RHAT	SYM	USPT	YEFB	YIDZ	YJDB
OMPR	PRIA	RHLB	SYN	UVRA	YEIC	YIEA	YJGA
OPDA	PROA	RHLE	SYP	UVRB	YEIE	YIEC	YJGB
OPPA	PROP	RHO	SYQ	UVRD	YFCA	YIEG	YPRA
OTC1	PROV	RIBG	SYS	UVRD	YFEB	YIEH	YPTF
OTC2	PROW	RIMJ	SYT	VISC	YFEC	YIEK	YZFB
OTSB	PSTA	RIMK	SYV	XERC	YFED	YIEL	
OXYR	PSTB	RIML	TIR	XPRB	YFFE	YIEO	
P30	PSTC	RLPA	TALB	XYLE	YFGA	YIEP	
PABA	PSPA	RNE	TDCA	XYLK	YFHA	YIFB	
PABB	PT1	RNPH	TDCC	YAAA	YFHC	YIFC	

This set of 971 paralogous proteins was further analyzed in two complementary ways. (i) We looked at the functional relatedness of the paired proteins, designating each pair as being related, different, or unknown (as in the case of open reading frames or proteins whose cellular function has not been characterized well enough to judge the level of similarity of function). Of the paired 971 proteins, 587 could be related by function to its (best) partner, only 12 were paired with another protein displaying an apparently totally different function, and 336 could not be assessed for lack of information on at least one partner of the pair. The extremely high percentage of similarity of functional relationship among paralogous gene pairs (60.45% of 971, and 98% of the 599 assessable proteins) shows that the sequence relationships between pairs are not accidental but have biological significance. We also used other ways of assessing functional relationships. These are summarized in Table 9. The assignment of the members of the 2,329 pairs to the functional categories reported here in Tables 2 and 3 was examined. Not all members of all pairs had assignments that characterized function, but for those pairs in which both members had been characterized, a large fraction registered as having similar functions (Table 9). Thus, these results strongly suggest that the genes coding for these proteins are paralogous, descendants of duplicate copies of ancestral genes residing in the same genome.

TABLE 9 Functional relationships among sequence-related proteins

Functional category	No. of pairs with identical assignment	Total no. of pairs ^a	% of pairs with related function
Physiological categories as listed in Table 1	450	1,636	27.5
Type of gene product as listed in Table 4	1,375	1,523	90.3
Enzymes that share the first two numbers of EC classification ^b	287	408	70.3

^aThe total number of sequence-related pairs for which both members bear assignments in Table 1 or 4.

^bEC numbers represent categorization of reactions over four levels of specification, assigned by the Enzyme Commission of the International Union of Biochemistry and Molecular Biology (2122).

(ii) Many of the proteins were found to be related to more than one other *E. coli* protein and thus are members of groups of interrelated proteins. Besides the 112 pairs (224 sequences), we could distinguish 38 triplets (113 sequences), 41 small groups (281 sequences), and 13 large families (353 sequences). These combinations are listed in Table 10. If each cluster and family were descended from one ancestral gene by duplication and divergence, one could begin to count the numbers of ancestral genes necessary to generate the *E. coli* genome. This leads to a dramatically small number of putative ancestral sequences. Indeed, the 747 sequences belonging to groups larger than pairs could originate from as few as 92 putative ancestral sequences. This number will undoubtedly fall further as additional genes are sequenced, providing partners for some of the single sequences and amalgamating some of the pairs into families. When the full sequence of the *E. coli* chromosome is known, we will be able to count the number of unique ancestral sequences required to generate *E. coli*.

TABLE 10 Families of paralogous genes

224 sequences having only partner, with PAM ^a values															
<i>aat/tyrB</i>	48.32	<i>cysP/sbp</i>	83.71	<i>glne/jycC</i>	222.42	<i>moaB/yaaG</i>	142.87	<i>slt/yafG</i>	154.82						
<i>aceE/htkA</i>	200.97	<i>cysQ/suhB</i>	162.26	<i>gipX/sucD</i>	198.81	<i>mtlD/rpsD</i>	247.56	<i>sodF/sodM</i>	90.78						
<i>ackA/yhaA</i>	104.54	<i>dacA/dacC</i>	46.04	<i>gppA/ppx</i>	100.59	<i>nagB/yieK</i>	179.56	<i>sspA/yibF</i>	167.57						
<i>acn/leuC</i>	172.72	<i>dapA/nanA</i>	176.95	<i>greA/greB</i>	124.38	<i>narJ/narW</i>	58.25	<i>pheS/yihI</i>	214.90						
<i>alr/dadX</i>	102.66	<i>lysA/speA</i>	166.07	<i>guaC/guaB</i>	116.02	<i>nlpA/yaeC</i>	46.03	<i>talB/yijG</i>	131.06						
<i>araD/fucA</i>	141.41	<i>dedA/yabl</i>	171.49	<i>hisA/hisF</i>	179.55	<i>nohA/nohB</i>	1.99	<i>topA/topB</i>	169.99						
<i>malS/amyA</i>	215.75	<i>sdhB/frdB</i>	123.35	<i>hms/stpA</i>	58.13	<i>nusG/rfah</i>	197.41	<i>trkG/trkH</i>	103.26						
<i>appC/cydA</i>	50.93	<i>dnaI/hydA</i>	245.97	<i>htrB/msbB</i>	179.47	<i>ogt/purA</i>	240.43	<i>ttk/hdK</i>	223.94						
<i>argA/argB</i>	192.23	<i>dnaA/dnaC</i>	159.80	<i>hypE/purM</i>	213.07	<i>pal/yfiB</i>	178.26	<i>uspA/yiiT</i>	118.75						
<i>argE/dapE</i>	155.27	<i>lig/yicF</i>	190.08	<i>ibpA/ibpB</i>	74.69	<i>pdxB/serA</i>	151.41	<i>yadD/yhgA</i>	67.22						
<i>ascB/bglB</i>	66.20	<i>dppA/oppA</i>	187.50	<i>icd/leuB</i>	129.09	<i>act/yijM</i>	152.86	<i>yafB/ydbC</i>	158.25						
<i>aslB/yidF</i>	143.37	<i>ecpD/fimC</i>	132.15	<i>ilvC/yptF</i>	228.87	<i>pheA/tyrA</i>	187.74	<i>yceF/yhdE</i>	119.78						
<i>asnC/lrp</i>	172.85	<i>edd/tivD</i>	142.49	<i>ilvE/pabC</i>	164.33	<i>potD/potF</i>	118.46	<i>yche/ydeB</i>	126.41						
<i>bioB/lipA</i>	196.37	<i>nth/mutY</i>	192.02	<i>inaA/rfaP</i>	157.51	<i>relA/spoT</i>	126.97	<i>yceI/ycaI</i>	170.33						
<i>bioF/kbl</i>	123.00	<i>exbD/tolR</i>	134.40	<i>gmk/phnN</i>	176.91	<i>prfA/prfB</i>	103.29	<i>yebB/yiiX</i>	157.38						
<i>cca/pcnB</i>	171.44	<i>fabA/yaeA</i>	174.51	<i>prs/pyrE</i>	218.26	<i>rfal/rfaI</i>	120.95	<i>yfeC/yfeD</i>	120.06						
<i>cdsA/hyaB</i>	239.19	<i>sepE/yifC</i>	197.10	<i>lexA/umuD</i>	125.85	<i>rfaQ/yibC</i>	221.06	<i>yhdG/yjbN</i>	193.77						
<i>gltA/yieH</i>	223.03	<i>fes/yieL</i>	226.06	<i>livJ/livK</i>	25.43	<i>rffM/ycaC</i>	203.83	<i>yhfD/yjU</i>	109.27						
<i>clpX/hslU</i>	90.45	<i>yaaD/slyD</i>	151.37	<i>malE/ugpB</i>	190.62	<i>ribG/yfhC</i>	125.39	<i>yicL/yihQ</i>	177.20						
<i>cpsB/yjcP</i>	210.22	<i>fmu/purN</i>	211.85	<i>marR/mprA</i>	167.01	<i>rimJ/rimL</i>	167.28	<i>yijP/yjdB</i>	178.47						
<i>cyp/fnr</i>	183.24	<i>fur/yjbK</i>	174.87	<i>metK/metX</i>	3.26	<i>rpsA/yaaS</i>	192.62								
<i>ppiB/ppiA</i>	55.50	<i>gapA/gapB</i>	94.82	<i>minD/mrp</i>	221.76	<i>ruvA/uvrC</i>	198.85								
<i>cysD/cysH</i>	162.21	<i>pgi/yicP</i>	225.43	<i>moaA/thiH</i>	194.88	<i>sdhL/sdhM</i>	28.39								
113 sequences which are part of a triplet															
<i>gnd/yihU/yhaE</i>		<i>aroF/aroG/aroH</i>		<i>coaA/udk/yggC</i>		<i>sdhA/frdA/nadB</i>		<i>fecB/fepB/fhuD</i>		<i>gyrB/parE/fliD</i>		<i>lon/recA/sms</i>		<i>proS/serS/thrS</i>	
<i>melA/celF/yidM</i>		<i>ansA/ansB/polB</i>		<i>cutE/cyoE/ubiA</i>		<i>dnaB/leuA/nfrB</i>		<i>fimD/htrE/yabG</i>		<i>hisB/yaeD/yihX</i>		<i>metB/metC/selA</i>		<i>tdh/yhdH/yjbG</i>	
<i>eda/fdhD/yidU</i>		<i>atpA/atpB/rho</i>		<i>cysI/mioC/recG</i>		<i>enC/pabB/trpE</i>		<i>galU/glgC/yfG</i>		<i>ispA/phoA/yhbD</i>		<i>argI/argF/pyrB</i>		<i>ybfD/ydcC/yhhI</i>	
<i>map/pepP/pepQ</i>		<i>cbgA/lacZ/uiaA</i>		<i>gadA/gadB/gcvP</i>		<i>fadB/menB/yaaL</i>		<i>genA/genF/cstA</i>		<i>pykF/pykA/upp</i>		<i>sohB/sppA/fabH</i>			
<i>argH/aspA/fumC</i>		<i>cpdB/ushA/yaaA</i>		<i>dodD/pfs/udp</i>		<i>fdnI/fdol/hyaC</i>		<i>glgB/glgX/malZ</i>		<i>lamB/yieC/yifI</i>		<i>gltX/glns/yadB</i>			
281 sequences belonging to small groups															
<i>yacB/fadR/ybgB/phnF/yidP/yidW/yieP/yihL</i>						<i>cysK/cysM/ilvA/tcbB/aslA/sdhD/sbm/ptr/phoU/trpB/yddC/yidJ</i>									
<i>aas/acs/entE/entF/fadD/plsC/plsB/ubiH/visC/yaaM</i>						<i>ddlA/ddlB/accC/carB/purD/gshB/rimK</i>									
<i>acrA/envC/emrA/dcp/prcC/yibH/yicR</i>						<i>deoR/glpR/gutR/fucR/yihW</i>									
<i>acrB/envD/glyA/nupC/secD/secF/rhaT/yiiI</i>						<i>ndh/gor/nirB/udhA/lpaA/trxC/bysI/pntA</i>									
<i>adhE/ald/betB/aldH/fucO/gabD/gldA/proA</i>						<i>entA/fabG/gutD/hdhA/envM</i>									
<i>adi/cadA/speC/speF/recE</i>						<i>era/hflX/thdF</i>									
<i>thrA/metL/lysC/smbA</i>						<i>fdoH/fdnH/narH/narY/hycB/hydN/dmsB/nrfC/yffe</i>									
<i>argD/bioA/gabT/hemL</i>						<i>fpr/fre/hmpA</i>									
<i>argT/artI/artJ/glnH/ygiF</i>						<i>fimB/fime/xerC/xprB</i>									
<i>asnB/glms/dapB/zwf/purF</i>						<i>fimF/fimG/fimA/htrA/htrH/phnJ</i>									
<i>bioC/cfa/prc/ubiG/yigO</i>						<i>fliA/rpoH/rpoD/rpoS/cheZ/otsB</i>									
<i>bisC/dmsA/fdhF/fdnG/fdoG/narG/narZ</i>						<i>fliC/fliG/lalaS/ydeK</i>									
<i>cysE/dapD/aroA/murZ/lacA/ftrA/lpxA/gcvT/kdsB/yieA</i>						<i>fucK/glpK/araB/txyB</i>									
<i>fumA/fumB/ttdA/ttdB</i>						<i>mukB/mutS/secA/hemX/sbcC/yidA</i>									
<i>galE/rfaD/rffE/yefA/yefB</i>						<i>nagR/yajF/yjA/yjcT</i>									
<i>gcl/ilvB/ilvG/ilvI/poxB/menD</i>						<i>nmpC/ompC/ompE/phoE</i>									
<i>glpA/glpD/murD/murE/murF/murC/folC</i>						<i>sucB/aceF/accB</i>									
<i>grpE/hepA/recN/hsdR/yicC/yiiG</i>						<i>mrdA/ftsI/mrcA/mrcB/alkA</i>									
<i>guaA/pabA/trpG/carA/ybiB</i>						<i>glgP/malP/moeB/thiF</i>									
<i>gyrA/parC/eflS/hisC/malY</i>						<i>pnp/rph/cpsG/yhbF</i>									
<i>helD/rep/uvrD/recD/recB/recC</i>						<i>lysS/lysU/aspS/asnS/glyQ/yjeA/umuC</i>									
<i>hflC/hflK/metE</i>						<i>yigK/chaA/nrfE</i>									
<i>fruK/pfrB/rbsK/yecC/yihV</i>						<i>hycC/nuoM/kup/mdoH/rarD/rodA/ftsW/yijE/yedA/yicL/yigM/yggA/ydeD/</i>									
<i>tsr/tar/trg/tap/metH/mopA</i>						<i>yhbE/ppa/fileS/leuS/metG/valS/cysS</i>									

(Table continues)

353 sequences belonging to large families
 abc/araG/artPbtuD/cydD/cysA/fecE/fepC/fhuC/fteE/glnQ/hisP/livF/livG/malK/malI/cydC/mglA/modC/msbA/phnC/phnK/phnL/phrA/potA/potG/proV/
 pstB/rbsA/ugpC/uvrA/yjgA/yabJ/ybbA/yddA/yhbG/jycW/yjgA/xseA
 ada/appY/araC/celD/envY/marA/melR/rhaR/rhaS/rob/soxS/yndL/yijO
 artM/artQ/cysT/cysW/hisM/glnP/malF/malG/modB/potB/potC/potH/potI/proW/pstA/pstC/ugpA/ugpE/phnE/yabK/yaeE/ybfB/yjbl/yjcF/kup
 ascG/cytR/ebgR/frruR/galR/galS/lacI/malI/purR/rbsB/rbsR/araF/mglB
 btuB/cirA/fecA/fepA/fhuA/fhuE
 btuC/fecC/fecD/fepD/fepG/fhuB/rfe/kefC/trkA/yjcE
 cynR/cysB/gcvA/iciA/ilvY/leuO/lysR/metR/nhaR/oxvR/tdcA/yafC/ybeF/yeiE/yfeB/yndZ/ffiG/nagA/rhaA
 cysN/fusA/tufA/tufB/infB/lepA/selB/yihK/yigN/tmaA
 btuR/dpbA/deaD/mfdI/priA/recG/recQ/rhlB/rhlE/srmB/uvrB
 arcA/baeR/basR/cheB/cheY/creB/evgA/fimZ/hydG/kdpE/narL/narP/ntrC/ompR/phoB/phoP/rcsB/tyrR/uhpA/rhlA/yfhA/yecB/yiiA/hemA/clpA/clpB/
 yjfb/ruvB/cadC/katA/surA/glyS
 arcB/baeS/barA/basS/cpxA/creC/envZ/evgS/hydH/kdpD/ntrB/phoQ/phoR/uspT/rcsC/cheA/polA/nusA/malT/narQ/narX/uhpB/creD/yddD
 appB/araE/araH/araJ/aroP/kdpA/atpB/bcr/betT/cadB/codB/cvpA/cydB/e mrB/exbB/fhuR/fucP/gabP/glpT/gltS/hypD/kgtP/lacY/livH/livM/lysP/
 melB/mglC/mveD/mraY/mtr/narI/narK/narV/nirC/nhaA/nhaB/nupG/panF/pheP/pntB/potE/proP/nagE/puiP/rbsC/rfaL/rffT/secY/tdcC/tnaB/
 tyrP/uhpC/uhpT/uidP/cylE/yaaI/yaaP/yaaU/yabE/yabM/ybdA/ycaD/ycaE/yceE/ygiB/ydeA/ydeE/yfcA/yggB/yhiD/yicE/yicK/yicM/yicO/yicQ/yidE/
 yidK/yidT/yndY/yieG/yieO/yifK/yihG/yihN/yihO/yihP/yihY/yjbB/yjcD/yjcG/yycV/yprA
 agp/kdpB/atpF/damX/dedD/deoC/dnaK/dnaX/fecI/ftsA/ftsN/ftsY/hisD/holB/mreB/mutL/pflI/ppa/pspA/rfpA/rne/ffh/tonB/tonY/yfgA/yhdF/yngT/yijL/yzfB
 cmtA/asd/glpF/glpG/gltB/gltP/ppsA/ptsI/bglF/ascF/frruA/ptsG/mitA/nagE/frdB/crr/cmtB/tesB/usb/ygiE/yhbI/yhiA/yndN/yidO/yiiI/yiiK/yijH/yijJ/yjcQ

^aPAM value, accepted point mutations (644).

To go a step farther in this analysis, we are reconstructing phylogenetic trees for each of the sequence-related groups and then using the putative ancestral sequences to extract other related sequences from databases of sequences. As long as the sequence relationships among distantly related proteins can be detected, one can continue to move earlier in the tree of descent, relating ancestral sequences for a given species to even earlier ancestral genes that fed many species, thereby progressively reducing the total number of ancestral sequences as one moves in the direction of the beginning of the tree. Ultimately, we will be able to approach the identification of a relatively small number of unique primitive ancestral sequences that gave rise to all contemporary genes. *E. coli* gene sequences will be very useful in this evolutionary context.

MAP RELATIONSHIPS AMONG FUNCTIONALLY RELATED *E. COLI* GENES

Some 20 years ago, a proposal was put forward that evolution of the *E. coli* genome might have occurred by successive duplications of the entire genome and that as a consequence, functionally and ancestrally related genes might be located either 90° or 180° from each other on the genetic map (2278, 2279). With many more genes now mapped than were at the time, one can test whether there is a tendency for genes related either by cellular function or by type of protein to cluster at 90° and 180° positions.

When the map positions of genes underlying each functional category as defined in Table 1 were examined, they did not lie at regular positions on the circular map. When map positions of genes for enzymes that catalyze similar reactions were examined, again no pattern of gene location was seen. For instance, phosphotransferase enzymes with an alcohol group as acceptor are enzymes with EC numbers beginning with 2.7.1. They were not clustered at 90° or 180° positions, nor were oxidoreductases acting on the CH-OH group of donors with NAD⁺ or NADP⁺ as the acceptor (EC numbers beginning 1.1.1.). Therefore, the idea of whole genome doubling (745, 1344, 1869, 2278, 2279) does not find support in current *E. coli* genetic data.

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