

The Genetic Map of *Salmonella typhimurium*, Edition VIII

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INTRODUCTION

We present a somewhat modified version of edition VIII of the genetic map of *Salmonella typhimurium* (official designation, *Salmonella enterica* serovar Typhimurium) strain LT2, which was published in 1995 (1717). We list a total of 1,160 genes; 1,081 of these have been located on the circular chromosome, and 29 of these are on pSLT, the 90-kb plasmid which is almost invariably found in LT2 lines; the remaining 50 genes are not yet mapped. The first edition of the map in 1965 contained 133 genes; later editions were published in 1967, 1970, 1972, 1978, and 1983, and edition VII, in 1988, listed a total of 750 genes (1721). A slightly modified version of edition VI of the map, presented originally in 1983, was published in the first edition of the present volumes (1718).

Strain LT2 is one of 25 different *S. typhimurium* isolates established by Lilleengen (1205) and designated LT1 to LT25; these strains represent 25 different phage sensitivity phenotypes. Many of these LT strains were used by Zinder and Lederberg for a study of genetic exchange, leading to the discovery of phage-mediated transduction (2236). M. Demerec obtained the LT strains from Zinder and began an exhaustive series of studies in the mid-1950s. The most important materials used were mutant strains derived from strain LT2, though a few were derived from strain LT7. Since the 1950s, strain LT2 has been the major focus of genetic and biochemical analysis, and thus the map we present here is derived primarily from work with LT2. However, more recently other strains have been used for specific reasons: e.g., some strains of *S. typhimurium* have been studied because they have higher levels of virulence than strain LT2; strain LT2 does not utilize histidine as sole carbon source, so other wild-type strains which do so have been used to study the *hut* operon.

All genes presently known to us are listed in Table 1 (p. 1907), with formerly used or alternative symbols in Table 2 (p. 1939). The references which describe these genes include a selection of the references from the first six editions which were presented in the first version of the present volumes (1718), those which were in edition VII published in 1988 (1721), and those which have been published since 1988 and which were included in the edition VIII published earlier (1717).

THE GENETIC MAP

The coordinate system used in the first four editions of the linkage map of *S. typhimurium* was determined by F-mediated conjugation; Hfr strains were used in interrupted conjugation experiments to place individual genes and P22-transduction linkage groups on a 138-min time-of-entry linkage map. In edition V, the map was changed to 100 units to correspond to the 100-min linkage map of *Escherichia coli* K-12. This was done to emphasize the similarity of the two genera and to facilitate comparisons. This 100-unit system was also used in editions VI and VII. In those editions, the 100 units of the map were based on "phage lengths" of the transducing phage P22 (1721). P22 can normally encapsulate about 45 kb of DNA; this is approximately 1% of the *Salmonella* chromosome. The map described here is the first edition in which we present a physical map of the chromosome with the interval between

genes based directly on the length of the DNA. We report these gene intervals as centisomes (Cs), each one of which represents 1% of the length of DNA in the chromosome, and we also present the DNA segments in kilobase pairs (kb).

This physical map of the chromosome is based on a low-resolution genomic cleavage map determined by digestion with rare-cutting endonucleases and separation of the resulting fragments with pulsed-field gel electrophoresis (PFGE). Preliminary cleavage maps used the enzymes *Xba*I (1224), *Bln*I (1739, 2163), and I-*Ceu*I (hereafter called *Ceu*I) (1223). The overall structure of the chromosome shown in Fig. 1 (p. 1957) is based on a summary of work with these three enzymes (1222), plus some additional unpublished work.

The genomic cleavage map shows the positions of 24 *Xba*I fragments, 12 *Bln*I fragments, and 7 *Ceu*I fragments on a circular molecule of 4,808 kb of DNA (1222). The positions of genes on this cleavage map were determined by three methods. (i) Strains with insertions of the transposon *Tn10* into known genes were analyzed. The presence of *Xba*I and *Bln*I sites in *Tn10* permitted the location of these insertions, and thus of the gene into which *Tn10* is inserted, through digestion of the DNA of the strain by the enzyme, followed by separation of the fragments by PFGE. A total of 109 independent strains with *Tn10* insertions were reported, but some of these were not in genes of known function (1222); together with unpublished work done recently, a total of 75 genes have been located on the physical map solely through analysis of *Tn10*-containing strains. (ii) A total of 12 genes could be placed on the map because their DNA sequence included a site for the endonucleases *Xba*I, *Bln*I, or *Ceu*I. (iii) In some situations, restriction mapping data or data from nucleotide sequences were used to correct or refine the locations of genes on the map. For example, a high-resolution restriction map for a 240-kb region spanning the 91 to 96 Cs region of the map located the positions of several genes (2166); these data were used to modify the locations of some genes in this interval.

The physically mapped *Tn10* insertions and genes (discussed above) were used to align genes whose positions were known only by linkage data, and also were used as “anchors” for DNA sequence (described in detail below).

The chromosome is a closed circle of DNA, and early editions of the linkage map were shown in this way. In editions from V to VII the linkage map was displayed not as a circle but as 10 linear 10-min intervals. The present edition is similar, but because the number of known genes has increased, it is shown as 20 linear 5-Cs intervals (Fig. 1). This figure integrates gene location information discovered by genetic linkage and by physical analyses. The position of any gene shown was determined using the data available in the following preference order: first, by the order of genes found in sequenced DNA segments; second, by *Tn10* or other physical anchors; third, by genetic linkage data; and, last, by extrapolation based on data from *E. coli* K-12 (see below). For display purposes, when gene orientation conflicts arose between physical and genetic data, preference was given to gene linkage information.

Most of the elements shown on the map are structural genes for proteins or, in a smaller number of cases, for rRNA or tRNA. We have not shown control elements for operons such as promoters, mRNA leaders, and terminators, nor have we shown the position of unnamed or poorly characterized chromosomal genes. We have not shown chromosomal elements such as repetitive extragenic palindromic (REP) sequences (771, 1423), but an exception is that we have indicated the positions of the six *IS200* sequences which are mapped on the chromosome of LT2 (1134, 1136, 1724).

NOMENCLATURE

We use the system of nomenclature for genes which was established by Demerec et al. (437). This system uses a three-letter designation for the gene or operon, e.g., *his* for mutations in the genes for histidine synthesis, followed by a capital letter, also in italics, designating the specific gene in that operon, e.g., *hisD* for a mutation in the gene for histidinol dehydrogenase. This system has become the de facto standard for bacterial genetics. Authors considering a three-letter designation for a new gene in *S. typhimurium* should check the published maps of *S. typhimurium* and *E. coli* to see whether the proposed name has been used previously; they are also encouraged to contact the *Salmonella* Genetic

Stock Center (SGSC) to see whether a proposed name has been used previously but not published. Allele number assignments should also be obtained from the SGSC. It is important to clear such numbers with the SGSC so that each mutation is identified by a unique allele number. A mutation is defined by its three-letter designation plus the allele number, i.e., the mutation *his-1* might be initially thought to be *hisDI*, based on its perceived enzyme defect, but is later changed to *hisE1*. Thus, there should be only one *his-1* mutation. Using assigned numbers is especially important for transposon insertions named by the “z- -” system proposed by Hong and Ames (824). In this case, the allele number may be the only identifier for a mutation, since all mutations mapped with “z- -” have a single series of allele numbers. As mapping is refined, a mutation’s “z- -” designation may change, but it retains its original allele number. It is therefore important that assigned allele numbers be used to avoid confusion of different laboratories using the same number for different insertions. It is also vital that strains be identified by a unique strain designation, which includes two or three capital letters (assigned for *Salmonella* strains by the SGSC to the laboratory, or by the *E. coli* Genetic Stock Center [CGSC] for *E. coli* strains) plus a number. The expanding use of the computer to keep records demands the use of correct strain designations; suffixes and phenotype designations after the strain designation, to refer to derivatives of a parent strain, are often not accepted by programs used for cataloging strains.

When possible, the same name should be used for homologous genes in related species such as *E. coli* and *Salmonella* spp. Many changes have been made in naming genes in these organisms to bring them into correspondence, and each edition of the maps has seen such changes. For example, a system of naming the genes for flagellar synthesis and function was proposed which recognizes the homology of these genera (891) and this system, now widely accepted, is used here. We encourage the trend to the use of these standardized names for *E. coli* and *S. typhimurium* for genes in other bacterial species as well when functional data and amino acid sequence data indicate that the genes are homologous.

PLASMID pSLT IN *S. TYPHIMURIUM* LT2

Because the plasmid content of strains of a species of bacteria is often extremely variable, the plasmids are not normally considered part of the genome; therefore, neither the F-factor in some lines of *E. coli* K-12 nor several types of plasmids frequently found in some wild-type *Salmonella* strains are treated as components of the normal genome. However, the original line of *S. typhimurium* LT2 contains a specific plasmid which we consider part of the genome. This plasmid has been called the virulence plasmid, the 90-kb plasmid, the 60-MDa plasmid, the cryptic plasmid, and pSLT (standing for salmonella LT); we use the last designation.

For two reasons, we consider this plasmid to be part of the normal genome of *S. typhimurium* LT2. The first is that the plasmid is an almost invariable part of the genome of LT2 lines. It is carried by all the lines of LT2 which we have tested, except for those few from which it has been intentionally eliminated. This is true even though LT2 has been in culture for many years and has been subjected to innumerable single-colony isolations. Genes on the plasmid which regulate replication, incompatibility, and partitioning (164, 242, 296) enable the plasmid to be maintained stably at low copy number. In addition, pSLT or a closely related plasmid is commonly found in independent *S. typhimurium* isolates from nature.

The second reason for considering pSLT to be part of the genome is that genes on the plasmid influence the phenotype in several ways, and thus mutations of genes on the plasmid may be mistaken for mutations of chromosomal genes. This influence of pSLT on the phenotype was first noted by Smith et al. (1837), who noted that it encoded Fin⁺ (fertility inhibition) properties, reducing the fertility of Hfr strains of *S. typhimurium*; special measures have been developed which restore fertility up to the level found in *E. coli* K-12 (1720). Many other genes have been detected due to their effect on phenotype. For example, mutations in the *traT* gene of pSLT cause an increase in outer membrane permeability, leading to an antibiotic-supersensitivity phenotype; this gene is listed in Table 1 (p. 1907). Other genes on pSLT, many of which influence the virulence of the strain, are also listed in Table 1 and are shown on a restriction map of pSLT in Fig. 1 (p. 1957).

SEQUENCED GENES OF *S. TYPHIMURIUM*

Gene identification can be largely based on open reading frames, codon usage distributions, and sequence-based evidence of homology (198, 1661). A significant amount of genomic DNA sequence has become available for *S. typhimurium*. By the end of 1994, we could assemble StySeq1, a nonredundant DNA sequence database modeled after the EcoSeq collection of *E. coli* genomic DNA sequences (1690). In fact, the extensive genomic sequence data available for *E. coli* (see, e.g., references 181 and 1853) cover close to two-thirds of the genome. Therefore, many *S. typhimurium* genes were identified at the sequence level as partial, but convincing, matches to one of the *E. coli* protein sequences in the EcoGene subset of SWISS-PROT (101).

StySeq1 has 197 contiguous sequence blocks (contigs) that do not overlap. Together, the nonredundant chromosomal genomic *S. typhimurium* StySeq1 DNA sequence collection is 548,508 bp in length. This represents 11.4% of the *Salmonella* chromosome, estimated to be 4,808 kb in length (1222). Eight contigs are greater than 10,000 bp in length. The longest contig, hisGstyM (Table 3 [p. 1940]), is 33,958 bp in length.

Of the 197 DNA sequences in this collection (Table 3), 191 are ordered and oriented as they might be on the *S. typhimurium* chromosome. This was accomplished in several ways: physical anchor, genetic pin, and extrapolation.

i) In the physical anchor method, if a Tn10 insertion, rare restriction site, or other direct physical link could be associated with one of the genes from StySeq, it was anchored and the positions of the other nearby genes were calculated based on a single base-pair anchor point per contig. Gene positions thus have high local precision (1-bp resolution) and coarse genomic map position accuracy, based on analysis by PFGE (ranging from 1,000 bp in some situations to over 10,000 bp, depending on the locations of restriction sites for the enzymes used). Unsequenced genes could also be anchored, and this information was taken into account in mapping the unsequenced genes depicted in Fig. 1. Sixty-two StySeq1 contigs were positioned in this way. (ii) In the genetic pin method, gene positions were assigned to a number of sequenced and unsequenced genes on the basis of linkage data. The positions of the anchors were used to realign conjugation and transduction mapping distances, allowing the integration of physical and genetic maps presented in Fig. 1. In turn, those genetic map positions were used to pin more sequences to the integrated genomic map. An additional 93 contigs in Table 3 were positioned by this approach. (iii) The extrapolation method was used to position a final 36 contigs by using map position information from *E. coli-Salmonella* gene pairs to extrapolate a position.

The aligned DNA sequences are ordered to coincide with the orientations of homologous sequences in the EcoSeq7 collection of aligned and oriented *E. coli* genes. Although some local inversions are likely to have occurred, most comparisons indicate a close correlation of the orientations and map positions of genes between *E. coli* and *S. typhimurium*, with one major exception. There is a large inversion of a chromosomal segment relative to the corresponding *E. coli* region with endpoints near 26 and 36 min on the genetic map (1721). We could localize this region on the physical map (Fig. 1), and this allowed us to set the orientation of genes in this region of *S. typhimurium* as being opposite to that of the *E. coli* homologs in this inverted segment.

Alignment of all but six of the StySeq1 contigs, at least as a best approximation subject to constant refinement, allowed the genes encoded in the DNA sequences to also be aligned. In this way, 523 protein-coding genes and 15 structural RNA genes were given genomic map positions based locally on DNA sequence information and globally on a combination of physical anchor points, genetic cross data, and extrapolation from the *E. coli* map. Fifty-one unnamed genes (described as *orf* or similar in GenBank entries) were given provisional names beginning with the letter "y" (1690); these genes were excluded from Table 1 but are listed in Table 3.

Until a larger proportion of the *S. typhimurium* genome is sequenced, the genetic linkage data will remain useful as the basis for the map. *E. coli* has a high-resolution genomic restriction map for the entire chromosome, whereas the high-resolution map of *S. typhimurium* is being assembled as parts

(2166). Nonetheless, several genes were physically positioned by DNA sequence and high-resolution restriction map data in the 91 to 96 Cs region of the *S. typhimurium* LT2 chromosome (2166) by using a single anchor.

Having access to both *E. coli* and *S. typhimurium* DNA sequence over the same region provides an opportunity to predict frameshift corrections and helps ensure the highest level of accuracy. Other organisms help identify probable new genes in *S. typhimurium* with homologs as well, but the comparison to *E. coli* involves enough preference for third-position changes to establish the correct frame for most protein-coding genes.

MAP REFINEMENT

If errors are detected in this work, we hope that this information will be transmitted to us to allow corrections. To assist in the preparation of future map editions or updates, we would appreciate receiving any information regarding the position and function of new genes, or refinements to the positions or roles of the genes described here. Electronic mail should be addressed to kesander@acs.ucalgary.ca and rudd@ncbi.nlm.nih.gov. StySeq1 and associated files can be retrieved in electronic form from the anonymous ftp site [ncbi.nlm.nih.gov](ftp://ncbi.nlm.nih.gov) in the /repository/Eco/Sty directory. Diskettes will be mailed on request to those without Internet access.

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TABLE 1 Genes of *S. typhimurium*.

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype ^a	Cs ^b	References ^c
<i>accA</i>		Acetyl-CoA carboxylase	6.0	1139, 1717
<i>aceA</i>	Acetate	Growth on acetate or fatty acids; isocitrate lyase (EC 4.1.3.1)	91.3	1717, 2128
<i>aceB</i>	Acetate	Growth on acetate or fatty acids; malate synthase (EC 4.1.3.2)	91.3	1717, 2128
<i>aceE</i>	Acetate	Acetate requirement; pyruvate dehydrogenase (pyruvate:cytochrome <i>b</i> ₁ oxidoreductase) (EC 1.2.2.2)	3.7	1140, 1717
<i>aceF</i>	Acetate	Acetate requirement; pyruvate dehydrogenase (pyruvate lipoate oxidoreductase) (EC 1.2.4.1)	3.7	1140, 1717
<i>aceK</i>	Acetate	Isocitrate dehydrogenase kinase/phosphatase	91.3	1717
<i>aciA</i>	Acid-inducible	pH-regulated gene; acid inducible	99.5	562, 1717
<i>aciB</i>	Acid-inducible	pH-regulated gene; acid inducible	92.4	562, 1717
<i>ack</i>	Acetate kinase	Acetate kinase (ATP:acetate phosphotransferase) (EC 2.7.2.1)	50.9	1130, 1183, 1717, 2073
<i>ada</i>		Inducible DNA repair system protecting against methylating and alkylating agents; <i>O</i> ⁶ -methylguanine DNA methyltransferase	50.1	720, 1717, 2078, 2181
<i>adhE</i>		Reduced survival in macrophages; CoA-linked acetaldehyde dehydrogenase and alcohol dehydrogenase	38.4	129, 1717
<i>adk</i>		Adenylate kinase; sensitivity to glycine betaine in high-osmolality media (EC 2.7.4.3)	11.6	707, 1717
<i>ahpC</i>	Alkyl hydroperoxide	Alkyl hydroperoxide reductase, C22 subunit	14.1	522, 1227, 1717, 1930, 1931
<i>ahpF</i>	Alkyl hydroperoxide	Alkyl hydroperoxide reductase, F52a subunit	14.1	522, 1717, 1930, 1931
<i>alaS</i>	Alanine	Alanine tRNA synthetase	62.0	1717
<i>alkB</i>	Alkylation	DNA repair system specific for alkylated DNA	50.1	720, 1717
<i>alr</i>	Alanine racemase	Biosynthetic alanine racemase (EC 5.1.1.1)	92.2	512, 520, 598, 599, 1717
<i>amiA</i>		<i>N</i> -Acetylmuramyl-L-alanine amidase activity; putative	53.2	1717, 2178
<i>amiB</i>		<i>N</i> -Acetylmuramyl-L-alanine amidase (EC 3.5.1.28)	95.0	1291, 1717
<i>amk</i>		AMP kinase	9.1	1717, 1721
<i>ampC</i>	Ampicillin	β-Lactamase; penicillin resistance (EC 3.5.2.6)	94.5	35, 1717
<i>ampD</i>	Ampicillin	β-Lactamase regulation; putative signalling protein	3.6	861, 1717
<i>amtA</i>		Resistance to 40 mM 3-amino-1,2,4-triazole in the presence of histidine	37.6	1717, 1718, 1721
<i>amyA</i>	Amylase	Cytoplasmic α-amylase (EC 3.2.1.1)	42.6	1008, 1607, 1717
<i>ana</i>		Anaerobic gas production	38.7	777, 1717
<i>aniB</i>	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	93.9	23, 1717
<i>aniC</i>	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	93.9	23, 1717
<i>aniD</i>	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	92.4	23, 1717
<i>aniF</i>	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	68.0	23, 1717
<i>aniG</i>	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	67.8	23, 1717
<i>aniH</i>	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	82.6	23, 1717
<i>aniI</i>	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	40.1	23, 1717
<i>ansB</i>		L-Asparaginase II; regulated by CRP and anaerobiosis	67.1	942, 1717
<i>apbA</i>		Alternative pyrimidine biosynthetic pathway; synthesis of thiamine in presence of exogenous purines	10.0	465, 1717
<i>apeB</i>	Acyl peptide esterase	Acyl amino acid esterase; hydrolyzes <i>N</i> -acetyl-L-phenylalanine-β-naphthyl ester	11.0	749, 1717
<i>apeE</i>	Acyl peptide esterase	Membrane-bound acyl amino acid esterase; hydrolyzes <i>N</i> -acetyl-L-phenylalanine-β-naphthyl ester	13.5	353, 1717, 1718, 1721
<i>apeR</i>	Acyl peptide esterase	<i>apeD</i> ; regulatory gene for <i>apeE</i>	85.0	1717, 1718, 1721
<i>aphA</i>		Nonspecific acid phosphatase II	NM	1717, 2043
<i>apt</i>		Adenine phosphoribosyltransferase	11.5	1717, 1718, 1721
<i>araA</i>	Arabinose	L-Arabinose isomerase (EC 5.3.1.4)	2.4	168, 831, 1162, 1163, 1208, 1209, 1596, 1717
<i>araB</i>	Arabinose	Ribulokinase (EC 2.7.1.16)	2.5	167, 311, 831, 1163, 1208, 1596, 1717
<i>araC</i>	Arabinose	Regulatory gene for arabinose catabolic enzymes	2.5	169, 345, 346, 831, 1149, 1161–1163, 1208, 1596, 1717
<i>araD</i>	Arabinose	L-Ribulose-phosphate 4-epimerase (EC 5.1.3.4)	2.4	831, 1163, 1207, 1208, 1595, 1596, 1695, 1717
<i>arcA</i>		Cytoplasmic DNA-binding component system for repression of genes during anaerobiosis	100.0	15, 56, 1717
<i>arcB</i>		Membrane-bound sensor of two-component system for repression of genes during anaerobiosis	72.4	15, 56, 1717
<i>argA</i>	Arginine	<i>argB</i> ; amino acid acetyltransferase (EC 2.3.1.1)	65.1	976, 1419, 1717, 1835, 2083

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype ^a	Cs ^b	References ^c
<i>argB</i>	Arginine	<i>argC</i> ; N-acetyl-γ-glutamate kinase (EC 2.7.2.8)	89.6	1717, 2083
<i>argC</i>	Arginine	<i>argH</i> ; N-acetyl-γ-glutamyl phosphate reductase (EC 1.2.1.38)	89.6	1717, 2083
<i>argD</i>	Arginine	<i>argG</i> ; acetylornithine aminotransferase (EC 2.6.1.11)	75.1	154, 1106, 1717, 2083
<i>argE</i>	Arginine	<i>argA</i> ; acetylornithine deacetylase (EC 3.5.1.16)	89.6	134, 187, 1717, 2083
<i>argG</i>	Arginine	<i>argE</i> ; argininosuccinate synthetase (EC 6.3.4.5)	72.0	1106, 1717, 2083
<i>argH</i>	Arginine	<i>argF</i> ; argininosuccinate lyase (EC 4.3.2.1)	89.6	577, 1717, 2083
<i>argI</i>	Arginine	Ornithine carbamoyltransferase (EC 2.1.3.3)	97.2	5, 264, 1013, 1016, 1717, 1978
<i>argP</i>	Arginine	Arginine transport	NM	1600, 1717
<i>argQ</i>	Arginine	Arginine tRNA ₂	62.0	173, 1717
<i>argR</i>	Arginine	L-Arginine regulation	73.4	615, 1015, 1019, 1020, 1240, 1242, 1717
<i>argS</i>	Arginine	Arginyl-tRNA synthetase (EC 6.1.1.19)	41.6	1539, 1717
<i>argT</i>	Arginine	Lysine-arginine-ornithine-binding protein	51.3	47, 73, 74, 762, 763, 1113, 1160, 1717, 1755, 1756, 1901
<i>argU</i>	Arginine	<i>fimU</i> ; arginine tRNA ₁ for rare codons (AGA and AGG); essential for fimbria expression	15.2	1717, 1975
<i>argV</i>	Arginine	Arginine tRNA ₂	62.0	173, 1717
<i>argX</i>	Arginine	<i>argT</i> , <i>argU</i> , <i>use</i> ; arginine tRNA ₁	85.6	201, 208, 264, 1241, 1717
<i>argY</i>	Arginine	Arginine tRNA ₂	62.0	173, 1717
<i>argZ</i>	Arginine	Arginine tRNA ₂	62.0	173, 1717
<i>aroA</i>	Aromatic	3-Enolpyruvylshikimate 5-phosphate synthetase	19.9	310, 322, 482, 655, 806–808, 1437, 1442, 1717, 1741, 1826, 1882
<i>aroB</i>	Aromatic	5-Dehydroquinate synthetase	75.7	655, 1437, 1717
<i>aroC</i>	Aromatic	<i>aroD</i> ; chorismate synthetase	52.0	655, 800, 1087, 1437, 1438, 1717, 1945, 1949
<i>aroD</i>	Aromatic	<i>aroE</i> ; 5'-dehydroquinate dehydratase (EC 4.2.1.10)	30.5	64, 655, 1437, 1717, 1776, 1846
<i>aroE</i>	Aromatic	<i>aroC</i> ; 5-dehydroshikimate reductase	74.4	655, 1437, 1717
<i>aroF</i>	Aromatic	Tyrosine-repressible DAHP synthetase	58.6	432, 1384, 1717, 1875
<i>aroG</i>	Aromatic	Phenylalanine-repressible DAHP synthetase	17.3	1717, 1875, 1933
<i>aroH</i>	Aromatic	Tryptophan-repressible DAHP synthetase	30.4	849, 1717
<i>aroP</i>	Aromatic	Aromatic amino acid transport	3.6	42, 868, 1717
<i>aroT</i>	Aromatic	Transport of tryptophan, phenylalanine, and tyrosine	39.3	1717, 2013, 2014
<i>asd</i>		Aspartate semialdehyde dehydrogenase (EC 1.2.1.11)	77.4	364, 605, 1717
<i>asm</i>		Unable to assimilate low levels of ammonia; deficient in glutamate synthase and glutamine synthase	70.5	445, 592, 1717
<i>asn</i>	Asparagine	Asparagine synthesis	82.4	957, 1717, 2240, 2241
<i>asnU</i>	Asparagine	Asparagine tRNA	44.1	1717
<i>aspA</i>	Aspartate	L-Aspartate ammonia-lyase (EC 4.3.1.1)	94.2	35, 1717
<i>aspC</i>	Aspartate	Aspartate aminotransferase (EC 2.6.1.1)	22.7	1717, 2072
<i>asrA</i>		Anaerobic sulfite reductase	57.1	850, 851, 1717
<i>asrB</i>		Anaerobic sulfite reductase	57.1	850, 851, 1717
<i>asrC</i>		Anaerobic sulfite reductase	57.1	850, 851, 1717
<i>ataA</i>	Attachment	<i>attP22 I</i> ; attachment site for prophage P22	7.8	100, 828, 948, 949, 1132, 1287, 1612, 1648, 1717, 2194
<i>atbA</i>	Attachment	<i>attP27 I</i> ; attachment site for prophage P27	12.7	100, 1212, 1717
<i>atbB</i>	Attachment	<i>attP27 II</i> ; second attachment site for prophage P27	8.1	100, 1717
<i>atcA</i>	Attachment	<i>attP221</i> ; attachment site for prophage P221	25.9	1717, 2209
<i>atdA</i>	Attachment	<i>attP14</i> ; attachment site for prophage P14 in group C <i>Salmonella</i> spp.	61.1	100, 1717
<i>atp</i>		<i>unc</i> , <i>unCA</i> ; membrane-bound (Mg ²⁺ , Ca ²⁺) ATPase	84.6	552, 553, 613, 957, 1717, 1883, 2240, 2241
<i>atrB</i>	Acid tolerance response	Defective in pre- but not post-acid shock-induced acid tolerance	32.2	548, 550, 552, 1717
<i>atrD</i>	Acid tolerance response	Defective in both pre- and post-acid shock-induced acid tolerance	68.1	548, 550, 1717
<i>atrF</i>	Acid tolerance response	Defective in both pre- and post-acid shock-induced acid tolerance	13.7	548, 550, 1717
<i>atrG</i>	Acid tolerance response	Defective in both pre- and post-acid shock-induced acid tolerance	NM	550, 1717
<i>atrR</i>	Acid tolerance response	<i>atrB</i> ; constitutive acid tolerance; <i>trans</i> -acting regulator of <i>atrB</i>	89.5	550, 1717
<i>ats</i>		Arylsulfatase	NM	1396, 1717, 2183
<i>att15</i>	Attachment	Attachment site for phage e15 in group E <i>Salmonella</i> spp.	46.3	1050, 1309, 1717
<i>att34</i>	Attachment	Attachment site for phage e34 in group E <i>Salmonella</i> spp.	5.7	1309, 1717
<i>attN</i>	Attachment	Attachment site for prophage N in <i>S. montevideo</i>	52.0	411, 1717
<i>avtA</i>		Alanine-valine transaminase, transaminase C (EC 2.6.1.66)	80.2	157, 1717, 2130

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<i>aziA</i>	Azide	Resistant to 3 mM sodium azide on L-methionine	3.4	341, 342, 536, 1717
<i>bfp</i>	Bundle-forming pili	Interbacterial linkage, adhesion to epithelial cells	NM	1717, 1854
<i>bioA</i>	Biotin	<i>bio</i> ; 7,8-diaminopelargonic acid synthetase	18.1	238, 1717, 1797, 1933
<i>bioB</i>	Biotin	Biotin synthetase	18.1	1717, 1797
<i>bioC</i>	Biotin	Block prior to pimeloyl-CoA	18.2	1717, 1797
<i>bioD</i>	Biotin	Dethiobiotin synthetase	18.2	1717, 1797
<i>bioF</i>	Biotin	7-Keto-8-aminopelargonic acid synthetase	18.1	1717, 1797
<i>birA</i>	Biotin repressor	Biotin-[acetyl-CoA carboxylase] holoenzyme synthetase	90.0	458, 1717
<i>brnQ</i>		<i>ilvT</i> ; branched-chain amino acid transport	8.9	1045, 1047, 1307, 1460, 1463, 1717
<i>btuB</i>	B ₁₂ utilization	<i>bfe</i> ; transport of cobalamins	89.7	706, 1372, 1373, 1649, 1650, 1717, 2114
<i>btuC</i>	B ₁₂ utilization	Transport of cobalamins	30.4	1717, 1846
<i>btuD</i>	B ₁₂ utilization	Transport of cobalamins	30.4	1717
<i>btuE</i>	B ₁₂ utilization	Transport of cobalamins	30.4	1717
<i>cadA</i>	Cadaverine	Lysine decarboxylase (EC 4.1.1.18)	56.2	562, 614, 1717
<i>cadC</i>	Cadaverine	Regulation of <i>cadA</i>	56.2	562, 1717
<i>capS</i>	Capsule	Capsular polysaccharide synthesis	31.1	1717, 1730
<i>carA</i>		<i>argD</i> , <i>ars</i> , <i>cap</i> , <i>pyrA</i> ; carbamyl phosphate synthase, glutamine (light) subunit (EC 2.7.2.9)	1.6	1-4, 264, 304, 311, 399, 728, 910, 944, 1023, 1035, 1242, 1243, 1419, 1459, 1717, 1838, 1978, 2197
<i>carB</i>		<i>pyrA</i> ; carbamyl phosphate synthase, ammonia (heavy) subunit (EC 2.7.2.9)	1.7	1-4, 264, 304, 311, 399, 728, 910, 944, 1023, 1035, 1242, 1243, 1419, 1459, 1717, 1838, 1978, 2197
<i>cbiA</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.7	1681, 1717
<i>cbiB</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.7	1681, 1717
<i>cbiC</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.7	1681, 1717
<i>cbiD</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.7	1681, 1717
<i>cbiE</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.7	1681, 1717
<i>cbiF</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.7	1681, 1717
<i>cbiG</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.6	1681, 1717
<i>cbiH</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.6	1681, 1717
<i>cbiJ</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.6	1681, 1717
<i>cbiK</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.6	1681, 1717
<i>cbiL</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.6	1681, 1717
<i>cbiM</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.6	1681, 1717
<i>cbiN</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.5	1681, 1717
<i>cbiO</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.5	1681, 1717
<i>cbiP</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.5	1681, 1717
<i>cbiQ</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.5	1681, 1717
<i>cbiT</i>		<i>cobI</i> ; synthesis of vitamin B ₁₂ adenosyl cobinamide precursor	43.7	1681, 1717
<i>cdd</i>		Cytidine deaminase (EC 3.5.4.5)	47.5	133, 930, 1016, 1717
<i>cheA</i>	Chemotaxis	<i>cheP</i> ; chemotaxis; ATP-dependent kinase; phosphorylates CheB and CheY	42.0	84-86, 354, 403, 429, 471, 1079, 1118, 1141, 1251, 1260-1263, 1265, 1352, 1717, 1876, 1909, 1916, 1919, 2001, 2002, 2069, 2102, 2176
<i>cheB</i>	Chemotaxis	<i>cheX</i> ; chemotaxis; bifunctional monomeric protein; C-terminal γ -carboxyl methylsterase and N-terminal transferase	41.9	196, 197, 407, 427-430, 608, 1028, 1118, 1148, 1251, 1616, 1717, 1807, 1808, 1839, 1916, 1917, 1919
<i>cheR</i>	Chemotaxis	Chemotaxis; S-adenosylmethionine-dependent methyltransferase	41.9	84-86, 196, 197, 347, 407, 427-430, 1079, 1118, 1148, 1251, 1717, 1873, 1876, 1917-1919, 1951, 2001, 2002, 2102
<i>cheS</i>	Chemotaxis	Chemotaxis	NM	85, 1148, 1717, 2102
<i>cheW</i>	Chemotaxis	Chemotaxis	42.0	85, 354, 429, 1118, 1148, 1717, 1804, 1911, 1919, 2102
<i>cheY</i>	Chemotaxis	<i>cheQ</i> ; chemotaxis; cytoplasmic protein; interacts at flagellar motor to reverse flagellar rotation	41.8	80, 84-86, 314, 354, 403, 427-430, 471, 1028, 1079, 1118, 1148, 1249-1251, 1260-1263, 1265, 1271, 1352, 1717, 1839, 1852, 1876, 1910, 1916, 1919, 2001, 2002, 2069, 2102

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<i>cheZ</i>	Chemotaxis	<i>cheT</i> ; chemotaxis; stimulates phospho-CheY dephosphorylation	41.8	85, 427–430, 471, 608, 1148, 1249, 1251, 1616, 1717, 1839, 1852, 1912, 1915, 1918, 1919, 2002, 2069, 2102
<i>chlF</i>	Chlorate	Resistance; may be part of <i>moe</i> operon	19.1	505, 1717, 1718, 1721, 1784, 1904, 1934
<i>chlG</i>	Chlorate	Resistance; affects nitrate reductase, tetrathionate reductase, chlorate reductase, and hydrogen lyase	56.8	1717, 1904, 1935
<i>cil</i>	Citrate lyase	Mutants unable to utilize citrate in anaerobic conditions without additional carbon sources	66.9	1105, 1717
<i>citA</i>	Citrate	Citrate carrier, different from TctI, TctII, TctIII transport systems	17.0	1717, 1795
<i>citB</i>	Citrate	Citrate carrier, different from TctI, TctII, TctIII transport systems	17.0	1717, 1795
<i>clid</i>	Chain length determinant	<i>rol</i> ; regulation of chain length in the O-units of the LPS	44.9	123, 124, 1717
<i>clmA</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	86.4	1717, 1750
<i>clmB</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	8.8	1717, 1750
<i>clmC</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	72.1	1717, 1750
<i>clmD</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	85.5	1717, 1750
<i>clmE</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	74.5	1717, 1750
<i>clmG</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	12.3	1717, 1721, 1750
<i>clmI</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	6.5	1717, 1750
<i>clmJ</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	32.4	1717, 1750
<i>clmK</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	62.4	1717, 1750
<i>clmM</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	99.1	1717, 1750
<i>clmN</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	46.9	1717, 1750
<i>clmP</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	81.1	1717, 1750
<i>clmQ</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	58.1	1717, 1750
<i>clmR</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	26.3	1717, 1750
<i>clmS</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	95.8	1717, 1750
<i>clmT</i>	Conditional-lethal mutation	Heat- or cold-sensitive mutation	51.0	1717, 1750
<i>cmk</i>		Cytidylate kinase (EC 2.7.4.14)	20.0	136, 1717
<i>coaA</i>	Coenzyme A	CoA synthesis; pantothenate kinase	90.3	15, 480, 1717
<i>cobA</i>	Cobalamin	<i>cobIV</i> ; ATP:corrinoid adenosyltransferase	38.0	515, 965, 1507, 1717, 1953, 1954
<i>cobB</i>	Cobalamin	DMB ribose phosphate phosphatase	20.6	1717, 2030
<i>cobC</i>	Cobalamin	DMB ribose phosphate phosphatase	15.6	669, 1498, 1509, 1717
<i>cobD</i>	Cobalamin	Synthesis of 1-amino-2-propanol moiety of vitamin B ₁₂	15.6	669, 1498, 1717
<i>cobF</i>	Cobalamin	Recessive regulator of <i>cbi</i> operon	26.9	57, 1717
<i>cobI</i>	Cobalamin	Operon encoding genes for synthesis of cobinamide intermediate of vitamin B ₁₂	43.6	514, 575, 951, 952, 1717
<i>cobII</i>	Cobalamin	Operon encoding genes for synthesis of DMB intermediate of vitamin B ₁₂	43.3	514, 951, 952, 1717
<i>cobIII</i>	Cobalamin	Operon encoding genes for joining cobinamide and DMB intermediates of vitamin B ₁₂	43.4	514, 951, 952, 1717
<i>cobJ</i>	Cobalamin	<i>cobII</i> ; synthesis of 5,6-DMB	43.3	513, 1717
<i>cobK</i>	Cobalamin	<i>cobII</i> ; synthesis of 5,6-DMB	43.3	513, 1717
<i>cobL</i>	Cobalamin	<i>cobII</i> ; synthesis of 5,6-DMB	43.3	513, 1717
<i>cobM</i>	Cobalamin	<i>cobII</i> ; synthesis of 5,6-DMB	43.3	513, 1717
<i>cobR</i>	Cobalamin	<i>cis</i> -Acting, dominant regulator for the <i>cbi</i> operon	44.0	57, 1717
<i>cobS</i>	Cobalamin	<i>cobIII</i> ; synthesis of the nucleotide loop that joins DMB to the corrin ring	43.5	513, 1508, 1681, 1717
<i>cobT</i>	Cobalamin	<i>cobIII</i> ; synthesis of DMB and transfer of ribose phosphate from NMN to DMB	43.4	513, 1508, 1717, 2030
<i>cobU</i>	Cobalamin	<i>cobIII</i> ; synthesis of the nucleotide loop that joins DMB to the corrin ring	43.5	513, 1507, 1508, 1681, 1717

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<i>cod</i>		Cytosine deaminase (EC 3.5.4.1)	72.8	134, 1015, 1717, 2127
<i>corA</i>	Cobalt resistance	Magnesium transport; cobalt resistance (high level)	85.8	630, 787, 788, 1717, 1843, 1847–1849
<i>corB</i>	Cobalt resistance	Magnesium transport; cobalt resistance (low level)	58.7	630, 1717
<i>corC</i>	Cobalt resistance	Magnesium transport; cobalt resistance (low level)	16.1	630, 703, 1717
<i>corD</i>	Cobalt resistance	<i>apaG</i> ; magnesium transport; cobalt resistance (low level)	2.1	630, 1717
<i>cpdB</i>		<i>cpd</i> ; 2', 3'-cyclic phosphodiesterase (EC 3.1.4.16)	69.5	30, 32, 210, 1221, 1704, 1717, 2027
<i>cpsB</i>	Capsule	M antigen capsular polysaccharide synthesis; homologous to <i>rfbM</i>	45.5	1717, 1903
<i>cpsG</i>	Capsule	<i>rfbL</i> ; M antigen capsular polysaccharide synthesis; homologous to <i>rfbK</i>	45.4	1717, 1903
<i>crp</i>		cAMP receptor protein	75.0	15, 32, 53, 187, 382, 441, 455, 825, 982, 1415, 1611, 1625, 1717, 1763, 1767, 2123
<i>crr</i>		Factor III for sugar transport by phosphotransferase IIB' (<i>ptsG</i>) system	52.9	373–376, 441, 531, 1322–1324, 1365, 1415, 1416, 1578, 1580, 1581, 1673, 1707, 1709, 1717, 1765, 1766, 1801, 2027
<i>cspA</i>	Cold shock protein	Transcriptional activation of cold shock promoters	80.0	1717
<i>cspG</i>	Cold shock protein	Transcriptional activation of cold shock promoters; putative	42.9	1661, 1717
<i>cutE</i>		<i>lnt</i> ; apolipoprotein <i>N</i> -acyltransferase	16.1	703, 1717
<i>cwd</i>	Cell wall defect	Sensitive to bile salts; mucoid	38.5	777, 1717
<i>cyaA</i>	cAMP	<i>cya</i> ; adenylate cyclase (EC 4.6.1.1)	85.7	32, 187, 455, 518, 825, 982, 1611, 1703, 1710, 1711, 1717, 2015, 2027, 2097, 2123, 2207
<i>cysA</i>	Cysteine	Sulfate-thiosulfate transport; chromate resistance	53.0	107, 117, 199, 316, 469, 470, 847, 873, 874, 976, 1005, 1368, 1375, 1416, 1469, 1532–1534, 1561, 1603, 1717, 2136
<i>cysB</i>	Cysteine	Regulation of L-cysteine transport and biosynthesis	37.7	106, 117, 292, 536, 847, 848, 874, 923–925, 1339, 1368, 1376, 1499–1501, 1503, 1504, 1716, 1717, 1821, 2135
<i>cysC</i>	Cysteine	Adenylylsulfate kinase (EC 2.7.1.25)	64.3	117, 438, 919, 1037–1039, 1375, 1603, 1717
<i>cysD</i>	Cysteine	Sulfate adenylyltransferases (EC 2.7.7.4)	64.3	117, 438, 919, 976, 1037–1039, 1368, 1375, 1603, 1717
<i>cysE</i>	Cysteine	Serine acetyltransferase (EC 2.3.1.30)	81.0	117, 137, 340, 446, 871, 875, 1087, 1095, 1097, 1107, 1368, 1500, 1717
<i>cysG</i>	Cysteine	Bifunctional protein: siroheme synthetase; uroporphyrinogen III methylase	75.5	117, 648, 794, 919, 951, 1717, 1867, 2169
<i>cysH</i>	Cysteine	Adenylylsulfate reductase (EC 1.8.99.2)	64.2	117, 438, 919, 1037–1039, 1235, 1376, 1499, 1502, 1503, 1505, 1549, 1717
<i>cysI</i>	Cysteine	Heme protein component of sulfite reductase	64.2	117, 438, 723, 794, 919, 1037–1039, 1235, 1376, 1499, 1502, 1503, 1505, 1717
<i>cysJ</i>	Cysteine	Flavoprotein component of sulfite reductase	64.2	117, 438, 723, 919, 1037–1039, 1235, 1236, 1376, 1499, 1502, 1503, 1505, 1549, 1717
<i>cysK</i>	Cysteine	<i>trz</i> ; resistance to 1,2,4-triazole; <i>O</i> -acetylserine sulfhydrylase A (EC 4.2.99.8)	52.8	266, 340, 368, 376, 536, 537, 871–874, 876, 1096, 1375, 1376, 1408, 1717, 2136
<i>cysL</i>	Cysteine	Resistance to selenate	53.1	872, 1717
<i>cysM</i>	Cysteine	<i>O</i> -Acetylserine sulfhydrylase B (EC 4.2.99.8)	53.0	537, 873, 874, 1375, 1408, 1717, 2135
<i>cysP</i>	Cysteine	Periplasmic thiosulfate-binding protein	53.1	846, 847, 1717
<i>cysQ</i>	Cysteine	Regulation of 3'-phosphoadenoside 5'-phosphosulfate pools; putative	69.5	1221, 1717
<i>cysU</i>	Cysteine	<i>cysAa</i> , <i>cysT</i> ; sulfate-thiosulfate transport	53.1	846, 847, 1717
<i>cysW</i>	Cysteine	<i>cysAb</i> ; sulfate-thiosulfate transport	53.1	847, 1717
<i>cysZ</i>	Cysteine	Sulfate transport; putative	52.8	266, 1717
<i>cytR</i>		Regulatory gene for <i>deo</i> operon and <i>udp</i> and <i>cdd</i> genes	88.6	1086, 1717

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<i>dadA</i>		<i>dad</i> ; D-histidine, D-methionine utilization; D-alanine dehydrogenase (EC 1.4.99.1)	41.1	1371, 1717, 2106, 2142, 2143
<i>dadB</i>		Catabolic alanine racemase (EC 5.1.1.1)	41.1	520, 599, 1717, 2105, 2106
<i>dadR</i>		Insensitivity of <i>dadA</i> to catabolite repression	41.1	1717, 2141, 2142
<i>dam</i>		DNA adenine methylase	75.6	659, 713, 1525, 1651, 1717
<i>dapA</i>	Diaminopimelate	Dihydropicolinate synthetase (EC 4.2.1.52)	54.0	1717, 1718, 1721
<i>dapB</i>	Diaminopimelate	Dihydropicolinate reductase	0.5	1717, 1718, 1721
<i>dapC</i>	Diaminopimelate	Tetrahydropicolinate succinylase	5.2	1717, 1718, 1721
<i>dapD</i>	Diaminopimelate	Succinyl-diaminopimelate aminotransferase	5.2	1717, 1718, 1721
<i>dapF</i>	Diaminopimelate	Diaminopimelate epimerase (EC 5.1.1.7)	5.4	1717, 1718, 1721
<i>dcd</i>		dCTP deaminase (EC 3.5.4.13)	45.9	132, 135, 1717
<i>dcm</i>		DNA cytosine methylation	43.1	659, 1717
<i>dcp</i>		Dipeptidyl carboxypeptidase	32.5	724, 1717, 2081
<i>dctA</i>		Transport of dicarboxylic acids	79.9	1010, 1011, 1531, 1717, 1943
<i>ddlA</i>	D-Alanine	D-Alanine:D-alanine ligase (EC 3.6.2.4)	8.7	413, 1062, 1717
<i>deoA</i>	Deoxyribose	<i>tpp</i> ; thymidine phosphorylase (EC 2.4.2.4)	99.0	175, 796, 798, 935, 936, 1643, 1659, 1717
<i>deoB</i>	Deoxyribose	<i>drm</i> ; phosphopentomutase (EC 2.7.5.6)	99.0	130, 796, 798, 935, 936, 1659, 1717
<i>deoC</i>	Deoxyribose	<i>dra</i> ; phosphodeoxyriboaldolase (EC 4.1.2.4)	99.0	130, 377, 796–799, 935–938, 1659, 1717
<i>deoD</i>	Deoxyribose	<i>pnu</i> , <i>pup</i> ; purine nucleoside phosphorylase (EC 2.4.2.1)	99.0	798, 935, 936, 1658, 1659, 1717
<i>deoK</i>	Deoxyribose	Deoxyribokinase	20.2	798, 1717, 1740
<i>deoP</i>	Deoxyribose	Deoxyribose transport	20.3	798, 1717
<i>deoR</i>	Deoxyribose	Constitutive for enzymes of <i>deoA</i> , <i>deoB</i> , <i>deoC</i> , and <i>deoD</i>	19.4	174, 611, 1717
<i>dgo</i>		D-Galactonate utilization	83.2	1717
<i>dgt</i>		dGTP triphosphohydrolase (EC 3.1.5.1)	5.1	964, 1717
<i>dhb</i>		2,3-Dihydroxybenzoic acid requirement	19.3	47, 118, 326, 1155, 1160, 1717, 1755, 1901
<i>dhuA</i>	D-Histidine	Utilization; increased activity of histidine-binding protein J	51.2	39–41, 45, 46, 49, 74, 763, 1091, 1110, 1154, 1717
<i>divA</i>	Division	<i>wrkA</i> ; septum initiation defect	88.4	341, 342, 369, 1717, 1736
<i>divC</i>	Division	<i>smoA</i> ; septum initiation defect	3.1	65, 1717
<i>divD</i>	Division	Round cell morphology	55.6	65, 68, 383, 1717, 2174
<i>dml</i>	D-Malate	Utilization	82.2	1717, 1902
<i>dnaA</i>	DNA	DNA initiation	83.6	94, 95, 97–99, 501, 731, 845, 957, 1311, 1313, 1717, 1818
<i>dnaB</i>	DNA	DNA synthesis	92.1	1311–1314, 1717, 2161
<i>dnaC</i>	DNA	DNA synthesis initiation and cell division uncoupling	98.8	12, 13, 135, 1063, 1174, 1311–1313, 1663, 1686, 1717, 1785, 1786, 1869–1871
<i>dnaE</i>	DNA	DNA synthesis	5.9	1139, 1311–1313, 1717
<i>dnaG</i>	DNA	DNA biosynthesis; DNA primase	70.0	509, 1313, 1686, 1717, 1738
<i>dnaJ</i>	DNA	DNA biosynthesis	0.3	1313, 1717
<i>dnaK</i>	DNA	DNA biosynthesis	0.3	522, 1313, 1717
<i>dnaL</i>	DNA	DNA biosynthesis	NM	1313, 1717
<i>dnaN</i>	DNA	DNA biosynthesis; DNA polymerase III, β -subunit	83.6	501, 1313, 1717
<i>dnaQ</i>	DNA	DNA biosynthesis	6.9	1138, 1200, 1312, 1313, 1717, 1820
<i>dnaX</i>	DNA	DNA biosynthesis	11.5	1313, 1717
<i>dnaY</i>	DNA	DNA biosynthesis	NM	1313, 1717
<i>dnaZ</i>	DNA	DNA biosynthesis	NM	501, 1313, 1686, 1717
<i>dor</i>		Deletion of r-determinants from plasmids	55.7	660, 853, 1688, 1717, 2107
<i>dpp</i>		Dipeptide permease	75.9	7, 495, 1717
<i>dsd</i>		D-Serine sensitivity; D-serine dehydratase (EC 4.2.1.14)	52.7	1717, 1718, 1721
<i>dum</i>		dUMP synthesis	NM	135, 1717
<i>earA</i>		Regulates expression of <i>aniG</i>	88.2	22, 1717
<i>earC</i>		<i>trans</i> -Acting regulatory protein for <i>aciA</i>	46.8	562, 1717
<i>eca</i>		Enterobacterial common-antigen synthesis	NM	50, 222, 454, 456, 490, 902, 1257, 1266, 1284, 1397, 1717, 1983, 2065, 2150–2152, 2206, 2231
<i>endA</i>		Endonuclease I	67.1	1717, 1769, 2220
<i>eno</i>	Enolase	Enolase (EC 4.2.1.11)	64.3	617, 1717
<i>ent</i>	Enterochelin	<i>asc</i> , <i>enb</i> ; enterochelin (dihydroxybenzoylserine trimer)	13.6	146, 305, 329, 1177, 1584, 1585, 1717, 2198
<i>envA</i>	Envelope	Cell division defect, chain formation	3.2	341, 595, 1717
<i>envD</i>	Envelope	Autolysis; drug sensitivity; alterations in cell morphology	17.1	65, 69, 1563, 1717

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<i>envZ</i>	Envelope	<i>ompB</i> , <i>tpdB</i> , <i>tpbA</i> ; positive regulation of tripeptide permease and outer membrane protein	76.0	146, 631, 632, 644, 765, 927, 959, 1201–1204, 1431, 1521, 1717, 1799, 2040
<i>eutA</i>	Ethanolamine utilization	Vitamin B ₁₂ adenosyltransferase; required for use of ethanolamine as sole carbon or nitrogen source	53.3	1670–1672, 1717, 1794
<i>eutB</i>	Ethanolamine utilization	Ethanolamine ammonia lyase, subunit I	53.3	525, 526, 1670–1672, 1717, 1794
<i>eutC</i>	Ethanolamine utilization	Ethanolamine ammonia lyase, subunit II	53.2	525, 526, 1670–1672, 1717, 1794
<i>eutD</i>	Ethanolamine utilization	CoA-dependent acetaldehyde dehydrogenase	53.3	1670–1672, 1717
<i>eutE</i>	Ethanolamine utilization	Acetaldehyde CoA reductase	53.3	1670–1672, 1717
<i>eutF</i>	Ethanolamine utilization	Ethanolamine permease or transcription factor for expression of <i>eut</i> operon	38.2	1506, 1717
<i>eutG</i>	Ethanolamine utilization	Function unknown	53.3	1717
<i>eutH</i>	Ethanolamine utilization	Function unknown	53.2	1717
<i>eutR</i>	Ethanolamine utilization	Positive regulatory gene for <i>eut</i> operon	53.2	1670–1672, 1717, 1794
<i>exbB</i>		Biopolymer uptake; outer membrane protein	69.1	1538, 1717
<i>fabB</i>	Fatty acid biosynthesis	β-Ketoacyl acyl carrier protein synthetase I (EC 2.3.1.41)	51.9	385, 824, 1717
<i>fabI</i>	Fatty acid biosynthesis	<i>envM</i> ; enoyl-(acyl carrier protein) reductase (EC 1.3.1.9)	37.6	1717, 2038
<i>fabZ</i>	Fatty acid biosynthesis	Fatty acid biosynthesis; putative	4.1	783, 1717
<i>fdhB</i>	Formate dehydrogenase-H	Required for formate dehydrogenase-H and -N	18.0	118, 326, 1717, 1904
<i>fdhF</i>	Formate dehydrogenase-H	<i>fhl</i> ; formate dehydrogenase-H	92.8	119, 1717, 1904
<i>fdhR</i>	Formate dehydrogenase-H	Positive regulator of <i>fdhF</i> expression	75.0	523, 1717
<i>fdhS</i>	Formate dehydrogenase-H	Positive regulator of <i>fdhF</i> expression	75.0	523, 1717
<i>fdnA</i>	Formate dehydrogenase-N	Mutants lack formate dehydrogenase-N and nitrate reductase	87.6	118, 120, 1553, 1717
<i>fdnB</i>	Formate dehydrogenase-N	Synthesis or activation of the cytochrome associated with formate dehydrogenase-N	87.7	118, 120, 1553, 1717, 1905
<i>fdnC</i>	Formate dehydrogenase-N	Synthesis or activation of the cytochrome associated with formate dehydrogenase-N	87.7	1553, 1717, 1905
<i>fdp</i>		Fructose-1,6-diphosphatase (EC 3.1.3.11)	99.2	1717, 1718, 1721
<i>fhlA</i>	Formate hydrogenlyase	Formate hydrogenlyase; putative	62.8	1359, 1717
<i>fhlD</i>	Formate hydrogenlyase	Mutants lack formate dehydrogenase H activity	81.8	119, 326, 1717
<i>fhuA</i>	Ferric hydroxamate uptake	Outer membrane receptor for ferrichrome	4.9	237, 1067, 1717
<i>fhuB</i>	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	4.9	237, 1067, 1717
<i>fhuC</i>	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	4.9	237, 1067, 1717
<i>fhuD</i>	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	5.0	237, 1067, 1717
<i>fic</i>		Filamentation in presence of cAMP in mutant	75.1	1717, 2026
<i>fimA</i>	Fimbriae	<i>pil</i> , <i>fim</i> ; major subunit protein of the fimbriae	15.0	349, 408, 532, 1227, 1228, 1473, 1599, 1717, 1926, 1974, 1997
<i>fimC</i>	Fimbriae	Fimbriae	15.0	795, 1717, 1975
<i>fimD</i>	Fimbriae	Fimbriae	15.1	1717, 1974, 1975
<i>fimF</i>	Fimbriae	Fimbriae	15.1	795, 1717, 1975
<i>fimH</i>	Fimbriae	Adhesin component of the fimbriae	15.1	1227, 1717, 1974, 1975
<i>fimI</i>	Fimbriae	Fimbriae	15.0	795, 1717, 1975
<i>fimW</i>	Fimbriae	Fimbriae	15.2	795, 1717, 1975
<i>fimY</i>	Fimbriae	Fimbriae	15.2	795, 1717, 1975
<i>fimZ</i>	Fimbriae	Fimbriae	15.1	795, 1717, 1975
<i>fis</i>	Factor for inversion stimulation	DNA-binding protein involved in site-specific inversion and recombination, gene regulation, and DNA replication	74.0	538, 1717
<i>flgA</i>	Flagella	<i>flaFI</i> ; flagellar synthesis; P-ring formation of the flagellar basal body	26.4	633, 887, 891, 1120, 1122–1124, 1226, 1264, 1717, 1969
<i>flgB</i>	Flagella	<i>flaFII</i> ; flagellar synthesis; function unknown	26.4	633, 781, 820, 887, 891, 972, 1102, 1120, 1122, 1264, 1717, 1969
<i>flgC</i>	Flagella	<i>flaFIII</i> ; flagellar synthesis; basal-body protein	26.4	633, 820, 887, 891, 892, 972, 1102, 1264, 1717, 1969

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<i>flgD</i>	Flagella	<i>flaFIV</i> ; flagellar synthesis; hook-capping protein to enable assembly of hook protein subunits	26.4	633, 812, 887, 891, 1115, 1120, 1264, 1468, 1717, 1969
<i>flgE</i>	Flagella	<i>flaFV</i> ; flagellar synthesis; hook protein	26.4	16, 17, 812, 823, 887, 891, 1120, 1125, 1264, 1377, 1461, 1717, 1969
<i>flgF</i>	Flagella	<i>flaFVI</i> ; flagellar synthesis; basal-body rod protein	26.5	16, 820, 823, 887, 891, 971, 972, 1102, 1120, 1264, 1717, 1969
<i>flgG</i>	Flagella	<i>flaFVII</i> ; flagellar synthesis; basal-body rod protein	26.5	16, 820, 823, 887, 891, 972, 1102, 1120, 1264, 1717
<i>flgH</i>	Flagella	<i>flaFVIII</i> ; flagellar synthesis; basal-body L-ring protein	26.5	887, 891, 971, 1120, 1264, 1717, 1969
<i>flgI</i>	Flagella	<i>flaFIX</i> ; flagellar synthesis; basal-body P-ring protein	26.5	16, 819, 887, 891, 971, 1120, 1264, 1717, 1969
<i>flgJ</i>	Flagella	<i>flaFX</i> ; flagellar synthesis; function unknown	26.5	887, 891, 971, 1120, 1264, 1717, 1969
<i>flgK</i>	Flagella	<i>flaW</i> ; flagellar synthesis; hook-associated protein 1	26.6	812, 813, 815–817, 821, 822, 891, 895, 994, 1264, 1717, 2189
<i>flgL</i>	Flagella	<i>flaU</i> ; flagellar synthesis; hook-associated protein 3	26.6	812, 813, 815–817, 821, 822, 891, 895, 994, 1264, 1717, 2189
<i>flgM</i>	Flagella	<i>flgR</i> , <i>mviS</i> , <i>rflB</i> ; negative regulator of σ^F	26.4	633–635, 1119, 1465, 1717, 1754
<i>flgN</i>	Flagella	Initiation of flagellar filament assembly	26.4	1124, 1717
<i>flhA</i>	Flagella	<i>flaC</i> ; flagellar synthesis; function unknown	41.7	354, 504, 887, 890, 891, 989, 1074, 1120, 1123, 1264, 1317, 1359, 1361, 1717, 2077, 2085, 2192
<i>flhB</i>	Flagella	<i>flaM</i> ; flagellar synthesis; assists <i>fliK</i> in hook length control	41.7	354, 471, 781, 887, 891, 1118, 1120–1122, 1264, 1361, 1717, 1873, 1915, 2192
<i>flhC</i>	Flagella	<i>flaE</i> ; flagellar synthesis; regulation of gene expression	42.1	354, 504, 635, 887, 890, 891, 989, 1074, 1118, 1120, 1264, 1317, 1717, 2077, 2192
<i>flhD</i>	Flagella	<i>flaK</i> ; flagellar synthesis; regulation of gene expression; putative flagellum-specific σ factor	42.1	354, 504, 635, 887, 890, 891, 989, 1074, 1118, 1120, 1122, 1264, 1317, 1717, 2077, 2192
<i>flhE</i>	Flagella	Function unknown; not essential for flagellar synthesis or function	41.7	1361, 1717
<i>fliA</i>	Flagella	<i>flaL</i> ; flagellar synthesis; alternative σ factor, σ^F , for flagellar expression	42.4	354, 504, 635, 887, 890, 891, 977, 989, 994, 1074, 1119, 1122, 1123, 1264, 1317, 1464, 1465, 1717, 1969, 2077, 2192
<i>fliB</i>	Flagella	<i>nml</i> ; flagellar synthesis; N-methylation of lysine residues in flagellin	42.5	891, 1026, 1076, 1264, 1717, 1924
<i>fliC</i>	Flagella	<i>H1</i> ; flagellar synthesis; phase 1 flagellin (filament structural protein)	42.5	274, 507, 508, 582, 583, 585, 634, 743, 814, 821, 829, 832, 881, 884–889, 891–894, 906, 913, 985–988, 994–997, 1001, 1116, 1117, 1157, 1264, 1265, 1278, 1305, 1318, 1454, 1465, 1471, 1556, 1717, 1802, 1804, 1806, 1840, 1841, 1928, 1966, 1967, 2025, 2115, 2116, 2191, 2192, 2208
<i>fliD</i>	Flagella	<i>flaV</i> ; flagellar synthesis; hook-associated protein 2	42.5	129, 813, 815–817, 821, 822, 891, 895, 993, 994, 1122, 1264, 1717, 2189
<i>fliE</i>	Flagella	<i>flaAI</i> ; flagellar synthesis; function unknown	42.7	354, 504, 829, 887, 890, 891, 989, 1074, 1102, 1120, 1122, 1264, 1317, 1392, 1607, 1717, 1803, 1965, 2077, 2190–2192
<i>fliF</i>	Flagella	<i>flaAIII.1</i> ; flagellar synthesis; basal-body M-ring protein	42.7	16, 424, 567, 891, 972, 1122, 1264, 1472, 1607, 1717, 2041, 2042, 2186

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<i>fliG</i>	Flagella	<i>flaAII.2</i> , <i>morC</i> , <i>cheV</i> ; flagellar synthesis; motor switching and energizing	42.7	354, 424, 471, 487, 504, 508, 567, 887, 890, 891, 907, 989, 1027, 1034, 1074, 1120, 1148, 1264, 1271, 1481, 1717, 2077, 2102, 2185, 2186, 2192
<i>fliH</i>	Flagella	<i>flaAII.3</i> ; flagellar synthesis; function unknown	42.8	424, 818, 891, 1264, 1717, 2085, 2186
<i>fliI</i>	Flagella	<i>flaAIII</i> ; flagellar assembly; may be ATPase in protein export pathway	42.8	354, 468, 471, 504, 818, 887, 890, 891, 989, 1074, 1120, 1264, 1717, 1877, 2077, 2085, 2186, 2192
<i>fliJ</i>	Flagella	<i>flaS</i> ; flagellar synthesis; function unknown	42.8	818, 891, 1120, 1264, 1717, 2085
<i>fliK</i>	Flagella	<i>flaR</i> ; flagellar synthesis; hook length control and replacement of <i>flgD</i> by <i>flgK</i>	42.8	17, 781, 818, 891, 1074, 1120, 1121, 1264, 1552, 1717, 1968, 2187
<i>fliL</i>	Flagella	<i>flaQI</i> ; flagellar synthesis; function unknown	42.8	818, 891, 1034, 1122, 1264, 1608, 1717
<i>fliM</i>	Flagella	<i>flaQII</i> , <i>cheC</i> , <i>cheU</i> ; flagellar synthesis; motor switching and energizing	42.8	429, 487, 504, 818, 887, 890, 891, 989, 1027–1029, 1034, 1120, 1148, 1264, 1271, 1317, 1481, 1717, 1852, 2102, 2192
<i>fliN</i>	Flagella	<i>flaN</i> ; flagellar synthesis; motor switching and energizing	42.8	354, 471, 504, 887, 890, 891, 907, 989, 1027, 1034, 1264, 1271, 1317, 1481, 1717, 2085, 2185, 2186, 2192
<i>fliO</i>	Flagella	<i>flaP</i> ; flagellar synthesis; function unknown	42.9	504, 887, 890, 891, 989, 1264, 1317, 1717, 2192
<i>fliP</i>	Flagella	<i>flaB</i> ; flagellar synthesis; function unknown	42.9	354, 504, 887, 890, 891, 989, 1074, 1264, 1317, 1717, 2077, 2192
<i>fliQ</i>	Flagella	<i>flaD</i> ; flagellar synthesis; function unknown	42.9	354, 504, 887, 890, 891, 989, 1074, 1264, 1317, 1717, 2077, 2185, 2192
<i>fliR</i>	Flagella	<i>flaX</i> ; flagellar synthesis; function unknown	42.9	891, 1264, 1717
<i>fliS</i>	Flagella	Member of axial family of structural proteins	42.6	1008, 1717
<i>fliT</i>	Flagella	Member of axial family of structural proteins	42.6	1008, 1717
<i>fliU</i>	Flagella	Flagellar function; part of basal body, or required for flagellin processing or export	42.5	457, 1717
<i>fliV</i>	Flagella	Flagellar function; part of basal body, or required for flagellin processing or export	42.5	457, 1717
<i>fljA</i>	Flagella	<i>rhl</i> ; flagellar synthesis; repressor of <i>fliC</i>	60.0	583, 891, 1123, 1264, 1717, 2188
<i>fljB</i>	Flagella	<i>H2</i> ; flagellar synthesis; phase 2 flagellin (filament structural protein)	60.1	487, 507, 508, 582, 634, 814, 884–889, 891–894, 896, 897, 985, 1116, 1117, 1157, 1264, 1278, 1318, 1471, 1556, 1717, 1796, 1802–1804, 1806, 1928, 1966, 1967, 1969, 1982, 2188, 2191, 2192, 2232, 2233
<i>flrB</i>	Fluoro-leucine resistance	Leucine or isoleucine regulation or both	16.4	20, 276, 574, 577, 589, 1717
<i>fnr</i>		<i>oxrA</i> ; anaerobic induction of genes for anaerobic metabolism, such as <i>pepT</i>	36.6	648, 942, 1230, 1717, 1904, 1940, 2165
<i>fol</i>	Folate	Trimethoprim resistance; tetrahydrofolate dehydrogenase	1.9	1023, 1717
<i>fpk</i>	Fructose	Fructose phosphate kinase	48.3	620, 1717
<i>frd</i>	Fumarate reductase	Fumarate reductase (EC 1.3.99.1)	NM	158, 1717
<i>fruA</i>	Fructose	Enzyme II ^{Fruc} of the phosphotransferase system	48.2	528, 619, 1717
<i>fruB</i>	Fructose	<i>fruF</i> ; enzyme III ^{Fruc} -modulator FPr tridomain fusion protein of the phosphotransferase system	48.1	528, 619, 620, 1717
<i>fruK</i>	Fructose	Fructose-1-phosphate kinase	48.1	528, 619, 1717
<i>fruR</i>	Fructose	Regulation of the fructose regulon; regulation of gluconeogenesis; may be the same as <i>ppsB</i>	3.0	323, 528, 619, 620, 1717, 2076
<i>ftsZ</i>		<i>sulB</i> ; essential for cell division	3.1	380, 1717
<i>fucA</i>	Fucose	<i>fuc</i> ; L-fucose utilization	65.1	1717
<i>fucI</i>	Fucose	L-Fucose utilization	65.1	1717
<i>fucK</i>	Fucose	L-Fucose utilization	65.1	1717
<i>fucP</i>	Fucose	L-Fucose utilization	65.1	1717
<i>fucR</i>	Fucose	L-Fucose utilization	65.1	1717

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<i>fumA</i>	Fumarate	Regulatory gene; putative	31.3	1652, 1717
<i>furA</i>	Ferrichrome	<i>fur</i> ; ferrichrome uptake, regulation of iron uptake; constitutive synthesis of iron-enterochelin	16.9	511, 549, 553, 554, 562, 613, 614, 1717
<i>fusA</i>	Fusidic acid	Protein chain elongation factor EF-G	74.7	958, 1717
<i>galE</i>	Galactose	UDP glucose 4-epimerase (EC 5.1.3.2)	17.8	584, 636, 653, 744, 834, 911, 1259, 1287, 1393, 1432, 1435, 1441, 1442, 1485, 1491, 1523, 1589, 1717, 1742, 2168
<i>galF</i>	Galactose	Modifier of UDP-glucose pyrophosphorylase	45.3	954, 1405, 1406, 1432, 1433, 1717
<i>galK</i>	Galactose	Galactokinase (EC 2.7.1.6)	17.8	31, 584, 834, 845, 1287, 1432, 1717, 1798
<i>galP</i>	Galactose	Specific galactose permease	67.0	1717, 1718, 1721
<i>galR</i>	Galactose	Regulation	65.3	1702, 1717
<i>galS</i>	Galactose	<i>mgID</i> ; <i>mgI</i> repressor and galactose ultrainduction factor	48.0	145, 1717
<i>galT</i>	Galactose	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	17.8	834, 1717
<i>galU</i>	Galactose	Glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	38.4	506, 777, 1406, 1485, 1717
<i>gapA</i>		Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	41.1	1152, 1717
<i>garA</i>	Gamma resistant	Resistant to γ and UV radiation; large cells; high RNA and protein content; may be equivalent to <i>rodA</i>	0.4	882, 1717
<i>garB</i>	Gamma resistant	Resistant to γ and UV radiation; large cells; high RNA and protein content	0.4	882, 1717
<i>gcv</i>	Glycine cleavage	<i>invD</i> ; defective in the glycine cleavage enzyme system	65.7	1717, 1893
<i>gdhA</i>		<i>gdh</i> ; glutamate dehydrogenase (EC 1.4.1.4)	29.1	105, 444, 445, 712, 778, 1351, 1675, 1717
<i>gleR</i>		Glycyl-leucyl-resistant regulatory gene for transport of branched-chain amino acids	8.1	1462, 1463, 1717
<i>glgA</i>	Glycogen	Glycogen synthase (EC 2.4.1.21)	77.2	1180, 1181, 1717, 1896
<i>glgC</i>	Glycogen	Glucose-1-phosphate adenyltransferase (EC 2.7.7.27)	77.2	1180, 1181, 1667, 1717, 1896
<i>glnA</i>	Glutamine	Glutamine synthetase (EC 6.3.1.2)	87.5	47, 163, 229, 230, 592, 593, 729, 933, 1066, 1088–1090, 1109, 1113, 1114, 1316, 1319, 1570, 1609, 1717, 2028, 2039, 2117
<i>glnD</i>	Glutamine	PIIA uridyl transferase	4.3	104, 1717
<i>glnE</i>	Glutamine	Covalent modification of glutamine synthetase; glutamine synthetase adenyltransferase (EC 2.7.2.42)	69.5	104, 1109, 1717
<i>glnH</i>	Glutamine	Periplasmic glutamine-binding protein	19.1	1113, 1717
<i>glnP</i>	Glutamine	High-affinity glutamine transport	19.1	89, 162, 163, 1717
<i>glpA</i>	Glycerol phosphate	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic) (EC 1.1.99.5)	49.6	1717, 1718, 1721
<i>glpD</i>	Glycerol phosphate	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (aerobic) (EC 1.1.1.8)	77.1	10, 1210, 1717
<i>glpK</i>	Glycerol phosphate	Glycerol kinase (EC 2.7.1.30)	88.5	1449, 1615, 1717, 1926
<i>glpQ</i>	Glycerol phosphate	Glycerol-3-phosphate diesterase	49.4	756, 1717
<i>glpR</i>	Glycerol phosphate	Regulatory gene for <i>glpD</i> , <i>glpK</i> , and <i>glpT</i>	77.1	1717, 1718, 1721
<i>glpT</i>	Glycerol phosphate	<i>sn</i> -Glycerol-3-phosphate transport	49.5	757, 1643, 1644, 1709, 1713, 1717
<i>gltA</i>	Glutamate	Requirement	17.1	1717, 1718, 1721
<i>gltB</i>	Glutamate	Glutamate synthetase (EC 2.6.1.53)	72.5	400, 581, 1269, 1717
<i>gltC</i>	Glutamate	Growth on glutamate as sole source of carbon	81.7	1717, 1718, 1721
<i>gltD</i>	Glutamate	Glutamate synthase, small subunit	72.7	400, 1269, 1717
<i>gltF</i>	Glutamate	Glutamate-specific transport system	0.1	35, 1717
<i>gltH</i>	Glutamate	Requirement	28.0	1717, 1718, 1721
<i>gltS</i>	Glutamate	Glutamate permease	81.7	35, 1717
<i>glyA</i>	Glycine	Serine hydroxymethyltransferase (EC 2.1.2.1)	56.0	1679, 1717, 1887–1890, 1943, 1944, 2048
<i>glyS</i>	Glycine	Glycyl-tRNA synthetase (EC 6.1.1.14)	80.1	1717, 1943, 1944
<i>glyT</i>	Glycine	<i>sufS</i> ; glycine tRNA ₂	90.0	1476, 1717
<i>gnd</i>		Phosphogluconate dehydrogenase (EC 1.1.1.43)	44.9	109, 165, 220, 682, 954, 975, 1398, 1475, 1621, 1717, 2154
<i>gpd</i>		Glucosamine-6-phosphate deaminase	NM	1711, 1717
<i>gpsA</i>		<i>sn</i> -Glycerol-3-phosphate dehydrogenase [NAD(P) ⁺] (EC 1.1.1.94)	81.0	1210, 1717
<i>gpt</i>		<i>gxu</i> ; guanine-hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	7.4	332, 665, 666, 833, 1483, 1484, 1648, 1717
<i>gsk</i>		Guanosine kinase	11.9	1717, 1718, 1721
<i>guaA</i>	Guanine	GMP synthetase (EC 6.3.4.1)	54.4	534, 611, 664, 1430, 1679, 1717, 1740
<i>guaB</i>	Guanine	IMP dehydrogenase (EC 1.1.1.205)	54.4	534, 611, 664, 943, 1430, 1679, 1717, 1740
<i>guaC</i>	Guanine	GMP reductase (EC 1.6.6.8)	3.5	148, 1717

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype ^a	Cs ^b	References ^c
<i>guaP</i>	Guanine	Guanine uptake	3.5	150, 1717
<i>gyrA</i>	Gyrase	<i>hisW</i> , <i>nalA</i> ; resistance or sensitivity to nalidixic acid; DNA gyrase	49.3	8, 9, 62, 178, 231, 232, 419, 420, 983, 1313, 1457, 1500, 1632, 1679, 1717, 1752, 2195
<i>gyrB</i>	Gyrase	<i>hisU</i> , <i>parA</i> ; DNA gyrase	83.3	62, 178, 203, 204, 232, 415–418, 983, 1252, 1455, 1457, 1679, 1717, 1752
<i>hemA</i>	Heme	Glutamyl-tRNA dehydrogenase	38.8	143, 493, 494, 497, 934, 1371, 1571, 1717, 1733, 1812, 2177
<i>hemB</i>	Heme	Heme deficient	8.7	1717, 1733, 2177
<i>hemC</i>	Heme	Heme deficient; urogen I synthase	85.7	1717, 1732, 2177
<i>hemD</i>	Heme	Heme deficient; uroporphyrinogen III cosynthase	85.7	1717, 1731, 2177
<i>hemE</i>	Heme	Accumulation of uroporphyrin III	90.6	449, 1717, 2177
<i>hemF</i>	Heme	Coproporphyrinogen III oxidase	53.2	1717, 2177, 2178
<i>hemG</i>	Heme	Defective in heme synthesis	86.5	1717, 2177
<i>hemH</i>	Heme	<i>visA</i> ; defective in heme synthesis	11.6	1717, 2177
<i>hemK</i>	Heme	Protoporphyrinogen oxidase; putative (EC 1.3.3.–)	38.8	493, 1717
<i>hemL</i>	Heme	Glutamate-1-semialdehyde aminotransferase	5.0	496, 497, 1717, 2177
<i>hemM</i>	Heme	Glutamyl tRNA dehydrogenase or subunit; putative	38.8	493, 1571, 1717
<i>hemN</i>	Heme	Oxygen-independent coproporphyrinogen III oxidase	86.7	1717, 2177, 2179
<i>hil</i>	Hyperinvasion locus	Hyperinvasion; essential for bacterial entry into epithelial cells	62.8	1158, 1359, 1717
<i>himA</i>		Integration host factor (IHF), α -subunit; site-specific recombination	30.3	1196, 1717
<i>himD</i>		Integration host factor (IHF), β -subunit; site-specific recombination	20.1	1455, 1717
<i>hin</i>	H inversion	<i>vh2</i> ; flagellar synthesis; regulation of flagellin gene expression by site-specific inversion of DNA	60.1	243, 244, 582, 643, 869, 884–887, 891, 998, 1116, 1117, 1157, 1256, 1264, 1556, 1717, 1772, 1802, 1823, 1981, 1982, 2188, 2232, 2234, 2235
<i>hisA</i>	Histidine	<i>N</i> -(5'-phospho-L-ribosylformimino)-5-amino-1-(5' -phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	44.8	26, 37, 165, 232, 280, 281, 335, 682, 736–738, 867, 908, 1071, 1073, 1231, 1295, 1296, 1301, 1610, 1717
<i>hisB</i>	Histidine	Imidazoleglycerol-phosphate dehydratase and histidinol phosphatase (EC 4.2.1.19, EC 3.1.3.15)	44.8	25, 37, 165, 217, 232, 280, 281, 319, 336, 736–738, 837–841, 1071, 1073, 1231, 1301, 1657, 1717, 1885
<i>hisC</i>	Histidine	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	44.8	24–26, 29, 37, 165, 232, 281, 645, 736–738, 754, 755, 916, 1071, 1073, 1231, 1301–1303, 1619, 1645, 1655–1657, 1717, 1777
<i>hisD</i>	Histidine	Histidinol dehydrogenase (EC 1.1.1.23)	44.7	24, 26, 29, 37, 54, 81, 113, 115, 141, 165, 171, 206, 232, 246, 247, 281, 336, 343, 674, 696, 737, 738, 867, 905, 916, 917, 1070, 1071, 1165, 1619, 1645, 1717, 1748, 1751, 1995, 2159, 2199, 2212–2216
<i>hisF</i>	Histidine	Cyclase	44.8	37, 165, 232, 280, 281, 318, 645, 736, 737, 1231, 1301, 1717
<i>hisG</i>	Histidine	ATP phosphoribosyltransferase (EC 2.4.2.17)	44.7	26, 27, 37, 38, 54, 81, 111–116, 165, 176, 177, 179, 188, 202, 225, 281, 300, 312, 337–339, 351, 372, 530, 597, 645–647, 737, 827, 967, 1055, 1057–1059, 1071, 1084, 1099, 1231, 1301, 1333, 1334, 1380, 1381, 1457, 1542–1545, 1590, 1647, 1682, 1692, 1717, 1770, 1771, 1782, 1842, 1900, 2084, 2086, 2092, 2134, 2149
<i>hisH</i>	Histidine	Amidotransferase (EC 2.4.2.–)	44.8	37, 65, 165, 232, 280, 281, 737, 1071, 1717

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<i>hisI</i>	Histidine	<i>hisE</i> , <i>hisIE</i> ; phosphoribosyl-AMP cyclohydrolase, phosphoribosyl-ATP pyrophosphatase (EC 3.5.4.19, EC 3.6.1.31)	44.8	37, 165, 232, 246, 280–282, 318, 645, 736, 737, 1231, 1301, 1717
<i>hisJ</i>	Histidine	Periplasmic histidine-binding protein J for high-affinity histidine transport system	51.2	39–41, 43, 45, 46, 49, 70, 73, 74, 258, 762, 766, 789, 1111, 1154, 1155, 1160, 1182, 1231, 1292, 1301, 1591, 1717, 2237
<i>hisM</i>	Histidine	Histidine transport; inner membrane protein	51.2	48, 762, 766, 1423, 1554, 1717
<i>hisP</i>	Histidine	High-affinity histidine transport; inner membrane protein	51.2	39–43, 45, 46, 48, 49, 70, 73, 74, 232, 637, 754, 766, 1110, 1160, 1591, 1679, 1717, 1760
<i>hisQ</i>	Histidine	Histidine transport; membrane protein	51.2	45, 46, 48, 70, 74, 762, 766, 1160, 1717
<i>hisR</i>	Histidine	tRNA structural gene	85.6	178, 201, 208, 232, 233, 282, 535, 1241, 1457, 1458, 1679, 1680, 1717, 1800, 1810
<i>hisS</i>	Histidine	Histidyl-tRNA synthetase (EC 6.1.1.21)	55.4	178, 232–235, 351, 433–436, 452, 453, 1179, 1189, 1320, 1678, 1679, 1717, 1811, 1942, 2173
<i>hisT</i>	Histidine	Pseudouridine modification of tRNA	51.8	178, 205, 206, 209, 232, 236, 241, 303, 376, 378, 379, 426, 966, 975, 1412, 1413, 1519, 1601, 1654, 1674, 1679, 1714, 1717, 2044
<i>hmpA</i>	Hemoprotein	Dihydropteridine reductase activity (EC 1.6.99.7)	56.0	1717, 1894
<i>hns</i>		<i>osmZ</i> , <i>bgIY</i> , <i>pilG</i> ; histone-like protein; DNA-binding nucleoid-associated protein	38.4	517, 770, 780, 877, 1299, 1516, 1717, 2036
<i>hpt</i>		Hypoxanthine phosphoribosyltransferase (not EC 2.4.2.8)(see <i>gpt</i>)	3.8	147, 148, 485, 486, 665, 833, 1484, 1637, 1717
<i>hsdL</i>	Host specificity	<i>hspLT</i> ; restriction-modification system	8.4	131, 153, 254, 350, 355, 359–361, 409, 421–423, 740, 741, 1470, 1717, 2031
<i>hsdM</i>	Host specificity	<i>hsdSB</i> ; restriction-modification system; modification component	98.5	253, 254, 256, 362, 588, 1100, 1417, 1717, 1787, 2031, 2065
<i>hsdS</i>	Host specificity	<i>hsdSB</i> ; restriction-modification system; specificity component	98.4	253, 254, 256, 362, 588, 1100, 1417, 1717, 1787, 2031, 2065
<i>hsdSA</i>	Host specificity	Restriction-modification system (operon)	97.6	131, 153, 254, 255, 350, 355, 359–361, 741, 1040, 1100, 1417, 1470, 1717, 1822, 2031, 2075
<i>htrA</i>	High temperature requirement	<i>degP</i> ; heat shock (stress)-regulated periplasmic protease; essential for survival in macrophages	5.1	129, 310, 964, 1717
<i>hupA</i>		Histonelike protein HU-2	90.7	773, 779, 1717
<i>hupB</i>		Histonelike protein HU-1	11.4	779, 1298, 1717
<i>hutC</i>	Histidine utilization	Repressor	17.9	161, 192, 238, 625, 714, 716, 717, 1272, 1326, 1573, 1717, 1831–1834, 2039
<i>hutG</i>	Histidine utilization	Formiminoglutamase (EC 3.5.3.8)	17.9	192, 238, 1272, 1326, 1717, 1831–1834, 2039
<i>hutH</i>	Histidine utilization	Histidine ammonia-lyase (EC 4.3.1.3)	17.9	192, 193, 238, 715, 1272, 1326, 1717, 1831–1834, 2039
<i>hutI</i>	Histidine utilization	Imidazolonepropionase (EC 3.5.2.7)	17.9	192, 193, 238, 1272, 1326, 1717, 1831–1834, 2039
<i>hutM</i>	Histidine utilization	Promoter for <i>hutIGC</i>	17.9	192, 195, 238, 625, 1272, 1326, 1717, 1831–1834, 2039
<i>hutP</i>	Histidine utilization	Promoter for <i>hutUH</i>	17.9	192, 195, 238, 372, 625, 1272, 1326, 1717, 1831–1834, 2039
<i>hutQ</i>	Histidine utilization	Promoter for <i>hutUH</i>	17.9	195, 238, 372, 625, 1272, 1326, 1717, 1831–1834, 2039
<i>hutR</i>	Histidine utilization	Catabolite insensitivity of <i>hutUH</i>	17.9	195, 238, 1272, 1326, 1717, 1831–1834, 2039
<i>hutU</i>	Histidine utilization	Urocanate hydratase (EC 4.2.1.49)	17.9	192, 193, 238, 1272, 1326, 1717, 1831, 2039
<i>hydA</i>	Hydrogenase	<i>aniA</i> , <i>fhIB</i> , <i>hyd</i> ; hydrogenase	62.5	119, 325, 1548, 1717

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<i>hydG</i>	Hydrogenase	Hydrogenase regulation	90.8	331, 1717
<i>hydH</i>	Hydrogenase	Hydrogenase regulation	90.7	331, 1717
<i>hyp</i>	Hydrophobic peptide auxotrophy	Hydrophobic polypeptide requirement	52.0	224, 1717
<i>icd</i>		Isocitrate dehydrogenase	27.6	553, 554, 1717
<i>iclR</i>		Constitutive expression of <i>aceBA</i> operon	91.2	606, 1414, 1717
<i>ilvA</i>	Isoleucine-valine	<i>ile</i> ; threonine deaminase (EC 4.2.1.16)	85.3	75, 79, 155, 156, 182, 184, 186, 261, 263, 272, 321, 415, 419, 420, 425, 472, 473, 642, 739, 802, 1185, 1233, 1248, 1717, 1737, 1874, 1985, 2103, 2104, 2224
<i>ilvB</i>	Isoleucine-valine	Acetohydroxy acid synthase I, valine sensitive, large subunit (EC 4.1.3.18)	82.3	404, 417, 419, 420, 642, 1143, 1145, 1478–1480, 1717, 1789, 1790, 2123
<i>ilvC</i>	Isoleucine-valine	<i>ilvA</i> ; keto-acid reductoisomerase (EC 1.1.1.86)	85.3	76, 79, 156, 182, 185, 415, 642, 803, 1048, 1717, 1792, 1793
<i>ilvD</i>	Isoleucine-valine	<i>ilvB</i> ; dihydroxyacid dehydratase (EC 4.2.1.19)	85.3	77–79, 155, 156, 182, 184, 186, 415, 419, 420, 472, 492, 642, 735, 1233, 1717
<i>ilvE</i>	Isoleucine-valine	<i>ilvC</i> ; branched-chain amino acid aminotransferase (EC 2.6.1.42)	85.2	79, 155, 156, 182, 184, 186, 350, 415, 419, 420, 472, 527, 642, 735, 1044, 1046, 1166, 1232, 1233, 1717
<i>ilvG</i>	Isoleucine-valine	Acetohydroxy acid synthase II, valine insensitive, large subunit (EC 4.1.3.18)	85.2	155, 156, 182, 184, 186, 404, 419, 420, 472, 735, 1142, 1145, 1232, 1233, 1478, 1480, 1587, 1717, 1747, 1789, 1790
<i>ilvH</i>	Isoleucine-valine	Acetohydroxy acid synthase III, valine sensitive, small subunit (EC 4.1.3.18)	3.0	419, 420, 1630, 1717, 1878, 2100
<i>ilvI</i>	Isoleucine-valine	Acetohydroxy acid synthase III, valine sensitive, large subunit (EC 4.1.3.18)	3.0	1630, 1717, 1878, 2100
<i>ilvL</i>	Isoleucine-valine	<i>ilvGMEDA</i> operon leader peptide	85.2	1153, 1717, 1986
<i>ilvM</i>	Isoleucine-valine	Acetohydroxy acid synthase II, valine insensitive, small subunit (EC 4.1.3.18)	85.2	404, 1232, 1233, 1717, 1747
<i>ilvN</i>	Isoleucine-valine	Acetohydroxy acid synthase II, valine sensitive, small subunit (EC 4.1.3.18)	82.3	404, 417, 1717
<i>ilvS</i>	Isoleucine-valine	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	1.0	179, 180, 321, 1717
<i>ilvY</i>	Isoleucine	Regulation of <i>ilvC</i>	85.3	183, 186, 1717
<i>incR</i>	Incompatibility	Required in <i>trans</i> with <i>parS</i>	pSL T	295, 296, 1717
<i>infC</i>		Protein chain initiation factor 3 (IF3)	30.2	1225, 1717
<i>inlA</i>	Inositol	Fermentation	92.7	185, 962, 1473, 1717, 1926, 1962
<i>inlB</i>	Inositol	Fermentation	56.5	1717, 1935
<i>inm</i>		Sensitivity to mutagenesis by nitrosoguanidine	80.6	367, 1717
<i>invA</i>	Invasion	Affects invasion but not attachment to cultured epithelial cells; sequence similarity to proteins for protein translocation	63.1	566, 600, 602–604, 639, 685, 970, 1359, 1517, 1717
<i>invD</i>	Invasion	Invasion-related function	NM	600, 603, 1717
<i>invE</i>	Invasion	Triggering of the endocytic uptake of <i>Salmonella</i> by epithelial cells; homologous to Mxic of <i>Shigella</i>	63.1	638, 639, 685, 1359, 1717
<i>invF</i>	Invasion	Defective in invasion but not in attachment to epithelial cells; similar to <i>araC</i>	63.2	1000, 1359, 1717
<i>invG</i>	Invasion	Defective in invasion of epithelial cells; member of PulA family of proteins for export of proteins lacking typical signal sequences	63.2	639, 1000, 1359, 1717
<i>invH</i>	Invasion	Defective in invasion of and attachment to epithelial cells	63.4	34, 1359, 1717
<i>iroA</i>	Iron-regulated locus	Induced by alkaline pH; undefined role in iron transport	60.6	554, 562, 1717
IS200I		Insertion sequence	65.8	170, 627, 1134–1136, 1717, 1724
IS200II		Insertion sequence	75.6	170, 627, 1134–1136, 1717, 1724
IS200II I		Insertion sequence	94.2	170, 627, 1134–1136, 1717, 1724
IS200I V		Insertion sequence	42.4	170, 627, 1134–1136, 1717, 1724
IS200 V		Insertion sequence	53.6	170, 627, 1134–1136, 1717, 1724
IS200 VI		Insertion sequence	22.3	170, 627, 1134–1136, 1717, 1724

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<i>katG</i>	Catalase	<i>cls</i> ; hydroperoxidase I (HPI) (EC 1.11.1.6)	89.4	522, 539, 1229, 1378, 1529, 1717, 1977, 1998
<i>kbl</i>		2-Amino-3-ketobutyrate CoA ligase (glycine acetyltransferase) (EC 2.3.1.29)	81.2	1717, 1814
<i>kdsA</i>		Ketodeoxyoctonate synthesis	38.7	279, 650, 651, 726, 732, 1167–1169, 1394, 1492, 1605, 1635–1638, 1640, 1641, 1717, 1937, 2093
<i>kdsB</i>		CMP ketodeoxyoctonate synthetase	20.2	279, 649–651, 1717
<i>lamB</i>	Lambda	Encodes a protein resembling the λ receptor	91.7	568, 1520, 1522, 1717
<i>lepA</i>		GTP-binding protein	57.6	1717, 2071
<i>lepB</i>		<i>lep</i> ; signal peptidase I	57.6	1717, 2070, 2071
<i>leuA</i>	Leucine	α -Isopropylmalate synthase (EC 4.1.3.12)	2.9	260, 278, 286, 287, 589, 621–623, 742, 760, 990, 1023, 1156, 1297, 1629, 1717, 1773, 2126
<i>leuB</i>	Leucine	β -Isopropylmalate dehydrogenase	2.9	58, 260, 262, 623, 760, 1297, 1717, 1773
<i>leuC</i>	Leucine	α -Isopropylmalate isomerase subunit	2.9	260, 590, 623, 689, 760, 1022, 1024, 1025, 1297, 1677, 1717
<i>leuD</i>	Leucine	α -Isopropylmalate isomerase subunit	2.9	260, 578, 590, 689, 1022, 1024, 1025, 1297, 1676, 1717, 1936
<i>leuS</i>	Leucine	Leucyl-tRNA synthetase (EC 6.1.1.4)	15.8	20, 21, 276, 760, 1717, 1906
<i>leuT</i>	Leucine	Leucine transport	39.4	1602, 1717, 2014
<i>leuU</i>	Leucine	<i>leuT</i> ; leucine tRNA	85.6	201, 208, 1717
<i>lev</i>	Levomycetin	Levomycetin resistance	NM	478, 1717
<i>lexA</i>		Regulatory gene for SOS functions	91.9	271, 618, 1399, 1717
<i>lgt</i>		<i>umpA</i> ; prolipoprotein diacylglyceryl transferase	64.9	609, 1717
<i>lig</i>	Ligase	DNA ligase	52.7	1313, 1535, 1717
<i>lip</i>	Lipoic acid	Requirement	15.3	1227, 1717, 1844
<i>livF</i>	Leucine, isoleucine, valine	<i>livG</i> ; high-affinity branched-chain amino acid transport; membrane component	77.5	1308, 1717
<i>livG</i>	Leucine, isoleucine, valine	<i>livF</i> ; high-affinity branched-chain amino acid transport	77.5	1308, 1717
<i>livH</i>	Leucine, isoleucine, valine	<i>livA</i> ; high-affinity branched-chain amino acid transport; membrane component	77.5	1306–1308, 1466, 1717
<i>livJ</i>	Leucine, isoleucine, valine	<i>livB</i> ; high-affinity branched-chain amino acid transport; membrane component	77.6	1308, 1467, 1717
<i>livK</i>	Leucine, isoleucine, valine	<i>livC</i> ; high-affinity branched-chain amino acid transport; membrane component	77.5	1308, 1467, 1717
<i>livM</i>	Leucine, isoleucine, valine	<i>livEF</i> ; high-affinity branched-chain amino acid transport; membrane component	77.5	1308, 1717
<i>livS</i>	Leucine, isoleucine, valine	<i>liv</i> ; regulatory gene; high-affinity branched-chain amino acid transport	19.2	1395, 1717
<i>lkyA</i>	Leaky	Leakage of periplasmic proteins	59.8	1717, 2118
<i>lkyB</i>	Leaky	Leakage of periplasmic proteins	59.8	1717, 2118
<i>lkyC</i>	Leaky	Leakage of periplasmic proteins	22.9	1717, 2118
<i>lkyD</i>	Leaky	Leakage of periplasmic proteins; morphology defect	22.9	298, 369, 594, 595, 1254, 1717, 1959, 2118, 2119
<i>lon</i>	Long form	<i>capR</i> ; ATP-dependent protease	11.1	302, 463, 1557, 1717, 1730, 2111
<i>lpd</i>		Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	3.8	10, 1140, 1210, 1717
<i>lpp</i>	Lipoprotein	Murein lipoprotein structural gene	30.6	1407, 1717, 2184
<i>lpxA</i>		UDP- <i>N</i> -acetylglucosamine acyltransferase	4.2	1717, 1757, 2090
<i>lpxD</i>		<i>ssc</i> , <i>omsA</i> , <i>firA</i> ; UDP-3- <i>O</i> -(<i>R</i> -3-hydroxymyristoyl)-glucosamine <i>N</i> -acyltransferase; antibiotic supersensitivity (EC 2.3.1.–)	4.0	750, 783, 785, 1687, 1717, 1757, 2089–2091
<i>lrp</i>		Leucine-responsive regulatory protein	19.1	1717, 2100
<i>lysA</i>	Lysine	<i>lys</i> ; requirement	65.4	371, 489, 1717, 1943, 1944
<i>lysS</i>	Lysine	Lysyl-tRNA synthetase (EC 6.1.1.6)	66.2	1009, 1717
<i>malE</i>	Maltose	<i>malB</i> ; maltose uptake; periplasmic maltose-binding protein	91.7	402, 1522, 1717
<i>malF</i>	Maltose	Maltose uptake; inner membrane protein	91.6	402, 1717, 1759
<i>malG</i>	Maltose	Maltose uptake; inner membrane protein	91.6	402, 569, 1717
<i>malK</i>	Maltose	Maltose uptake; inner membrane protein	91.7	402, 1717, 1760, 2094, 2095
<i>malM</i>	Maltose	Possible periplasmic protein; function unknown	91.7	1717, 1759
<i>malQ</i>	Maltose	Amylomaltase (EC 1.2.1.25)	77.0	10, 1709, 1711, 1717, 1722
<i>malT</i>	Maltose	Regulation of maltose genes	76.8	1521, 1717
<i>manA</i>	Mannose	<i>pmi</i> ; mannose-6-phosphate isomerase (EC 5.3.1.8)	31.3	356, 357, 565, 692, 1287, 1652, 1697, 1717, 1921, 2145
<i>mdh</i>		Malate dehydrogenase (EC 1.1.1.37)	73.4	1240, 1717

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<i>melA</i>	Melibiose	α -Galactosidase (EC 3.2.1.22)	93.8	1709, 1712, 1717, 1851
<i>melB</i>	Melibiose	Melibiose carrier protein	93.8	1108, 1370, 1712, 1717
<i>mem</i>	Membrane	Sugar transport and membrane protein defective	80.8	1577, 1717
<i>mena</i>	Menaquinone	Menaquinone deficient; defective in trimethylamine oxide reduction; grows on vitamin K ₁	88.5	1126, 1129, 1717
<i>menB</i>	Menaquinone	Biosynthesis; grows on vitamins K ₁ and K ₅	50.1	344, 414, 1126, 1127, 1129, 1664, 1717
<i>menC</i>	Menaquinone	Biosynthesis	50.1	414, 1127, 1129, 1717
<i>menD</i>	Menaquinone	Biosynthesis	50.1	414, 1127, 1129, 1717
<i>menE</i>	Menaquinone	<i>O</i> -Succinyl benzoic acid-CoA synthase	50.1	414, 1127, 1664, 1717
<i>metA</i>	Methionine	<i>metI</i> ; homoserine transsuccinylase (EC 2.3.1.46)	91.1	92, 308, 1150, 1294, 1668, 1683, 1684, 1717, 1829, 1830
<i>metB</i>	Methionine	Cystathionine γ -synthase (EC 4.2.99.9)	89.3	92, 699, 1004, 1653, 1683, 1684, 1717, 1829, 1830, 2047, 2050, 2051
<i>metC</i>	Methionine	Cystathionine γ -lyase (EC 4.4.1.1)	69.1	431, 1385, 1537, 1538, 1683, 1684, 1717, 1830
<i>metD</i>	Methionine	<i>metP</i> ; high-affinity methionine transport	5.5	89–91, 93, 384, 697, 1567, 1717, 1791
<i>metE</i>	Methionine	Tetrahydropteroyltriglutamate methyltransferase (EC 2.1.1.14)	86.1	294, 1564, 1565, 1717, 1732, 1735, 1768, 1829, 1830, 2056–2058, 2131, 2171, 2172
<i>metF</i>	Methionine	5,10-Methylenetetrahydrofolate reductase (EC 1.1.99.15)	89.4	92, 386, 1717, 1829, 1830, 1891, 1892, 2131
<i>metG</i>	Methionine	Methionyl-tRNA synthetase	47.1	72, 92, 307, 690, 691, 1653, 1717, 1829, 1830
<i>metH</i>	Methionine	Vitamin B ₁₂ -dependent homocysteine- <i>N</i> ⁵ -metylenetetrahydrofolate transmethylase	91.3	92, 265, 320, 1474, 1565, 1717, 1891, 2005, 2053, 2055, 2056, 2058, 2131, 2132, 2171, 2172
<i>metJ</i>	Methionine	Methionine analog resistant; transcriptional repressor of <i>metE</i> and <i>metR</i>	89.3	92, 93, 306, 307, 386, 1151, 1685, 1717, 1735, 1891, 1944, 2050–2052, 2132, 2172
<i>metK</i>	Methionine	Methionine analog resistant; <i>S</i> -adenosylmethionine synthetase	67.0	86, 93, 162, 306, 307, 791–793, 1150, 1151, 1362, 1685, 1717, 1735, 1944, 2220
<i>metL</i>	Methionine	Aspartokinase II-homoserine dehydrogenase II	89.4	1717, 2050
<i>metR</i>	Methionine	Transcriptional activator of <i>metE</i> and <i>metH</i>	86.1	221, 265, 386, 758, 1294, 1564, 1717, 2054, 2056–2058, 2172
<i>mglA</i>	Methyl galactoside	Membrane-bound protein for methylgalactoside transport	48.0	145, 1391, 1633, 1717
<i>mglB</i>	Methyl galactoside	Galactose-binding protein	48.0	145, 1327, 1390, 1391, 1575, 1633, 1717, 1938, 2149, 2238, 2239
<i>mglC</i>	Methyl galactoside	Membrane-bound transport protein	48.0	145, 1391, 1633, 1717
<i>mglE</i>	Methyl galactoside	Transport	NM	145, 1391, 1633, 1717
<i>mgtA</i>	Magnesium transport	Magnesium transport	96.7	787, 1717, 1847–1849
<i>mgtB</i>	Magnesium transport	Magnesium transport	82.1	614, 787, 1717, 1847–1850
<i>mgtC</i>	Magnesium transport	Magnesium transport	82.1	1717, 1850
<i>miaA</i>		Deficient in the nucleotide ms ² io ⁶ AA, a modified base present in some tRNAs	95.0	189, 211, 251, 510, 975, 1717
<i>miaE</i>		Lack of tRNA (ms ² io ⁶ A37) hydroxylase	97.2	1558, 1717
<i>min</i>	Mimicells	Cell division	NM	1717, 1996
<i>moaA</i>	Molybdenum	<i>chlA</i> ; molybdenum-containing factor; biosynthesis of molybdopterin	19.0	344, 505, 1717, 1784, 1904, 1933
<i>mob</i>	Molybdenum	<i>chlB</i> ; molybdenum-containing factor; biosynthesis of molybdopterin guanine dinucleotide	86.4	289, 291, 293, 1717, 1784, 1904
<i>modC</i>	Molybdenum	<i>chlD</i> ; molybdenum uptake	18.3	31, 1717, 1784, 1904, 1933
<i>moeA</i>	Molybdenum	<i>chlE</i> ; molybdenum-containing factor; biosynthesis of molybdopterin	19.1	505, 1717, 1784, 1904, 1934
<i>motA</i>	Motility	Nonmotile but flagellate	42.1	471, 502–504, 887, 912, 1074, 1118, 1717, 2192
<i>motB</i>	Motility	Nonmotile but flagellate	42.0	471, 502–504, 887, 912, 1074, 1118, 1717, 2192
<i>mre</i>	Mecillinam resistance	<i>bac</i> , <i>envB</i> ; round cell morphology; mecillinam resistance	73.6	63, 64, 66–68, 383, 1482, 1717
<i>mscL</i>	Mechanosensitive channel	Large-conductance mechanosensitive channel	74.5	1541, 1717
<i>mta</i>	meso-Tartaric acid	Utilization of and resistance to meso-tartaric acid	NM	1315, 1717, 2137

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<i>mtlA</i>	Mannitol	D-Mannitol phosphotransferase enzyme IIA	80.4	159, 221, 676, 1176, 1580, 1706, 1711, 1717, 1723
<i>mtlD</i>	Mannitol	Mannitol-1-phosphate dehydrogenase (EC 1.1.1.17)	80.4	159, 947, 1717
<i>murB</i>		UDP- <i>N</i> -acetylenolpyruvoylglucosamine reductase	90.0	458, 1717
<i>murI</i>		Glutamate synthase	89.7	1717, 2114
<i>mutG</i>	Mutator	Increased frequency of mutation in host chromosome, not in P22	NM	705, 1717
<i>mutH</i>	Mutator	Mutations inactivate methyl-directed mismatch repair	65.5	713, 1234, 1526, 1618, 1717, 1780, 1781
<i>mutL</i>	Mutator	Mutations inactivate methyl-directed mismatch repair	95.0	1043, 1291, 1525, 1526, 1618, 1717, 1780, 1781, 2221
<i>mutS</i>	Mutator	Mutations inactivate methyl-directed mismatch repair	63.9	709, 710, 1525, 1526, 1618, 1717, 1780, 1781, 2221
<i>mutU</i>	Mutator	Increased frequency of mutation	NM	1618, 1717
<i>mutY</i>	Mutator	<i>mutB</i> ; increased frequency of mutation with alkylating agents	67.2	448, 713, 1239, 1717, 1780
<i>mviA</i>	Mouse virulence	Mutants have increased virulence in Ity ^s , not in Ity ^f mice	38.9	144, 1717
<i>mviM</i>	Mouse virulence	<i>mviB</i> ; affects the virulence of cells in mice	26.3	1717
<i>mviN</i>	Mouse virulence	Affects the virulence of cells in mice	26.3	1717
<i>mviS</i>	Mouse virulence	Affects the virulence of cells in mice	26.3	284, 1717
<i>nadA</i>	Nicotinamide	<i>nicA</i> ; requirement; quinolinic acid synthetase	17.2	110, 546, 559–561, 563, 811, 1220, 1717, 1862, 2017, 2226–2228
<i>nadB</i>	Nicotinamide	<i>nic</i> ; L-aspartate oxidase	57.8	110, 370, 546, 561, 563, 810, 811, 1220, 1717, 2226, 2228
<i>nadC</i>	Nicotinamide	Quinolinic acid PRPP phosphoribosyl transferase	3.6	110, 546, 561, 810, 811, 861, 868, 1220, 1717
<i>nadD</i>	Nicotinamide	NAMN:ATP-ADP transferase	15.5	110, 317, 860, 862, 863, 1717
<i>nadE</i>	Nicotinamide	Essential biosynthetic gene, unsupplementable; NAD synthetase	29.5	865, 1717
<i>nadF</i>	Nicotinamide	NAD kinase I	14.7	317, 1717
<i>nadG</i>	Nicotinamide	NAD kinase II; quinolinate sensitive	74.9	317, 1717
<i>nadR</i>	Nicotinamide	<i>nadI</i> , <i>pnuA</i> ; NMN transport and repression of transcription of <i>nadA</i> , <i>nadB</i> ; bifunctional enzyme	99.9	370, 558, 563, 811, 1717, 2226, 2228, 2229
<i>nagA</i>	<i>N</i> -Acetylglucosamine	<i>nag</i> ; nonutilization	16.5	129, 1393, 1717, 1738
<i>nalB</i>	Nalidixic acid	Resistance or sensitivity	61.6	1429, 1717
<i>nanH</i>	Neuraminidase	Sialidase (EC 3.2.2.18)	23.7	843, 844, 1717, 2003, 2101
<i>nap</i>	Nonspecific acid phosphatase	Deficiency for nonspecific acid phosphatase I	NM	640, 641, 1662, 1717, 2043
<i>nar</i>	Nitrate reductase	<i>chIC</i> ; nitrate reductase (operon) (EC 1.7.99.4)	38.6	121, 289, 290, 1131, 1646, 1717, 1904
<i>narK</i>	Nitrate reductase	Regulatory gene for <i>nar</i> operon	38.6	826, 1717
<i>ndk</i>		Nucleoside diphosphate kinase (EC 2.7.4.6)	55.5	1717, 1718, 1721
<i>neaA</i>	Neamine	Neamine resistance	74.1	540, 1717
<i>newD</i>		Substitute gene for <i>leuD</i>	8.0	591, 1022, 1024, 1132, 1133, 1648, 1717, 1936
<i>nfnB</i>		<i>nfsI</i> ; sensitivity to nitrofurantoin	13.6	1717, 2108
<i>nhoA</i>		<i>N</i> -Hydroxyarylamine <i>O</i> -acetyltransferase (EC 2.3.1.118)	104.0	1717, 2109
<i>nirB</i>	Nitrite reductase	NADH-nitrite oxidoreductase apoprotein, subunit I (EC 1.6.6.4)	75.2	648, 1717, 2169
<i>nirC</i>	Nitrite reductase	Nitrite transport; putative (EC 1.6.6.4)	75.5	1717, 2169
<i>nirD</i>	Nitrite reductase	NADH-nitrite oxidoreductase apoprotein, subunit II	75.5	1717, 2169
<i>nirP</i>	Nitrite reductase	Nitrite permease	7.5	648, 1717
<i>nit</i>	Nitrogen	Nitrogen metabolism	30.1	239, 445, 1717
<i>nlpD</i>		Lipoprotein precursor	63.7	1085, 1717
<i>nmpC</i>	New membrane protein	Outer membrane porin protein	38.7	826, 1717
<i>nol</i>	Norleucine	Norleucine resistance; possible defect in valine uptake or regulation	64.5	790, 1717
<i>nrda</i>		Ribonucleoside diphosphate reductase, α -subunit (R1) (EC 1.17.4.1)	49.3	977, 1313, 1717, 1904
<i>nrdb</i>		Ribonucleoside diphosphate reductase, β -subunit (R2) (EC 1.17.4.1)	49.4	977, 1717, 1904
<i>nrde</i>		Ribonucleoside-diphosphate reductase subunit (EC 1.17.4.1)	61.3	977, 1717
<i>nrdf</i>		Ribonucleoside-diphosphate reductase subunit (EC 1.17.4.1)	61.4	977, 1717
<i>nsiA</i>	Nicotinamide starvation inducible	NAD metabolism regulation	77.8	556, 1717
<i>ntrB</i>	Nitrogen regulation	<i>glnR</i> ; regulation of <i>glnA</i> expression and other nitrogen-controlled genes	87.3	47, 1088–1090, 1109, 1112, 1113, 1316, 1319, 1440, 1717, 2117
<i>ntrC</i>	Nitrogen regulation	<i>glnR</i> ; regulation of <i>glnA</i> expression and other nitrogen-controlled genes	87.2	47, 1088–1090, 1112, 1316, 1319, 1440, 1515, 1570, 1717, 1756, 2117
<i>nuoD</i>		NADH ubiquinone oxidoreductase	51.0	71, 1717
<i>nuoE</i>		NADH ubiquinone oxidoreductase	51.0	71, 1717
<i>nuoF</i>		NADH ubiquinone oxidoreductase	51.0	71, 1717
<i>nuoG</i>		NADH ubiquinone oxidoreductase	51.0	71, 1717

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<i>nusA</i>	N utilization	Transcription termination; does not support transcription antitermination of N protein of λ	72.0	388, 1717
<i>nuvA</i>		Uridine thiolation factor A activity	9.5	1093, 1717
<i>oadA</i>		Oxalacetate decarboxylase, α -subunit (EC 4.1.1.3)	NM	1717, 2158
<i>oadB</i>		Oxalacetate decarboxylase, β -subunit (EC 4.1.1.3)	NM	1717, 2158
<i>oadG</i>		Oxalacetate decarboxylase, γ -subunit (EC 4.1.1.3)	NM	1717, 2158
<i>oafA</i>	O-antigen factor	<i>O-5, ofi</i> ; LPS O-factor 5, acetyl group	50.7	1052, 1287, 1717, 1921
<i>oafC</i>	O-antigen factor	Determines factor 1 in LPS of group E <i>Salmonella</i> spp.	15.2	1287, 1309, 1566, 1717, 1921
<i>oafR</i>	O-antigen factor	Synthesis of LPS O-antigen 122	12.7	1280, 1287, 1717, 1921
<i>ogt</i>		<i>O-6-Alkylguanine-DNA-alkyltransferase</i>	36.6	1717
<i>ompA</i>	Outer membrane protein	Outer membrane protein 33K	24.3	146, 412, 573, 1237, 1431, 1510, 1717, 1719, 1799, 1925, 2040
<i>ompC</i>	Outer membrane protein	Outer membrane protein 36K	49.1	146, 309, 462, 644, 670, 959, 984, 1237, 1424, 1431, 1450, 1510, 1521, 1717, 1799, 2020, 2021, 2040, 2225
<i>ompD</i>	Outer membrane protein	Outer membrane protein 34K	33.7	146, 462, 644, 959, 1237, 1431, 1450, 1518, 1717, 1799, 2020, 2021, 2040
<i>ompF</i>	Outer membrane protein	Outer membrane protein 35K	22.8	309, 462, 644, 670, 984, 1450, 1597, 1717, 1734, 2040
<i>ompH</i>	Outer membrane protein	Outer membrane protein 16K, cationic	4.0	782, 783, 1080, 1081, 1717
<i>ompR</i>	Outer membrane protein	<i>ompB, tppA</i> ; positive regulation of tripeptide permease and of outer membrane protein	76.0	146, 309, 462, 602, 631, 632, 644, 765, 927, 959, 1201–1204, 1431, 1521, 1717, 1799, 2040
<i>opdA</i>	Oligopeptidase	<i>optA</i> ; endoprotease which hydrolyzes <i>N</i> -acetyl-L-Ala ₄ ; required for normal phage P22 growth	79.7	364–366, 1717, 2080
<i>oppA</i>	Oligopeptide permease	Oligopeptide-binding protein	38.4	662, 765, 767, 768, 775–777, 804, 921, 1175, 1717, 1886, 1990
<i>oppB</i>	Oligopeptide permease	Oligopeptide transport system	38.3	662, 765, 768, 775, 777, 804, 1555, 1717
<i>oppC</i>	Oligopeptide permease	Oligopeptide transport system	38.3	662, 765, 768, 775, 777, 804, 1555, 1717
<i>oppD</i>	Oligopeptide permease	Oligopeptide transport system	38.3	662, 765, 768, 775, 777, 804, 1717
<i>oppF</i>	Oligopeptide permease	Oligopeptide transport system	38.3	607, 775, 777, 1717
<i>orf11</i>		Putative role in fimbria production	pSL T	580, 1717
<i>orf7</i>		Putative role in fimbria production	pSL T	580, 1717
<i>orf9</i>		Putative role in fimbria production	pSL T	580, 1717
<i>orfE</i>		Function unknown; locates downstream of <i>spv</i> operon of pSLT	pSL T	702, 1717
<i>orgA</i>	Oxygen-regulated gene	Noninvasive mutant in low oxygen	62.9	969, 1717
<i>oriC</i>	Origin	<i>poh</i> ; origin of replication of chromosome	84.9	957, 1717, 1788, 2240, 2241
<i>osmB</i>		Osmotically inducible lipoprotein; resistance to osmotic stress	37.6	1717, 2006
<i>oxdA</i>	Oxygen dependent	Gene activity controlled by <i>fnr</i>	67.8	1717, 1940
<i>oxdB</i>	Oxygen dependent	Gene activity controlled by <i>fnr</i>	93.2	1717, 1940
<i>oxiA</i>	Oxygen inducible	Induced by anaerobiosis	9.2	23, 929, 1717
<i>oxiB</i>	Oxygen inducible	Induced by anaerobiosis	25.8	23, 1717
<i>oxiC</i>	Oxygen inducible	Induced by anaerobiosis	35.3	23, 1717
<i>oxiE</i>	Oxygen inducible	Induced by anaerobiosis	89.4	23, 1717
<i>oxrF</i>	Oxygen regulation	Regulates expression of <i>aniH</i>	NM	22, 1717
<i>oxrG</i>	Oxygen regulation	Regulates expression of <i>aniC, aniI</i>	89.4	22, 562, 1717
<i>oxyR</i>	Oxidative stress resistant	Transcriptional activator of oxidative stress response genes	89.6	333, 334, 522, 1164, 1378, 1529, 1717, 1929, 1931, 1932, 1998, 2164
<i>pabA</i>	<i>p</i> -Aminobenzoate	Requirement; <i>p</i> -aminobenzoate synthase	75.1	1003, 1717
<i>pabB</i>	<i>p</i> -Aminobenzoate	<i>p</i> -Aminobenzoate synthetase, component I (EC 4.1.3.–)	41.6	661, 1717
<i>pagC</i>	<i>phoP</i> -activated gene	<i>ail, lom</i> ; <i>phoP</i> -activated gene for virulence	NM	1355, 1358, 1598, 1717
<i>panB</i>	Pantothenic acid	Ketopantohydroxymethyl transferase (EC 4.1.2.12)	4.6	396, 440, 1568, 1588, 1717
<i>panC</i>	Pantothenic acid	Pantothenate synthetase (EC 6.3.2.1)	4.5	396, 440, 1568, 1588, 1717
<i>panD</i>	Pantothenic acid	Ketopantoic acid reductase	4.6	1144, 1488, 1588, 1717
<i>panE</i>	Pantothenic acid	Ketopantoic acid reductase	NM	1588, 1717

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<i>panR</i>	Pantothenic acid	Pantothenate excretion; suppression of the thiamine requirement of the <i>purF</i> mutation	4.6	467, 1717
<i>panT</i>	Pantothenic acid	Pantothenate transport	NM	1717, 1718, 1721
<i>parA</i>	Partition	Partitioning; homologous to <i>parA</i> of phage P1	pSL T	295, 296, 1717
<i>parB</i>	Partition	Partitioning; homologous to <i>parB</i> in phage P1	pSL T	295, 296, 1717
<i>parC</i>	Partition	<i>clmF</i> ; defect in nucleoid segregation; topoisomerase IV subunit; similar to <i>gyrA</i>	69.3	11, 1252, 1717, 1749, 1750, 1752
<i>parE</i>	Partition	<i>clmF</i> ; defect in nucleoid segregation; topoisomerase IV subunit; similar to <i>gyrB</i>	69.4	1252, 1717, 1749, 1752, 1872
<i>parF</i>	Partition	<i>clmF</i> ; partitioning of nucleoid; topoisomerase	69.3	1252, 1717, 1749, 1872
<i>parS</i>	Partition	<i>incL</i> ; partitioning of pSLT	pSL T	295, 296, 1717
<i>pasA</i>		6-Aminonicotinic acid sensitive	92.9	551, 557, 1717
<i>pasB</i>		6-Aminonicotinic acid sensitive	70.1	551, 557, 1717
<i>pasC</i>		6-Aminonicotinic acid sensitive	23.4	551, 557, 1717
<i>pasD</i>		6-Aminonicotinic acid sensitive	17.9	557, 1717
<i>pasE</i>		6-Aminonicotinic acid sensitive	56.8	557, 1717
<i>pbpA</i>	Penicillin-binding protein	Round cell morphology; mecillinam resistance; penicillin-binding protein 2	15.4	383, 1717
<i>pckA</i>		Phosphoenolpyruvate carboxykinase (ATP) activity (EC 4.1.1.49)	76.0	1201, 1717
<i>pckB</i>		<i>pck</i> ; phosphoenolpyruvate carboxykinase (ATP) activity (EC 4.1.1.49)	14.5	283, 1717
<i>pclA</i>	Permissive for <i>cly</i>	Permissive for lytic growth of P22 <i>cly</i>	NM	1717, 2156
<i>pclB</i>	Permissive for <i>cly</i>	Permissive for lytic growth of P22 <i>cly</i>	NM	1717, 2156
<i>pclC</i>	Permissive for <i>cly</i>	Permissive for lytic growth of P22 <i>cly</i>	NM	1717, 2156
<i>pde</i>	Phosphodiesterase	2',3'-Cyclic nucleotide 2'-phosphodiesterase	95.5	1717, 2043
<i>pduA</i>	Propanediol utilization	Propanediol utilization	43.8	15, 194, 315, 950, 1717
<i>pduB</i>	Propanediol utilization	Propanediol utilization	43.8	15, 194, 315, 950, 1717
<i>pduC</i>	Propanediol utilization	Propanediol dehydratase	43.9	15, 194, 950, 1717
<i>pduD</i>	Propanediol utilization	Propanediol dehydratase	44.0	15, 194, 950, 1717
<i>pduE</i>	Propanediol utilization	Vitamin B ₁₂ adenosyltransferase	44.0	15, 194, 950, 1717
<i>pduF</i>	Propanediol utilization	Facilitated diffusion of propanediol	43.8	15, 194, 315, 950, 1717
<i>pduG</i>	Propanediol utilization	Propanediol utilization	44.0	15, 194, 950, 1717
<i>pduH</i>	Propanediol utilization	Propanediol utilization	44.0	15, 194, 950, 1717
<i>pdxB</i>	Pyridoxine	Requirement	51.8	824, 1717
<i>pefA</i>	Plasmid-encoded fimbriae	Fimbrial biosynthesis; fimbrial/pilin shaft subunits	pSL T	580, 1649, 1717
<i>pefB</i>	Plasmid-encoded fimbriae	Fimbrial biosynthesis; fimbrial regulatory protein	pSL T	580, 1649, 1717
<i>pefC</i>	Plasmid-encoded fimbriae	Fimbrial biosynthesis; outer membrane protein	pSL T	580, 1649, 1717
<i>pefD</i>	Plasmid-encoded fimbriae	Fimbrial biosynthesis; sequence related to periplasmic chaperones	pSL T	580, 1649, 1717
<i>pefI</i>	Plasmid-encoded fimbriae	Short polypeptide related in sequence to <i>papI</i> and <i>sfaC</i> of <i>E. coli</i>	pSL T	580, 1649, 1717
<i>pefK</i>	Plasmid-encoded fimbriae	<i>orf5</i> ; fimbrial biosynthesis	pSL T	580, 1649, 1717
<i>pefL</i>	Plasmid-encoded fimbriae	<i>orf6</i> ; fimbrial biosynthesis	pSL T	580, 1649, 1717
<i>pefS</i>	Plasmid-encoded fimbriae	<i>orf8</i> ; homologous to <i>dsbA</i> of <i>E. coli</i>	pSL T	580, 1649, 1717
<i>pepA</i>	Peptidase	Peptidase A; similar to aminopeptidase A of <i>E. coli</i>	97.4	632, 1340, 1341, 1346, 1350, 1620, 1717, 2204, 2205
<i>pepB</i>	Peptidase	Peptidase B; aminopeptidase	55.8	675, 1341, 1350, 1620, 1717, 2204, 2205
<i>pepD</i>	Peptidase	<i>ptdD</i> ; peptidase D; a dipeptidase, carnosinase	7.3	828, 1049, 1340, 1341, 1346, 1620, 1717, 2204, 2205
<i>pepE</i>	Peptidase	α -Aspartyl dipeptidase; peptidase E; splits Asp-X peptide bonds	91.4	288, 363, 1717
<i>pepM</i>	Peptidase	Peptidase M; aminopeptidase that removes N-terminal methionine from proteins	4.3	1345, 1349, 1382, 1717, 2153
<i>pepN</i>	Peptidase	<i>ptdN</i> ; peptidase N; an aminopeptidase, naphthylamidase	24.4	226, 1340, 1341, 1343, 1350, 1620, 1717, 2204, 2205
<i>pepP</i>	Peptidase	<i>ptdP</i> ; peptidase P; splits X-Pro peptide bonds	66.6	921, 1321, 1342, 1350, 1717, 2200
<i>pepQ</i>	Peptidase	Peptidase Q; splits X-Pro dipeptides	86.2	921, 1321, 1342, 1350, 1717, 2200
<i>pepT</i>	Peptidase	Peptidase T; a tripeptidase	27.3	1347, 1717, 1939, 1941
<i>pfkA</i>		6-Phosphofructokinase (EC 2.7.1.11)	88.2	1717, 1718, 1721
<i>pfl</i>		Pyruvate formate lyase	19.5	806, 808, 1546, 1717, 2165
<i>pgi</i>	Phosphoglucose	<i>oxrC</i> , <i>pasA</i> ; regulation of fermentative or biosynthetic enzymes;	91.4	565, 928, 1424, 1717

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	isomerase	glucosephosphate isomerase (EC 5.3.1.9)		
<i>pgn</i>		Poor growth on nutrient plates	3.6	868, 1717
<i>pgtA</i>	Phosphoglycerate	Activator of phosphoglycerate transport	52.1	953, 1713, 1717, 2016, 2201, 2217
<i>pgtB</i>	Phosphoglycerate	Protein for signal transmission for phosphoglycerate transport	52.1	953, 1713, 1717, 2201, 2217
<i>pgtC</i>	Phosphoglycerate	Protein for signal transmission for phosphoglycerate transport	52.1	953, 1713, 1717, 2201, 2217
<i>pgtE</i>	Phosphoglycerate	Outer membrane protease E (E protein) precursor (EC 3.4.21.-)	52.0	683, 1717
<i>pgtP</i>	Phosphoglycerate	Transporter for phosphoglycerate transport	52.2	654, 953, 1713, 1717, 2201, 2217
<i>pheA</i>	Phenylalanine	Chorismate mutase (EC 5.4.99.5)	58.3	655, 1437, 1717, 1993
<i>pheR</i>	Phenylalanine	Regulation of <i>pheA</i>	67.7	657, 658, 1717, 1875
<i>pheT</i>	Phenylalanine	Phenylalanyl-tRNA synthetase, β -subunit	30.3	1196, 1717
<i>phoE</i>	Phosphate	Phosphate limitation-inducible outer membrane pore protein	7.6	1717, 1868
<i>phoN</i>	Phosphate	Nonspecific acid phosphatase	94.2	1007, 1031–1033, 1355, 1717, 2043, 2125
<i>phoP</i>	Phosphate	Phosphorylated transcriptional activator; regulator of expression of <i>phoN</i> and virulence genes	27.4	33, 140, 533, 552, 601, 686, 1031–1033, 1354–1357, 1717, 2125
<i>phoQ</i>		Membrane sensor kinase; environmental response regulator in conjunction with PhoP	27.4	33, 686, 1354–1357, 1717
<i>phoS</i>	Phosphatase	Periplasmic phosphate-binding protein	NM	125, 1717, 1746, 2180
<i>phrB</i>	Photoreactivation	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	16.9	1195, 1717
<i>phsA</i>		<i>aniE</i> , <i>phs</i> ; hydrogen sulfide production	44.3	19, 344, 542, 1717, 2087, 2088
<i>phsB</i>		Iron sulfur subunit; electron transfer	44.2	1717
<i>phsC</i>		Membrane-anchoring protein	44.2	1717
<i>phsD</i>		Cytochrome <i>c</i> -containing subunit; electron transfer	44.2	1717
<i>phsE</i>		Function unknown	44.2	1717
<i>phsF</i>		Function unknown	NM	1717
<i>pig</i>	Pigment	Brownish colonies	56.5	1717, 1926
<i>pldA</i>		Outer membrane phospholipase A	86.0	240, 1717
<i>ply</i>	Phage lysogeny	<i>pox</i> ; control of P22 lysogeny	94.6	1717, 1718, 1721
<i>pmrA</i>		Polymyxin B resistance; regulation of transcription	93.5	1238, 1665, 1717, 2059–2063
<i>pmrB</i>		Polymyxin B resistance; sensor protein (EC 2.7.3.-)	93.5	1665, 1717
<i>pmrD</i>		Polymyxin B resistance	50.1	1664, 1717
<i>pncA</i>	Pyridine nucleotide cycle	Nicotinamide deamidase (EC 3.5.1.19)	28.9	559, 560, 778, 860, 1042, 1220, 1717
<i>pncB</i>	Pyridine nucleotide cycle	Nicotinic acid phosphoribosyltransferase (EC 2.4.2.11)	23.2	555, 559, 560, 810, 1041, 1042, 1220, 1717, 2082
<i>pncC</i>	Pyridine nucleotide cycle	NMN deamidase; mutations fail to use NMN as a pyridine source	88.8	1717
<i>pncH</i>	Pyridine nucleotide cycle	Nicotinamide used as sole nitrogen source	29.0	778, 1717
<i>pncX</i>	Pyridine nucleotide cycle	6-Aminonicotinamide resistant	29.0	778, 860, 1717
<i>pnuA</i>	Pyridine nucleotide uptake	NMN uptake deficient	99.7	558, 1042, 1717, 1718, 1861, 1864, 1865
<i>pnuB</i>	Pyridine nucleotide uptake	Growth on lower than normal levels of NMN	99.7	1717, 1864, 1865
<i>pnuC</i>	Pyridine nucleotide uptake	NMN uptake deficient	17.2	563, 1717, 1864, 1865, 2017, 2227, 2228
<i>pnuD</i>	Pyridine nucleotide uptake	Restores ability to use NMN to a <i>pnuC</i> mutant	64.0	1717, 1865
<i>pnuE</i>	Pyridine nucleotide uptake	Failure to use exogenous NAD; periplasmic NAD pyrophosphatase	88.3	1536, 1717
<i>pnuF</i>	Pyridine nucleotide uptake	Mutations allow use of quinolinate as pyridine source	2.7	1717
<i>pnuG</i>	Pyridine nucleotide uptake	Mutations allow use of quinolinate as pyridine source	38.9	1717
<i>pnuH</i>	Pyridine nucleotide uptake	Mutations allow use of quinolinate as pyridine source	56.1	1717
<i>pocR</i>		Positive regulator for <i>cob</i> and <i>pdu</i> genes	43.8	15, 194, 315, 1669, 1717
<i>polA</i>	Polymerase	<i>atrC</i> ; DNA nucleotidyltransferase (EC 2.7.7.7)	86.5	454, 499, 550, 708, 713, 902, 903, 909, 1077, 1234, 1267, 1268, 1717, 1897, 2133, 2150, 2231
<i>potA</i>	Polyamine transport	Spermidine and putrescine transport; membrane-associated protein	27.3	1347, 1717
<i>poxA</i>	Pyruvate oxidase	Hypersensitivity to antimicrobial agents; lower levels of pyruvate oxidase and acetolactate synthase deficiency in α -ketobutyrate metabolism	94.6	1717, 1895, 2022, 2023, 2074

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<i>ppc</i>		Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	89.6	92, 768, 804, 1270, 1700, 1717, 1824, 2008
<i>ppiA</i>		Peptidyl-prolyl <i>cis-trans</i> isomerase A precursor (EC 5.2.1.8)	75.1	1717, 2026
<i>ppsA</i>		Phosphoenolpyruvate synthase	30.5	322, 620, 1717, 1846
<i>ppsB</i>		Deficiency in phosphoenolpyruvate synthase; may be identical to <i>fruR</i>	3.3	277, 1717
<i>praA</i>		Phage P221 receptor function	93.8	1451, 1452, 1717
<i>praB</i>		Phage P221 receptor function	64.7	1451, 1452, 1717
<i>prbA</i>		Phage ES18 receptor function	93.8	1717, 1718, 1721
<i>prbB</i>		Phage ES18 receptor function	35.5	1717, 1718, 1721
<i>prc</i>		Reduced survival in macrophages; similar to <i>prc</i> protease of <i>E. coli</i>	41.6	129, 1717
<i>prdB</i>		Phage PH51 receptor function	35.6	1717, 1718, 1721
<i>prfA</i>		Protein release factor 1 (RF1)	38.8	493, 494, 498, 1717
<i>prfB</i>		<i>supT</i> , <i>supK</i> ; protein release factor 2 (RF2)	66.2	87, 1009, 1622, 1623, 1717, 2046
<i>prgH</i>	<i>phoP</i> -repressed gene	Influences mouse virulence; defective in macrophage invasion	62.9	140, 1717
<i>prh</i>		Phage HK009 receptor function	94.0	1717, 1718, 1721
<i>prk</i>		Phage HK068 receptor function	35.4	1717, 1718, 1721
<i>proA</i>	Proline	Glutamate to glutamic- γ -semialdehyde	7.8	301, 828, 920, 948, 949, 1132, 1133, 1137, 1275, 1367, 1612, 1648, 1717, 1836, 1845
<i>proB</i>	Proline	Glutamate to glutamic- γ -semialdehyde	7.8	301, 828, 920, 948, 949, 1132, 1133, 1137, 1275, 1367, 1612, 1717, 1836, 1845
<i>proC</i>	Proline	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	8.9	218, 920, 1367, 1717, 1836, 1845
<i>proL</i>	Proline	<i>sufB</i> , <i>proW</i> ; frameshift suppressor affecting proline tRNA and correcting +1 frameshifts at runs of C in mRNA	49.1	1717, 1879
<i>proM</i>	Proline	<i>proT</i> ; proline tRNA	85.6	201, 208, 1717
<i>proP</i>	Proline	Proline permease II; glycine betaine and proline; low affinity	93.5	55, 267, 269, 397, 479, 984, 1329, 1717
<i>proV</i>	Proline	<i>proU</i> ; high-affinity transport system for glycine betaine and proline; binding protein	61.4	70, 268, 397, 400, 475, 479, 764, 772, 984, 1424, 1513, 1514, 1717, 1908, 1964
<i>proW</i>	Proline	<i>proU</i> ; high-affinity transport system for glycine betaine and proline; hydrophobic membrane component	61.4	397, 400, 984, 1424, 1513, 1514, 1717, 1908
<i>proX</i>	Proline	<i>proU</i> ; high-affinity transport system for glycine betaine and proline; glycine betaine-binding protein	61.4	397, 400, 984, 1424, 1513, 1514, 1717, 1908
<i>proY</i>	Proline	Proline transport system	9.0	1717
<i>proZ</i>	Proline	Proline transport system	77.7	491, 1717
<i>prpA</i>	Propionate	<i>prp</i> ; propionate metabolism	95.7	1717, 1721
<i>prpB</i>	Propionate	Propionate metabolism	8.2	1717
<i>prsA</i>		<i>prsB</i> ; phosphoribosylpyrophosphate synthetase	38.9	213, 493, 733, 734, 955, 956, 1524, 1571, 1572, 1717
<i>psiA</i>		Phosphate starvation inducible	75.8	564, 1717
<i>psiB</i>		Phosphate starvation inducible	88.9	564, 1717
<i>psiC</i>		Phosphate starvation inducible	10.1	564, 1717
<i>psiD</i>		Phosphate starvation inducible	93.8	564, 1717
<i>psiR</i>		Regulates <i>psiC</i> activity	84.8	564, 1717
<i>pss</i>		Outer membrane proteins which protect against oxidative intraleukocyte killing	94.3	1717, 1907
<i>psuA</i>		Suppressor of polarity	NM	1717, 1718, 1721
<i>pta</i>	Phosphotransacetylase	Acetyl-CoA:orthophosphate acetyltransferase (EC 2.3.1.8)	50.8	1130, 1183, 1717, 2073, 2080
<i>ptsF</i>	Phosphotransferase system	<i>fruA</i> ; fructose phosphotransferase enzyme IIa	48.8	620, 1078, 1580, 1701, 1705, 1706, 1711, 1717
<i>ptsG</i>	Phosphotransferase system	<i>glu</i> , <i>gpt</i> ; glucose phosphotransferase enzyme IIB'-factor III (<i>crr</i>) system (methyl- β -D-glucoside)	26.9	212, 676, 1328, 1574, 1576, 1580, 1626, 1693, 1694, 1701, 1706, 1711, 1717, 1764, 1920, 2068
<i>ptsH</i>	Phosphotransferase system	<i>carB</i> ; phosphohistidine protein-hexose phosphotransferase (EC 2.7.1.69)	52.9	142, 266, 373, 375, 681, 722, 774, 1038, 1078, 1289, 1366, 1375, 1574, 1580-1583, 1701, 1705, 1706, 1708, 1710, 1711, 1717, 1762, 1763, 1801, 2112, 2121

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<i>ptsI</i>	Phosphotransferase system	<i>carA</i> ; enzyme I of the phosphotransferase system	52.9	266, 373, 375, 676, 722, 1038, 1078, 1104, 1199, 1289, 1366, 1375, 1574, 1580–1582, 1701, 1705, 1706, 1708, 1710–1712, 1717, 1762, 1763, 1801, 2120, 2122
<i>ptsJ</i>	Phosphotransferase system	Enzyme I* of the phosphotransferase system, not expressed in wild type	52.9	324, 1717
<i>ptsM</i>	Phosphotransferase system	<i>manA</i> ; mannose-glucose phosphotransferase enzyme IIA (2-deoxyglucose)	NM	1580, 1626, 1703, 1706, 1711, 1717, 1920
<i>purA</i>	Purine	Adenylosuccinate synthetase (EC 6.3.4.4)	95.1	149, 664, 668, 1715, 1717
<i>purB</i>	Purine	Adenylosuccinate lyase (EC 4.3.2.2)	27.5	656, 664, 667, 1717
<i>purC</i>	Purine	Phosphoribosylaminoimidazole-succinocarboxamide synthetase (EC 6.3.2.6)	54.0	664, 1679, 1717
<i>purD</i>	Purine	Phosphoribosylglycinamide synthetase (EC 6.3.1.13)	90.8	129, 330, 482, 664, 1717, 2129
<i>purE</i>	Purine	Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21)	12.6	664, 1065, 1484, 1717, 2012
<i>purF</i>	Purine	Amidophosphoribosyltransferase (EC 2.4.2.14)	51.7	464, 466, 467, 611, 664, 1065, 1717, 2129
<i>purG</i>	Purine	Phosphoribosylglycinamidase synthetase (EC 6.3.5.3)	56.3	664, 1679, 1717
<i>purH</i>	Purine	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	90.8	330, 482, 664, 1717
<i>purI</i>	Purine	Phosphoribosylaminoimidazole synthetase (EC 6.3.3.1)	54.5	405, 1679, 1717
<i>purJ</i>	Purine	IMP cyclohydrolase (EC 3.5.4.10)	90.8	668, 1717
<i>purN</i>	Purine	Cryptic <i>purF</i> analog; synthesis of phosphoribosylamine	4.7	1717, 1721
<i>purR</i>	Purine	Constitutive high expression of <i>pur</i> genes	30.7	1717, 1721
<i>putA</i>	Proline utilization	<i>putB</i> ; bifunctional enzyme; proline oxidase and pyrroline-5-carboxylate dehydrogenase	25.6	28, 70, 398, 442, 443, 718, 719, 1290, 1330, 1331, 1496, 1497, 1613, 1614, 1717, 1745
<i>putP</i>	Proline utilization	Major L-proline permease	25.7	55, 70, 269, 397, 451, 479, 719, 1290, 1329, 1330, 1353, 1401, 1455, 1497, 1717
<i>pyrB</i>	Pyrimidine	Aspartate carbamoyltransferase (EC 2.1.3.2)	96.9	139, 335, 399, 541, 543, 544, 940, 944–946, 1013, 1016, 1335, 1336, 1459, 1717, 1770, 1838, 1979, 1980, 2147, 2197
<i>pyrC</i>	Pyrimidine	Dihydroorotase (EC 3.5.2.3)	26.2	139, 264, 940, 944, 1016–1018, 1421, 1459, 1717, 1770, 1838, 1858–1860, 2037, 2147, 2197
<i>pyrD</i>	Pyrimidine	Dihydroorotate oxidase (EC 1.3.3.1)	24.1	139, 264, 576, 940, 944, 1016, 1018, 1459, 1717, 1770, 1838, 1858, 1859, 2037, 2147, 2197
<i>pyrE</i>	Pyrimidine	Orotate phosphoribosyltransferase (EC 2.4.2.10)	81.4	139, 166, 944–946, 1016, 1018, 1087, 1107, 1259, 1420, 1422, 1459, 1717, 1723, 1770, 1838, 2147, 2197
<i>pyrF</i>	Pyrimidine	Orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	37.6	139, 292, 940, 1016, 1087, 1371, 1459, 1716, 1717, 1770, 1838, 2006, 2007, 2147, 2197
<i>pyrG</i>	Pyrimidine	CTP synthetase	64.4	133, 931, 1418, 1459, 1717
<i>pyrH</i>	Pyrimidine	UMP kinase	4.4	904, 940, 941, 987, 1014, 1419, 1717, 2222
<i>pyrI</i>	Pyrimidine	Regulatory polypeptide for aspartate transcarbamoylase, regulatory subunit (EC 2.1.3.2)	96.9	541, 944, 1336, 1717
<i>pyrL</i>	Pyrimidine	Aspartate transcarbamoylase leader peptide	96.9	1336, 1717
<i>qor</i>		Quinoline reductase	92.1	1409, 1717
<i>rbsB</i>	Ribose	<i>rbsP</i> ; ribose-binding protein	85.0	18, 1383, 1717, 1938, 2149
<i>rck</i>	Resistance to complement killing	17-kDa outer membrane protein; sequence similarity to <i>pagC</i>	pSL	580, 711, 745, 746, 1717
<i>recA</i>	Recombination	Recombination deficient; degrades DNA	T	62.2
				50, 108, 222, 250, 454, 456, 473, 490, 660, 698, 864, 902, 1186, 1234, 1257, 1266, 1397, 1487, 1511, 1617, 1717, 1753, 1820, 1857, 1983, 2150–2152, 2206, 2231

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<i>recB</i>	Recombination	Recombination deficient; exonuclease V (EC 3.1.11.15)	65.2	250, 473, 490, 864, 1274, 1277, 1617, 1717, 1835, 1857, 1983
<i>recC</i>	Recombination	Recombination deficient; exonuclease V (EC 3.1.11.15)	65.3	250, 473, 490, 864, 1274, 1277, 1617, 1717, 1835, 1983
<i>recD</i>	Recombination	Endonuclease component of RecBCD enzyme	65.2	1274, 1337, 1617, 1717
<i>recF</i>	Recombination	UV sensitive; recombination defective in <i>recB sbcBC</i> background	83.5	1717, 1726
<i>recJ</i>	Recombination	UV sensitive; recombination defective in <i>recB sbcBC</i> background	66.2	1274, 1276, 1717
<i>recN</i>	Recombination	Recombination defective in <i>recB sbcBC</i> background	58.2	1717
<i>recQ</i>	Recombination	Recombination deficient; DNA helicase activity	86.0	240, 1717
<i>relA</i>	RNA relaxed	RC; regulation of RNA synthesis	64.6	82, 416, 911, 1093, 1300, 1413, 1586, 1689, 1714, 1717, 1783, 1899, 2154
<i>repB</i>	Replication	Plasmid partitioning	pSL T	580, 1717
<i>repC</i>	Replication	Plasmid partitioning	pSL T	580, 1717
<i>rfaB</i>	Rough	UDP-D-galactose:LPS α -1,6-D-galactosyltransferase (EC 2.1.4.–)	81.4	228, 992, 1061, 1717, 2160
<i>rfaC</i>	Rough	LPS core defect; LPS heptosyltransferase I	81.3	215, 223, 224, 727, 1288, 1486, 1717, 1719, 1758, 1884, 1922, 1959
<i>rfaD</i>	Rough	D-Glycero-D-manno-heptose epimerase (EC 5.1.3.–)	81.2	852, 992, 1170, 1288, 1717, 1758, 1814, 1922
<i>rfaE</i>	Rough	LPS core defect; proximal heptose deficient	78.5	39, 44, 215, 586, 624, 629, 725, 727, 752, 981, 1246, 1247, 1255, 1282, 1288, 1410, 1489–1491, 1493, 1494, 1604, 1717, 1719, 1742, 1743, 1825, 1884, 1921, 1922, 1927, 1959, 1989
<i>rfaF</i>	Rough	LPS core defect; ADP-heptose–LPS heptosyltransferase II	81.2	138, 725, 752, 786, 845, 852, 981, 1107, 1259, 1288, 1489, 1490, 1493, 1494, 1717, 1723, 1744, 1758, 1814, 1922, 1950
<i>rfaG</i>	Rough	LPS core defect; glucose I transferase	81.4	216, 228, 392, 506, 786, 981, 992, 1107, 1246, 1247, 1273, 1282, 1288, 1388, 1485, 1489, 1490, 1493, 1494, 1697, 1717, 1723, 1742, 1921, 1922, 2145
<i>rfaH</i>	Rough	Deficient in LPS core synthesis and in F-factor expression; transcription control factor	86.1	228, 391, 393, 521, 1211, 1246, 1247, 1288, 1489, 1490, 1493, 1494, 1717, 1725, 1921, 1923, 2145
<i>rfaI</i>	Rough	LPS core defect; LPS 1,3-galactosyltransferase (EC 2.4.1.44)	81.4	228, 285, 991, 992, 1288, 1717, 1814
<i>rfaJ</i>	Rough	LPS core defect; LPS 1,2-glucosyltransferase	81.4	228, 285, 786, 991, 992, 1246, 1247, 1282, 1288, 1489, 1490, 1493, 1494, 1717, 1742, 1814, 1921, 2145
<i>rfaK</i>	Rough	LPS core defect; LPS 1,2-N-acetylglucosaminetransferase (EC 2.4.1.56)	81.3	981, 1060, 1213, 1246, 1247, 1258, 1282, 1288, 1489, 1490, 1493, 1494, 1717, 1758
<i>rfaL</i>	Rough	LPS core defect; O-antigen ligase	81.3	786, 1060, 1246, 1247, 1258, 1282, 1288, 1387, 1489, 1490, 1493, 1494, 1523, 1717, 1742, 1921, 2144
<i>rfaP</i>	Rough	LPS core defect; heptose phosphorylation	81.4	474, 751, 981, 1061, 1385, 1717, 1921
<i>rfaY</i>	Rough	LPS core defect	81.3	1060, 1258, 1717, 1758, 1814
<i>rfaZ</i>	Rough	LPS core defect	81.3	1060, 1258, 1717, 1758
<i>rfaA</i>	Rough	<i>musA, musB</i> ; LPS side chain defect; glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)	45.2	219, 220, 516, 954, 960, 974, 1030, 1050–1052, 1187, 1214, 1247, 1253, 1282, 1288, 1389, 1433, 1434, 1453, 1491, 1639, 1717, 1921, 1922, 1950, 2079, 2110

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<i>rfbB</i>	Rough	LPS side chain defect; dTDP-D-glucose-4,6-dehydratase (EC 4.2.1.46)	45.3	219, 220, 954, 1184, 1247, 1279, 1288, 1304, 1433, 1434, 1666, 1717, 1921, 2099
<i>rfbC</i>	Rough	LPS side chain defect; dTDP-4-dehydroxyrhamnose 3,5-epimerase (EC 5.1.3.13)	45.2	954, 1218, 1304, 1717
<i>rfbD</i>	Rough	LPS side chain defect; NADPH:dTDP-4-dehydroxyrhamnose reductase (EC 1.1.1.133)	45.3	219, 220, 954, 1053, 1054, 1218, 1247, 1288, 1304, 1433, 1434, 1717, 1921
<i>rfbF</i>	Rough	LPS side chain defect; glucose-1-phosphate cytidyltransferase (EC 2.7.7.33)	45.2	219, 220, 954, 1215, 1216, 1247, 1288, 1433, 1434, 1717, 1921
<i>rfbG</i>	Rough	LPS side chain defect; CDP-glucose-4,6-dehydratase (EC 4.2.1.45)	45.2	219, 220, 954, 1216, 1218, 1247, 1433, 1434, 1717, 1921
<i>rfbH</i>	Rough	LPS side chain defect; CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	45.1	219, 220, 954, 1216, 1218, 1247, 1400, 1433, 1434, 1717, 1921, 2218
<i>rfbI</i>	Rough	LPS side chain defect; CDP-6-deoxy- Δ 3,4-glucoseen reductase	45.2	954, 1216, 1717
<i>rfbJ</i>	Rough	LPS side chain defect; CDP-abequose synthase (EC 4.2.1.-)	45.1	220, 954, 1216, 1218, 1219, 1717
<i>rfbK</i>	Rough	LPS side chain defect; phosphomannomutase (EC 5.4.2.8)	45.0	219, 220, 954, 1218, 1247, 1433, 1434, 1717, 1921
<i>rfbM</i>	Rough	LPS side chain defect; mannose-1-phosphate guanylyltransferase (EC 2.7.7.22)	45.0	219, 220, 954, 1218, 1247, 1433, 1434, 1717, 1921
<i>rfbN</i>	Rough	LPS side chain defect; rhamnosyltransferase	45.0	219, 220, 954, 1218, 1696, 1697, 1717
<i>rfbP</i>	Rough	<i>rfbT</i> ; bifunctional enzyme; undecaprenyl-phosphate galactosephosphotransferase; may also relocate O-antigen from cytoplasmic to periplasmic face of cytoplasmic membrane	44.9	219, 954, 1218, 1247, 1287, 1433, 1717, 1921, 2098, 2144
<i>rfbU</i>	Rough	LPS side chain defect; mannosyltransferase	45.0	954, 1218, 1717
<i>rfbV</i>	Rough	LPS side chain defect; abequosyltransferase; putative	45.1	954, 1717
<i>rfbX</i>	Rough	LPS side chain defect; rhamnosyltransferase; putative (EC 2.4.1.-)	45.1	954, 1717
<i>rfc</i>	Rough	<i>rouC</i> ; O-antigen polymerase	35.7	356, 358, 652, 1247, 1287, 1404, 1411, 1433, 1453, 1559, 1717, 1921, 1952
<i>rfe</i>	Rough	Defect in synthesis of enterobacterial common antigen, the T1 antigen, and O-side chains of <i>Salmonella</i> groups L and C1	85.4	245, 932, 981, 1187, 1188, 1281, 1283-1285, 1717
<i>rffM</i>	Rough	<i>rff</i> ; synthesis of enterobacterial common antigen; UDP-N-acetyl-D-mannosaminuronic acid transferase (EC 2.4.1.-)	85.6	459, 1187, 1188, 1241, 1284, 1286, 1325, 1717
<i>rffT</i>	Rough	<i>rff</i> ; synthesis of enterobacterial common antigen; 4- α -L-fucosyl transferase (EC 2.4.1.-)	85.5	459, 1188, 1241, 1284, 1286, 1717
<i>rft</i>	Rough	“Transient” T1 forms	16.2	160, 245, 801, 1287, 1717, 1729
<i>rfu</i>	Rough	“Transient” T1 forms	NM	245, 1717, 1730
<i>rhaA</i>	Rhamnose	L-Rhamnose isomerase (EC 5.3.1.14)	88.1	36, 500, 1439, 1473, 1715, 1717
<i>rhaB</i>	Rhamnose	L-Rhamnulokinase (EC 2.7.1.5)	88.1	36, 500, 1439, 1473, 1715, 1717
<i>rhaD</i>	Rhamnose	L-Rhamnulose-1-phosphate aldolase (EC 4.1.2.19)	88.1	36, 500, 1439, 1473, 1715, 1717
<i>rhaR</i>	Rhamnose	<i>rhaC1</i> ; regulation	88.1	36, 500, 1439, 1473, 1715, 1717
<i>rhaS</i>	Rhamnose	<i>rhaC2</i> ; regulation	88.1	36, 500, 1439, 1473, 1715, 1717
<i>rhaT</i>	Rhamnose	L-Rhamnose transport	88.1	36, 500, 1439, 1473, 1715, 1717
<i>rhlB</i>		RNA helicase; putative	85.4	582, 1360, 1717
<i>rho</i>		<i>psu</i> ; polarity suppressor; transcription terminator factor Rho	85.3	339, 835, 836, 1158, 1717
<i>rna</i>	RNase	<i>rnsA</i> ; RNase I	15.2	52, 248, 299, 1172, 1495, 1717, 2113
<i>rnc</i>	RNase	RNase III	57.6	52, 1172, 1495, 1717, 1963
<i>rnhA</i>	RNase H	RNase H (EC 3.1.26.4)	6.9	918, 1717
<i>rnhB</i>	RNase H	RNase HII (EC 3.1.26.4)	5.9	1139, 1717
<i>mnpA</i>	RNase P	RNase P, protein component (EC 3.1.26.5)	83.8	1692, 1717
<i>mnpB</i>	RNase P	RNase P, RNA subunit, M1 RNA	71.1	96, 1717
<i>rodA</i>	Rod	Round cell morphology; mecillinam resistance	15.4	65, 68, 383, 1717
<i>rph</i>	RNase PH	tRNA nucleotidyltransferase; RNase PH (EC 2.7.7.56)	81.5	1422, 1717
<i>rplA</i>	Ribosomal protein, large	50S ribosomal subunit protein L1	90.1	1717, 2230
<i>rplE</i>	Ribosomal protein, large	50S ribosomal subunit protein L5	74.6	297, 1717

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<i>rplJ</i>	Ribosomal protein, large	50S ribosomal subunit protein L10	90.2	1551, 1717, 1971, 2018, 2230
<i>rplK</i>	Ribosomal protein, large	50S ribosomal subunit protein L11	90.1	1717, 2230
<i>rplL</i>	Ribosomal protein, large	50S ribosomal subunit protein L7/L12	90.2	1717, 1971, 2018, 2230
<i>rplS</i>	Ribosomal protein, large	50S ribosomal subunit protein L19	57.9	1717
<i>rplX</i>	Ribosomal protein, large	50S ribosomal subunit protein L24	74.6	297, 1717
<i>rpoA</i>	RNA polymerase	<i>oxrB</i> ; RNA polymerase, α -subunit (EC 2.7.7.6)	74.5	523, 1230, 1717
<i>rpoB</i>	RNA polymerase	<i>rif</i> ; RNA polymerase, β -subunit (EC 2.7.7.6)	90.2	98, 214, 585, 945, 946, 1419, 1717, 1970, 1971, 2018, 2019, 2024, 2210
<i>rpoC</i>	RNA polymerase	RNA polymerase, β' -subunit (EC 2.7.7.6)	90.2	214, 585, 945, 946, 1717, 1971, 2018, 2019, 2210, 2211
<i>rpoD</i>	RNA polymerase	RNA polymerase, σ^{70} subunit	70.0	509, 753, 1717, 1738
<i>rpoE</i>	RNA polymerase	RNA polymerase, σ^E subunit	57.7	1717
<i>rpoN</i>	RNA polymerase	<i>glnF</i> , <i>ntrA</i> ; RNA polymerase, σ^{54} subunit (EC 2.7.7.6)	72.2	230, 524, 581, 612, 1090, 1112, 1316, 1319, 1569, 1570, 1717, 2117
<i>rpoS</i>	RNA polymerase	<i>katF</i> ; RNA polymerase, σ^S subunit	63.6	519, 522, 1085, 1448, 1477, 1717, 1932
<i>rpsD</i>	Ribosomal protein, small	30S ribosomal subunit protein S4	74.5	1230, 1717
<i>rpsE</i>	Ribosomal protein, small	<i>spcA</i> ; 30S ribosomal subunit protein S5	74.6	1717, 2182
<i>rpsG</i>	Ribosomal protein, small	30S ribosomal subunit protein S7	74.7	958, 1717
<i>rpsL</i>	Ribosomal protein, small	<i>strA</i> ; 30S ribosomal subunit protein S12	74.7	859, 870, 958, 1717, 1984, 2032, 2034, 2182
<i>rpsP</i>	Ribosomal protein small	30S ribosomal subunit protein S16	57.9	1717
<i>rpsU</i>	Ribosomal protein, small	30S ribosomal subunit protein S21	70.0	509, 1717
<i>rjfB</i>		5S rRNA gene of <i>rrnB</i> operon	90.0	458, 1717
<i>rrnA</i>	rRNA	rRNA operon	87.0	52, 257, 1171–1173, 1495, 1717, 1819
<i>rrnB</i>	rRNA	rRNA operon	90.0	52, 257, 1171–1173, 1495, 1717, 1819
<i>rrnC</i>	rRNA	rRNA operon	85.0	52, 257, 1171–1173, 1495, 1717, 1819
<i>rrnD</i>	rRNA	rRNA operon	74.3	257, 1171, 1495, 1717, 1819
<i>rrnE</i>	rRNA	rRNA operon	90.9	52, 257, 1171–1173, 1495, 1717, 1819
<i>rrnG</i>	rRNA	rRNA operon	58.1	257, 1171, 1717, 1819
<i>rrnH</i>	rRNA	rRNA operon	6.2	52, 257, 1171, 1495, 1717, 1819
<i>rsk</i>		Binding site for a regulatory element for virulence traits	pSL T	1717, 2066, 2067
<i>samA</i>	<i>Salmonella</i> mutagenesis	Mutagenesis by UV and mutagens; related to <i>umuDC</i> operon	pSL T	1064, 1443, 1444, 1717
<i>samB</i>	<i>Salmonella</i> mutagenesis	Mutagenesis by UV and mutagens; related to <i>umuDC</i> operon	pSL T	1064, 1443, 1444, 1717
<i>sapA</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.1	1540, 1717
<i>sapB</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.2	1540, 1717
<i>sapC</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.2	686, 1540, 1717
<i>sapD</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.2	686, 1540, 1717
<i>sapE</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	3.4	686, 1717
<i>sapF</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.2	1540, 1717
<i>sapI</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	38.7	686, 1717
<i>sapJ</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	87.7	686, 1717

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<i>sapK</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	87.7	686, 1717
<i>sapL</i>		Resistance to antimicrobial peptides melittin and protamine	44.1	686, 1717
<i>sapM</i>	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	6.6	686, 1717
<i>sbcB</i>	Suppressor of <i>recBC</i>	Suppressor of <i>recBC</i> mutations	41.6	151, 1717
<i>sbcC</i>	Suppressor of <i>recBC</i>	Suppressor of <i>recBC</i> mutations	9.2	151, 1717
<i>sbcD</i>	Suppressor of <i>recBC</i>	Suppressor of <i>recBC</i> mutations	9.2	151, 1717
<i>sbcE</i>	Suppressor of <i>recBC</i>	Unstable suppressor of <i>recBC</i> mutations	57.0	1717
<i>sbp</i>	Sulfate-binding protein	Periplasmic sulfate-binding protein	88.3	616, 914, 1560, 1561, 1717
<i>selA</i>	Selenium	<i>fdhA</i> ; selenium metabolism; biosynthesis of selenoproteins	80.3	118, 325, 326, 1092, 1547, 1717, 1905
<i>selB</i>	Selenium	<i>fdhA</i> ; selenium metabolism; translation factor necessary for biosynthesis of selenoproteins	80.3	1717, 1905
<i>selC</i>	Selenium	<i>fdhC</i> ; selenium metabolism; selenocysteine tRNA	81.5	118, 1717, 1905
<i>selD</i>	Selenium	<i>selA</i> ; selenium metabolism; biosynthesis of selenoproteins and selenocysteine tRNA	29.0	1717, 1905
<i>serA</i>	Serine	Phosphoglycerate dehydrogenase (EC 1.1.1.95)	66.8	1717, 2045, 2220
<i>serB</i>	Serine	Phosphoserine phosphatase (EC 3.1.3.3)	99.5	558, 1717, 2045
<i>serC</i>	Serine	Requirement	19.6	680, 806, 808, 1717
<i>serD</i>	Serine	Requirement for pyridoxine plus L-serine or glycine	47.2	1717, 1718, 1721
<i>serV</i>	Serine	Serine tRNA ₃	62.0	173, 1717
<i>sgdA</i>	Suppressor of gyrase	Restores <i>his</i> attenuation in <i>gyrA</i> mutants and suppresses other <i>gyrA</i> phenotypes	62.0	173, 1717
<i>sidC</i>	Siderochrome	Siderochrome utilization; ferrichrome transport; albomycin resistance	3.8	1244, 1245, 1717
<i>sidF</i>	Siderochrome	Siderochrome utilization; ferrichrome transport; albomycin resistance	3.8	1244, 1245, 1717
<i>sidK</i>	Siderochrome	Siderochrome utilization; albomycin resistance; receptor of phage ES18 in <i>S. typhimurium</i> and of T5 in <i>S. paratyphi B</i>	5.0	227, 673, 1244, 1245, 1717
<i>sinR</i>	<i>Salmonella</i> insert regulator	Protein in the LysR family of transcription regulators; gene is unique to <i>Salmonella</i>	104.0	688, 1717
<i>slt</i>		Soluble lytic transglycosylase	99.9	1717
<i>slyA</i>	Salmolysin	<i>cyx</i> ; hemolysin, required for survival in macrophages and for virulence	30.8	1197, 1198, 1717
<i>smoB</i>	Smooth	Smooth colony morphology in histidine-constitutive mutants	98.6	34, 1717
<i>smpB</i>	Small protein	Reduced survival in macrophages	59.5	129, 1717
<i>sms</i>		Repair of endogenous alkylation damage; putative; similarity with ATP-dependent proteases Lon and RecA	99.9	563, 1717
<i>smvA</i>		Methyl viologen resistant	38.6	826, 1717
<i>sodB</i>		Iron superoxide dismutase; putative (EC 1.15.1.1)	30.7	1717
<i>spaK</i>	Surface presentation of antigens	<i>invB</i> ; reduced invasion; secretory pathway	63.1	483, 600, 603, 685, 970, 1359, 1717
<i>spaL</i>	Surface presentation of antigens	<i>invC</i> ; reduced invasion; secretory pathway, homologous to <i>spa</i> in <i>Shigella</i>	63.1	483, 600, 603, 639, 685, 1359, 1717
<i>spaM</i>	Surface presentation of antigens	<i>invI</i> ; reduced invasion; secretory pathway	63.1	352, 685, 1310, 1359, 1717
<i>spaN</i>	Surface presentation of antigens	<i>invJ</i> ; reduced invasion; secretory pathway	63.0	352, 685, 1310, 1359, 1717
<i>spaO</i>	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	685, 1359, 1717
<i>spaP</i>	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	685, 1359, 1717
<i>spaQ</i>	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	685, 1359, 1717
<i>spaR</i>	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	685, 1359, 1717
<i>spaS</i>	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	685, 1359, 1717
<i>spaT</i>	Surface presentation of antigens	Reduced invasion; secretory pathway	62.9	685, 1359, 1717
<i>spcB</i>	Spectinomycin	Nonribosomal resistance	74.5	1717, 2182
<i>spoT</i>	Spot	Guanosine 5'-diphosphate, 3'-diphosphate pyrophosphatase	81.6	418, 1689, 1691, 1717
<i>spvA</i>	<i>Salmonella</i> plasmid virulence	<i>mkaB</i> , <i>vsdB</i> ; hydrophilic protein, 28 kDa, outer membrane protein	pSL	387, 701, 702, 1085, 1717, 1988
<i>spvB</i>	<i>Salmonella</i> plasmid virulence	<i>vsdC</i> , <i>mkaA</i> , <i>mkfB</i> ; hydrophilic protein, 66 kDa, cytoplasmic protein	pSL	387, 701, 702, 1085, 1447, 1448, 1456, 1717, 1987, 1988
<i>spvC</i>	<i>Salmonella</i> plasmid virulence	<i>virA</i> , <i>mkaD</i> , <i>mkfA</i> , <i>vsdD</i> ; hydrophilic protein, 28 kDa	pSL	387, 700–702, 1085, 1445, 1446, 1717, 1988
<i>spvD</i>	<i>Salmonella</i> plasmid virulence	<i>virB</i> , <i>vsdE</i> ; hydrophilic protein, 25 kDa	pSL	701, 702, 1085, 1445, 1717

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<i>spvR</i>	<i>Salmonella</i> plasmid virulence	<i>mkaC</i> , <i>vsdA</i> ; regulation of the <i>spv</i> operon; member of LysR family of positive regulatory proteins	pSL T	270, 387, 702, 1085, 1094, 1717, 1988
<i>srlA</i>	Sorbitol	D-Glucitol-specific enzyme II of the phosphotransferase system	62.5	1717, 1728
<i>srlB</i>	Sorbitol	D-Glucitol-specific enzyme III of the phosphotransferase system	62.5	1717, 1728
<i>srlC</i>	Sorbitol	<i>gut</i> ; regulatory gene	62.4	1056, 1717, 1728
<i>srlD</i>	Sorbitol	Sorbitol-6-phosphate dehydrogenase (EC 1.1.1.140)	62.5	1717, 1721
<i>srlM</i>	Sorbitol	DNA-binding protein which activates transcription of the <i>srl</i> operon	62.5	1717, 1721
<i>srlR</i>	Sorbitol	Regulatory gene	62.5	1717, 1721
<i>ssb</i>	Single-strand binding	Single-strand DNA-binding protein	92.3	1313, 1717
<i>stiA</i>	Starvation inducible	<i>sinA</i> ; induced by starvation for carbon source or other requirements	35.8	547, 1717, 1863, 1866
<i>stiB</i>	Starvation inducible	Induced by starvation for carbon source or other requirements	NM	1717, 1863, 1866
<i>stiC</i>	Starvation inducible	Induced by starvation for carbon source or other requirements	78.2	1717, 1863, 1866
<i>stiD</i>	Starvation inducible	Induced by starvation for carbon source or other requirements	35.9	1717, 1863, 1866
<i>stiE</i>	Starvation inducible	Induced by starvation for carbon source or other requirements	44.0	1717, 1863, 1866
<i>stiF</i>	Starvation inducible	Induced by starvation for carbon source or other requirements	NM	1717, 1863, 1866
<i>stiG</i>	Starvation inducible	Induced by starvation for carbon source or other requirements	88.2	1717, 1863, 1866
<i>stiH</i>	Starvation inducible	Induced by starvation for carbon source or other requirements	57.4	1717, 1863, 1866
<i>stn</i>	Salmonella toxin	<i>stx</i> ; enterotoxin	NM	328, 329, 1584, 1717
<i>strB</i>	Streptomycin	Low-level resistance plus auxotrophy; nonribosomal	55.7	1530, 1679, 1717, 2173
<i>strC</i>	Streptomycin	Streptomycin resistance; nonribosomal	NM	672, 1717
<i>sucA</i>	Succinate	<i>lys</i> , <i>suc</i> ; succinate requirement; α -ketoglutarate dehydrogenase, decarboxylase component	17.1	1140, 1717
<i>sufA</i>	Suppressor of frameshifts	Suppressor affecting proline tRNA and correcting +1 frameshifts at runs of C in the mRNA	79.9	1069, 1103, 1643, 1644, 1717
<i>sufB</i>	Suppressor of frameshifts	<i>sufC</i> ; recessive suppressor of +1 frameshifts at runs of C in the mRNA	16.8	1069, 1103, 1643, 1644, 1717, 1879
<i>sufD</i>	Suppressor of frameshifts	Frameshift suppressor affecting glycine tRNA and correcting +1 frameshifts at runs of G in the mRNA	65.8	1069, 1642–1644, 1717
<i>sufE</i>	Suppressor of frameshifts	Frameshift suppressor correcting +1 frameshifts at runs of G in the mRNA	90.7	1069, 1643, 1644, 1717
<i>sufF</i>	Suppressor of frameshifts	Recessive frameshift suppressor correcting +1 frameshifts at runs of G in the mRNA	12.4	1643, 1644, 1717
<i>sufG</i>	Suppressor of frameshifts	<i>sufI</i> ; frameshift suppressor correcting +1 frameshifts at runs of A in the mRNA	16.6	1069, 1072, 1717
<i>sufH</i>	Suppressor of frameshifts	Suppressor	53.2	1069, 1717
<i>sufI</i>	Suppressor of frameshifts	Suppressor	12.5	1069, 1717
<i>sulA</i>	Suppressor of <i>lon</i>	Lacks SOS-induced filamentation	24.4	572, 628, 1717
<i>sumA</i>	Suppressor of missense	Suppressor	95.2	1717, 1718, 1721
<i>supC</i>	Suppressor	Ochre suppressor	38.6	1717, 2157
<i>supD</i>	Suppressor	Amber suppressor; serine insertion	42.9	200, 570, 866, 1717, 2157
<i>supE</i>	Suppressor	<i>supY</i> ; amber suppressor; glutamine insertion	16.7	152, 200, 206, 866, 1717, 2157
<i>supG</i>	Suppressor	Ochre suppressor; lysine insertion	NM	1717, 2157
<i>supJ</i>	Suppressor	<i>supH</i> ; amber suppressor; leucine insertion	85.1	200, 663, 1717, 2157
<i>supQ</i>	Suppressor	Suppressor of nonsense and deletion mutations of <i>leuD</i>	7.9	591, 1022, 1024, 1025, 1132, 1133, 1717, 1936
<i>supR</i>	Suppressor	Amber suppressor; haploid lethal	85.1	1348, 1717
<i>supS</i>	Suppressor	UGA suppressor; haploid lethal	85.1	1348, 1717
<i>supU</i>	Suppressor	Suppressor of UGA mutations; may be due to alteration of ribosome structure	74.8	968, 1717
<i>tar</i>	Taxis-associated receptor	Chemotaxis transduction polypeptide; aspartate receptor	41.9	401, 427, 428, 545, 1338, 1348, 1369, 1698, 1717, 2096
<i>tcp</i>		Transmembrane receptor for citrate (attractant) and phenol (repellent)	NM	1717, 2193
<i>tctA</i>	Tricarboxylate transport	Membrane protein	60.9	883, 898–901, 1717, 1856, 2138–2140
<i>tctB</i>	Tricarboxylate transport	Membrane protein	60.8	1717, 2138–2140
<i>tctC</i>	Tricarboxylate transport	Tricarboxylate-binding protein	60.8	83, 900, 1717, 1855, 1856, 1972, 1973, 2138–2140
<i>tctD</i>	Tricarboxylate transport	Regulatory protein	60.8	1717, 2138–2140
<i>tctIII</i>	Tricarboxylate transport	Transport	17.6	1717, 1718, 1721
<i>tctIII</i>	Tricarboxylate transport	<i>triM</i> , <i>triR</i> ; transport	1.3	900, 1717
<i>tdcB</i>		Catabolic threonine dehydratase	70.9	1036, 1717
<i>tdk</i>		Thymidine kinase (EC 2.7.1.21)	38.4	134, 824, 1717
<i>tesA</i>		<i>apeA</i> ; thioesterase I (EC 3.1.2.–)	12.3	327, 749, 1344, 1350, 1717

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<i>thiA</i>	Thiamine	<i>thiG</i> ; thiamine or thiazole moiety	90.5	824, 1144, 1717
<i>thiC</i>	Thiamine	<i>thiA</i> ; thiamine or pyrimidine moiety	90.5	1717, 1718, 1721
<i>thiD</i>	Thiamine	Thiamine requirement	50.5	1717, 1718, 1721
<i>thiE</i>	Thiamine	Thiazole type	55.2	1717, 1718, 1721
<i>thiF</i>	Thiamine	Thiazole type	55.3	1717, 1718, 1721
<i>thiH</i>	Thiamine	<i>thiB</i> ; thiamine requirement	56.6	1717, 1718, 1721
<i>thiI</i>	Thiamine	<i>thiC</i> ; thiazole type	10.5	1717, 1718, 1721
<i>thrA</i>	Threonine	<i>thrC</i> , <i>thrD</i> ; aspartokinase I and homoserine dehydrogenase I (EC 2.7.2.4, EC 1.1.1.3)	0.0	642, 939, 1717, 1947
<i>thrB</i>	Threonine	<i>thrA</i> ; homoserine kinase (EC 2.7.1.39)	0.0	642, 1717, 1947
<i>thrC</i>	Threonine	<i>thrB</i> ; threonine synthase (EC 4.2.99.2)	0.1	642, 1717, 1947
<i>thrT</i>	Threonine	<i>sufJ</i> ; threonine tRNA	90.0	205, 207, 209, 231, 1068, 1069, 1717
<i>thrW</i>	Threonine	Threonine tRNA ₂ ; sequence contains attachment site for prophage P22; see <i>ataA</i>	7.8	1178
<i>thyA</i>	Thymine	Requirement	65.3	489, 976, 1717, 1835
<i>tip</i>	Taxis-involved protein	Methyl-accepting chemotaxis protein, aspartate receptor	NM	1699, 1717
<i>tkt</i>		Transketolase (EC 2.2.1.1)	NM	484, 1717
<i>tlpA</i>		Prokaryotic coiled-coil protein	pSL T	878, 1082, 1717
<i>tlpB</i>		<i>tlp</i> ; loss of protease II	40.4	748, 1717
<i>tlr</i>		Thiolutin resistance; P22 development at high temperature	NM	978–980, 1717
	T-one	<i>chr</i> ; regulates levels of some outer membrane proteins; resistance to ES18; determines a salmonellocin; affects iron transport	38.2	146, 227, 237, 381, 461, 730, 777, 1717, 1925
<i>tonB</i>				
<i>topA</i>	Topoisomerase	<i>supX</i> , <i>top</i> ; DNA topoisomerase I	37.7	313, 476, 477, 579, 587, 602, 671, 764, 983, 1175, 1206, 1386, 1487, 1511, 1512, 1592–1594, 1631, 1632, 1717, 1752, 1976, 2029, 2195
<i>topB</i>	Topoisomerase	DNA topoisomerase III (EC 5.99.1.2)	29.1	105, 1717
<i>tor</i>		Trimethylamine oxide reductase	82.5	1126–1128, 1717
<i>tpdB</i>	Tripeptide permease	Resistance to alafosfalin; tripeptide permease	32.1	309, 632, 765, 927, 928, 1424, 1717
<i>tpdB</i>	Tripeptide permease	Regulator of tripeptide permease	4.7	928, 1717
<i>traT</i>	Transfer	Membrane protein cross-reacts immunologically with TraT protein of F plasmid; restores permeability mutants to normal	pSL T	1628, 1717, 1955–1958, 1960, 1961, 2064
<i>treA</i>	Trehalose	<i>tre</i> ; utilization	40.2	1579, 1580, 1717, 1880
<i>treR</i>	Trehalose	Trehalose regulation	96.6	1717
<i>trkA</i>	Transport of potassium	<i>sapG</i> ; potassium uptake protein	74.4	686, 1541, 1717
<i>trmA</i>		tRNA (m ⁵ U54) methyltransferase (EC 2.1.1.35)	89.7	704, 1717
<i>trmD</i>		tRNA (m ¹ G37) methyltransferase (EC 2.1.1.31)	57.9	172, 1717
<i>trpA</i>	Tryptophan	<i>trpC</i> ; tryptophan synthetase, α -subunit (EC 4.2.1.20)	38.1	14, 51, 102, 127, 190, 292, 389, 394, 439, 447, 450, 721, 880, 1002, 1193, 1194, 1332, 1364, 1374, 1425, 1428, 1717, 1761, 1828, 1881, 1902, 2155, 2202, 2219
<i>trpB</i>	Tryptophan	<i>trpD</i> ; tryptophan synthetase, β -subunit (EC 4.2.1.20)	38.1	51, 102, 127, 190, 249, 390, 394, 439, 450, 721, 880, 1012, 1364, 1374, 1717, 1761, 1775, 1828, 1992
<i>trpC</i>	Tryptophan	<i>trpE</i> ; <i>N</i> -(5-phosphoribosyl) anthranilate isomerase and indole-3-glycerol phosphate synthase (EC 5.1.3.24, EC 4.1.1.48)	38.1	102, 103, 127, 190, 394, 439, 678, 830, 1192, 1374, 1627, 1717, 1775
<i>trpD</i>	Tryptophan	<i>trpB</i> ; anthranilate phosphoribosyltransferase (EC 2.4.2.18)	38.0	103, 126–128, 190, 191, 394, 439, 460, 677, 678, 693, 694, 830, 879, 1146, 1147, 1293, 1374, 1402, 1403, 1426, 1660, 1717, 1948, 1993, 1994
<i>trpE</i>	Tryptophan	<i>trpA</i> ; anthranilate synthase (EC 4.1.3.27)	38.0	103, 126, 128, 191, 273, 275, 311, 394, 410, 571, 587, 677–679, 693, 694, 1028, 1147, 1159, 1190, 1191, 1293, 1374, 1402, 1403, 1427, 1624, 1660, 1717, 1991, 1992, 1994, 2203
<i>trpR</i>	Tryptophan	Resistance to 5-methyltryptophan; derepression of tryptophan enzymes	99.9	103, 1717, 1946

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype ^a	Cs ^b	References ^c
<i>trxA</i>	Thioredoxin	Thioredoxin	85.3	1083, 1717
<i>tsr</i>		Chemotaxis receptor; serine specificity	98.5	1717, 1721
<i>tsx</i>	T-six	Nucleoside uptake; receptor for phage T6 (in <i>E. coli</i>)	9.1	1717
<i>ttr</i>		Tetrathionate reductase	40.0	291, 1717
<i>tufA</i>		Protein chain elongation factor EF-Tu	74.7	6, 88, 596, 854–858, 958, 1717, 2032–2035
<i>tufB</i>		Protein chain elongation factor EF-Tu	90.1	88, 854–858, 1717, 2032, 2034, 2035
<i>tyn</i>		Tyramine oxidase	NM	1396, 1717
<i>tyrA</i>	Tyrosine	Requirement	58.3	1717, 1875, 1993
<i>tyrR</i>	Tyrosine	Regulator gene for <i>aroF</i> and <i>tyrA</i>	37.1	432, 658, 1437, 1717, 1875
<i>tyrS</i>	Tyrosine	Tyrosyl-tRNA synthetase	30.9	1197, 1198, 1717
<i>tyrT</i>	Tyrosine	<i>supC</i> , <i>supF</i> ; ochre suppressor; tyrosine tRNA ₁	38.4	200, 211, 510, 866, 1717, 2157
<i>tyrU</i>	Tyrosine	<i>supM</i> ; ochre suppressor; tyrosine tRNA ₂	90.0	1717, 2157
<i>ubiF</i>	Ubiquinone	<i>cad</i> ; deficient in ubiquinone synthesis; accumulates 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	16.3	1021, 1717, 2223
<i>ubiG</i>	Ubiquinone	Ubiquinone synthesis	49.3	1717
<i>ubiX</i>	Ubiquinone	Growth stimulation by <i>p</i> -hydroxybenzoic acid; 3-octaprenyl-4-hydroxybenzoate decarboxylase	51.3	73, 74, 122, 842, 1717
<i>udk</i>		Uridine kinase (EC 2.7.1.48)	45.7	134, 1717, 2146
<i>udp</i>		Uridine phosphorylase (EC 2.4.2.3)	86.3	133, 1418, 1717
<i>uhpA</i>		Utilization of hexose phosphate	82.1	915, 1717
<i>uhpB</i>		Utilization of hexose phosphate	82.0	915, 1717
<i>uhpC</i>		Utilization of hexose phosphate	82.0	915, 1717
<i>uhpT</i>		Hexosephosphate transport	82.0	485, 486, 915, 1637, 1717
<i>umuC</i>		Induction of mutations by UV; error-prone repair	42.9	488, 759, 1064, 1443, 1444, 1717, 1774, 1817, 1820, 1827, 2009–2011
<i>umuD</i>		Induction of mutations by UV; error-prone repair	42.9	1064, 1443, 1444, 1717, 1774, 1820, 1827, 2009–2011, 2167
<i>upp</i>		Uracil phosphoribosyltransferase (EC 2.4.2.9)	54.2	133, 1717, 2146
<i>urs</i>	Uracil	Uracil catabolism defect	35.2	1717, 2128
<i>UshA</i>	UDP sugar hydrolase	UDP-sugar hydrolase (5'-nucleotidase); silent gene in <i>Salmonella</i> spp. of subgenus I	12.2	258, 259, 481, 1363, 1717, 2004
<i>UshB</i>	UDP sugar hydrolase	Inner membrane-associated UDP-sugar hydrolase	88.3	258, 259, 481, 616, 1717
<i>usp</i>	Ureidosuccinate	Permeability to ureidosuccinate	NM	1717, 2223
<i>uvrA</i>	UV	Repair of UV damage to DNA; exinuclease ABC, subunit A	92.3	59–61, 406, 1075, 1101, 1717, 1898, 2016
<i>uvrB</i>	UV	Repair of UV damage to DNA; exinuclease ABC, subunit B	18.4	50, 60, 902, 903, 1234, 1397, 1717, 1815, 1933, 1983
<i>uvrC</i>	UV	Repair of UV damage to DNA; exinuclease ABC, subunit C	42.2	1717, 1816
<i>uvrD</i>	UV	Repair of UV damage to DNA; helicase II (EC 3.6.1.–)	85.8	1234, 1526–1528, 1717, 1780, 1781, 2148, 2231
<i>valS</i>	Valine	Valyl-tRNA synthetase (EC 6.1.1.9)	97.3	1539, 1717
<i>viaA</i>		<i>ViA</i> ; <i>Vi</i> antigen (in <i>S. typhi</i>)	50.3	961, 963, 1717, 1851
<i>xylA</i>	D-Xylose	Xylose isomerase (EC 5.3.1.5)	80.0	626, 1717, 1722, 1723, 1778, 1779
<i>xylB</i>	D-Xylose	Xylulokinase (EC 2.7.1.17)	80.0	626, 1717, 1778, 1779
<i>xylR</i>	D-Xylose	Regulation	80.0	626, 1717, 1778, 1779
<i>xylT</i>	D-Xylose	Transport	80.0	626, 1379, 1717, 1778, 1779

^aAbbreviations: CoA, coenzyme A; cAMP, cyclic AMP; CRP, cAMP receptor protein; DAHP, 3-deoxy-D-arabinoheptulosonic acid 7-phosphate; DMB, dimethylbenzimidazole; HP, hydrogen peroxide; LPS, Lipopolysaccharide; NAMN, nicotinic acid, mononucleotide; NMN, nicotinamide mononucleotide; PRPP, phosphoribosyl pyrophosphate

^bMap position in centisomes (Cs) indicates the location of the gene on the map in Fig. 1, from 0 to 100 Cs. NM indicates that gene is on the chromosome, but the map position is not known. The symbol pSLT indicates that the gene is on pSLT, the 90-kb plasmid of LT2; a map of pSLT is shown in Fig. 1 (p. 1957).

^cReference 1721 refers to edition VII of the linkage map, in which other references to the indicated gene are given. Also, there are many papers cited in reference 1718 which have important information on the genes of *S. typhimurium*.

TABLE 2 Alternative gene symbols^a

Former or alternative symbol	Current symbol	Former or alternative symbol	Current symbol
<i>ail</i>	<i>pagC</i>	<i>cobI</i>	<i>cbiQ</i>
<i>aniA</i>	<i>hydA</i>	<i>cobI</i>	<i>cbiT</i>
<i>aniE</i>	<i>phsA</i>	<i>cobII</i>	<i>cobJ</i>
<i>apaG</i>	<i>corD</i>	<i>cobII</i>	<i>cobK</i>
<i>apeA</i>	<i>tesA</i>	<i>cobII</i>	<i>cobL</i>
<i>apeD</i>	<i>apeR</i>	<i>cobII</i>	<i>cobM</i>
<i>argA</i>	<i>argE</i>	<i>cobIII</i>	<i>cobS</i>
<i>argB</i>	<i>argA</i>	<i>cobIII</i>	<i>cobT</i>
<i>argC</i>	<i>argB</i>	<i>cobIII</i>	<i>cobU</i>
<i>argD</i>	<i>carA</i>	<i>cobIV</i>	<i>cobA</i>
<i>argE</i>	<i>argG</i>	<i>cpd</i>	<i>cpdB</i>
<i>argF</i>	<i>argH</i>	<i>cya</i>	<i>cyaA</i>
<i>argG</i>	<i>argD</i>	<i>cysAa</i>	<i>cysU</i>
<i>argH</i>	<i>argC</i>	<i>cysAb</i>	<i>cysW</i>
<i>argT</i>	<i>argX</i>	<i>cysT</i>	<i>cysU</i>
<i>argU</i>	<i>argX</i>	<i>cyx</i>	<i>slyA</i>
<i>aroC</i>	<i>aroE</i>	<i>dad</i>	<i>dadA</i>
<i>aroD</i>	<i>aroC</i>	<i>degP</i>	<i>htrA</i>
<i>aroE</i>	<i>aroD</i>	<i>dra</i>	<i>deoC</i>
<i>ars</i>	<i>carA</i>	<i>drm</i>	<i>deoB</i>
<i>asc</i>	<i>ent</i>	<i>enb</i>	<i>ent</i>
<i>atbR</i>	<i>atrR</i>	<i>envB</i>	<i>mre</i>
<i>atrC</i>	<i>polA</i>	<i>envM</i>	<i>fabI</i>
<i>attP14</i>	<i>atdA</i>	<i>fdhA</i>	<i>selA</i>
<i>attP22 I</i>	<i>ataA</i>	<i>fdhA</i>	<i>selB</i>
<i>attP221</i>	<i>atcA</i>	<i>fdhC</i>	<i>selC</i>
<i>attP27 I</i>	<i>atbA</i>	<i>fhl</i>	<i>fdhF</i>
<i>attP27 II</i>	<i>atbB</i>	<i>fhlB</i>	<i>hydA</i>
<i>bac</i>	<i>mre</i>	<i>fim</i>	<i>fimA</i>
<i>bfe</i>	<i>btuB</i>	<i>fimU</i>	<i>argU</i>
<i>bgly</i>	<i>hns</i>	<i>firA</i>	<i>lpxD</i>
<i>bio</i>	<i>bioA</i>	<i>flaAI</i>	<i>fliE</i>
<i>cad</i>	<i>ubiF</i>	<i>flaAII.2</i>	<i>fliG</i>
<i>cap</i>	<i>carA</i>	<i>flaAII.3</i>	<i>fliH</i>
<i>capR</i>	<i>lon</i>	<i>flaAII.I</i>	<i>fliF</i>
<i>carA</i>	<i>ptsI</i>	<i>flaAIII</i>	<i>fliI</i>
<i>carB</i>	<i>ptsH</i>	<i>flaB</i>	<i>fliP</i>
<i>cheC</i>	<i>fliM</i>	<i>flaC</i>	<i>fliA</i>
<i>cheP</i>	<i>cheA</i>	<i>flaD</i>	<i>fliQ</i>
<i>cheQ</i>	<i>cheY</i>	<i>flaE</i>	<i>fliC</i>
<i>cheT</i>	<i>cheZ</i>	<i>flaFI</i>	<i>fliG</i>
<i>cheU</i>	<i>fliM</i>	<i>flaFII</i>	<i>fliB</i>
<i>cheV</i>	<i>fliG</i>	<i>flaFIII</i>	<i>fliC</i>
<i>cheX</i>	<i>cheB</i>	<i>flaFIV</i>	<i>fliD</i>
<i>chlA</i>	<i>moaA</i>	<i>flaFIX</i>	<i>fliI</i>
<i>chlB</i>	<i>mob</i>	<i>flaFV</i>	<i>fliE</i>
<i>chlC</i>	<i>nar</i>	<i>flaFVI</i>	<i>fliF</i>
<i>chlD</i>	<i>modC</i>	<i>flaFVII</i>	<i>fliG</i>
<i>chlE</i>	<i>moeA</i>	<i>flaFVIII</i>	<i>fliH</i>
<i>chr</i>	<i>tonB</i>	<i>flaFX</i>	<i>fliJ</i>
<i>clmF</i>	<i>parC</i>	<i>flaK</i>	<i>fliD</i>
<i>clmF</i>	<i>parE</i>	<i>flaL</i>	<i>fliA</i>
<i>clmF</i>	<i>parF</i>	<i>flaM</i>	<i>fliB</i>
<i>cls</i>	<i>katG</i>	<i>flaN</i>	<i>fliN</i>
<i>cobI</i>	<i>cbiA</i>	<i>flaP</i>	<i>fliO</i>
<i>cobI</i>	<i>cbiB</i>	<i>flaQI</i>	<i>fliL</i>
<i>cobI</i>	<i>cbiC</i>	<i>flaQII</i>	<i>fliM</i>
<i>cobI</i>	<i>cbiD</i>	<i>flaR</i>	<i>fliK</i>
<i>cobI</i>	<i>cbiE</i>	<i>flaS</i>	<i>fliJ</i>
<i>cobI</i>	<i>cbiF</i>	<i>flaU</i>	<i>fliL</i>
<i>cobI</i>	<i>cbiG</i>	<i>flaV</i>	<i>fliD</i>
<i>cobI</i>	<i>cbiH</i>	<i>flaW</i>	<i>fliK</i>
<i>cobI</i>	<i>cbiJ</i>	<i>flaX</i>	<i>fliR</i>
<i>cobI</i>	<i>cbiK</i>	<i>flgR</i>	<i>fliM</i>
<i>cobI</i>	<i>cbiL</i>	<i>fruA</i>	<i>ptsF</i>
<i>cobI</i>	<i>cbiM</i>	<i>fruF</i>	<i>fruB</i>
<i>cobI</i>	<i>cbiN</i>	<i>fuc</i>	<i>fucA</i>
<i>cobI</i>	<i>cbiO</i>	<i>fur</i>	<i>furA</i>
<i>cobI</i>	<i>cbiP</i>	<i>gdh</i>	<i>gdhA</i>

TABLE 2 Continued

Former or alternative symbol	Current symbol	Former or alternative symbol	Current symbol
<i>glnF</i>	<i>rpoN</i>	<i>ompB</i>	<i>envZ</i>
<i>glnR</i>	<i>ntrB</i>	<i>ompB</i>	<i>ompR</i>
<i>glnR</i>	<i>ntrC</i>	<i>omsA</i>	<i>lpxD</i>
<i>glu</i>	<i>ptsG</i>	<i>optA</i>	<i>opdA</i>
<i>gpt</i>	<i>ptsG</i>	<i>orf5</i>	<i>pefK</i>
<i>gut</i>	<i>srlC</i>	<i>orf6</i>	<i>pefL</i>
<i>gxcu</i>	<i>gpt</i>	<i>orf8</i>	<i>pefS</i>
<i>H1</i>	<i>fliC</i>	<i>osmZ</i>	<i>hns</i>
<i>H2</i>	<i>fliB</i>	<i>oxrA</i>	<i>fur</i>
<i>hisE</i>	<i>hisI</i>	<i>oxrB</i>	<i>rpoA</i>
<i>hisIE</i>	<i>hisI</i>	<i>oxrC</i>	<i>pgt</i>
<i>hisU</i>	<i>gyrB</i>	<i>para</i>	<i>gyrB</i>
<i>hisW</i>	<i>gyrA</i>	<i>pasA</i>	<i>pgi</i>
<i>hsdSB</i>	<i>hsdM</i>	<i>pck</i>	<i>pckB</i>
<i>hsdSB</i>	<i>hsdS</i>	<i>phs</i>	<i>phsA</i>
<i>hspLT</i>	<i>hsdL</i>	<i>pil</i>	<i>fimA</i>
<i>hyd</i>	<i>hydA</i>	<i>pilG</i>	<i>hns</i>
<i>ile</i>	<i>ilvA</i>	<i>pmi</i>	<i>mana</i>
<i>ilvA</i>	<i>ilvC</i>	<i>pnu</i>	<i>deoD</i>
<i>ilvB</i>	<i>ilvD</i>	<i>pnuA</i>	<i>nadR</i>
<i>ilvC</i>	<i>ilvE</i>	<i>poh</i>	<i>oriC</i>
<i>ilvT</i>	<i>brnQ</i>	<i>pox</i>	<i>ply</i>
<i>incl</i>	<i>parS</i>	<i>proT</i>	<i>proM</i>
<i>invB</i>	<i>spaK</i>	<i>proU</i>	<i>proV</i>
<i>invC</i>	<i>spaL</i>	<i>proU</i>	<i>proW</i>
<i>invD</i>	<i>gcv</i>	<i>proU</i>	<i>proX</i>
<i>invI</i>	<i>spaM</i>	<i>proW</i>	<i>proL</i>
<i>invJ</i>	<i>spaN</i>	<i>prp</i>	<i>prpA</i>
<i>katF</i>	<i>rpoS</i>	<i>prsB</i>	<i>prsA</i>
<i>lep</i>	<i>lepB</i>	<i>psu</i>	<i>rho</i>
<i>leuT</i>	<i>leuU</i>	<i>ptdD</i>	<i>pepD</i>
<i>liv</i>	<i>livS</i>	<i>ptdN</i>	<i>pepN</i>
<i>livA</i>	<i>livH</i>	<i>ptdP</i>	<i>pepP</i>
<i>livB</i>	<i>livJ</i>	<i>pup</i>	<i>deoD</i>
<i>livC</i>	<i>livK</i>	<i>putB</i>	<i>putA</i>
<i>livEF</i>	<i>livM</i>	<i>pyrA</i>	<i>carA</i>
<i>livF</i>	<i>livG</i>	<i>pyrA</i>	<i>carB</i>
<i>livG</i>	<i>livF</i>	<i>rbsP</i>	<i>rbsB</i>
<i>lnt</i>	<i>cutE</i>	<i>RC</i>	<i>relA</i>
<i>lom</i>	<i>pagC</i>	<i>rflB</i>	<i>cpsG</i>
<i>lys</i>	<i>lysA</i>	<i>rflBT</i>	<i>rflBP</i>
<i>lys</i>	<i>sucA</i>	<i>rff</i>	<i>rffM</i>
<i>malB</i>	<i>malE</i>	<i>rff</i>	<i>rffT</i>
<i>manA</i>	<i>ptsM</i>	<i>rflB</i>	<i>fliM</i>
<i>metI</i>	<i>metA</i>	<i>rhaC1</i>	<i>rhaR</i>
<i>metP</i>	<i>metD</i>	<i>rhaC2</i>	<i>rhaS</i>
<i>nglD</i>	<i>galS</i>	<i>rhl</i>	<i>fliA</i>
<i>mkaA</i>	<i>spvB</i>	<i>rif</i>	<i>rpoB</i>
<i>mkaB</i>	<i>spvA</i>	<i>rnsA</i>	<i>rna</i>
<i>mkaC</i>	<i>spvR</i>	<i>rol</i>	<i>clD</i>
<i>mkaD</i>	<i>spvC</i>	<i>rouC</i>	<i>rflC</i>
<i>mkfA</i>	<i>spvC</i>	<i>sapG</i>	<i>trkA</i>
<i>mkfB</i>	<i>spvB</i>	<i>selA</i>	<i>selD</i>
<i>motC</i>	<i>fliG</i>	<i>sinA</i>	<i>stiA</i>
<i>musA</i>	<i>rflA</i>	<i>smoA</i>	<i>divC</i>
<i>musB</i>	<i>rflA</i>	<i>spcA</i>	<i>rpsE</i>
<i>mutB</i>	<i>mutY</i>	<i>ssc</i>	<i>lpxD</i>
<i>mviB</i>	<i>mviM</i>	<i>strA</i>	<i>rpsL</i>
<i>mviS</i>	<i>fliM</i>	<i>stx</i>	<i>stn</i>
<i>nadI</i>	<i>nadR</i>	<i>suc</i>	<i>sucA</i>
<i>nag</i>	<i>nagA</i>	<i>sufB</i>	<i>proL</i>
<i>nalA</i>	<i>gyrA</i>	<i>sufC</i>	<i>sufB</i>
<i>nfsI</i>	<i>nfsB</i>	<i>suff</i>	<i>thrT</i>
<i>nic</i>	<i>nadB</i>	<i>sufS</i>	<i>glyT</i>
<i>nicA</i>	<i>nadA</i>	<i>sulB</i>	<i>ftsZ</i>
<i>nml</i>	<i>fliB</i>	<i>supC</i>	<i>tyrT</i>
<i>ntrA</i>	<i>rpoN</i>	<i>supF</i>	<i>tyrT</i>
<i>O-5</i>	<i>oafA</i>	<i>supH</i>	<i>supJ</i>
<i>ofi</i>	<i>oafA</i>	<i>supI</i>	<i>sufG</i>

(Table continues)

TABLE 2 Continued

Former or alternative symbol	Current symbol	Former or alternative symbol	Current symbol
<i>supK</i>	<i>prfB</i>	<i>thrC</i>	<i>thrA</i>
<i>supM</i>	<i>tyrU</i>	<i>thrD</i>	<i>thrA</i>
<i>supT</i>	<i>prfB</i>	<i>tlp</i>	<i>tlpB</i>
<i>supX</i>	<i>topA</i>	<i>top</i>	<i>topA</i>
<i>supY</i>	<i>supE</i>	<i>tpp</i>	<i>deoA</i>
<i>thiA</i>	<i>thiC</i>	<i>tppA</i>	<i>envZ</i>
<i>thiB</i>	<i>thiH</i>	<i>tppA</i>	<i>ompR</i>
<i>thiC</i>	<i>thiI</i>	<i>tppB</i>	<i>envZ</i>
<i>thiG</i>	<i>thiA</i>	<i>tre</i>	<i>treA</i>
<i>thrA</i>	<i>thrB</i>	<i>triM</i>	<i>tctIII</i>
<i>thrB</i>	<i>thrC</i>	<i>triR</i>	<i>tctIII</i>

TABLE 2 Continued

Former or alternative symbol	Current symbol	Former or alternative symbol	Current symbol
<i>trpA</i>	<i>trpE</i>	<i>Via</i>	<i>viaA</i>
<i>trpB</i>	<i>trpD</i>	<i>virA</i>	<i>spvC</i>
<i>trpC</i>	<i>trpA</i>	<i>virB</i>	<i>spvD</i>
<i>trpD</i>	<i>trpB</i>	<i>visA</i>	<i>hemH</i>
<i>trpE</i>	<i>trpC</i>	<i>vsdA</i>	<i>spvR</i>
<i>trz</i>	<i>cysK</i>	<i>vsdB</i>	<i>spvA</i>
<i>umpA</i>	<i>lgt</i>	<i>vsdC</i>	<i>spvB</i>
<i>unc</i>	<i>atp</i>	<i>vsdD</i>	<i>spvC</i>
<i>uncA</i>	<i>atp</i>	<i>vsdE</i>	<i>spvD</i>
<i>use</i>	<i>argX</i>	<i>wrkA</i>	<i>divA</i>
<i>vh2</i>	<i>hin</i>		

^aThe alternative symbols have been used in past publications. It is recommended that their use be abandoned and that the current symbols, listed and described in Table 1 and in the associated references, be used in the future.

TABLE 3 Sequenced genes of *S. typhimurium*^a

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
STCARAB	(+)	78000	1.622	SP	1,886	X13200	
<i>carA</i>	(+)	78696	1.637	W	382	SG10032/P14845	1035
<i>carB</i>	(+)	79863	1.661	F	8	SG10033/P14846	1035
araDstyM	(+)	115391	2.400	MG	5,947	SS1001	
STYARABAD	(-)	115392	2.400	C	4,790	M11047	
<i>araD</i>	(-)	115954	2.412	W	248	SG10015/P06190	1207
<i>araA</i>	(-)	116841	2.430	W	500	SG10012/P06189	1209
<i>araB</i>	(-)	118354	2.462	W	569	SG10013/P06188	1208
STYARALC	(+)	120053	2.497	C	1,286	J01797	
<i>araC</i>	(+)	120404	2.504	W	281	SG10014/P03022	345, 346
leuDstyM	(+)	137999	2.870	MP	6,168	SS1020	
STLEUD	(-)	138000	2.870	C	1,074	X02528	
<i>leuD</i>	(-)	138454	2.880	W	201	SG10198/P04787	578
STLEUC	(-)	139053	2.892	C	1,432	X51476	
<i>leuC</i>	(-)	139070	2.892	W	464	SG10197/P15717	1677
STLEUB	(-)	140445	2.921	C	1,122	X53376	
<i>leuB</i>	(-)	140467	2.922	W	359	SG10196/P37412	58
STYLEUA	(-)	141545	2.944	C	1,569	X51583	
<i>leuA</i>	(-)	141546	2.944	W	522	SG10195/P15875	623, 1629
STYLEUOP	(-)	143024	2.975	C	497	J01807	
STYLEUP	(-)	143313	2.981	C	855	M12892	
STILVIHO	(+)	144299	3.001	SG	348	X68562	
STFRURG	(+)	144721	3.010	SG	2,497	X55456	
<i>ilvI</i>	(+)	144722	3.010	F	52	SG10129/P40811	926
<i>ilvH</i>	(+)	144904	3.014	W	163	SG10182/P21622	926
<i>fruR</i>	(+)	145679	3.030	W	334	SG10133/P21930	926, 2076
STYNADC	(-)	172126	3.580	SG	1,403	L07292	
<i>nadC</i>	(-)	172264	3.583	W	297	SG10242/P30012	861
<i>ampD</i>	(+)	173245	3.603	F	94	SG10010/P30013	861
ompHstyM	(+)	193281	4.020	MG	2,332	SS1025	
STYOMPH	(+)	193282	4.020	C	992	J05101	
<i>ompH</i>	(+)	193593	4.026	W	161	SG10265/P16974	782, 1080, 1081
STYSSCA	(+)	194063	4.036	C	1,551	M35193	
<i>lpxD</i>	(+)	194082	4.037	W	341	SG10209/P18482	783, 784, 1757, 2089

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>fabZ</i>	(+)	195213	4.060	F	134	SG10096/P21773	783
STLPXGNA	(+)	200974	4.180	SG	812	Z25462	
<i>lpxA</i>	(+)	200975	4.180	W	262	SG10208/P32200	2089
STPEPMG	(-)	205782	4.280	SG	1,811	X55778	
<i>glnD</i>	(-)	206054	4.286	F	201	SG10144/P23679	1382
<i>pepM</i>	(-)	206623	4.297	W	264	SG10283/P10882	1382, 2153
STYHEML	(-)	240400	5.000	SG	1,658	M60064	
<i>hemL</i>	(-)	240548	5.003	W	426	SG10152/P21267	496
STSPHSPG	(+)	245000	5.096	SH	1,980	X54548	
<i>dgt</i>	(+)	245001	5.096	F	87	SG10473/P40733	964
<i>htrA</i>	(+)	245395	5.104	W	475	SG10173/P26982	964
STYPOL3A	(+)	284000	5.907	SP	3,763	M26046	
<i>rnhB</i>	(+)	284001	5.907	F	55	SG10493/P40675	1139
<i>dnaE</i>	(+)	284159	5.910	W	1,160	SG10087/P14567	1139
<i>accA</i>	(+)	287654	5.983	F	36	SG10496/P40674	1139
rnhAstyM	(+)	329999	6.864	MH	927	SS1031	
STDNAQRN	(-)	330000	6.864	C	545	X57159	
<i>rnhA</i>	(-)	330001	6.864	W	155	SG10360/P23329	
STYPOL3E	(+)	330473	6.873	C	454	M26045	
<i>dnaQ</i>	(+)	330532	6.875	F	100	SG10090/P14566	1138
STGHPT	(+)	356273	7.410	SG	845	X63336	
<i>gpt</i>	(+)	356466	7.414	W	152	SG10147/P26972	
<i>yafA</i>	(+)	357013	7.425	F	35	SG10415/P37722	
STPHOE	(-)	365408	7.600	SG	1,232	X68023	
<i>phoE</i>	(-)	365413	7.600	W	350	SG10291/P30705	1868
STYP22ATB	(+)	375000	7.800	SG	320	M10894	
<i>proA</i>	(+)	375001	7.800	F	23	SG10301/P40861	1178
<i>thrW (ataA)</i>	(+)	375188	7.803	W	RNA	SG30013/tRNA	
STYDDLDA	(-)	420000	8.735	SH	1,197	M20793	
<i>ddlA</i>	(-)	420004	8.736	W	364	SG10084/P15051	413
brnQstyM	(+)	429999	8.943	MG	2,645	SS1003	
STYBRNQ	(+)	430000	8.943	C	1,603	D00332	
<i>brnQ</i>	(+)	430220	8.948	W	439	SG10029/P14931	1460
STPROY	(+)	431457	8.974	C	1,188	X74420	
<i>proY</i>	(+)	431551	8.976	W	292	SG10314/P37460	
STTSXOMP	(-)	435000	9.047	SH	2,244	Z26657	
<i>yajD</i>	(+)	435015	9.048	W	109	SG10517/P40777	
<i>tsx</i>	(-)	435987	9.068	W	287	SG10516/P40776	
STU09529	(+)	480000	9.983	SH	1,030	U09529	
<i>apbA</i>	(+)	480102	9.985	W	281	SG10001/P37402	
STHUPB	(+)	547831	11.394	SH	478	X07844	
<i>hupB</i>	(+)	547951	11.397	W	90	SG10175/P05515	1298
STYADK	(+)	555324	11.550	SG	1,590	L26246	
<i>adk</i>	(+)	555536	11.554	W	214	SG10003/P37407	
<i>hemH</i>	(+)	556409	11.573	F	168	SG10151/P37408	
STUSHA0	(+)	585614	12.180	SG	2,607	X04651	
<i>ushA</i>	(+)	585780	12.183	W	550	SG10412/P06196	259
<i>ybaK</i>	(-)	587549	12.220	W	159	SG10416/P37174	259
STNITRD	(-)	652330	13.568	SG	1,690	X17250	
<i>nfnB</i>	(-)	653069	13.583	W	217	SG10246/P15888	2108
STYAHPCFA	(+)	678000	14.101	SP	2,610	J05478	
<i>ahpC</i>	(+)	678166	14.105	W	187	SG10004/P19479	922, 1998, 1999
<i>ahpF</i>	(+)	678971	14.122	W	521	SG10005/P19480	922, 1999

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
STYFIMCLUS	(+)	721200	15.000	SG	12,168	L19338	
<i>fimA</i>	(+)	722263	15.022	W	185	SG10275/P37921	
<i>fimI</i>	(+)	722934	15.036	W	164	SG10508/P37922	
<i>fimC</i>	(+)	723472	15.047	W	230	SG10504/P37923	
<i>fimD</i>	(+)	724195	15.062	W	870	SG10505/P37924	
<i>fimH</i>	(+)	726822	15.117	W	335	SG10507/P37925	
<i>fimF</i>	(+)	727839	15.138	W	172	SG10506/P37926	
<i>fimZ</i>	(-)	728403	15.150	W	210	SG10099/P26319	1974
<i>fimY</i>	(-)	729639	15.176	W	240	SG10098/P26318	1974
<i>fimW</i>	(-)	730853	15.201	W	198	SG10509/P37928	
<i>argU</i>	(+)	731705	15.218	W	RNA	SG30004/tRNA	
STU12808	(-)	750048	15.600	SG	1,124	U12808	
<i>cobC</i>	(-)	750261	15.604	W	234	SG10479/P39701	
STPHRG	(+)	814000	16.930	SH	1,353	X60662	
<i>phrB</i>	(+)	814001	16.930	W	450	SG10295/P25078	1195
STYCITA	(+)	815437	16.960	SG	2,119	D90203	
<i>citB</i>	(+)	815438	16.960	F	58	SG10059/P37463	1795
<i>citA</i>	(+)	815667	16.965	W	434	SG10058/P24115	1795
STYNADAPCU	(+)	826000	17.180	SP	2,330	M85180	
<i>nadA</i>	(+)	826142	17.183	W	365	SG10241/P24519	563
<i>pnuC</i>	(+)	827209	17.205	W	322	SG10306/P24520	563
STYGALOPA	(-)	856000	17.804	SP	3,219	M33681	
<i>galK</i>	(-)	856001	17.804	W	380	SG10137/P22713	834
<i>galT</i>	(-)	857147	17.828	W	348	SG10138/P22714	834
<i>galE</i>	(-)	858206	17.850	W	337	SG10135/P22715	834
STYBIOAB	(+)	871000	18.116	SP	117	M21923	
<i>bioA</i>	(-)	871001	18.116	F	5	SG10026/P12677	1797
<i>bioB</i>	(+)	871103	18.118	F	5	SG10027/P12678	1797
STU02273	(+)	920000	19.135	SH	495	U02273	
<i>lrp</i>	(+)	920001	19.135	W	164	SG10210/P37403	
STYAROAPM	(+)	956000	19.884	SG	1,332	M10947	
<i>aroA</i>	(+)	956027	19.884	W	427	SG10019/P07637	1882
STOMPFGGE	(-)	1094000	22.754	SH	1,306	Z31594	
<i>ompF</i>	(-)	1094013	22.754	W	363	SG10264/P37432	
STYPNCB	(-)	1114000	23.170	SP	1,837	M55986	
<i>pncB</i>	(-)	1114398	23.178	W	400	SG10305/P22253	2082
STYNEUR	(+)	1140000	23.710	SP	1,803	M55342	
<i>nanH</i>	(+)	1140263	23.716	W	382	SG10244/P29768	395, 843, 2003
<i>yedD</i>	(-)	1141482	23.741	F	106	SG10500/P40784	843
STPYRDDD	(+)	1160000	24.126	SP	1,286	X55636	
<i>pyrD</i>	(+)	1160149	24.130	W	336	SG10326/P25468	576
sulAstyM	(+)	1169999	24.334	MG	2,236	SS1032	
STOMPA	(-)	1170000	24.334	C	1,400	X02006	
<i>ompA</i>	(-)	1170148	24.338	W	350	SG10263/P02936	573
STYSULA	(-)	1171364	24.363	C	874	M16324	
<i>sulA</i>	(-)	1171557	24.367	W	169	SG10386/P08847	572
putAstyM	(+)	1229999	25.582	MP	6,077	SS1029	
STPUTA	(-)	1230000	25.582	C	4,102	X70843	
<i>putA</i>	(-)	1230140	25.585	W	1,320	SG10321/P10503	28, 719
STPUTPA	(-)	1234022	25.666	C	546	X12569	
STPUTP	(+)	1234473	25.675	C	1,604	X52573	
<i>putP</i>	(+)	1234524	25.676	W	502	SG10322/P10502	719, 1353
STPYRC	(-)	1260000	26.206	SP	1,672	X03928	
<i>pyrC</i>	(-)	1260209	26.211	W	348	SG10325/P06204	1421
<i>yceB</i>	(-)	1261363	26.235	F	103	SG10459/P40822	1421
mviMstyM	(+)	1264987	26.310	MP	15,013	SS1008	

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
STYFLGA	(-)	1264988	26.310	C	4,943	D25292	
STMVIMN	(+)	1264989	26.310	C	3,120	Z26133	
<i>mviM</i>	(+)	1265263	26.316	W	307	SG10239/P37168	
<i>mviN</i>	(+)	1266451	26.340	W	524	SG10240/P37169	
STU03631	(+)	1268096	26.375	C	893	U03631	
<i>flgN</i>	(-)	1268107	26.375	W	140	SG10113/P37406	1754
<i>flgM</i>	(-)	1268534	26.384	W	97	SG10112/P26477	633, 1754
<i>flgA</i>	(-)	1268919	26.392	W	219	SG10503/P40131	1124
STYFLG	(+)	1269578	26.406	C	1,000	D13703	
STFLGBC	(+)	1269700	26.408	C	878	X52093	
<i>flgB</i>	(+)	1269735	26.409	W	138	SG10101/P16437	820, 973, 1122
<i>flgC</i>	(+)	1270155	26.418	W	134	SG10102/P16438	820, 973, 1122
STYFLGD	(+)	1270377	26.422	C	1,147	D25293	
<i>flgD</i>	(+)	1270571	26.426	W	232	SG10103/P16321	812, 1115
STFLGE	(+)	1271235	26.440	C	1,320	X51737	
<i>flgE</i>	(+)	1271296	26.441	W	403	SG10104/P16322	812
STFLGFG	(+)	1272467	26.466	C	1,687	X52094	
<i>flgF</i>	(+)	1272528	26.467	W	251	SG10105/P16323	812, 820, 973
<i>flgG</i>	(+)	1273297	26.483	W	260	SG10106/P16439	820, 973
STYFLGH	(+)	1274076	26.499	C	2,947	M24466	
<i>flgH</i>	(+)	1274137	26.500	W	232	SG10107/P15929	820, 971
<i>flgI</i>	(+)	1274847	26.515	W	365	SG10108/P15930	819, 971
<i>flgJ</i>	(+)	1275944	26.538	W	316	SG10109/P15931	812, 971
STFLGK	(+)	1276878	26.557	C	1,765	X51738	
<i>flgK</i>	(+)	1276959	26.559	W	553	SG10110/P15932	812, 971, 973
STFLGL	(+)	1278574	26.593	C	1,427	X51739	
<i>flgL</i>	(+)	1278635	26.594	W	317	SG10111/P16326	812
STPTSG	(+)	1293000	26.893	SP	1,434	X74629	
<i>ptsG</i>	(+)	1293001	26.893	W	477	SG10316/P37439	
STYPEPT	(+)	1312178	27.292	SG	2,551	M62725	
<i>potA</i>	(-)	1312179	27.292	F	63	SG10489/P40790	1347
<i>pepT</i>	(+)	1312618	27.301	W	409	SG10284/P26311	1347
STYPHOPQ	(-)	1315063	27.352	SG	2,190	M24424	
<i>phoQ</i>	(-)	1315084	27.352	W	451	SG10294/P14147	1355
<i>phoP</i>	(-)	1316439	27.380	W	224	SG10293/P14146	684, 1355
STYGDHA	(-)	1401000	29.139	SP	1,603	M24021	
<i>topB</i>	(+)	1401001	29.139	F	49	SG10495/P40687	105
<i>gdhA</i>	(-)	1401180	29.143	W	447	SG10140/P15111	105
STYINFCA	(+)	1450000	30.158	SH	570	L11254	
<i>infC</i>	(+)	1450019	30.158	W	180	SG10185/P33321	1225
STHIMA	(+)	1458747	30.340	SG	420	X16739	
<i>pheT</i>	(+)	1458748	30.340	F	17	SG10290/P15434	1196
<i>himA</i>	(+)	1458808	30.341	W	99	SG10155/P15430	1196
STU09502	(-)	1475000	30.678	SH	376	U09502	
<i>sodB</i>	(-)	1475001	30.678	F	56	SG10514/P40726	
STU03842	(+)	1482000	30.824	SG	714	U03842	
<i>slyA</i>	(+)	1482167	30.827	W	146	SG10526/P40676	1197
STPMIPHI	(-)	1502500	31.250	SG	1,650	X57117	
<i>manA</i>	(-)	1502544	31.251	W	391	SG10217/P25081	1652
<i>fumA</i>	(+)	1503919	31.280	F	38	SG10462/P40720	1652
STYDCP	(+)	1562000	32.488	SP	2,841	M84575	
<i>ydfG</i>	(-)	1562001	32.488	F	96	SG10499/P40864	724
<i>dcp</i>	(+)	1562427	32.496	W	680	SG10083/P27236	724
STYRFC	(-)	1714533	35.660	SG	1,750	M60066	
<i>rfc</i>	(-)	1714600	35.661	W	407	SG10352/P26479	358
STFNR	(+)	1761000	36.626	SP	1,360	U05668	
<i>ogt</i>	(+)	1761001	36.626	F	115	SG10262/P37429	
<i>fnr</i>	(+)	1761546	36.638	W	250	SG10131/P37428	
STSAP	(+)	1785400	37.134	SG	5,714	X74212	

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>sapA</i>	(+)	1785516	37.136	W	549	SG10377/P36634	1540
<i>sapB</i>	(+)	1787162	37.171	W	321	SG10378/P36668	1540
<i>sapC</i>	(+)	1788114	37.190	W	296	SG10379/P36669	1540
<i>sapD</i>	(+)	1789004	37.209	W	330	SG10380/P36636	1540
<i>sapF</i>	(+)	1789998	37.230	W	268	SG10381/P36638	1540
STYENVVM	(+)	1805000	37.542	SH	1,656	M31806	
<i>ycjE</i>	(+)	1805259	37.547	W	99	SG10440/P16656	2038
<i>fabI</i>	(+)	1805676	37.556	W	262	SG10095/P16657	2038
STPYRF	(-)	1808000	37.604	SP	1,459	X05382	
<i>osmB</i>	(+)	1808001	37.604	F	20	SG10272/P37723	2006
<i>yciH</i>	(-)	1808185	37.608	W	108	SG10419/P20770	2006
<i>pyrF</i>	(-)	1808966	37.624	W	245	SG10328/P07691	2006
STYCYSB	(-)	1810000	37.646	SP	1,759	M15040	
<i>cysB</i>	(-)	1810342	37.653	W	324	SG10072/P06614	1501
<i>topA</i>	(-)	1811727	37.682	F	10	SG10515/P40686	1501
STYATPCA	(-)	1824636	37.950	SG	993	L08890	
<i>cobA</i>	(-)	1824854	37.955	W	196	SG10031/P31570	515, 1953
<i>trpEstyM</i>	(+)	1827293	38.005	MP	6,783	SS1035	
STYTRPOP	(+)	1827294	38.005	C	105	M10673	
STYTRPEA	(+)	1827370	38.007	C	294	M24960	
STYTRPE	(+)	1827547	38.011	C	1,563	J01812	
<i>trpE</i>	(+)	1827548	38.011	W	520	SG10392/P00898	1159, 1191, 1426, 2203
STYTRPDC1	(+)	1829109	38.043	C	1,596	M30285	
<i>trpD</i>	(+)	1829110	38.043	W	531	SG10399/P00905	830, 1426
STYTRPDC2	(+)	1830709	38.076	C	1,359	M30286	
<i>trpC</i>	(+)	1830710	38.076	W	452	SG10398/P00910	830
STYTRPCBI	(+)	1832031	38.104	C	82	M24299	
STYTRPBA	(+)	1832077	38.105	C	2,000	J01810	
<i>trpB</i>	(+)	1832078	38.105	W	397	SG10397/P00933	390, 880, 1428, 1761
<i>trpA</i>	(+)	1833271	38.130	W	268	SG10396/P00929	
STTONB	(+)	1838098	38.230	SG	950	X56434	
<i>tonB</i>	(+)	1838219	38.233	W	242	SG10391/P25945	730, 1006
<i>yciA</i>	(-)	1839007	38.249	F	13	SG10418/P25944	730
STOPPAF	(-)	1840000	38.270	SP	6,006	X05491	
<i>oppF</i>	(-)	1840244	38.275	W	334	SG10271/P08007	775
<i>oppD</i>	(-)	1841245	38.295	W	335	SG10270/P04285	769, 775
<i>oppC</i>	(-)	1842264	38.317	W	302	SG10269/P08006	775, 1555
<i>oppB</i>	(-)	1843187	38.336	W	306	SG10268/P08005	775, 1555
<i>oppA</i>	(-)	1844229	38.358	W	542	SG10267/P06202	775, 776
<i>hns-styM</i>	(+)	1846388	38.402	MG	926	SS1009	
STYOSMZ	(+)	1846389	38.402	C	909	M37891	
STHNS	(+)	1846489	38.405	C	827	X14375	
<i>hns</i>	(+)	1846767	38.410	W	137	SG10171/P17428	877, 1299
STYNARK	(+)	1856000	38.602	SH	4,183	D26057	
<i>narK</i>	(-)	1856001	38.602	F	130	SG10245/P37593	
<i>smvA</i>	(+)	1857300	38.629	W	496	SG10384/P37594	
<i>nmpC</i>	(-)	1859335	38.672	F	282	SG10249/P37592	
<i>prfAstyM</i>	(+)	1863999	38.769	MP	5,845	SS1028	
STYHEMAPRF	(-)	1864000	38.769	C	3,341	J04243	
<i>hemK</i>	(-)	1864001	39.769	F	77	SG10534/P40816	493
<i>prfA</i>	(-)	1864231	38.773	W	360	SG10309/P13654	493
<i>hemA</i>	(-)	1865354	38.797	W	418	SG10149/P13581	493
STYPRS	(+)	1866603	38.823	C	2,060	M77236	
<i>hemM</i>	(+)	1866928	38.830	W	207	SG10153/P30752	493, 1571
<i>ychB</i>	(+)	1867548	38.842	W	283	SG10417/P30753	213, 1571
STYPRSA	(+)	1868101	38.854	C	1,740	M19488	
<i>prsA</i>	(+)	1868665	38.866	W	315	SG10315/P15849	213
STYDADB	(-)	1975000	41.077	SP	1,140	K02119	
<i>dadB</i>	(-)	1975010	41.078	W	356	SG10082/P06191	2105
STYGAPA	(+)	1977000	41.119	SH	882	M63369	

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>gapA</i>	(+)	1977001	41.119	F	294	SG10139/P24165	1152
STYPABB	(+)	2000000	41.597	SH	1,815	M22079	
<i>pabB</i>	(+)	2000207	41.602	W	454	SG10274/P12680	661
<i>flhEstyM</i>	(+)	2003810	41.677	MP	5,097	SS1004	
STYFLHB	(-)	2003811	41.677	C	4,023	D32203	
<i>flhE</i>	(-)	2004025	41.677	W	130	SG10528/P40728	1361
<i>flhA</i>	(-)	2004417	41.689	W	692	SG10529/P40729	1361
<i>flhB</i>	(-)	2006488	41.732	W	383	SG10530/P40727	1361
STYCHEZ	(-)	2007000	41.743	C	1,506	M16691	
<i>cheZ</i>	(-)	2007833	41.760	W	214	SG10057/P07800	1915
STYCHEY	(-)	2008456	41.773	C	452	M12131	
<i>cheY</i>	(-)	2008488	41.774	W	129	SG10056/P06657	761, 1910, 1913, 1914
STYCHER	(-)	2012629	41.860	SG	896	J02757	
<i>cheB</i>	(-)	2012630	41.860	W	349	SG10053/P04042	761, 1807, 1808
<i>cheR</i>	(-)	2012635	41.860	W	288	SG10054/P07801	1809
tar-styM	(+)	2015513	41.920	MG	4,475	SS1033	
STYTAR	(-)	2015514	41.920	C	1,922	J01809	
<i>tar</i>	(-)	2015540	41.921	W	552	SG10387/P02941	1698
STYCHEW	(-)	2017195	41.955	C	770	J02656	
<i>cheW</i>	(-)	2017439	41.960	W	167	SG10055/P06110	1912
STYCHEA	(-)	2017939	41.970	C	2,050	J03611	
<i>cheA</i>	(-)	2017963	41.971	W	671	SG10052/P09384	1909
STYFLIA	(-)	2040000	42.429	SG	1,244	D00497	
<i>fliA</i>	(-)	2040321	42.436	W	239	SG10114/P17168	1464
<i>fliCstyM</i>	(+)	2043999	42.512	MP	14,084	SS1010	
STYFLGHI1	(-)	2044000	42.512	C	1,485	M11332	
<i>fliC</i>	(-)	2044001	42.513	W	490	SG10115/P06179	812, 986
STFLID	(+)	2045409	42.542	C	1,766	X51740	
<i>fliD</i>	(+)	2045730	42.548	W	467	SG10116/P16328	812
STYFLGPRO	(+)	2047047	42.576	C	965	M85241	
<i>fliS</i>	(+)	2047148	42.578	W	135	SG10127/P26609	1008
<i>fliT</i>	(+)	2047555	42.586	W	122	SG10128/P26611	1008
STYFTAA	(+)	2047894	42.593	C	1,700	L01643	
<i>amyA</i>	(+)	2047995	42.596	W	494	SG10011/P26613	1008, 1606
STYAMYA	(+)	2049418	42.625	C	2,940	L13280	
<i>yedD</i>	(-)	2049519	42.627	W	141	SG10420/Q06399	1607
<i>yedE</i>	(+)	2050130	42.640	W	401	SG10421/Q06400	1607
<i>yedF</i>	(+)	2051332	42.665	W	77	SG10422/P31065	1607
STYFLIE	(-)	2052299	42.685	C	647	M84993	
<i>fliE</i>	(-)	2052337	42.686	W	104	SG10117/P26462	971, 1392
STYFLIG	(+)	2052807	42.696	C	2,755	M24462	
<i>fliF</i>	(+)	2052868	42.697	W	560	SG10118/P15928	971
<i>fliG</i>	(+)	2054543	42.732	W	331	SG10119/P15933	567, 1034, 2085
STYFLIHJ	(+)	2055430	42.750	C	2,654	M62408	
<i>fliH</i>	(+)	2055531	42.752	W	235	SG10120/P15934	1034, 2085
<i>fliI</i>	(+)	2056238	42.767	W	456	SG10121/P26465	468, 2085
<i>fliJ</i>	(+)	2057630	42.796	W	147	SG10122/P26463	2085
STYFLIL	(+)	2058550	42.815	SG	2,013	M24463	
<i>fliK</i>	(+)	2058551	42.815	F	10	SG10123/P26416	1034, 2085
<i>fliL</i>	(+)	2058671	42.818	W	155	SG10124/P26417	1034
<i>fliM</i>	(+)	2059143	42.827	W	334	SG10125/P26418	1034
<i>fliN</i>	(+)	2060144	42.848	W	137	SG10126/P26419	1034
STYUMUDC	(-)	2062151	42.890	SG	2,574	M57431	
<i>cspG</i>	(-)	2062152	42.890	W	40	SG10445/P39818	
<i>umuC</i>	(-)	2062825	42.904	W	422	SG10410/P22494	1827, 2010
<i>umuD</i>	(-)	2064096	42.930	W	139	SG10411/P22493	1827, 2010, 2167
cobTstyM	(+)	2086671	43.400	MP	22,490	SS1005	
STYCOB	(-)	2086672	43.400	C	2,760	L35477	
<i>asnT?</i>	(+)	2087023	43.407	W	RNA	SG30008/tRNA	
<i>yeeG</i>	(-)	2087325	43.414	W	309	SG10484/P40680	
<i>cobT</i>	(-)	2088332	43.435	W	366	SG10062/Q05603	1681
STYVB12AA	(-)	2088675	43.442	C	17,442	L12006	
<i>cobS</i>	(-)	2089429	43.457	W	247	SG10061/Q05602	1681

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>cobU</i>	(-)	2090169	43.473	W	180	SG10063/Q05599	1681
<i>cbiP</i>	(-)	2090711	43.484	W	506	SG10048/Q05597	1681
<i>cbiO</i>	(-)	2092228	43.516	W	271	SG10047/Q05596	1681
<i>cbiQ</i>	(-)	2093052	43.533	W	225	SG10049/Q05598	1681
<i>cbiN</i>	(-)	2093716	43.547	W	93	SG10046/Q05595	1681
<i>cbiM</i>	(-)	2093999	43.552	W	245	SG10045/Q05594	1681
<i>cbiL</i>	(-)	2094733	43.568	W	237	SG10044/Q05593	1681
<i>cbiK</i>	(-)	2095443	43.582	W	264	SG10043/Q05592	1681
<i>cbiJ</i>	(-)	2096240	43.599	W	263	SG10042/Q05591	1681
<i>cbiH</i>	(-)	2097028	43.615	W	241	SG10041/Q05590	1681
<i>cbiG</i>	(-)	2097753	43.630	W	351	SG10040/Q05631	1681
<i>cbiF</i>	(-)	2098789	43.652	W	257	SG10039/Q05630	1681
<i>cbiT</i>	(-)	2099546	43.668	W	192	SG10050/Q05632	1681
<i>cbiE</i>	(-)	2100114	43.680	W	201	SG10038/Q05629	1681
<i>cbiD</i>	(-)	2100713	43.692	W	379	SG10037/Q05628	1681
<i>cbiC</i>	(-)	2101852	43.716	W	210	SG10036/Q05601	1681
<i>cbiB</i>	(-)	2102495	43.729	W	319	SG10035/Q05600	1681
<i>cbiA</i>	(-)	2103451	43.749	W	459	SG10034/P29946	1634, 1681
STYPDUC	(-)	2105401	43.790	C	3,761	L31414	
<i>pocR</i>	(-)	2105428	43.790	W	303	SG10307/Q05587	1681
<i>pduF</i>	(-)	2106556	43.814	W	264	SG10281/P37451	
<i>pduA</i>	(+)	2107876	43.841	W	97	SG10278/P37448	
<i>pduB</i>	(+)	2108266	43.849	W	233	SG10279/P37449	
<i>pduC</i>	(+)	2108986	43.864	F	59	SG10280/P37450	
STYPBCDEF	(-)	2124655	44.190	SG	3,282	L31538	
<i>phsE</i>	(-)	2125087	44.199	W	390	SG10300/P37604	
<i>phsD</i>	(-)	2126288	44.224	W	84	SG10299/P37603	
<i>phsC</i>	(-)	2126542	44.229	W	199	SG10298/P37602	
<i>phsB</i>	(-)	2127138	44.242	W	198	SG10297/P37601	
<i>phsA</i>	(-)	2127731	44.254	F	68	SG10296/P37600	
hisGstyM	(+)	2148461	44.685	MP	33,958	SS1013	
STYHISOGD	(+)	2148462	44.685	C	4,443	J01804	
STHISOP	(+)	2149090	44.698	C	7,439	X13464	
<i>hisG</i>	(+)	2149366	44.704	W	299	SG10162/P00499	281, 337, 1266, 1562
<i>hisD</i>	(+)	2150368	44.725	W	434	SG10160/P10370	281, 695
<i>hisC</i>	(+)	2151669	44.752	W	359	SG10159/P10369	281
<i>hisB</i>	(+)	2152745	44.774	W	354	SG10158/P10368	281
<i>hisH</i>	(+)	2153809	44.796	W	194	SG10163/P10376	281
<i>hisA</i>	(+)	2154393	44.809	W	246	SG10157/P10372	281
<i>hisF</i>	(+)	2155115	44.824	W	258	SG10161/P10374	281
<i>hisI</i>	(+)	2155885	44.840	W	203	SG10164/P10367	281, 318
SECLDB	(-)	2156446	44.851	C	2,948	Z17278	
<i>clt</i>	(-)	2156576	44.854	W	327	SG10060/Q04866	123, 124
<i>yefA</i>	(-)	2157699	44.877	W	388	SG10439/Q04873	123
STYGND A	(-)	2158970	44.904	C	1,705	M64332	
<i>gnd</i>	(-)	2159104	44.906	W	468	SG10146/P14062	954, 1621
SERFBB	(-)	2160340	44.932	C	22,080	X56793	
<i>rfbP</i>	(-)	2160674	44.939	W	476	SG10351/P26406	954
<i>rfbK</i>	(-)	2162176	44.970	W	477	SG10349/P26405	954
<i>rfbM</i>	(-)	2163596	45.000	W	479	SG10350/P26404	954
<i>rfbN</i>	(-)	2165036	45.030	W	314	SG10455/P26403	954
<i>rfbU</i>	(-)	2165981	45.050	W	353	SG10446/P26402	954
<i>rfbV</i>	(-)	2167361	45.078	W	333	SG10454/P26401	954
<i>rfbX</i>	(-)	2168367	45.099	W	430	SG10453/P26400	954
<i>rfbJ</i>	(-)	2169741	45.128	W	299	SG10348/P22716	954, 2175
<i>rfbH</i>	(-)	2170668	45.147	W	437	SG10452/P26398	954
<i>rfbG</i>	(-)	2172008	45.175	W	359	SG10347/P26397	954
<i>rfbF</i>	(-)	2173092	45.197	W	257	SG10346/P26396	954
<i>rfbI</i>	(-)	2173862	45.213	W	330	SG10451/P26395	954
<i>rfbC</i>	(-)	2174860	45.234	W	183	SG10450/P26394	954
<i>rfbA</i>	(-)	2175412	45.246	W	292	SG10449/P26393	954
<i>rfbD</i>	(-)	2176338	45.265	W	299	SG10344/P26392	954
<i>rfbB</i>	(-)	2177237	45.284	W	361	SG10345/P26391	954
<i>galF</i>	(-)	2178699	45.314	W	297	SG10136/P26390	954
<i>yefK</i>	(-)	2179770	45.336	W	467	SG10448/P26389	954
<i>yefL</i>	(-)	2181184	45.366	W	406	SG10447/P26388	954
STCPSBG	(-)	2185000	45.445	SH	3,069	X59886	
<i>cpsG</i>	(-)	2185011	45.445	W	456	SG10067/P26341	1903
<i>cpsB</i>	(-)	2186492	45.476	W	480	SG10066/P26340	1903

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>mglBsty</i>	(-)	2307000	47.983	SH	1,810	SS3004	
<i>mglA</i>	(-)	2307001	47.983	F	42	SG10228/P23924	145
<i>mglB</i>	(-)	2307259	47.988	W	332	SG10229/P23905	145
<i>galS</i>	(-)	2308754	48.019	F	18	SG10521/P41030	145
STFRUF	(+)	2310725	48.060	SG	1,610	X14243	
<i>yeiO</i>	(-)	2310726	48.060	F	22	SG10423/P33027	619
<i>fruB</i>	(+)	2311160	48.069	W	376	SG10132/P17127	619
STRNAP	(+)	2360247	49.090	SG	1,041	X63777	
<i>yejM</i>	(+)	2360248	49.090	F	190	SG10463/P40709	1879
<i>proL</i>	(+)	2360895	49.103	W	RNA	SG30015/tRNA	
STGYRA	(-)	2367940	49.250	SG	261	X78977	
<i>gyrA</i>	(-)	2367941	49.250	F	86	SG10148/P37411	
STNRDABA	(+)	2370000	49.293	SH	4,967	X72948	
<i>ubiG</i>	(+)	2370001	49.293	F	209	SG10405/P37431	977
<i>nrdA</i>	(+)	2370987	49.313	W	761	SG10250/P37426	977
<i>nrdB</i>	(+)	2373385	49.363	F	122	SG10251/P37427	977
STU02281	(-)	2408808	50.100	SG	1,329	U02281	
<i>pmrD</i>	(-)	2409096	50.106	W	85	SG10304/P37589	
<i>menE</i>	(-)	2409451	50.113	F	228	SG10221/P37418	
STYADA	(-)	2411000	50.146	SH	1,266	D90221	
<i>alkB</i>	(-)	2411001	50.146	F	24	SG10006/P37462	720
<i>ada</i>	(-)	2411078	50.147	W	352	SG10002/P26189	720
STYNUOD	(-)	2449676	50.950	SG	3,950	L22504	
<i>nuoG</i>	(-)	2449677	50.950	F	612	SG10257/P33900	71
<i>nuoF</i>	(-)	2451586	50.990	W	431	SG10256/P33901	71
<i>nuoE</i>	(-)	2452878	51.017	W	166	SG10255/P33903	71
<i>nuoD</i>	(-)	2453381	51.027	F	81	SG10254/P33902	71
<i>hisPstyM</i>	(+)	2459999	51.165	MP	5,228	SS1014	
STYHIS3P	(-)	2460000	51.165	C	789	M32273	
STYHISTO	(-)	2460578	51.177	C	4,483	J01805	
<i>hisP</i>	(-)	2460899	51.183	W	258	SG10168/P02915	766
<i>hisM</i>	(-)	2461686	51.200	W	235	SG10167/P02912	766
<i>hisQ</i>	(-)	2462390	51.214	W	228	SG10169/P02913	766
<i>hisJ</i>	(-)	2463259	51.233	W	260	SG10165/P02910	762, 766, 805
<i>argT</i>	(-)	2464279	51.254	W	260	SG10018/P02911	762, 999
STYARGTR	(-)	2465061	51.270	C	467	J01798	
<i>ubiX</i>	(-)	2465352	51.276	F	58	SG10481/P40787	763
<i>pgtAstyM</i>	(+)	2501999	52.038	MP	7,612	SS1027	
STYPGTA	(-)	2502000	52.038	C	2,680	M13923	
<i>pgtE</i>	(-)	2502268	52.044	W	296	SG10288/P06185	683, 2217
<i>pgtA</i>	(-)	2503374	52.067	W	415	SG10285/P06184	2201, 2217
STYPGTBC	(-)	2504534	52.091	C	3,388	M21279	
<i>pgtB</i>	(-)	2504611	52.093	W	593	SG10286/P37433	953, 2201
<i>pgtC</i>	(-)	2506615	52.134	W	397	SG10287/P37591	953, 2201
STYPGTP	(+)	2507601	52.155	C	2,011	M21278	
<i>pgtP</i>	(+)	2508243	52.168	W	406	SG10289/P12681	654
<i>cysZstyM</i>	(+)	2538995	52.808	MP	11,006	SS1006	
STYCYSPS	(+)	2538995	52.808	C	3,812	M21450	
<i>cysZ</i>	(+)	2539214	52.812	W	290	SG10081/P12673	266
<i>cysK</i>	(+)	2540250	52.834	W	323	SG10078/P12674	266
<i>ptsH</i>	(+)	2541605	52.862	W	85	SG10317/P07006	266, 1583, 1762, 2121
STYENZI	(+)	2541910	52.868	C	1,728	M76176	
<i>ptsI</i>	(+)	2541911	52.868	W	575	SG10318/P12654	266, 1199, 1762
<i>STCRR</i>	(+)	2543473	52.901	C	733	X05210	
<i>crr</i>	(+)	2543679	52.905	W	169	SG10069/P02908	1416
STU11243	(+)	2544185	52.916	C	4,471	U11243	
<i>yfeI</i>	(-)	2544573	52.924	W	287	SG10475/P40192	
<i>ptsJ</i>	(+)	2545519	52.943	W	430	SG10474/P40193	
<i>yfeJ</i>	(+)	2546826	52.971	W	170	SG10476/P40194	
<i>yfeK</i>	(+)	2547623	52.987	W	120	SG10477/P40195	
<i>yfeL</i>	(+)	2547998	52.995	W	179	SG10478/P40196	
STCYSM	(-)	2548650	53.009	C	1,351	X59595	

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>cysM</i>	(-)	2548668	53.009	W	303	SG10079/P29848	
<i>cysA</i>	(-)	2549647	53.029	F	117	SG10518/P40860	
<i>cysPsty</i>	(-)	2553600	53.112	SH	1,401	SS3006	
<i>cysU</i>	(-)	2553601	53.112	F	15	SG10520/P41032	846, 847
<i>cysP</i>	(-)	2553645	53.112	W	338	SG10519/P40131	846, 847
<i>yfeF</i>	(-)	2554819	53.137	F	60	SG10424/P37441	846, 847
STYHEMF	(+)	2556414	53.170	SG	2,398	L19503	
<i>amiA</i>	(+)	2556641	53.175	W	289	SG10008/P33772	2178
<i>hemF</i>	(+)	2557513	53.193	W	299	SG10150/P33771	
STYEUTBC	(-)	2560000	53.245	SP	2,526	J05518	
<i>eutC</i>	(-)	2560149	53.248	W	286	SG10093/P19265	526
<i>eutB</i>	(-)	2561028	53.266	W	452	SG10092/P19264	526
STGLYAG	(-)	2691000	55.969	SP	1,903	X15816	
<i>glyA</i>	(-)	2691238	55.974	W	417	SG10145/P06192	1894, 2049
<i>hmpA</i>	(+)	2692817	56.007	F	29	SG10170/P26353	1894
STYASRABC	(+)	2745368	57.100	SG	3,360	M57706	
<i>asrA</i>	(+)	2745678	57.106	W	347	SG10021/P26474	851
<i>asrB</i>	(+)	2746725	57.128	W	272	SG10022/P26475	851
<i>asrC</i>	(+)	2747554	57.145	W	337	SG10023/P26476	851
STLEPG	(-)	2770000	57.612	SH	1,294	X54933	
<i>lepB</i>	(-)	2770196	57.616	W	324	SG10194/P23697	2071
<i>lepA</i>	(-)	2771187	57.637	F	35	SG10193/P23698	2071
STU05669	(-)	2776000	57.737	SH	744	U05669	
<i>rpoE</i>	(-)	2776024	57.738	W	191	SG10370/P37401	
STGENES	(-)	2782000	57.862	SG	2,169	X74933	
<i>rplS</i>	(-)	2782029	57.862	W	115	SG10365/P36240	
<i>trmD</i>	(-)	2782417	57.871	W	255	SG10395/P36245	
<i>yjA</i>	(-)	2783229	57.887	W	183	SG10425/P36246	
<i>rpsP</i>	(-)	2783799	57.899	W	82	SG10375/P36242	
STYAROF	(-)	2817488	58.600	SG	1,235	M31302	
<i>aroF</i>	(-)	2817489	58.600	W	356	SG10020/P21307	1384
STHINZ	(+)	2889127	60.090	SG	1,149	V01370	
<i>hin</i>	(+)	2889227	60.092	W	190	SG10156/P03013	529, 747, 1805, 2235
STYTCTD	(+)	2924000	60.815	SP	829	M28368	
<i>tctD</i>	(+)	2924155	60.819	W	224	SG10388/P22104	2140
nrdEstyM	(+)	2947999	61.314	MP	5,654	SS1024	
STNRD	(+)	2948000	61.314	C	4,894	X73226	
<i>nrdE</i>	(+)	2948863	61.332	W	714	SG10252/Q08698	977
<i>nrdF</i>	(+)	2950991	61.377	W	319	SG10253/P17424	977, 1908
STPROVW	(+)	2951644	61.390	C	2,010	X52693	
<i>proV</i>	(+)	2952305	61.404	W	400	SG10312/P17328	977, 1514, 1908
<i>proW</i>	(+)	2953500	61.429	F	51	SG10313/P17327	1908
STTRNADNA	(-)	2980960	62.000	SG	650	X64175	
<i>argQ</i>	(-)	2980961	62.000	W	RNA	SG30002/tRNA	
<i>argZ</i>	(-)	2981210	62.005	W	RNA	SG30015/tRNA	
<i>argY</i>	(-)	2981349	62.008	W	RNA	SG30006/tRNA	
<i>argV</i>	(-)	2981488	62.011	W	RNA	SG30005/tRNA	
<i>serV</i>	(-)	2981568	62.013	W	RNA	SG30012/tRNA	
STU16278	(+)	3018943	62.790	SG	1,085	U16278	
<i>fhlA</i>	(+)	3018944	62.790	W	253	SG10480/P40734	
STYORG	(+)	3022790	62.870	SG	1,898	L33855	
<i>orgA</i>	(+)	3022998	62.874	W	412	SG10502/P40823	969
spaTstyM	(+)	3026612	62.950	MG	12,917	SS1018	
STSPA	(-)	3026613	62.950	C	6,387	X73525	
<i>spaT</i>	(-)	3026614	62.950	F	32	SG10472/P40703	685
<i>spaS</i>	(-)	3026848	62.954	W	356	SG10471/P40702	685
<i>spaR</i>	(-)	3027905	62.976	W	263	SG10470/P40701	685

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>spaQ</i>	(-)	3028700	62.993	W	82	SG10469/P40704	685
<i>spaP</i>	(-)	3028986	62.999	W	224	SG10468/P40700	685
<i>spaO</i>	(-)	3029650	63.013	W	303	SG10467/P40699	685
<i>spaN</i>	(-)	3030561	63.032	W	336	SG10466/P40613	685
<i>spaM</i>	(-)	3031571	63.053	W	147	SG10465/P40612	685
STU08279	(-)	3031903	63.060	C	1,835	U08279	
<i>spaL</i>	(-)	3031996	63.061	W	432	SG10464/P39444	483, 685
<i>spaK</i>	(-)	3033284	63.088	C	134	SG10532/P39443	483
STYINVA	(-)	3033677	63.096	C	2,176	M90846	
<i>invA</i>	(-)	3033712	63.097	W	665	SG10186/P35657	604
STYEPI	(-)	3035753	63.140	C	1,313	M90714	
<i>invE</i>	(-)	3035794	63.140	W	372	SG10187/P35671	638, 1000
STU08280	(-)	3036700	63.159	C	2,830	U08280	
STINVGE	(-)	3036896	63.163	C	1,736	X75302	
<i>invG</i>	(-)	3036909	63.164	W	562	SG10188/P35672	1000
<i>invF</i>	(-)	3038594	63.199	W	216	SG10130/P39437	1000
STINVH	(-)	3047000	63.374	SG	884	Z17242	
<i>invH</i>	(-)	3047328	63.380	W	147	SG10189/P37423	34
STKATFR	(-)	3060000	63.644	SH	1,574	X77752	
<i>rpoS</i>	(-)	3060278	63.650	W	330	SG10372/P37400	1085
<i>nlpD</i>	(-)	3061333	63.672	F	98	SG10513/P40827	1085
STU16303	(+)	3073265	63.920	SP	3,141	U16303	
<i>mutS</i>	(+)	3073812	63.931	W	854	SG10237/P10339	348, 709, 710
STYCYSIHA	(+)	3085080	64.166	SG	6,050	M23007	
<i>cysJ</i>	(+)	3085470	64.174	W	599	SG10077/P38039	1498, 1505
<i>cysI</i>	(+)	3087269	64.211	W	570	SG10076/P17845	1098, 1505
<i>cysH</i>	(+)	3089063	64.248	W	244	SG10075/P17853	1505
<i>ygcC</i>	(-)	3089885	64.265	W	317	SG10485/P40722	1505
STYLGTX	(-)	3120392	64.900	SG	1,473	L13259	
<i>lgt</i>	(-)	3120516	64.903	W	291	SG10201/Q07293	609, 1727
<i>ygdF</i>	(-)	3121606	64.925	F	85	SG10426/P37178	609
STYPRF2	(-)	3180492	66.150	SG	1,351	M38590	
<i>lysS</i>	(-)	3180493	66.150	F	31	SG10211/P28354	1009
<i>prfB</i>	(-)	3180595	66.152	W	365	SG10310/P28353	1009
<i>recJ</i>	(-)	3181797	66.177	F	14	SG10332/P28355	1061
SEANSBSQA	(-)	3227000	67.117	SH	147	X69868	942
STY MUTB	(+)	3230495	67.190	SG	1,170	M86634	
<i>mutY</i>	(+)	3230568	67.192	W	350	SG10238/Q05869	448
metCsty	(+)	3322000	69.093	SP	2,186	SS3002	
<i>exbB</i>	(-)	3322001	69.093	F	110	SG10094/P18950	1538
<i>metC</i>	(+)	3322583	69.105	W	395	SG10223/P18949	1538
<i>yghB</i>	(+)	3323910	69.133	F	92	SG10427/P18951	1538
parFstyM	(+)	3328097	69.220	MG	6,409	SS1026	
STU09309	(-)	3328098	69.220	C	3,184	U09309	
<i>ygiK</i>	(+)	3328407	69.226	W	435	SG10523/P40800	
<i>ygiJ</i>	(-)	3329771	69.255	W	465	SG10522/P40799	
STYPARCF	(-)	3330980	69.280	C	3,527	M68936	
<i>parF</i>	(-)	3331242	69.285	W	245	SG10303/P26974	
<i>parC</i>	(-)	3332236	69.306	W	752	SG10276/P26973	1252
STYPARE	(-)	3337000	69.405	SG	1,981	L05544	
<i>parE</i>	(-)	3337037	69.406	W	630	SG10277/P31598	1872
STCPDB	(-)	3341079	69.490	SG	1,311	X54009	
<i>cpdB</i>	(-)	3341080	69.490	F	250	SG10065/P26265	1221
<i>cysQ</i>	(+)	3342097	69.511	F	98	SG10080/P26264	1221
STYUGDOP	(+)	3365000	69.988	SH	4,631	M14427	
<i>ygiD</i>	(-)	3365001	69.988	F	44	SG10491/P40731	509
<i>rpsU</i>	(+)	3365359	69.995	W	71	SG10376/P02379	509
<i>dnaG</i>	(+)	3365810	70.004	W	581	SG10088/P07362	509
<i>rpoD</i>	(+)	3367705	70.044	W	615	SG10369/P07336	509

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tdcBsty	(-)	3410000	70.923	SH	72	SS3008	
<i>tdcB</i>	(-)	3410001	70.923	F	24	SG10390/P11954	1036
STYM1R1	(-)	3420000	71.131	SG	555	M10888	
<i>rnpB</i>	(-)	3420128	71.134	W	RNA	SG30001/M1-RNA	96
STYM1R2	(-)	3420705	71.146	SG	225	M10889	
STYNUSAINF	(-)	3459700	71.963	SH	228	M28868	
STYNUSA	(-)	3460000	71.963	SH	1,503	M61008	
<i>nusA</i>	(-)	3460001	71.963	W	500	SG10258/P37430	388
STYSIG54	(+)	3473299	72.240	SG	1,955	M68571	
<i>rpoN</i>	(+)	3473375	72.242	W	477	SG10371/P26979	1569
<i>yhbH</i>	(+)	3474831	72.272	W	95	SG10428/P26983	1569
mdh-styM	(+)	3528999	73.399	MP	2,075	SS1022	
STYLT2MDH	(-)	3529000	73.399	C	1,122	M95049	
<i>mdh</i>	(-)	3529064	73.400	W	312	SG10218/P25077	1240
STYARGR	(+)	3529934	73.418	C	1,141	M75913	
<i>argR</i>	(+)	3530415	73.428	W	156	SG10017/P37170	1242
STU03101	(+)	3559000	74.022	SH	1,757	U03101	
<i>yhdG</i>	(+)	3559286	74.028	W	321	SG10429/P37405	
<i>fis</i>	(+)	3560260	74.049	W	98	SG10100/P37404	
STSAPG	(+)	3578215	74.422	SG	1,785	X80501	
<i>trkA</i>	(+)	3578464	74.427	W	458	SG10533/P39445	1541
<i>mscL</i>	(+)	3579980	74.459	F	7	SG10531/P39446	1541
STYRPOA	(-)	3582000	74.501	SG	1,065	M77750	
<i>rpoA</i>	(-)	3582041	74.502	W	329	SG10367/P00574	1230
<i>rpsD</i>	(-)	3583056	74.523	F	2	SG10525/NA	1230
STYSPCA	(-)	3587806	74.622	SH	201	M36266	
<i>rplE</i>	(-)	3587807	74.622	F	43	SG10362/P37436	
<i>rplX</i>	(-)	3587951	74.625	F	18	SG10366/P37438	
tufAstyM	(+)	3589171	74.650	MG	3,963	SS1036	
STTUFA	(-)	3589172	74.650	C	1,281	X55116	
<i>tufA</i>	(-)	3589198	74.651	W	394	SG10403/P21694	2035
STRPSG	(-)	3590382	74.675	C	2,753	X64591	
<i>fusA</i>	(-)	3590454	74.677	W	704	SG10134/P26229	958
<i>rpsG</i>	(-)	3592665	74.723	W	156	SG10373/P26230	958
STYRPSL	(-)	3592944	74.728	C	605	M68548	
<i>rpsL</i>	(-)	3593051	74.731	W	124	SG10374/P02367	859
STYCRP	(+)	3604000	74.958	SP	959	M13773	
<i>crp</i>	(+)	3604283	74.964	W	210	SG10068/P06170	1767
STYPABAA	(-)	3610327	75.090	SG	1,669	M32355	
<i>argD</i>	(-)	3610328	75.090	F	17	SG10488/P40732	2026
<i>pabA</i>	(-)	3610464	75.093	W	187	SG10273/P06193	1003, 2026
<i>fic</i>	(-)	3611059	75.105	W	200	SG10097/P20751	2026
<i>yhfG</i>	(-)	3611651	75.118	W	55	SG10430/P37771	2026
<i>ppiA</i>	(-)	3611914	75.123	F	26	SG10308/P20753	2026
STYCYSA	(+)	3629000	75.478	SP	5,280	M64606	
<i>nirD</i>	(+)	3629001	75.478	F	67	SG10487/P40789	2169
<i>nirC</i>	(+)	3629469	75.488	W	269	SG10248/P25926	2169
<i>cysG</i>	(+)	3630290	75.505	W	457	SG10074/P25924	2169
<i>yhfI</i>	(+)	3631997	75.541	W	416	SG10437/P25927	2169
<i>yhfJ</i>	(+)	3633433	75.571	W	264	SG10438/P25928	2169
STENVZ	(-)	3653599	75.990	SG	3,293	X12374	
<i>pckA</i>	(+)	3653600	75.990	F	287	SG10497/P41033	1201
<i>envZ</i>	(-)	3654543	76.010	W	450	SG10091/P08982	1201
<i>ompR</i>	(-)	3655892	76.038	W	239	SG10266/P08981	1201
glgAstyM	(+)	3712737	77.220	MG	1,838	SS1011	
STYGLGC	(-)	3712738	77.220	C	1,410	M17363	

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>gIa</i>	(-)	3712739	77.220	F	29	SG10141/P05416	1181
<i>gIc</i>	(-)	3712826	77.222	W	431	SG10142/P05415	1181
STGLGCG	(-)	3714118	77.249	C	458	X59281	
livFstyM	(+)	3723795	77.450	MG	7,630	SS1021	
STYLIV	(-)	3723796	77.450	C	4,072	D12589	
<i>yhhV</i>	(-)	3723797	77.450	F	68	SG10457/P40819	1308
<i>livF</i>	(-)	3724127	77.457	W	237	SG10202/P30294	1308
<i>livG</i>	(-)	3724842	77.472	W	255	SG10203/P30293	1308
<i>livM</i>	(-)	3725606	77.488	W	425	SG10207/P30296	1308
<i>livH</i>	(-)	3726880	77.514	W	308	SG10204/P30295	1308
STYLIVBC	(-)	3727808	77.533	C	3,618	D00478	
<i>livK</i>	(-)	3727866	77.535	W	369	SG10206/P17216	1467
<i>livJ</i>	(-)	3729975	77.579	W	365	SG10205/P17215	1467
STYOPDA	(+)	3832000	79.700	SP	2,842	M84574	
<i>opaA</i>	(+)	3832603	79.713	W	239	SG10266/P08981	364
STYCSPSA	(+)	3848000	80.033	SH	481	L23115	
<i>cspA</i>	(+)	3848268	80.039	W	70	SG10070/P37410	
STCYSE	(-)	3892557	80.960	SG	1,497	X59594	
<i>cysE</i>	(-)	3892627	80.961	W	273	SG10073/P29847	
<i>gpsA</i>	(-)	3893535	80.980	F	171	SG10456/P40716	
kbl-styM	(+)	3903999	81.198	MP	10,168	SS1019	
STRFADF	(+)	3904000	81.198	C	2,700	U06472	
<i>kbl</i>	(-)	3904001	81.198	F	162	SG10191/P37419	1814
<i>rfaD</i>	(+)	3904690	81.212	W	310	SG10335/P37420	1814
<i>rfaF</i>	(+)	3906016	81.240	W	348	SG10336/P37421	1814
STYRFAC	(+)	3906070	81.241	C	1,574	M95927	
<i>rfaC</i>	(+)	3906672	81.254	W	317	SG10334/P26469	1258, 1813
STYRFALK	(+)	3907310	81.267	C	4,280	M73826	
<i>rfaL</i>	(+)	3907665	81.274	W	404	SG10340/P26471	1258
<i>rfaK</i>	(-)	3908936	81.301	W	381	SG10339/P26470	1258
<i>rfaZ</i>	(-)	3910182	81.327	W	269	SG10343/P26473	1258
<i>rfaY</i>	(-)	3911141	81.347	C	232	SG10342/P26472	1258
<i>rfaYsty</i>	(-)	3911590	81.356	C	2,578	SS3007	
<i>rfaJ</i>	(-)	3911935	81.363	W	336	SG10338/P19817	285
<i>rfaI</i>	(-)	3912891	81.383	W	337	SG10337/P19816	285
<i>rfaB</i>	(-)	3913910	81.404	F	81	SG10333/Q06994	285
S56361	(-)	3914809	81.423	SP	815	S56361	
<i>rfaB</i>	(-)	3914810	81.423	F	70	SG10333/Q06994	1061
<i>yibR</i>	(-)	3915089	81.429	W	77	SG10512/P40824	1061
<i>rfaP</i>	(-)	3915354	81.434	F	89	SG10341/Q06995	1061
pyrEstyM	(+)	3915999	81.448	MG	1,047	SS1030	
STOPPRBST	(-)	3916000	81.448	C	645	Z19547	
<i>pyrE</i>	(-)	3916001	81.448	W	213	SG10327/P08870	1422, 1739
M28333	(+)	3916462	81.457	C	585	M28333	
<i>rph</i>	(+)	3916463	81.457	F	108	SG10361/P26155	1422
STYUHPABCT	(-)	3940637	81.960	SG	5,465	M89480	
<i>uhpT</i>	(-)	3940837	81.964	W	463	SG10409/P27670	915
<i>uhpC</i>	(-)	3942369	81.996	W	442	SG10408/P27669	915
<i>uhpB</i>	(-)	3943707	82.024	W	500	SG10407/P27668	915
<i>uhpA</i>	(-)	3945209	82.055	W	196	SG10406/P27667	915
STYMGTCB	(+)	3946406	82.080	SG	4,586	M57715	
<i>mgtC</i>	(+)	3947009	82.093	W	231	SG10232/P22037	1850
<i>mgtB</i>	(+)	3947924	82.112	W	908	SG10231/P22036	1850
STRECF	(-)	4012276	83.450	SG	1,068	X62505	
<i>recF</i>	(-)	4012277	83.450	W	355	SG10331/P24900	1009
STYDNAA	(-)	4019488	83.600	SG	1,946	M17352	
<i>dnaN</i>	(-)	4019489	83.600	F	64	SG10089/P26464	1818
<i>dnaA</i>	(-)	4019679	83.604	W	466	SG10085/P35891	1818
STYORI	(+)	4080550	84.870	SG	552	J01808	

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
rbsBsty	(+)	4085357	84.970	SH	891	SS3005	
<i>rbsB</i>	(+)	4085358	84.970	W	297	SG10330/P02926	252
STYILVPA	(+)	4098000	85.233	SP	329	J01806	
<i>ilvL</i>	(+)	4098120	85.235	W	32	SG10183/P03060	1153, 1986
ilvEsty	(+)	4098500	85.243	SP	927	SS3001	
<i>ilvE</i>	(+)	4098501	85.243	W	308	SG10181/P15168	527
ilvAstyM	(+)	4099499	85.264	MP	1,756	SS1017	
STYILVAPRI	(+)	4099500	85.264	C	240	M25498	
<i>ilvD</i>	(+)	4099501	85.264	F	68	SG10458/P40810	1233
STYILVA	(+)	4099711	85.269	C	1,545	M26670	
<i>ilvA</i>	(+)	4099712	85.269	W	514	SG10179/P20506	1985
STYILVYCR	(+)	4100000	85.275	SP	378	K03522	
<i>ilvY</i>	(-)	4100001	85.275	F	42	SG10184/P05988	2124
<i>ilvC</i>	(+)	4100295	85.281	F	28	SG10180/P05989	2124
Z21789	(+)	4102040	85.317	SG	2,558	Z21789	
<i>rhlB</i>	(-)	4102041	85.317	F	56	SG10498/P40863	1360
<i>trxA</i>	(+)	4102391	85.324	W	109	SG10402/P00274	880, 1083, 1194, 1428, 1436, 1761
<i>rho</i>	(+)	4103139	85.340	W	419	SG10359/P26980	1083, 1360
STYCARABA	(+)	4112282	85.530	SG	4,378	M95047	
<i>rffT</i>	(+)	4112283	85.530	F	426	SG10354/P37458	
<i>rffM</i>	(+)	4113560	85.557	W	246	SG10353/P37457	
<i>yifK</i>	(+)	4114507	85.576	W	461	SG10431/P37456	
<i>argX</i>	(+)	4115995	85.607	W	RNA	SG30007/tRNA	
<i>hisR</i>	(+)	4116125	85.610	W	RNA	SG30009/tRNA	
<i>leuU</i>	(+)	4116222	85.612	W	RNA	SG30010/tRNA	
<i>proM</i>	(+)	4116351	85.615	W	RNA	SG30011/tRNA	
cyaAstyM	(+)	4120000	85.691	SG	1,661	SS1002	
STCYAG	(+)	4120001	85.691	C	489	X55783	
<i>hemC</i>	(-)	4120001	85.691	F	16	SG10571/NA	
cyaAsty	(+)	4120404	85.699	C	1,257	SS3009	
<i>cyaA</i>	(+)	4120404	85.699	F	419	SG10071/Q05878	809, 2015
		4120001	85.691	F			
STYCRA	(+)	4126226	85.820	SG	1,921	L11043	
<i>uvrD</i>	(+)	4126227	85.820	F	13	SG10414/Q05311	1843
<i>corA</i>	(+)	4126740	85.831	W	316	SG10064/P31138	1843
<i>yigF</i>	(-)	4127739	85.851	W	126	SG10432/P31139	1843
STPLDA	(+)	4133000	85.961	SH	1,254	X76900	
<i>YigI</i>	(-)	4133001	85.961	F	25	SG10461/P40725	240
<i>PldA</i>	(+)	4133241	85.966	W	289	SG10302/P37442	240
<i>RecQ</i>	(+)	4134194	85.986	F	22	SG10460/P40724	240
STYMETR	(-)	4137284	86.050	SG	1,203	M17356	
<i>metR</i>	(-)	4137397	86.052	W	276	SG10227/P05984	1564
<i>metE</i>	(+)	4138479	86.075	F	2	SG10483/NA	1564
STHEMN	(+)	4165170	86.630	SG	3,055	U06779	
<i>yihI</i>	(+)	4165987	86.647	W	171	SG10433/P37130	2179
<i>hemN</i>	(+)	4166691	86.662	W	457	SG10154/P37129	2179
glnAstyM	(+)	4208423	87.530	MP	1,965	SS1012	
STYGLNA2	(-)	4208424	87.530	C	395	J01803	
<i>glnA</i>	(-)	4208754	87.536	W	469	SG10143/P06201	933, 2196
STYGLNA	(-)	4208756	87.537	C	1,407	M14536	
STYGLNA1	(-)	4210121	87.565	C	120	J01802	
STYGLNAA	(-)	4210201	87.567	C	188	M11196	
STRHABC2	(-)	4234406	88.070	SG	2,816	X57299	
<i>rhaA</i>	(-)	4234407	88.070	F	70	SG10355/P27031	1439
<i>rhaB</i>	(-)	4234615	88.074	W	489	SG10356/P27030	1439
<i>rhaS</i>	(+)	4236372	88.111	W	277	SG10357/P27029	1439
STYRHAT	(-)	4237806	88.141	SG	2,388	M85157	
<i>rhaR</i>	(+)	4237807	88.141	F	106	SG10524/P40865	2000

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>rhaT</i>	(-)	4238124	88.147	W	344	SG10358/P27135	2000
STUSHB	(+)	4247000	88.332	SH	1,453	X13380	
<i>sbp</i>	(+)	4247001	88.332	W	311	SG10382/P02906	616, 914, 1560, 1561
<i>ushB</i>	(+)	4247358	88.339	W	251	SG10051/P26219	616
STMETJ	(-)	4295000	89.330	SP	656	X01961	
<i>metJ</i>	(-)	4295063	89.332	W	104	SG10226/P06203	2051
<i>metB</i>	(+)	4295645	89.344	F	4	SG10482/NA	2051
metFstyM	(+)	4296999	89.372	MP	3,726	SS1023	
STMETF	(+)	4297000	89.372	C	1,735	X07689	
<i>metF</i>	(+)	4297435	89.381	W	296	SG10224/P11003	2178
STKATG	(+)	4298339	89.400	C	2,387	X53001	
<i>katG</i>	(+)	4298490	89.403	W	727	SG10190/P17750	1229
trmAstyM	(+)	4310371	89.650	MG	2,604	SS1034	
STYTRMA	(-)	4310372	89.650	C	639	M57569	
<i>trmA</i>	(-)	4310373	89.650	F	102	SG10394/P22038	704
STYBTUB	(+)	4310480	89.652	C	2,496	M89481	
<i>btuB</i>	(+)	4311049	89.664	W	614	SG10030/P37409	2114
<i>murI</i>	(+)	4312838	89.701	F	46	SG10494/P40723	2114
STYMURBIRA	(+)	4326000	89.975	SP	1,746	L14816	
<i>rifB</i>	(+)	4326018	89.975	W	RNA	SG30014/rRNA	
<i>murB</i>	(+)	4326317	89.982	W	342	SG10235/P37417	458
<i>birA</i>	(+)	4327342	90.003	W	135	SG10028/P37416	458
STTUFB	(+)	4329681	90.052	SG	1,308	X55117	
<i>tufB</i>	(+)	4329772	90.053	W	394	SG10404/P21694	2035
STRPLJL	(+)	4334412	90.150	SG	1,131	X53072	
<i>rplJ</i>	(+)	4334602	90.154	W	165	SG10363/P17352	1550, 1551, 2230
<i>rplL</i>	(+)	4335166	90.166	W	121	SG10364/P18081	1550, 2230
STRPOB	(+)	4338258	90.230	SG	4,185	X04642	
<i>rpoB</i>	(+)	4338279	90.230	W	1,342	SG10368/P06173	1217, 1971
STYHUPA	(+)	4360500	90.693	SH	584	M22975	
<i>hupA</i>	(+)	4360711	90.697	W	90	SG10174/P15148	773
hydGstyM	(+)	4362999	90.745	MP	4,784	SS1016	
STYHYDGG	(+)	4363000	90.745	C	2,088	M64988	
<i>hydH</i>	(+)	4363001	90.745	F	208	SG10177/P37461	331
<i>hydG</i>	(+)	4363635	90.758	W	441	SG10176/P25852	331
STYPURHD	(-)	4364597	90.778	C	3,187	M66160	
<i>purD</i>	(-)	4364957	90.785	W	429	SG10319/P26977	330
<i>purH</i>	(-)	4366258	90.812	F	508	SG10320/P26978	330
STYMETA	(+)	4379126	91.080	SG	671	M74188	
<i>yjaB</i>	(-)	4379127	91.080	F	102	SG10486/P40677	1294
<i>metA</i>	(+)	4379591	91.090	F	69	SG10222/P37413	1294
STICLR	(-)	4387011	91.244	SG	950	X52950	
<i>iclR</i>	(-)	4387086	91.246	W	274	SG10178/P17430	606
metHsty	(+)	4388000	91.265	SH	1,373	SS3003	
<i>metH</i>	(+)	4388261	91.270	F	371	SG10225/P37586	2055
U01246	(-)	4392589	91.360	SG	1,088	U01246	
<i>yjbB</i>	(+)	4392590	91.360	F	52	SG10492/P40730	363
<i>pepE</i>	(-)	4392824	91.365	W	229	SG10282/P36936	363
STMAL	(-)	4403243	91.582	SP	8,590	X54292	
<i>malG</i>	(-)	4403507	91.587	W	296	SG10214/P26468	569, 1759
<i>malF</i>	(-)	4404412	91.606	W	514	SG10213/P26467	1759
<i>malE</i>	(-)	4407203	91.664	W	396	SG10212/P19576	402, 1759
<i>malK</i>	(+)	4407639	91.673	W	369	SG10215/P19566	402, 1759
<i>lamB</i>	(+)	4408837	91.698	W	452	SG10192/P26466	568, 1759
<i>malM</i>	(+)	4410368	91.730	W	305	SG10216/P26478	1759
STLEXA	(+)	4420513	91.941	SP	921	X63002	

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>lexA</i>	(+)	4420626	91.943	W	202	SG10200/P29831	618, 1399
dnaBstyM	(+)	4429257	92.123	MP	3,155	SS1007	
STYDNABA	(+)	4429258	92.123	C	2,013	J03390	
<i>qor</i>	(-)	4429259	92.123	F	168	SG10511/P40783	1726, 2161
<i>dnaB</i>	(+)	4429827	92.135	W	471	SG10086/P10338	2161
STYALR	(+)	4431213	92.163	C	1,200	M12847	
<i>alr</i>	(+)	4431274	92.165	W	359	SG10007/P06655	598
STYUVRA	(-)	4435524	92.253	SP	3,623	M93014	
<i>uvrA</i>	(-)	4435800	92.259	W	941	SG10413/P37434	
<i>ssb</i>	(+)	4438874	92.323	F	91	SG10385/P37435	
STYPMTRAB	(-)	4494834	93.487	SP	3,824	L13395	
<i>proP</i>	(+)	4494835	93.487	F	17	SG10510/P40862	1665
<i>pmrB</i>	(-)	4495055	93.491	W	356	SG10025/P36557	1665
<i>pmrA</i>	(-)	4496135	93.514	W	222	SG10024/P36556	1665
<i>yjdB</i>	(-)	4496800	93.527	W	547	SG10434/P36555	1665
STMELB	(+)	4507574	93.752	SP	1,714	X62101	
<i>melA</i>	(+)	4507575	93.752	F	43	SG10219/P30877	1370
<i>melB</i>	(+)	4507790	93.756	W	476	SG10220/P30878	1370
STPHON	(-)	4529711	94.212	SP	1,408	X63599	
<i>phoN</i>	(-)	4529821	94.214	W	250	SG10292/P26976	687, 1007
STYMUTL	(+)	4566000	94.967	SP	2,446	M29687	
<i>amiB</i>	(+)	4566001	94.967	F	100	SG10009/P26366	1291
<i>mutL</i>	(+)	4566313	94.973	W	618	SG10236/P14161	1291
<i>miaA</i>	(+)	4568160	95.012	F	95	SG10233/P37724	1291
STU07843	(+)	4645490	96.620	SG	4,989	U07843	
<i>treR</i>	(-)	4645965	96.630	W	315	SG10393/P36674	
<i>mgtA</i>	(+)	4647296	96.658	F	42	SG10228/P23924	
STPYRBIG	(-)	4658000	96.880	SP	1,812	X05641	
<i>pyrI</i>	(-)	4658031	96.881	W	153	SG10329/P08421	1336
<i>pyrB</i>	(-)	4658505	96.891	W	311	SG10324/P08420	1336
<i>pyrL</i>	(-)	4659476	96.911	W	33	SG10323/P08522	1336
STMIAE	(+)	4672000	97.171	SP	4,531	X73368	
<i>argI</i>	(-)	4672001	97.171	F	218	SG10016/Q08016	1558
<i>yjgD</i>	(+)	4672820	97.188	W	138	SG10435/Q08019	1558
<i>miaE</i>	(+)	4673248	97.197	W	270	SG10234/Q08015	1558
<i>yjgA</i>	(-)	4674295	97.219	W	162	SG10441/Q08020	1558
<i>yjgM</i>	(-)	4674890	97.231	W	167	SG10442/Q08021	1558
<i>yjgN</i>	(+)	4675726	97.249	F	268	SG10443/Q08022	
hsdSstyM	(+)	4732999	98.440	MP	3,010	SS1015	
STHSDS	(-)	4733000	98.440	C	1,650	Y00524	
<i>hsdS</i>	(-)	4733016	98.440	W	469	SG10172/P06187	588, 610
STYHSDMB	(-)	4734420	98.470	C	1,590	L02506	
<i>hsdM</i>	(-)	4734421	98.470	W	529	SG10501/P40813	
STYNADR	(+)	4800788	99.850	SG	2,496	M85181	
<i>sms</i>	(+)	4800789	99.850	F	298	SG10444/P24517	563
<i>nadR</i>	(+)	4801836	99.872	W	409	SG10243/P24518	563, 2229
STYTRPR	(+)	4804154	99.920	SG	748	L13768	
<i>slt</i>	(+)	4804155	99.920	F	54	SG10490/P39434	
<i>trpR</i>	(+)	4804411	99.925	W	108	SG10401/P37444	
<i>yjyX</i>	(-)	4804799	99.933	F	35	SG10436/P39432	
STY326F	(+)	ND ^h	ND	S	326	D12814	
STYNHOA	(+)	ND	ND	S	2,134	D90301	
<i>nhoA</i>	(+)	ND	ND	W	281	SG10247/Q00267	2109
<i>yzzJ</i>	(-)	ND	ND	F	132	SG10500/P40788	1558
STYOADGABA	(+)	ND	ND	S	4,053	M96434	
<i>oadG</i>	(+)	ND	ND	W	83	SG10261/Q03032	2158
<i>oadA</i>	(+)	ND	ND	W	591	SG10259/Q03030	2158

Locus	Ori ^b	Left end ^c	Cs	Code ^d	Length ^e	Accession no. ^f	Reference(s) ^g
<i>oadB</i>	(+)	ND	ND	W	433	SG10260/Q03031	2158
STYSINRPHO	(+)	ND	ND	S	4,880	L04307	
<i>SinR</i>	(+)	ND	ND	W	315	SG10383/P37459	688
STYTCPCHEM	(+)	ND	ND	S	1,840	L06029	
<i>Tcp</i>	(+)	ND	ND	W	547	SG10389/Q02755	2193
SEANSP	(+)	ND	ND	S	1,887	U04851	
<i>AnsPn</i>	(+)	ND	ND	W	497	SG10527/P40812	

^aGenBank LOCUS field, StySeq contig name, or gene name. The StySeq contigs are generally composites created by merging overlapping GenBank entries and are usually named using the first gene present in the contig. This gene name is followed by the organism code "sty" and an "M" to denote a merged (melded) contig. Three-letter gene names have a "-" instead of a fourth letter, following the conventions established for the EcoSeq data collection. The LOCUS and contig names are mnemonic, but they are subject to change and therefore one should use the accession numbers for retrieval and identification purposes.

^bOri, orientation of genes on the chromosome: (+), clockwise; (-), counterclockwise. Orientation of GenBank entries on the chromosome: (+), 5' to 3' is the clockwise direction; (-), 5' to 3' is the counterclockwise direction. If the orientation is unknown, the orientation of the corresponding *E. coli* sequence is used as the default orientation (see text). All melded contigs are constructed to be in the (+) orientation.

^cLeft end denotes the genomic coordinate (base pairs) of the left (counterclockwise) end of an aligned DNA sequence entry or gene in base pairs and centisomes. A centisome is a physical map unit equal to 1% of a chromosome's length. We estimate 1 Cs for the chromosome of *S. typhimurium* to be 48,080 bp. For genetically pinned genes, the estimated centisome value is used to calculate a left-end genomic coordinate in base pairs. We do not mean to imply that genomic positions are known to single-base-pair accuracy. In contrast, the relative positions of genes within a contig are known to single-base-pair accuracy. Persons wishing to quote a centisome map position for *S. typhimurium* genes should use the centisome values presented in Table 1.

^dCodes: P, physically anchored contig; G, genetically pinned; H, roughly located by using mapping information from the homologous chromosome of *E. coli*; M, melded StySeq; S, single StySeq (GenBank) entry; C, constituent GenBank sequence used in assembly of a StySeq meld; W, whole gene sequence; F, fragment of a gene, partial sequence. StySeq master contigs are preceded by blank lines and have two codes.

^eLength, number of base pairs for DNA sequences or the number of codons (amino acids) for genes. The number of codons is not given for the structural RNA genes, labeled "RNA."

^fGenBank, SWISS-PROT, and StyGene (SG) accession numbers; completely overlapping (redundant) GenBank entries omitted here are listed in the SWISS-PROT records. Structural RNA genes do not have corresponding SWISS-PROT records; the type of structural RNA gene is indicated instead.

^gDNA sequence and characterization citations from SWISS-PROT. Additional sequence-related references, including unpublished sources, can be obtained from GenBank and SWISS-PROT records. Additional references are also present in Table 1

^hND, not done.

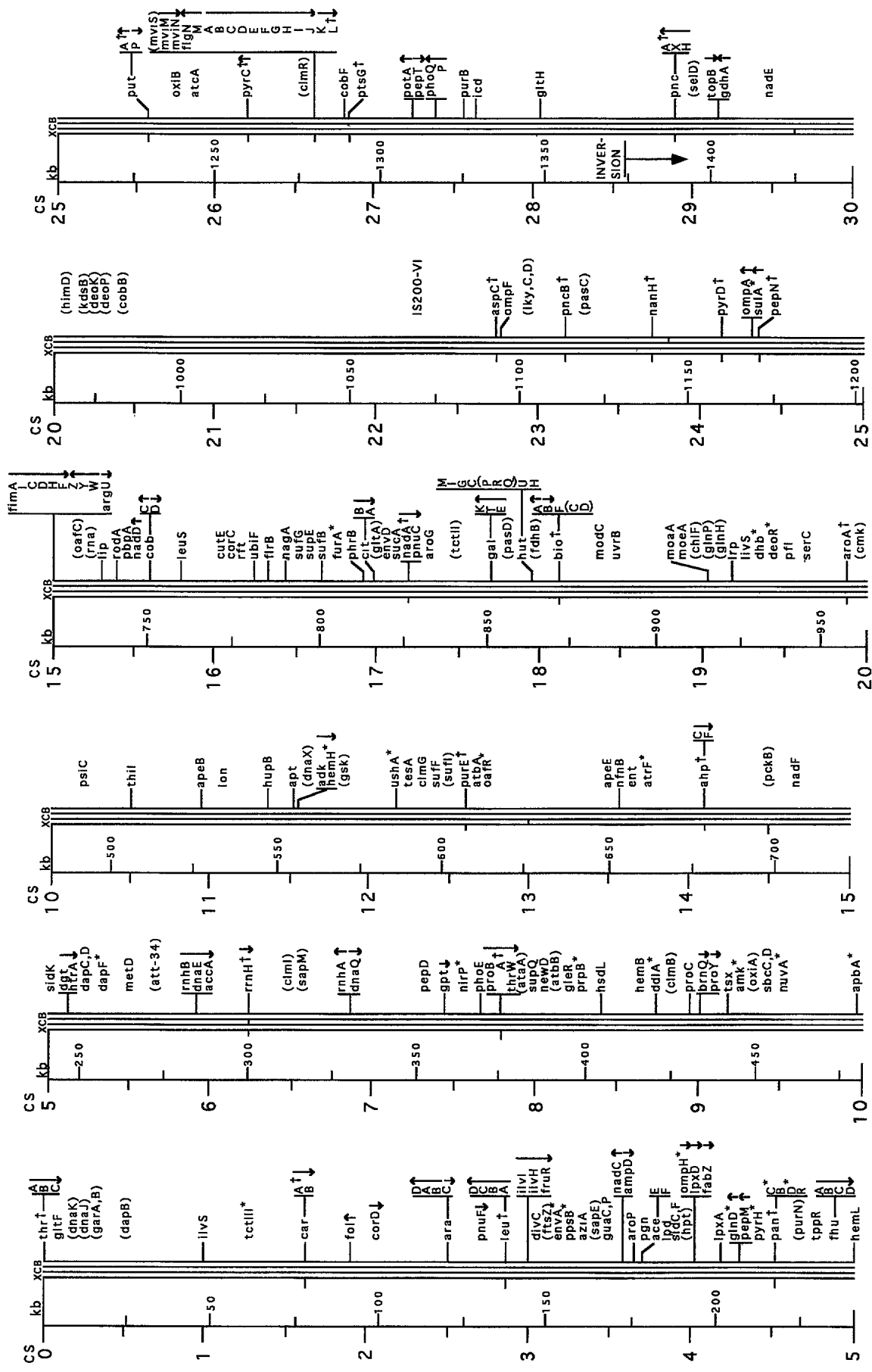


FIGURE 1 Continued

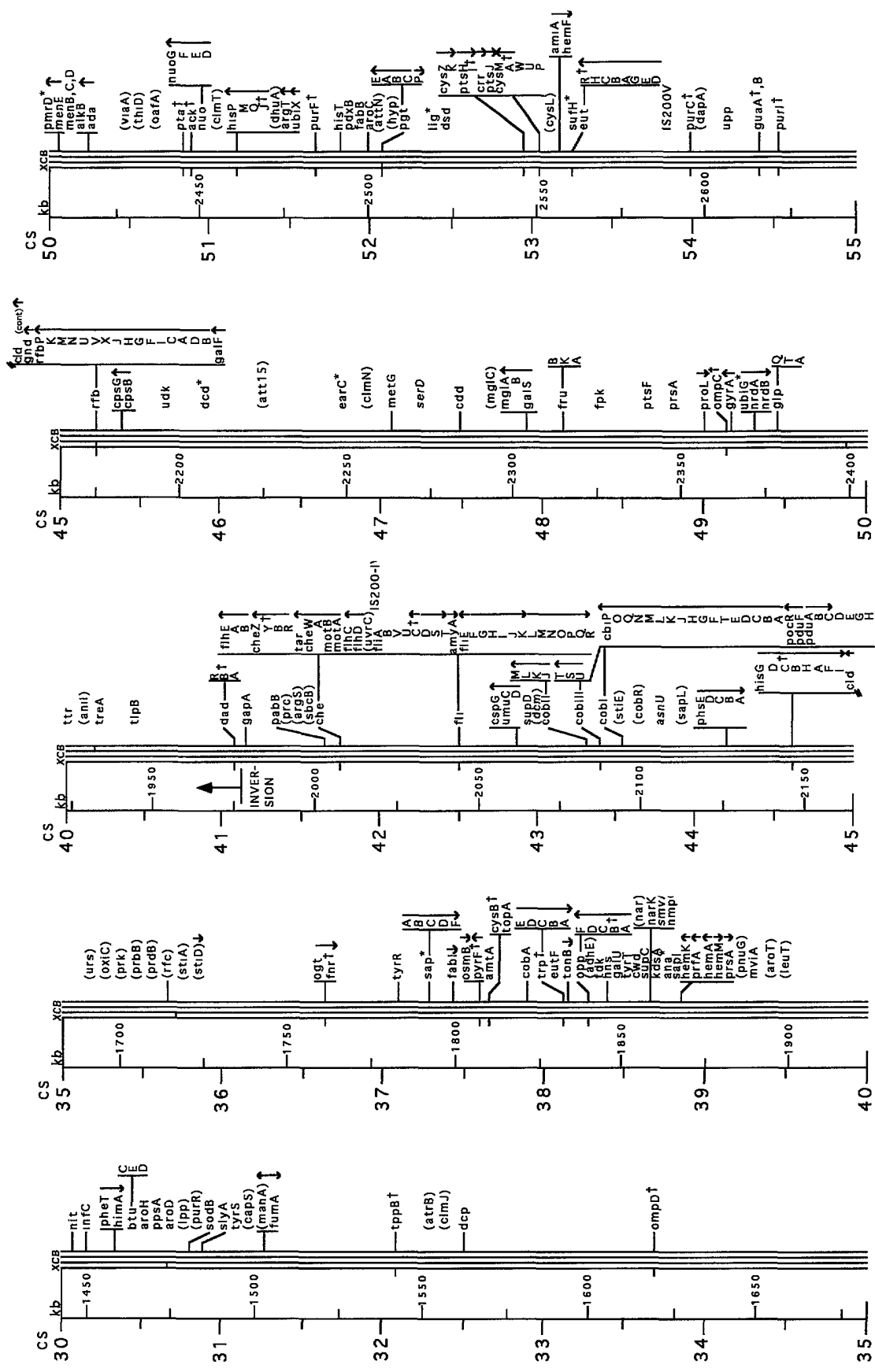


FIGURE 1 Continued

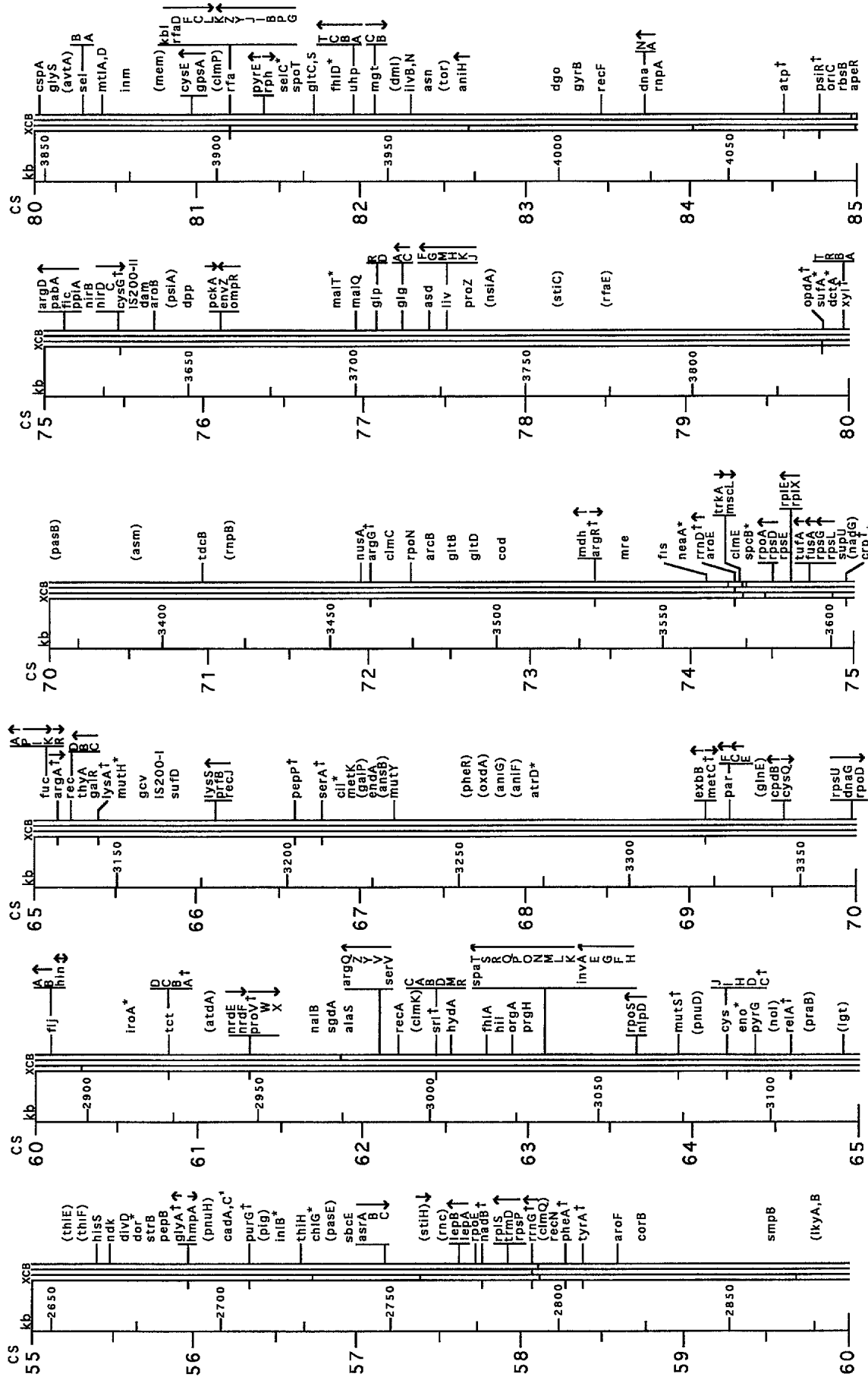


FIGURE 1 Continued

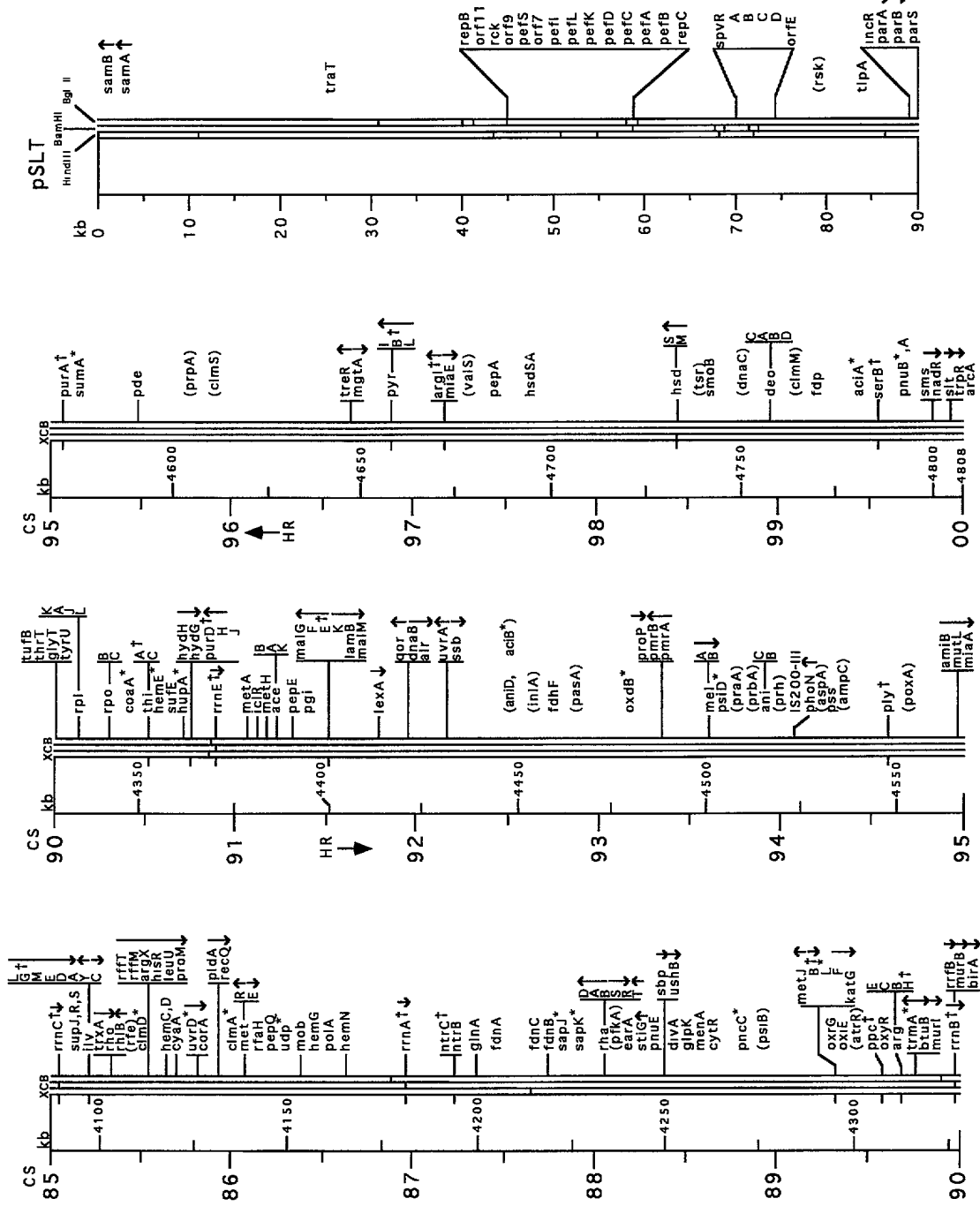


FIGURE 1 Continued

FIGURE 1 Genetic map of *S. typhimurium* LT2. The gene designations used here are described in Table 1. The map is shown as 20 linear segments, representing the circular chromosome, and one linear segment representing the circular plasmid pSLT. The chromosome is composed of 100 centisomes (Cs); a scale covering 5 Cs is shown to the left of each segment. The scale is also designated in kilobases (Kb); the entire chromosome is designated as 4,808 kb (1222). In the middle of each segment are vertical lines which show the restriction maps for the endonucleases *Xba*I, *Ceu*I, and *Bln*I, indicated by X, C, and B, respectively; a horizontal line indicates a restriction site. These sites were determined from PFGE (1222, 1224, 2162, 2163). The position of many genes around the chromosome were anchored using PFGE, through the *Xba*I map, and *Bln*I sites in Tn10 transposons which had transposed into these genes (1224, 1224, 2162). Genes which have been mapped in this way are indicated by a short horizontal bar to the left of the *Xba*I map, and the gene named is flagged with a superscript †; e.g., the *carAB* genes at 1.6 Cs, the *leu* genes at 2.8 Cs, and the *pan* genes at 4.5 Cs have been mapped through analysis of Tn10 insertions in these genes (1222). Other genes are anchored through a specific restriction site which falls into a known gene; e.g., *Ceu*I sites are found only in the *rrn* genes; thus, at 6.2 Cs the *Ceu*I site indicates the location of the *rrnH* operon, at 58.1 Cs it indicates the location of the *rrnG* operon, and so on. In these cases, too we show a short horizontal bar to the left of the *Xba*I map. The locations of the genes between these fixed points are based on several types of data (see the text). In many cases, the location is based on phage-mediated transduction; the distance between genes was determined by assuming that the lengths of P22 and P1 transducing fragments are 1 and 2 Cs, respectively, and applying the formula developed by Wu (2170) to convert the percentage of joint transduction to map distance in centisomes, with modifications as described in Fig. 2 of Sanderson and Roth (1721). Parentheses around a gene symbol indicate that the location of the gene is known only approximately, usually from conjugation studies or sequence comparison with *E. coli*. An asterisk indicates that the gene has been mapped more precisely, usually by phage-mediated transduction, but that its position with respect to adjacent markers is not known. Arrows to the extreme right of the genes and operons indicate the direction or mRNA transcription at these loci. The endpoints of the region of the chromosome inverted with respect to *E. coli* are indicated by the word “inversion: and by arrows. The region of the chromosome for which high-resolution restriction mapping data have been published (2166) is delimited by the letters HR.

LITERATURE CITED

1. **Abd-el-al, A., and J. L. Ingraham.** 1969. Cold sensitivity and other phenotypes resulting from mutation in *pyrA* gene. *J. Biol. Chem.* **244**:4039–4045.
2. **Abdelal, A. T. H., E. Griego, and J. L. Ingraham.** 1976. Arginine-sensitive phenotype of mutations in *pyrA* *Salmonella typhimurium*: role of ornithine carbamyl transferase in the assembly of mutant carbamyl phosphate synthetase. *J. Bacteriol.* **128**:105–113.
3. **Abdelal, A. T. H., E. Griego, and J. L. Ingraham.** 1978. Arginine auxotrophic phenotype of mutations in *pyrA* of *Salmonella typhimurium*: role of *N*-acetylornithine in the maturation of mutant carbamylphosphate synthetase. *J. Bacteriol.* **134**:528–536.
4. **Abdelal, A. T. H., and J. L. Ingraham.** 1975. Carbamylphosphate synthetase from *Salmonella typhimurium*. *J. Biol. Chem.* **250**:4410–4417.
5. **Abdelal, A. T. H., E. H. Kennedy, and O. Nainan.** 1977. Ornithine transcarbamylase from *Salmonella typhimurium*: purification, subunit composition, kinetic analysis, and immunological cross-reactivity. *J. Bacteriol.* **129**:1387–1396.
6. **Abdulkarim, F., T. M. Tuohy, R. H. Buckingham, and D. Hughes.** 1991. Missense substitutions lethal to essential functions of EF-Tu. *Biochimie* **73**:1457–1464.
7. **Abouhamad, W. N., M. Manson, M. M. Gibson, and C. F. Higgins.** 1991. Peptide transport and chemotaxis in *Escherichia coli* and *Salmonella typhimurium*: characterization of the dipeptide permease (Dpp) and the dipeptide-binding protein. *Mol. Microbiol.* **5**:1035–1047.
8. **Abshire, K. Z., and F. C. Neidhardt.** 1993. Analysis of proteins synthesized by *Salmonella*

- typhimurium* during growth within a host macrophage. *J. Bacteriol.* **175**:3734–3743.
9. **Abshire, K. Z., and F. C. Neidhardt.** 1993. Growth rate paradox of *Salmonella typhimurium* within host macrophages. *J. Bacteriol.* **175**:3744–3748.
 10. **Aceves-Pina, E., M. V. Ortega, and M. Artis.** 1974. Linkage of the *Salmonella typhimurium* chromosomal loci encoding for the cytochrome-linked L- α -glycerophosphate dehydrogenase and amylomaltase activities. *Arch. Microbiol.* **101**:59–70.
 11. **Adams, D. E., E. M. Shekhtman, E. L. Zechiedrich, M. B. Schmid, and N. R. Cozzarelli.** 1992. The role of topoisomerase IV in partitioning bacterial replicons and the structure of catenated intermediates in DNA replication. *Cell* **71**:277–288.
 12. **Ahmed, N., and R. J. Rowbury.** 1971. A temperature-sensitive cell division component in a mutant of *Salmonella typhimurium*. *J. Gen. Microbiol.* **67**:107–115.
 13. **Ahmed, N., and R. J. Rowbury.** 1974. Studies of septation and separation in a mutant of *Salmonella typhimurium*. *Z. Allg. Mikrobiol.* **14**:455–463.
 14. **Ahmed, S. A., H. Kawasaki, R. Bauerle, H. Morita, and E. W. Miles.** 1988. Site-directed mutagenesis of the α subunit of tryptophan synthase from *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.* **151**:672–678.
 15. **Ailion, M., T. A. Bobik, and J. R. Roth.** 1993. Two global regulatory systems (Crp and Arc) control the cobalamin/propanediol regulon of *Salmonella typhimurium*. *J. Bacteriol.* **175**:7200–7208.
 16. **Aizawa, S.-I., G. E. Dean, C. J. Jones, R. M. Macnab, and S. Yamaguchi.** 1985. Purification and characterization of the flagellar hook-basal body complex of *Salmonella typhimurium*. *J. Bacteriol.* **161**:836–849.
 17. **Aizawa, S.-I., S. Kato, S. Asakura, H. Kagawa, and S. Yamaguchi.** 1980. *In-vitro* polymerization of polyhook protein from *Salmonella* SJW 880. *Biochim. Biophys. Acta* **625**:291–303.
 18. **Aksamit, R. R., and D. E. Koshland, Jr.** 1974. Identification of the ribose binding protein as the receptor for ribose chemotaxis in *Salmonella typhimurium*. *Biochemistry* **13**:4473–4478.
 19. **Alami, N., and P. C. Hallenbeck.** 1992. Mutations that affect the regulation of *phs* in *Salmonella typhimurium*. *J. Gen. Microbiol.* **138**:1117–1122.
 20. **Alexander, R. R., and J. M. Calvo.** 1969. A *Salmonella typhimurium* locus involved in the regulation of isoleucine, valine, and leucine biosynthesis. *Genetics* **61**:539–556.
 21. **Alexander, R. R., J. M. Calvo, and M. Freundlich.** 1971. Mutants of *Salmonella typhimurium* with an altered leucyl-transfer ribonucleic acid synthetase. *J. Bacteriol.* **106**:213–220.
 22. **Aliabadi, Z., Y. K. Park, J. L. Slonczewski, and J. W. Foster.** 1988. Novel regulatory loci controlling oxygen- and pH-regulated gene expression in *Salmonella typhimurium*. *J. Bacteriol.* **170**:842–851.
 23. **Aliabadi, Z., F. Warren, S. Mya, and J. W. Foster.** 1986. Oxygen-regulated stimulons of *Salmonella typhimurium* identified by Mu d (*APlac*) operon fusions. *J. Bacteriol.* **165**:780–786.
 24. **Alifano, P., M. S. Ciampi, A. G. Nappo, C. B. Bruni, and M. S. Carlomagno.** 1988. *In vivo* analysis of the mechanisms responsible for strong transcriptional polarity in a “sense” mutant within an intercistronic region. *Cell* **55**:351–360.
 25. **Alifano, P., C. Piscitelli, V. Blasi, F. Rivellini, A. G. Nappo, C. B. Bruni, and M. S. Carlomagno.** 1992. Processing of a polycistronic mRNA requires a 5′ cis element and active translation. *Mol. Microbiol.* **6**:787–798.
 26. **Alifano, P., F. Rivellini, D. Limauro, C. B. Bruni, and M. S. Carlomagno.** 1991. A consensus motif common to all Rho-dependent prokaryotic transcription terminators. *Cell* **64**:553–563.
 27. **Allen, J. D., and S. M. Parsons.** 1979. Nitrocellulose filter binding: quantitation of the histidyl-tRNA-ATP phosphoribosyltransferase complex. *Anal. Biochem.* **92**:22–30.
 28. **Allen, S. W., A. Senti-Willis, and S. R. Maloy.** 1993. DNA sequence of the *putA* gene from *Salmonella typhimurium*: a bifunctional membrane-associated dehydrogenase that binds DNA. *Nucleic Acids Res.* **21**:1676.
 29. **Aloj, S., C. B. Bruni, H. Edelhoch, and M. M. Rechler.** 1973. Physical studies comparing a genetically fused enzyme of the histidine operon with its component enzymes. *J. Biol. Chem.* **248**:5880–5886.

30. **Alper, M. D., and B. N. Ames.** 1975. Cyclic 3',5'-adenosine monophosphate phosphodiesterase mutants of *Salmonella typhimurium*. *J. Bacteriol.* **122**:1081–1090.
31. **Alper, M. D., and B. N. Ames.** 1975. Positive selection of mutants with deletions of the *gal-chl* region of the *Salmonella* chromosome as a screening procedure of mutagens that cause deletions. *J. Bacteriol.* **121**:259–266.
32. **Alper, M. D., and B. N. Ames.** 1978. Transport of antibiotics and metabolite analogs by systems under cyclic AMP control: positive selection of *Salmonella typhimurium cya* and *crp* mutants. *J. Bacteriol.* **133**:149–157.
33. **Alpuche Aranda, C. M., J. A. Swanson, W. P. Loomis, and S. I. Miller.** 1992. *Salmonella typhimurium* activates virulence gene transcription within acidified macrophage phagosomes. *Proc. Natl. Acad. Sci. USA* **89**:10079–10083.
34. **Altmeyer, R. M., J. K. McNern, J. C. Bossio, I. Rosenshine, B. B. Finlay, and J. E. Galan.** 1993. Cloning and molecular characterization of a gene involved in *Salmonella* adherence and invasion of cultured epithelial cells. *Mol. Microbiol.* **7**:89–98.
35. **Alvarez-Jacobs, J., M. de la Garza, and M. V. Ortega.** 1986. Biochemical and genetic characterization of L-glutamate transport and utilization in *Salmonella typhimurium* LT-2 mutants. *Biochem. Genet.* **24**:195–205.
36. **Al-Zarban, S., L. Heffernan, J. Nishitani, L. Ransome, and G. Wilcox.** 1984. Positive control of the L-rhamnose genetic system in *Salmonella typhimurium* LT2. *J. Bacteriol.* **158**:603–608.
37. **Ames, B. N., and P. E. Hartman.** 1963. The histidine operon. *Cold Spring Harbor Symp. Quant. Biol.* **24**:349–356.
38. **Ames, B. N., T. H. Tsang, M. Buck, and M. F. Christman.** 1983. The leader mRNA of the histidine attenuator region resembles tRNA^{His}: possible general regulatory implications. *Proc. Natl. Acad. Sci. USA* **80**:5240–5242.
39. **Ames, G. F.** 1973. Resolution of bacterial proteins by polyacrylamide gel electrophoresis on slabs. *J. Biol. Chem.* **249**:634–644.
40. **Ames, G. F., and J. Lever.** 1970. Components of histidine transport: histidine-binding proteins and *hisP* protein. *Proc. Natl. Acad. Sci. USA* **66**:1096–1103.
41. **Ames, G. F., and J. E. Lever.** 1972. The histidine-binding protein J is a component of histidine transport. Identification of its structural gene, *hisJ*. *J. Biol. Chem.* **247**:4309–4316.
42. **Ames, G. F., and J. R. Roth.** 1968. Histidine and aromatic permeases of *Salmonella typhimurium*. *J. Bacteriol.* **96**:1742–1749.
43. **Ames, G. F., and E. N. Spudich.** 1976. Protein-protein interaction in transport: periplasmic histidine-binding protein J interacts with P protein. *Proc. Natl. Acad. Sci. USA* **73**:1877–1881.
44. **Ames, G. F., E. N. Spudich, and H. Nikaido.** 1974. Protein composition of the outer membrane of *Salmonella typhimurium*: effect of lipopolysaccharide mutations. *J. Bacteriol.* **117**:406–416.
45. **Ames, G. F.-L., D. P. Biek, and E. N. Spudich.** 1978. Duplications of histidine transport genes in *Salmonella typhimurium* and their use for the selection of deletion mutants. *J. Bacteriol.* **136**:1094–1108.
46. **Ames, G. F.-L., and K. Nikaido.** 1978. Identification of a membrane protein as a histidine transport component in *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **75**:5447–5451.
47. **Ames, G. F.-L., and K. Nikaido.** 1985. Nitrogen regulation in *Salmonella typhimurium*. Identification of an *ntnC* protein-binding site and definition of a consensus binding sequence. *EMBO J.* **4**:539–547.
48. **Ames, G. F.-L., K. Nikaido, A. Hobson, and B. Malcolm.** 1985. Overproduction of the membrane-bound components on the histidine permease from *Salmonella typhimurium*: identification of the M protein. *Biochimie* **67**:149–154.
49. **Ames, G. F.-L., K. D. Noel, H. Taber, E. N. Spudich, K. Nikaido, J. Afong, and F. Ardeshir.** 1977. Fine-structure map of the histidine transport genes in *Salmonella typhimurium*. *J. Bacteriol.* **129**:1289–1297.
50. **Amsden, A. B., D. K. Small, and R. F. Gomez.** 1977. Complex medium toxicity to some DNA repair deficient strains of *Salmonella typhimurium*. *Can. J. Microbiol.* **23**:1494–1496.

51. **Anderson, K. S., E. W. Miles, and K. A. Johnson.** 1991. Serine modulates substrate channeling in tryptophan synthase. A novel intersubunit triggering mechanism. *J. Biol. Chem.* **266**:8020–8033.
52. **Anderson, P., and J. Roth.** 1981. Spontaneous tandem genetic duplications in *Salmonella typhimurium* arise by unequal recombinations between mRNA (*rrn*) cistrons. *Proc. Natl. Acad. Sci. USA* **78**:3113–3117.
53. **Anderson, R. P., and I. Pastan.** 1973. The cyclic AMP receptor of *Escherichia coli*: immunological studies in extracts of *Escherichia coli* and other organisms. *Biochim. Biophys. Acta* **320**:577–578.
54. **Anderson, R. P., and J. R. Roth.** 1978. Tandem chromosomal duplications in *Salmonella typhimurium*: fusion of histidine genes to novel promoters. *J. Mol. Biol.* **119**:147–166.
55. **Anderson, R. R., R. Menzel, and J. M. Wood.** 1980. Biochemistry and regulation of a second L-proline transport system in *Salmonella typhimurium*. *J. Bacteriol.* **141**:1071–1076.
56. **Andersson, D. I.** 1992. Involvement of the Arc system in redox regulation of the Cob operon in *Salmonella typhimurium*. *Mol. Microbiol.* **6**:1491–1494.
57. **Andersson, D. I., and J. R. Roth.** 1989. Mutations affecting regulation of cobinamide biosynthesis in *Salmonella typhimurium*. *J. Bacteriol.* **171**:6726–6733.
58. **Andreadis, A., and E. R. Rosenthal.** 1992. The nucleotide sequence of *leuB* from *Salmonella typhimurium*. *Biochim. Biophys. Acta* **1129**:228–230.
59. **Andreeva, I. V., and A. A. Kiryushkina.** 1994. Contribution of *Salmonella albona* *uvr-12* gene in the excision repair pathway. *Genetics (USSR)* **9**:177–180.
60. **Andreeva, I. V., A. A. Kiryushkina, and A. M. Amerkhanova.** 1972. Genetic basis of UV-resistance in *Salmonella*. II. *uvrB*-mutants of *Salmonella albona*. *Genetics (USSR)* **8**(11):117–122.
61. **Andreeva, I. V., A. A. Kiryushkina, V. N. Pokrovsky, and A. G. Skavronskaya.** 1972. Genetic basis for UV-resistance in *Salmonella*. I. Location of *uvrA* gene on *Salmonella typhimurium* chromosome. *Genetics (USSR)* **8**(4):117–122.
62. **Anton, D. N.** 1968. Histidine regulatory mutants in *Salmonella typhimurium*. V. Two new classes of histidine regulatory mutants. *J. Mol. Biol.* **33**:533–546.
63. **Anton, D. N.** 1968. Osmotic-sensitive mutant of *Salmonella typhimurium*. *J. Bacteriol.* **109**:1273–1283.
64. **Anton, D. N.** 1978. Genetic control of defective cell shape and osmotic sensitivity in a mutant *Salmonella typhimurium*. *Mol. Gen. Genet.* **160**:277–286.
65. **Anton, D. N.** 1979. Positive selection of mutants with cell envelope defects of a *Salmonella typhimurium* strain hypersensitive to the products of genes *hisF* and *hisH*. *J. Bacteriol.* **137**:1271–1281.
66. **Anton, D. N.** 1981. *envB* mutations confer UV-sensitivity to *Salmonella typhimurium* and UV-resistance to *Escherichia coli*. *Mol. Gen. Genet.* **181**:150–152.
67. **Anton, D. N.** 1987. Conditional transduction of *Salmonella typhimurium envB* mutations. *J. Bacteriol.* **169**:1767–1771.
68. **Anton, D. N., A. T. de Micheli, and A. M. Palermo.** 1983. Isolation of round-cell mutants of *Salmonella typhimurium*. *Can. J. Microbiol.* **29**:170–173.
69. **Anton, D. N., and L. V. Orce.** 1976. Envelope mutation promoting autolysis in *Salmonella typhimurium*. *Mol. Gen. Genet.* **144**:97–105.
70. **Antonucci, T. K., and D. L. Oxender.** 1986. The molecular biology of amino-acid transport in bacteria. *Adv. Microb. Physiol.* **28**:145–180.
71. **Archer, C. D., X. Wang, and T. Elliott.** 1994. Mutants defective in the energy-conserving NADH dehydrogenase of *Salmonella typhimurium* identified by a decrease in energy-dependent proteolysis after carbon starvation. *Proc. Natl. Acad. Sci. USA* **90**:9877–9881.
72. **Archibald, E. R., and L. S. Williams.** 1973. Regulation of methionyl-transfer ribonucleic acid synthetase formation in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **114**:1007–1013.
73. **Ardeshir, F., and G. F.-L. Ames.** 1980. Cloning of the histidine transport genes from *Salmonella typhimurium* and characterization of an analogous transport system in *Escherichia coli*. *J. Supramol. Struct.* **13**:117–130.

74. **Ardeshir, F., C. F. Higgins, and G. F.-L. Ames.** 1981. Physical map of the *Salmonella typhimurium* histidine transport operon: correlation with the genetic map. *J. Bacteriol.* **147**:401–409.
75. **Arfin, S. M., T. Miner, and G. W. Hatfield.** 1974. Synthesis of branched-chain aminoacyl-transfer ribonucleic acid synthetases in a *Salmonella typhimurium* mutant with an altered biosynthetic L-threonine deaminase. *J. Bacteriol.* **120**:604–607.
76. **Armstrong, F. B., C. J. R. Hedgecock, J. B. Reary, D. Whitehouse, and C. H. G. Crout.** 1974. Stereochemistry of the reductoisomerase and α,β -dihydroxyacid dehydratase-catalysed steps in valine and isoleucine biosynthesis. *J. Chem. Soc. Chem. Commun.* **9**:351–352.
77. **Armstrong, F. B., and H. Ishiwa.** 1971. Isoleucine-valine mutants of *Salmonella typhimurium*. *Genetics* **67**:171–182.
78. **Armstrong, F. B., U. S. Muller, J. B. Reary, D. Whitehouse, and D. H. G. Crout.** 1977. Stereoselectivity and stereospecificity of the α,β -dihydroxyacid dehydratase from *Salmonella typhimurium*. *Biochim. Biophys. Acta* **498**:282–293.
79. **Armstrong, F. B., and R. P. Wagner.** 1964. Isoleucine-valine requiring mutants of *Salmonella typhimurium*. *Genetics* **50**:957–965.
80. **Artymiuk, P. J., D. W. Rice, E. M. Mitchell, and P. Willett.** 1990. Structural resemblance between the families of bacterial signal-transduction proteins and of G proteins revealed by graph theoretical techniques. *Protein Eng.* **4**:39–43.
81. **Artz, S., D. Holzschu, P. Blum, and R. Shand.** 1983. Use of M13mp phages to study gene regulation, structure and function: cloning and recombinational analysis of genes of the *Salmonella typhimurium* histidine operon. *Gene* **26**:147–158.
82. **Artz, S. W., and J. R. Broach.** 1975. Histidine regulation in *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **72**:3453–3457.
83. **Ashton, D. M., G. D. Sweet, J. M. Somers, and W. W. Kay.** 1980. Citrate transport in *Salmonella typhimurium*: studies with 2-fluoro-L-erythro-citrate as a substrate. *Can. J. Biochem.* **58**:797–803.
84. **Aswad, D., and D. E. Koshland, Jr.** 1974. Role of methionine in bacterial chemotaxis. *J. Bacteriol.* **118**:640–645.
85. **Aswad, D., and D. E. Koshland, Jr.** 1975. Isolation, characterization and complementation of *Salmonella typhimurium* chemotaxis mutants. *J. Mol. Biol.* **97**:225–235.
86. **Aswad, D. W., and D. E. Koshland, Jr.** 1975. Evidence for an S-adenosylmethionine requirement in the chemotactic behavior of *Salmonella typhimurium*. *J. Mol. Biol.* **97**:207–223.
87. **Atkins, J. F., and S. Ryce.** 1974. UGA and non-triplet suppressor reading of the genetic code. *Nature (London)* **249**:527–530.
88. **Aulin, M. R., and D. Hughes.** 1990. Overproduction of release factor reduces spontaneous frameshifting and frameshift suppression by mutant elongation factor Tu. *J. Bacteriol.* **172**:6721–6726.
89. **Ayling, P. D.** 1981. Methionine sulfoxide is transported by high-affinity methionine and glutamine transport systems in *Salmonella typhimurium*. *J. Bacteriol.* **148**:514–520.
90. **Ayling, P. D., and E. S. Bridgeland.** 1970. Methionine transport systems in *Salmonella typhimurium*. *Heredity* **25**:687–688.
91. **Ayling, P. D., and E. S. Bridgeland.** 1972. Methionine transport in wild-type and transport-defective mutants of *Salmonella typhimurium*. *J. Gen. Microbiol.* **73**:127–141.
92. **Ayling, P. D., and K. F. Chater.** 1968. The sequence of four structural and two regulatory methionine genes in the *Salmonella typhimurium* map. *Genet. Res.* **12**:341–354.
93. **Ayling, P. D., T. Mojica-a, and T. Klopotoski.** 1979. Methionine transport in *Salmonella typhimurium*: evidence for at least one low-affinity transport system. *J. Gen. Microbiol.* **114**:227–246.
94. **Backhaus, H., and H. Schmieger.** 1979. Bacterial DNA synthesized under phage control in a DNA defective *Salmonella* mutant and packaged into a special fraction of transducing particles of phage P-22. *Mol. Gen. Genet.* **171**:301–306.
95. **Backhaus, H., and H. Schmieger.** 1979. Replication and maturation of phage P-22 in a mutant of *Salmonella typhimurium* temperature sensitive in initiation of DNA replication. *Mol. Gen. Genet.*

- 171:295–300.
96. **Baer, M., and S. Altman.** 1985. A catalytic RNA and its gene from *Salmonella typhimurium*. *Science* **228**:999–1002.
 97. **Bagdasarian, M., M. Hryniewicz, M. Zdzienicka, and M. Bagdasarian.** 1975. Integrative suppression of a *dnaA* mutation in *Salmonella typhimurium*. *Mol. Gen. Genet.* **139**:213–231.
 98. **Bagdasarian, M., M. Izakowska, and M. Bagdasarian.** 1977. Suppression of the DnaA phenotype by mutations in the *rpoB* cistron of ribonucleic acid polymerase in *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **130**:577–582.
 99. **Bagdasarian, M., M. Zdzienicka, and M. Bagdasarian.** 1972. Temperature sensitive initiation of DNA synthesis in a mutant of *Salmonella typhimurium*. *Mol. Gen. Genet.* **117**:129–142.
 100. **Bagdian, G. B., and P. H. Makela.** 1971. Antigenic conversion by P27. I. Mapping of the prophage attachment site on the *Salmonella* chromosome. *Virology* **43**:403–411.
 101. **Bairoch, A., and B. Boeckmann.** 1994. The SWISS-PROT protein sequence data bank: current status. *Nucleic Acids Res.* **22**:3578–3580.
 102. **Balbinder, E., A. J. Blume, A. Weber, and H. Tamaki.** 1968. Polar and antipolar mutants in the tryptophan operon of *Salmonella typhimurium*. *J. Bacteriol.* **95**:2217–2229.
 103. **Balbinder, E., R. Callahan III, P. P. McCann, C. Cordaro, A. R. Weber, A. M. Smith, and R. Angelosanto.** 1970. Regulatory mutants of the tryptophan operon of *Salmonella typhimurium*. *Genetics* **66**:31–53.
 104. **Bancroft, S., S. G. Rhee, C. Neumann, and S. Kustu.** 1978. Mutations that alter the covalent modification of glutamine synthetase in *Salmonella typhimurium*. *J. Bacteriol.* **134**:1046–1055.
 105. **Bansal, A., M. A. Dayton, H. Zalkin, and R. F. Colman.** 1989. Affinity labeling of a glutamyl peptide in the coenzyme binding site of NADP⁺-specific glutamate dehydrogenase of *Salmonella typhimurium* by 2-[(4-bromo-2,3-dioxobutyl)thio]-1,N6-ethenoadenosine 2',5'-bisphosphate. *J. Biol. Chem.* **264**:9827–9835.
 106. **Baptist, E. W., S. G. Hallquist, and N. M. Kredich.** 1982. Identification of the *Salmonella typhimurium* *cysB* gene product by two-dimensional protein electrophoresis. *J. Bacteriol.* **151**:495–499.
 107. **Baptist, E. W., and N. M. Kredich.** 1977. Regulation of L-cystine transport in *Salmonella typhimurium*. *J. Bacteriol.* **131**:111–118.
 108. **Barbe, J., A. Villaverde, and R. Guerrero.** 1983. Indirect induction of SOS functions in *Salmonella typhimurium*. *Antonie Van Leeuwenhoek J. Microbiol. Serol.* **49**:471–484.
 109. **Barcak, G. J., and R. E. Wolf, Jr.** 1988. Comparative nucleotide sequence analysis of growth-rate-regulated *gnd* alleles from natural isolates of *Escherichia coli* and from *Salmonella typhimurium* LT-2. *J. Bacteriol.* **170**:372–379.
 110. **Barker, R. M., and A. A. Yousuf.** 1985. Clonal relationships among naturally occurring nicotinamide-requiring *Salmonella typhimurium*. *Genet. Res.* **46**:241–250.
 111. **Barnes, W. M.** 1978. DNA sequence from the histidine operon control region: seven histidine codons in a row. *Proc. Natl. Acad. Sci. USA* **75**:4281–4285.
 112. **Barnes, W. M.** 1978. DNA sequencing by partial ribo substitution. *J. Mol. Biol.* **119**:83–100.
 113. **Barnes, W. M.** 1979. Construction of an M-13 histidine transducing phage: a single stranded cloning vehicle with one *EcoRI* site. *Gene* **5**:127–140.
 114. **Barnes, W. M.** 1980. DNA cloning with single-stranded phage vectors, p. 185–200. In J. K. Setlow and A. Hollaender (ed.), *Genetic Engineering*, vol. 2. Plenum Publishing Corp., New York.
 115. **Barnes, W. M.** 1981. Cloning and restriction map of the first part of the histidine operon of *Salmonella typhimurium*. *J. Bacteriol.* **147**:124–134.
 116. **Barnes, W. M., and E. Tuley.** 1983. DNA sequence changes of mutations in the histidine operon control region that decrease attenuation. *J. Mol. Biol.* **165**:443–459.
 117. **Barrett, E. L., and G. W. Chang.** 1979. Cysteine auxotrophs of *Salmonella typhimurium* which grow without cysteine in a hydrogen/carbon dioxide atmosphere. *J. Gen. Microbiol.* **115**:513–516.
 118. **Barrett, E. L., C. E. Jackson, H. T. Fukumoto, and G. W. Chang.** 1979. Formate dehydrogenase mutants of *Salmonella typhimurium*: a new medium for their isolation and new mutant

- classes. *Mol. Gen. Genet.* **177**:95–101.
119. **Barrett, E. L., H. S. Kwan, and J. Macy.** 1984. Anaerobiosis, formate, nitrate, and *pyrA* are involved in the regulation of formate hydrogenlyase in *Salmonella typhimurium*. *J. Bacteriol.* **158**:972–977.
 120. **Barrett, E. L., and D. L. Riggs.** 1982. *Salmonella typhimurium* mutants defective in the formate dehydrogenase linked to nitrate reductase. *J. Bacteriol.* **149**:554–560.
 121. **Barrett, E. L., and D. L. Riggs.** 1982. Evidence for a second nitrate reductase activity that is distinct from the respiratory enzyme in *Salmonella typhimurium*. *J. Bacteriol.* **150**:563–571.
 122. **Bar-Tana, J., D. J. Howlett, and R. Hertz.** 1980. Ubiquinone synthetic pathway in flagellation in *Salmonella typhimurium*. *J. Bacteriol.* **143**:637–643.
 123. **Bastin, D. A., G. Stevenson, P. K. Brown, A. Haase, and P. R. Reeves.** 1993. Repeat unit polysaccharides of bacteria: a model for polymerization resembling that of ribosomes and fatty acid synthetase, with a novel mechanism for determining chain length. *Mol. Microbiol.* **7**:725–734.
 124. **Batchelor, R. A., P. Alifano, E. Biffali, S. I. Hull, and R. A. Hull.** 1992. Nucleotide sequences of the genes regulating O-polysaccharide antigen chain length (*rol*) from *Escherichia coli* and *Salmonella typhimurium*: protein homology and functional complementation. *J. Bacteriol.* **174**:5228–5236.
 125. **Bauer, K., R. Benz, J. Brass, and W. Boos.** 1985. *Salmonella typhimurium* contains an anion-selective outer membrane porin induced by phosphate starvation. *J. Bacteriol.* **161**:813–816.
 126. **Bauerle, R., J. Hess, and S. French.** 1987. Anthranilate synthase-anthranilate phosphoribosyltransferase complex and subunits of *Salmonella typhimurium*. *Methods Enzymol.* **142**:366–386.
 127. **Bauerle, R. H., and P. Margolin.** 1966. The functional organization of the tryptophan gene cluster in *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **56**:111–118.
 128. **Bauerle, R. H., and P. Margolin.** 1966. A multifunctional enzyme complex in the tryptophan pathway of *Salmonella typhimurium*: comparison of polarity and pseudopolarity mutations. *Cold Spring Harbor Symp. Quant. Biol.* **31**:203–214.
 129. **Baumler, A. J., J. G. Kusters, I. Stojiljkovic, and F. Heffron.** 1994. *Salmonella typhimurium* loci involved in survival within macrophages. *Infect. Immun.* **62**:1623–1630.
 130. **Beacham, I. R., A. Eisenstark, P. T. Barth, and R. H. Pritchard.** 1968. Deoxynucleoside-sensitive mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **102**:112–127.
 131. **Beacham, I. R., and S. Garrett.** 1981. Transfer of RP4::Mu to *Salmonella typhimurium*. *J. Gen. Microbiol.* **124**:255–228.
 132. **Beck, C. F., A. R. Eisenshardt, and J. Neuhard.** 1975. Deoxycytidine triphosphate deaminase of *Salmonella typhimurium*. *J. Biol. Chem.* **250**:609–616.
 133. **Beck, C. F., and J. L. Ingraham.** 1971. Location on the chromosome of *Salmonella typhimurium* of genes governing pyrimidine metabolism. *Mol. Gen. Genet.* **111**:303–316.
 134. **Beck, C. F., J. L. Ingraham, and J. Neuhard.** 1972. Location on the chromosome of *Salmonella typhimurium* of genes governing pyrimidine metabolism. II. Uridine kinase, cytosine deaminase, and thymidine kinase. *Mol. Gen. Genet.* **115**:208–215.
 135. **Beck, C. F., J. Neuhard, and E. Thomassen.** 1977. Thymidine-requiring mutants of *Salmonella typhimurium* that are defective in deoxyuridine 5'-phosphate synthesis. *J. Bacteriol.* **129**:305–316.
 136. **Beck, C. F., J. Neuhard, E. Thomassen, J. L. Ingraham, and E. Kleker.** 1974. *Salmonella typhimurium* mutants defective in cytidine monophosphate kinase (*cmk*). *J. Bacteriol.* **120**:1370–1379.
 137. **Becker, M. A., N. M. Kredich, and G. Tomkins.** 1969. The purification and characterization of O-acetylserine sulfhydrylase-A from *Salmonella typhimurium*. *J. Biol. Chem.* **244**:2418–2427.
 138. **Beckmann, I., T. B. Subbaiah, and B. A. D. Stocker.** 1964. Rough mutants of *Salmonella typhimurium*. II. Serological and chemical investigations. *Nature (London)* **201**:1299–1301.
 139. **Beckwith, J. R., A. B. Pardee, R. Austrian, and F. Jacob.** 1962. Coordination of the synthesis of the enzymes in the pyrimidine pathway of *Escherichia coli*. *J. Mol. Biol.* **5**:618–634.
 140. **Behlau, I., and S. I. Miller.** 1993. A PhoP-repressed gene promotes *Salmonella typhimurium*

- invasion of epithelial cells. *J. Bacteriol.* **175**:4475–4484.
141. **Benamira, M., U. Singh, and L. J. Marnett.** 1992. Site-specific frameshift mutagenesis by a propanodeoxyguanosine adduct positioned in the (CpG)₄ hot-spot of *Salmonella typhimurium* *hisD3052* carried on an M13 vector. *J. Biol. Chem.* **267**:22392–22400.
 142. **Beneski, D. A., A. Nakazawa, N. Weigel, P. E. Hartman, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Isolation and characterization of a phosphocarrier protein HPr from wild type and mutants of *Salmonella typhimurium*. *J. Biol. Chem.* **257**:14492–14498.
 143. **Benjamin, W. H., Jr., P. Hall, and D. E. Briles.** 1991. A *hemA* mutation renders *Salmonella typhimurium* avirulent in mice, yet capable of eliciting protection against intravenous infection with *S. typhimurium*. *Microb. Pathog.* **11**:289–295.
 144. **Benjamin, W. H., Jr., J. Yother, P. Hall, and D. E. Briles.** 1991. The *Salmonella typhimurium* locus *mviA* regulates virulence in Itys but not Ityr mice: functional *mviA* results in avirulence; mutant (nonfunctional) *mviA* results in virulence. *J. Exp. Med.* **174**:1073–1083.
 145. **Benner-Luger, D., and W. Boos.** 1988. The *mglB* sequence of *Salmonella typhimurium* LT2; promoter analysis by gene fusions and evidence for a divergently oriented gene coding for the *mgl* repressor. *Mol. Gen. Genet.* **214**:579–587.
 146. **Bennett, R. L., and L. I. Rothfield.** 1976. Genetic and physiological regulation of intrinsic proteins of the outer membrane of *Salmonella typhimurium*. *J. Bacteriol.* **127**:498–504.
 147. **Benson, C. E., and J. S. Gots.** 1975. Genetic modification of substrate specificity of hypoxanthine phosphoribosyltransferase in *Salmonella typhimurium*. *J. Bacteriol.* **121**:77–82.
 148. **Benson, C. E., and J. S. Gots.** 1975. Regulation of GMP reductase in *Salmonella typhimurium*. *Biochim. Biophys. Acta* **403**:47–57.
 149. **Benson, C. E., and J. S. Gots.** 1976. Occurrence of a regulatory deficiency of purine biosynthesis among *purA* mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **145**:31–36.
 150. **Benson, C. E., D. L. Hornick, and J. S. Gots.** 1980. Genetic separation of purine transport from phosphoribosyltransferase activity in *Salmonella typhimurium*. *J. Gen. Microbiol.* **121**:357–364.
 151. **Benson, N., and J. R. Roth.** 1994. Suppressors of *recB* mutations in *Salmonella typhimurium*. *Genetics* **138**:11–28.
 152. **Benson, N., P. Sugiono, S. Bass, L. V. Mendelman, and P. Youderian.** 1986. General selection for specific DNA-binding activities. *Genetics* **114**:1–14.
 153. **Benzinger, R., and I. Kleber.** 1971. Transfection of *Escherichia coli* and *Salmonella typhimurium* spheroplasts: host-controlled restriction of infective bacteriophage P22 deoxyribonucleic acid. *J. Virol.* **8**:197–202.
 154. **Berg, C. M., and J. J. Rossi.** 1974. Proline excretion and indirect suppression in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **118**:928–939.
 155. **Berg, C. M., and K. J. Shaw.** 1981. Organization and regulation of the *ilvGEDA* operon in *Salmonella typhimurium*. *J. Bacteriol.* **145**:984–989.
 156. **Berg, C. M., K. J. Shaw, L. Sarokin, and D. E. Berg.** 1981. Probing the organization and regulation of bacterial operons with transposons, p. 121–123. In D. Schlessinger (ed.), *Microbiology—1981*. American Society for Microbiology, Washington, D.C.
 157. **Berg, C. M., W. A. Whalen, and L. B. Archambault.** 1983. Role of alanine-valine transaminase in *Salmonella typhimurium* and analysis of an *avtA::Tn5* mutant. *J. Bacteriol.* **155**:1009–1014.
 158. **Bergstrom, S., F. P. Lindberg, O. Olsson, and S. Normark.** 1983. Comparison of the overlapping *frd* and *ampC* operons of *Escherichia coli* with the corresponding DNA sequences in other gram-negative bacteria. *J. Bacteriol.* **155**:1297–1305.
 159. **Berkowitz, D.** 1971. D-Mannitol utilization in *Salmonella typhimurium*. *J. Bacteriol.* **105**:232–240.
 160. **Berst, M., C. G. Hellerqvist, B. Lindberg, O. Luderitz, S. Svensson, and O. Westphal.** 1969. Structural investigations on T1 lipopolysaccharides. *Eur. J. Biochem.* **11**:353–359.
 161. **Best, E. A., and R. A. Bender.** 1990. Cloning of the *Klebsiella aerogenes nac* gene, which encodes a factor required for nitrogen regulation of the histidine utilization (*hut*) operons in

- Salmonella typhimurium*. *J. Bacteriol.* **172**:7043–7048.
162. **Betteridge, P. R., and P. D. Ayling.** 1975. The role of methionine transport-defective mutations in resistance to methionine sulfoximine in *Salmonella typhimurium*. *Mol. Gen. Genet.* **138**:41–52.
 163. **Betteridge, P. R., and P. D. Ayling.** 1976. The regulation of glutamine transport and glutamine synthetase in *Salmonella typhimurium*. *J. Gen. Microbiol.* **95**:324–334.
 164. **Beyer, W., and L. Geue.** 1992. Characterization of the virulence regions in the plasmids of three live *Salmonella* vaccines. *Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis.* **277**:10–21.
 165. **Bhaduri, S., T. Kasai, D. Schlessinger, and H. J. Raskas.** 1980. pMB-9 plasmids bearing the *Salmonella typhimurium* *his* operon and *gnd* gene. *Gene* **8**:239–254.
 166. **Bhatia, M. B., A. Vinitsky, and C. Grubmeyer.** 1990. Kinetic mechanism of orotate phosphoribosyltransferase from *Salmonella typhimurium*. *Biochemistry* **29**:10480–10487.
 167. **Bhattacharya, A. K., and M. Chakravorty.** 1971. Induction and repression of L-arabinose isomerase in *Salmonella typhimurium*. *J. Bacteriol.* **106**:107–112.
 168. **Bhattacharya, A. K., and M. Chakravorty.** 1974. Effect of antibiotics and antimetabolites on the induction of L-arabinose isomerase in *Salmonella typhimurium*. *Curr. Sci.* **43**:499–503.
 169. **Bhattacharya, A. K., and M. Chakravorty.** 1975. Isolation and characterization of an L-arabinose negative mutant of *Salmonella typhimurium*. *Indian J. Exp. Biol.* **13**:244–246.
 170. **Bisercic, M., and H. Ochman.** 1993. Natural populations of *Escherichia coli* and *Salmonella typhimurium* harbor the same classes of insertion sequences. *Genetics* **133**:449–454.
 171. **Bitar, K. G., F. R. Firca, and J. C. Loper.** 1977. Histidinol dehydrogenase from *Salmonella typhimurium* and *Escherichia coli*. *Biochim. Biophys. Acta* **493**:429–440.
 172. **Bjork, G. R., P. M. Wikstrom, and A. S. Bystrom.** 1989. Prevention of translational frameshifting by the modified nucleoside 1-methylguanosine. *Science* **244**:986–989.
 173. **Blanc-Potard, A.-B., and L. Bossi.** 1994. Phenotypic suppression of DNA gyrase deficiencies by a deletion lowering the gene dosage of a major tRNA in *Salmonella typhimurium*. *J. Bacteriol.* **176**:2216–2226.
 174. **Blank, J., and P. Hoffee.** 1972. Regulatory mutants of the *deo* regulon in *Salmonella typhimurium*. *Mol. Gen. Genet.* **116**:291–298.
 175. **Blank, J. G., and P. A. Hoffee.** 1975. Purification and properties of thymidine phosphorylase from *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **168**:259–265.
 176. **Blasi, F., S. M. Aloj, and R. F. Goldberger.** 1971. Effect of histidine on the enzyme which catalyzes the first step of histidine biosynthesis in *Salmonella typhimurium*. *Biochemistry* **10**:1409–1417.
 177. **Blasi, F., R. W. Barton, J. S. Kovach, and R. F. Goldberger.** 1971. Interaction between the first enzyme for histidine biosynthesis and histidyl transfer ribonucleic acid. *J. Bacteriol.* **106**:508–513.
 178. **Blasi, F., and C. B. Bruni.** 1981. Regulation of the histidine operon: translation-controlled transcription termination (a mechanism common to several biosynthetic operons). *Curr. Top. Cell. Regul.* **19**:1–45.
 179. **Blasi, F., C. B. Bruni, A. Avitabile, R. G. Deeley, R. F. Goldberger, and M. M. Meyers.** 1973. Inhibition of transcription of the histidine operon *in vitro* by the first enzyme of the histidine pathway. *Proc. Natl. Acad. Sci. USA* **70**:2692–2696.
 180. **Blatt, J. M., and H. E. Umbarger.** 1972. On the role of isoleucyl-tRNA synthetase in multivalent repression. *Biochem. Genet.* **6**:99–118.
 181. **Blattner, F. R., V. Burland, G. Plunkett, H. J. Sofia, and D. L. Daniels.** 1993. Analysis of the *Escherichia coli* genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes. *Nucleic Acids Res.* **21**:5408–5417.
 182. **Blazey, D. L., and R. O. Burns.** 1979. Genetic organization of the *Salmonella typhimurium* *ilv* gene cluster. *Mol. Gen. Genet.* **177**:1–11.
 183. **Blazey, D. L., and R. O. Burns.** 1980. Gene *ilvY* of *Salmonella typhimurium*. *J. Bacteriol.* **142**:1015–1018.
 184. **Blazey, D. L., and R. O. Burns.** 1982. Transcriptional activity of the transposable element Tn10 in the *Salmonella typhimurium* *ilvGEDA* operon. *Proc. Natl. Acad. Sci. USA* **79**:5011–5015.

185. **Blazey, D. L., and R. O. Burns.** 1984. Regulation of *Salmonella typhimurium* *ilvYC* genes. *J. Bacteriol.* **159**:951–957.
186. **Blazey, D. L., R. Kim, and R. O. Burns.** 1981. Molecular cloning and expression of the *ilvGEDAY* genes from *Salmonella typhimurium*. *J. Bacteriol.* **147**:452–462.
187. **Blum, P., L. Blaha, and S. Artz.** 1986. Reversion and immobilization of phage Mud1 cts (Ap^f *lac*) insertion mutations in *Salmonella typhimurium*. *Mol. Gen. Genet.* **202**:327–330.
188. **Blum, P., D. Holzschu, H. S. Kwan, D. Riggs, and S. Artz.** 1989. Gene replacement and retrieval with recombinant M13mp bacteriophages. *J. Bacteriol.* **171**:538–546.
189. **Blum, P. H.** 1988. Reduced *leu* operon expression in a *miaA* mutant of *Salmonella typhimurium*. *J. Bacteriol.* **170**:5125–5133.
190. **Blume, A. J., and E. Balbinder.** 1966. The tryptophan operon of *Salmonella typhimurium*. Fine structure analysis by deletion mapping and abortive transduction. *Genetics* **53**:577–592.
191. **Blume, A. J., A. Weber, and E. Balbinder.** 1968. Analysis of polar and nonpolar tryptophan mutants by depression kinetics. *J. Bacteriol.* **95**:2230–2241.
192. **Blumenberg, M., and B. Magasanik.** 1979. A study in evolution: the histidine utilization genes of enteric bacteria. *J. Mol. Biol.* **135**:23–38.
193. **Blumenberg, M., and B. Magasanik.** 1981. Physical maps of *Klebsiella aerogenes* and *Salmonella typhimurium* *hut* genes. *J. Bacteriol.* **145**:664–667.
194. **Bobik, T. A., M. Ailion, and J. R. Roth.** 1992. A single regulatory gene integrates control of vitamin B¹² synthesis and propanediol degradation. *J. Bacteriol.* **174**:2253–2266.
195. **Bochner, B. R., and M. A. Savageau.** 1979. Inhibition of growth by imidazol(on)e propionic acid. Evidence *in-vivo* for coordination of histidine catabolism with the catabolism of other amino acids. *Mol. Gen. Genet.* **168**:87–96.
196. **Borczuk, A., A. Staub, and J. Stock.** 1986. Demethylation of bacterial chemoreceptors is inhibited by attractant stimuli in the complete absence of the regulatory domain of the demethylating enzyme. *Biochem. Biophys. Res. Commun.* **141**:918–923.
197. **Borczuk, A., A. Stock, and J. Stock.** 1987. *S*-Adenosylmethionine may not be essential for signal transduction during bacterial chemotaxis. *J. Bacteriol.* **169**:3295–3300.
198. **Borodovsky, M., E. V. Koonin, and K. E. Rudd.** 1994. New genes in old sequence: a strategy for finding genes in the bacterial genome. *Trends Biochem. Sci.* **19**:309–313.
199. **Borum, P. R., and K. J. Monty.** 1976. Regulatory mutants and control of cysteine biosynthetic enzymes in *Salmonella typhimurium*. *J. Bacteriol.* **125**:94–101.
200. **Bossi, L.** 1983. Context effects: translation of UAG codon by suppressor tRNA is affected by the sequence following UAG in the message. *J. Mol. Biol.* **164**:73–87.
201. **Bossi, L.** 1983. The *hisR* locus of *Salmonella*: nucleotide sequence and expression. *Mol. Gen. Genet.* **192**:163–170.
202. **Bossi, L., and M. S. Ciampi.** 1981. DNA sequences at the sites of three insertions of the transposable element Tn5 in the histidine operon of *Salmonella*. *Mol. Gen. Genet.* **183**:406–408.
203. **Bossi, L., M. S. Ciampi, and R. Cortese.** 1978. Characterization of a *Salmonella typhimurium* *hisU* mutant defective in tRNA precursor processing. *J. Bacteriol.* **134**:612–620.
204. **Bossi, L., and R. Cortese.** 1977. Biosynthesis of tRNA in histidine regulatory mutants of *Salmonella typhimurium*. *Nucleic Acids Res.* **4**:1945–1956.
205. **Bossi, L., T. Kohno, and J. R. Roth.** 1982. Genetic characterization of the *sufJ* suppressor in *Salmonella typhimurium*. *Genetics* **103**:31–42.
206. **Bossi, L., and J. R. Roth.** 1980. The influence of codon context on genetic code translation. *Nature (London)* **286**:123–127.
207. **Bossi, L., and D. M. Smith.** 1984. Suppressor *sufJ*: a novel type of tRNA mutant that induces translational frameshifting. *Proc. Natl. Acad. Sci. USA* **81**:6105–6109.
208. **Bossi, L., and D. M. Smith.** 1984. Conformational change in the DNA associated with an unusual promoter mutation in a tRNA operon of *Salmonella*. *Cell* **39**:643–652.
209. **Bossi, M., and J. R. Roth.** 1981. Four-base codons ACCA, ACCU, and ACCC are recognized by frameshift suppressor *sufJ*. *Cell* **25**:489–496.

210. **Botsford, J. L.** 1984. Cyclic AMP phosphodiesterase in *Salmonella typhimurium*: characteristics and physiological function. *J. Bacteriol.* **160**:826–830.
211. **Boudadloun, F., T. Srichaiyo, L. A. Isaksson, and G. R. Bjork.** 1986. Influence of modification next to the anticodon in tRNA on codon context sensitivity of translational suppression and accuracy. *J. Bacteriol.* **166**:1022–1027.
212. **Bouma, C. L., N. D. Meadow, E. W. Stover, and S. Roseman.** 1987. II-B^{Glc}, a glucose receptor of the bacterial phosphotransferase system: molecular cloning of *ptsG* and purification of the receptor from an overproducing strain of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **84**:930–934.
213. **Bower, S. G., B. Hove-Jensen, and R. L. Switzer.** 1988. Structure of the gene encoding phosphoribosylpyrophosphate synthetase (*prsA*) in *Salmonella typhimurium*. *J. Bacteriol.* **170**:3243–3248.
214. **Boyd, D. H., L. M. Porter, B. S. Young, and A. Wright.** 1979. The *in-vitro* detection of defects in temperature sensitive RNA polymerases from mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **173**:279–288.
215. **Brade, H., H. Moll, and E. T. Rietschel.** 1985. Structural investigations on the inner core region of lipopolysaccharides from *Salmonella minnesota* rough mutants. *Biomed. Mass. Spectrom.* **12**:602–609.
216. **Brade, L., F. E. Nano, S. Schlecht, S. Schramek, and H. Brade.** 1987. Antigenic and immunogenic properties of recombinants from *Salmonella typhimurium* and *Salmonella minnesota* rough mutants expressing in their lipopolysaccharide a genus-specific chlamydial epitope. *Infect. Immun.* **55**:482–486.
217. **Brady, D. R., and L. L. Houston.** 1973. Some properties of the catalytic sites of imidazoleglycerol phosphate dehydratase-histidinol phosphate phosphatase, a bifunctional enzyme from *Salmonella typhimurium*. *J. Biol. Chem.* **248**:2588–2592.
218. **Brady, R. A., and L. N. Csonka.** 1988. Transcriptional regulation of the *proC* gene of *Salmonella typhimurium*. *J. Bacteriol.* **170**:2379–2382.
219. **Brahmbhatt, H. N., N. B. Quigley, and P. R. Reeves.** 1986. Cloning part of the region encoding biosynthetic enzymes for surface antigen (O-antigen) of *Salmonella typhimurium*. *Mol. Gen. Genet.* **203**:172–176.
220. **Brahmbhatt, H. N., P. Wyk, N. B. Quigley, and P. R. Reeves.** 1988. Complete physical map of the *rfb* gene cluster encoding biosynthetic enzymes for the O antigen of *Salmonella typhimurium* LT2. *J. Bacteriol.* **170**:98–102.
221. **Bramley, H. F., and H. L. Kornberg.** 1987. Sequence homologies between proteins of bacterial phosphoenolpyruvate-dependent sugar phosphotransferase systems: identification of possible phosphate-carrying histidine residues. *Proc. Natl. Acad. Sci. USA* **84**:4777–4780.
222. **Brana, H., and J. Hubacek.** 1977. Virulence of *Salmonella typhimurium* infected with the R plasmid and relation with the *rec* mutation. *Folia Microbiol.* **22**:451.
223. **Branes, L. V., and W. W. Kay.** 1983. Lipopolysaccharide core mutants of *Salmonella typhimurium* containing D-glycero-D-manno-heptose. *J. Bacteriol.* **154**:1462–1466.
224. **Branes, L. V., J. M. Somers, and W. W. Kay.** 1981. Hydrophobic peptide auxotrophy in *Salmonella typhimurium*. *J. Bacteriol.* **147**:986–996.
225. **Brashear, W. T., and S. M. Parsons.** 1975. Evidence against a covalent intermediate in the adenosine triphosphate phosphoribosyltransferase reaction of histidine biosynthesis. *J. Biol. Chem.* **250**:6885–6890.
226. **Braun, V., K. Gunthner, K. Hantke, and L. Zimmermann.** 1983. Intracellular activation of albomycin in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **156**:308–315.
227. **Braun, V., K. Hantke, and W. Stauder.** 1977. Identification of the *sid* outer membrane protein in *Salmonella typhimurium* strain SL1027. *Mol. Gen. Genet.* **155**:227–230.
228. **Brazas, R., E. Davie, A. Farewell, and L. I. Rothfield.** 1991. Transcriptional organization of the *rfaGBIJ* locus of *Salmonella typhimurium*. *J. Bacteriol.* **173**:6168–6173.
229. **Brenchley, J. E., C. A. Baker, and L. G. Patil.** 1975. Regulation of the ammonia assimilatory enzymes in *Salmonella typhimurium*. *J. Bacteriol.* **124**:182–189.

230. **Brenchley, J. E., D. M. Bedwell, S. M. Dendinger, and J. M. Kuchta.** 1980. Analysis of mutations affecting the regulation of nitrogen utilization in *Salmonella typhimurium*, p. 79–93. In J. Mora and R. Palacios (ed.), *Glutamine: Metabolism, Enzymology and Regulation*. International Symposium on Glutamine: Metabolism, Enzymology and Regulation, Queretaro, Mexico. Academic Press, Inc., New York.
231. **Brenchley, J. E., and J. L. Ingraham.** 1973. Characterization of a cold-sensitive *hisW* mutant of *Salmonella typhimurium*. *J. Bacteriol.* **114**:528–536.
232. **Brenner, M., and B. N. Ames.** 1971. The histidine operon and its regulations, p. 349–387. In H. J. Vogel (ed.), *Metabolic Regulation*, vol. 5 in D. Greenberg (ed.), *Metabolic Pathways*. Academic Press, Inc., New York.
233. **Brenner, M., and B. N. Ames.** 1972. Histidine regulation in *Salmonella typhimurium*. IX. Histidine transfer ribonucleic acid of the regulatory mutants. *J. Biol. Chem.* **247**:1080–1088.
234. **Brenner, M., F. DeLorenzo, and B. N. Ames.** 1970. Energy charge and protein synthesis. Control of aminoacyl transfer ribonucleic acid synthesis. *J. Biol. Chem.* **245**:450–452.
235. **Brenner, M., J. A. Lewis, D. S. Straus, R. DeLorenzo, and B. N. Ames.** 1972. Histidine regulation in *Salmonella typhimurium*. XIV. Interaction of the histidyl transfer ribonucleic acid synthetase with histidine transfer ribonucleic acid. *J. Biol. Chem.* **247**:4333–4339.
236. **Bresalier, R. S., A. A. Rizzino, and M. Freundlich.** 1975. Reduced maximal levels of derepression of the isoleucine-valine and leucine enzymes in *hisT* mutants of *Salmonella typhimurium*. *Nature* (London) **253**:279–280.
237. **Brewer, S., M. Tolley, I. P. Trayer, G. C. Barr, C. J. Dorman, K. Hannavy, C. F. Higgins, J. S. Evans, B. A. Levine, and M. R. Wormald.** 1990. Structure and function of X-Pro dipeptide repeats in the TonB proteins of *Salmonella typhimurium* and *Escherichia coli*. *J. Mol. Biol.* **216**:883–895.
238. **Brill, W. J., and B. Magasanik.** 1969. Genetic and metabolic control of histidase and urocanase in *Salmonella typhimurium*, strain 15–59. *J. Biol. Chem.* **244**:5392–5402.
239. **Broach, J., C. Neumann, and S. Kustu.** 1976. Mutant strains (*nit*) of *Salmonella typhimurium* with a pleiotropic defect in nitrogen metabolism. *J. Bacteriol.* **128**:86–98.
240. **Brok, R. G., E. Brinkman, R. van Boxtel, A. C. Bekkers, H. M. Verheij, and J. Tommassen.** 1994. Molecular characterization of enterobacterial *pldA* genes encoding outer membrane phospholipase A. *J. Bacteriol.* **176**:861–870.
241. **Brown, B. A., S. R. Lax, L. Liang, B. J. Dabney, L. L. Spremulli, and J. M. Ravel.** 1977. Repression of the tyrosine, lysine, and methionine biosynthetic pathways in a *hisT* mutant of *Salmonella typhimurium*. *J. Bacteriol.* **129**:1168–1170.
242. **Brown, D. J., J. E. Olsen, and M. Bisgaard.** 1992. *Salmonella enterica*: infection, cross infection and persistence within the environment of a broiler parent stock unit in Denmark. *Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis.* **277**:129–138.
243. **Bruist, M. F., A. C. Glasgow, R. C. Johnson, and M. I. Simon.** 1987. Fis binding to the recombinational enhancer of the Hin DNA inversion system. *Genes Dev.* **1**:762–772.
244. **Bruist, M. F., and M. I. Simon.** 1984. Phase variation and the Hin protein: in vivo activity measurements, protein overproduction, and purification. *J. Bacteriol.* **159**:71–79.
245. **Bruneteau, M., W. A. Volk, P. P. Singh, and O. Luderitz.** 1974. Structural investigations on the *Salmonella* T2 lipopolysaccharide. *Eur. J. Biochem.* **43**:501–508.
246. **Bruni, C. B., M. S. Carlomagno, S. Formisano, and G. Paoletta.** 1986. Primary and secondary structural homologies between the HIS4 gene product of *Saccharomyces cerevisiae* and the *hisIE* and *hisD* gene products of *Escherichia coli* and *Salmonella typhimurium*. *Mol. Gen. Genet.* **203**:389–396.
247. **Bruni, C. B., R. G. Martin, and M. M. Rechler.** 1972. COOH-terminal amino acid sequence of histidinol dehydrogenase from a *Salmonella typhimurium* mutant. *J. Biol. Chem.* **247**:6671–6678.
248. **Bruni, C. B., M. M. Rechler, and R. G. Martin.** 1973. *Salmonella typhimurium* mutants lacking ribonuclease I: effect on the polarity of histidine mutants. *J. Bacteriol.* **113**:1207–1212.
249. **Brzovic, P. S., A. M. Kayastha, E. W. Miles, and M. F. Dunn.** 1992. Substitution of glutamic acid 109 by aspartic acid alters the substrate specificity and catalytic activity of the beta-subunit in the

- tryptophan synthase holoenzyme complex from *Salmonella typhimurium*. *Biochemistry* **31**:1180–1190.
250. **Buchmeier, N. A., C. J. Lipps, M. Y. So, and F. Heffron.** 1993. Recombination-deficient mutants of *Salmonella typhimurium* are avirulent and sensitive to the oxidative burst of macrophages. *Mol. Microbiol.* **7**:933–936.
251. **Buck, M., and B. N. Ames.** 1984. A modified nucleotide in tRNA as a possible regulator of aerobiosis: synthesis of *cis*-2-methyl-thioribosylzeatin in the tRNA of *Salmonella*. *Cell* **36**:523–531.
252. **Buckenmeyer, G. K., and M. A. Hermodson.** 1983. The amino acid sequence of D-ribose-binding protein from *Salmonella typhimurium* ST1. *J. Biol. Chem.* **258**:12957.
253. **Bullas, L. R., and C. Colson.** 1975. DNA restriction and modification systems in *Salmonella*. *Mol. Gen. Genet.* **139**:177–188.
254. **Bullas, L. R., C. Colson, and B. Neufeld.** 1980. DNA restriction and modification systems in *Salmonella*: chromosomally located systems of different serotypes. *J. Bacteriol.* **141**:275–292.
255. **Bullas, L. R., C. Colson, and A. Van Pel.** 1976. DNA restriction and modification systems in *Salmonella*. IV. SQ, a new system derived by recombination between the SB system of *Salmonella typhimurium* and of *Salmonella potsdam*. *J. Gen. Microbiol.* **95**:166–172.
256. **Bullas, L. R., and J.-I. Ryu.** 1983. *Salmonella typhimurium* LT2 strains which are $r^- m^+$ for all three chromosomally located systems of DNA restriction and modification. *J. Bacteriol.* **156**:471–474.
257. **Burgin, A. B., K. Parodos, D. J. Lane, and N. R. Pace.** 1990. The excision of intervening sequences from *Salmonella* 23S ribosomal RNA. *Cell* **60**:405–414.
258. **Burns, D. M., and I. R. Beacham.** 1985. Rare codons in *E. coli* and *S. typhimurium* signal sequences. *FEBS Lett.* **189**:318–324.
259. **Burns, D. M., and I. R. Beacham.** 1986. Identification and sequence analysis of a silent gene (*ushA*⁰) in *Salmonella typhimurium*. *J. Mol. Biol.* **192**:163–175.
260. **Burns, R. O., J. Calvo, P. Margolin, and H. E. Umbarger.** 1966. Expression of the leucine operon. *J. Bacteriol.* **91**:1570–1576.
261. **Burns, R. O., J. G. Hofler, and G. H. Luginbuhl.** 1979. Threonine deaminase from *Salmonella typhimurium* substrate specific patterns in an activator site deficient form of the enzyme. *J. Biol. Chem.* **254**:1074–1079.
262. **Burns, R. O., H. E. Umbarger, and S. R. Gross.** 1963. The biosynthesis of leucine. III. The conversion of α -hydroxy- β -carboxyisocaproate to α -ketoisocaproate. *Biochemistry* **2**:1053–1058.
263. **Burns, R. O., and M. H. Zarlengo.** 1969. Threonine deaminase from *Salmonella typhimurium*. I. Purification and properties. *J. Biol. Chem.* **243**:178–185.
264. **Bussey, L. B., and J. L. Ingraham.** 1982. A regulatory gene (*use*) affecting the expression of *pyrA* and certain other pyrimidine genes. *J. Bacteriol.* **151**:144–152.
265. **Byerly, K. A., M. L. Urbanowski, and G. V. Stauffer.** 1991. The *metR* binding site in the *Salmonella typhimurium methH* gene: DNA sequence constraints on activation. *J. Bacteriol.* **173**:3547–3553.
266. **Byrne, C. R., R. S. Monroe, K. A. Ward, and N. M. Kredich.** 1988. DNA sequences of the *cysK* regions of *Salmonella typhimurium* and *Escherichia coli* and linkage of the *cysK* regions to *ptsH*. *J. Bacteriol.* **170**:3150–3157.
267. **Cairney, J., I. R. Booth, and C. F. Higgins.** 1985. *Salmonella typhimurium proP* gene encodes a transport system for the osmoprotectant betaine. *J. Bacteriol.* **164**:1218–1223.
268. **Cairney, J., I. R. Booth, and C. F. Higgins.** 1985. Osmoregulation of gene expression in *Salmonella typhimurium*: *proU* encodes an osmotically induced betaine transport system. *J. Bacteriol.* **164**:1224–1232.
269. **Cairney, J., C. F. Higgins, and I. R. Booth.** 1984. Proline uptake through the major transport system of *Salmonella typhimurium* is coupled to sodium ions. *J. Bacteriol.* **160**:22–27.
270. **Caldwell, A. L., and P. A. Gulig.** 1991. The *Salmonella typhimurium* virulence plasmid encodes a positive regulator of a plasmid-encoded virulence gene. *J. Bacteriol.* **173**:7176–7185.
271. **Calero, S., X. Garriga, and J. Barbe.** 1991. One-step cloning system for isolation of bacterial *lexA*-like genes. *J. Bacteriol.* **173**:7345–7350.

272. **Calhoun, D. H., and G. W. Hatfield.** 1973. Autoregulation: a role for a biosynthetic enzyme in the control of gene expression. *Proc. Natl. Acad. Sci. USA* **70**:2757–2761.
273. **Caligiuri, M. G., and R. Bauerle.** 1991. Identification of amino acid residues involved in feedback regulation of the anthranilate synthase complex from *Salmonella typhimurium*. Evidence for an amino-terminal regulatory site. *J. Biol. Chem.* **266**:8328–8335.
274. **Calladine, C. R.** 1975. Construction of bacterial flagella. *Nature (London)* **255**:121–124.
275. **Callahan, R., III, M. M. Dooley, and E. Ballbinder.** 1978. A mutation to 5-methyltryptophan-dependence in the tryptophan (*trp*) operon of *Salmonella typhimurium*. II. Studies of 5-methyltryptophan-dependent mutants and their revertants. *Mol. Gen. Genet.* **165**:129–143.
276. **Calvo, J. M., M. Freundlich, and H. E. Umbarger.** 1969. Regulation of branched-chain amino acid biosynthesis in *Salmonella typhimurium*: isolation of regulatory mutants. *J. Bacteriol.* **97**:1272–1282.
277. **Calvo, J. M., M. Goodman, M. Salgo, and N. Kapes.** 1971. *Salmonella* locus affecting phosphoenolpyruvate synthase activity identified by deletion analysis. *J. Bacteriol.* **106**:286–288.
278. **Calvo, J. M., and H. E. Worden.** 1970. A multisite-mutation map of the leucine operon of *Salmonella typhimurium*. *Genetics* **64**:199–214.
279. **Capobianco, J. O., R. P. Darveau, R. C. Goldman, P. A. Lartey, and A. G. Pernet.** 1987. Inhibition of exogenous 3-deoxy-D-manno-octulosonate incorporation into lipid A precursor of toluene-treated *Salmonella typhimurium*. *J. Bacteriol.* **169**:4030–4035.
280. **Carlomagno, M. S., F. Blasi, and C. B. Bruni.** 1983. Gene organization in the distal part of the *Salmonella typhimurium* histidine operon and determination and sequence of the operon transcription terminator. *Mol. Gen. Genet.* **191**:413–420.
281. **Carlomagno, M. S., L. Chiariotti, P. Alifano, A. G. Nappo, and C. B. Bruni.** 1988. Structure and function of the *Salmonella typhimurium* and *Escherichia coli* K-12 histidine operons. *J. Mol. Biol.* **203**:585–606.
282. **Carlomagno, M. S., A. Riccio, and C. B. Bruni.** 1985. Convergently functional, rho-independent terminator in *Salmonella typhimurium*. *J. Bacteriol.* **163**:362–368.
283. **Carrillo-Castaneda, G., and M. V. Ortega.** 1970. Mutants of *Salmonella typhimurium* lacking phosphoenolpyruvate carboxykinase and α -ketoglutarate dehydrogenase activities. *J. Bacteriol.* **100**:524–530.
284. **Carsiotis, M., B. A. Stocker, and I. A. Holder.** 1989. *Salmonella typhimurium* virulence in a burned-mouse model. *Infect. Immun.* **57**:2842–2846.
285. **Carstenius, P., J. I. Flock, and A. Lindberg.** 1990. Nucleotide sequence of *rfaI* and *rfaJ* genes encoding lipopolysaccharide glycosyl transferases from *Salmonella typhimurium*. *Nucleic Acids Res.* **18**:6128.
286. **Carter, P. W., J. M. Bartkus, and J. M. Calvo.** 1986. Transcription attenuation in *Salmonella typhimurium*: the significance of rare leucine codons in the *leu* leader. *Proc. Natl. Acad. Sci. USA* **83**:8127–8131.
287. **Carter, P. W., D. L. Weiss, H. L. Weith, and J. M. Calvo.** 1985. Mutations that convert the four leucine codons of the *Salmonella typhimurium leu* leader to four threonine codons. *J. Bacteriol.* **162**:943–949.
288. **Carter, T. H., and C. G. Miller.** 1984. Aspartate-specific peptidases in *Salmonella typhimurium*: mutants deficient in peptidase E. *J. Bacteriol.* **159**:453–459.
289. **Casse, F.** 1970. Mapping of gene *chl-B* controlling membrane-bound nitrate-reductase and formic hydrogenylase activities in *Escherichia coli* K-12. *Biochem. Biophys. Res. Commun.* **39**:429–436.
290. **Casse, F., M. Chippaux, and M.-C. Pascal.** 1973. Isolation from *Salmonella typhimurium* LT2 of mutants lacking specifically nitrate reductase activity and mapping of the *chl-C* gene. *Mol. Gen. Genet.* **124**:247–251.
291. **Casse, F., M.-C. Pascal, and M. Chippaux.** 1972. A mutant of *Salmonella typhimurium* deficient in tetrathionate reductase activity. *Mol. Gen. Genet.* **119**:71–74.
292. **Casse, F., M.-C. Pascal, and M. Chippaux.** 1973. Comparison between the chromosomal maps of *Escherichia coli* and *Salmonella typhimurium*. Length of the inverted segment in the *trp* region.

- Mol. Gen. Genet.* **124**:213–257.
293. **Casse, F., M.-C. Pascal, M. Chippaux, and J. Ratouchniak.** 1972. Mapping of the *chlB* gene in *Salmonella typhimurium* LT2. *Mol. Gen. Genet.* **119**:67–70.
294. **Cauthen, S. E., M. A. Foster, and D. D. Woods.** 1966. Methionine synthesis by extracts of *Salmonella typhimurium*. *Biochem. J.* **98**:630–635.
295. **Cerin, H., and J. Hackett.** 1989. Molecular cloning and analysis of the incompatibility and partition functions of the virulence plasmid of *Salmonella typhimurium*. *Microb. Pathog.* **7**:85–99.
296. **Cerin, H., and J. Hackett.** 1993. The *parVP* region of the *Salmonella typhimurium* virulence plasmid pSLT contains four loci required for incompatibility and partition. *Plasmid* **30**:30–38.
297. **Cerretti, D. P., L. C. Mattheakis, K. R. Kearney, L. Vu, and M. Nomura.** 1988. Translational regulation of the *spc* operon in *Escherichia coli*. Identification and structural analysis of the target site for S8 repressor protein. *J. Mol. Biol.* **204**:309–329.
298. **Chakraborti, A. S., K. Ishidate, W. R. Cook, J. Zrike, and L. I. Rothfield.** 1986. Accumulation of a murein-membrane attachment site fraction when cell division is blocked in *lkyD* and *cha* mutants of *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **168**:1422–1429.
299. **Chakravorty, M., T. Suryanarayana, and A. K. Datta.** 1975. A ribonuclease I deficient mutant (MB24) of *Salmonella typhimurium*. *Indian J. Biochem. Biophys.* **12**:153–157.
300. **Chan, C. L., and R. Landick.** 1989. The *Salmonella typhimurium* *his* operon leader region contains an RNA hairpin-dependent transcription pause site. Mechanistic implications of the effect on pausing of altered RNA hairpins. *J. Biol. Chem.* **264**:20796–20804.
301. **Chan, R. K., and D. Bostein.** 1976. Specialized transduction by bacteriophage P-22 in *Salmonella typhimurium*: genetic and physical structure of the transducing genomes and the prophage attachment site. *Genetics* **83**:433–458.
302. **Chang, G. W., and K. Fenton.** 1974. A simple method for measuring protein degradation in bacteria. *Anal. Biochem.* **59**:185–189.
303. **Chang, G. W., J. R. Roth, and B. N. Ames.** 1971. Histidine regulation in *Salmonella typhimurium*. VII. Mutations of the *hisT* gene. *J. Bacteriol.* **108**:410–414.
304. **Charlier, D., M. Roovers, D. Gigot, N. Huysveld, A. Pierard, and N. Glansdorff.** 1993. Integration host factor (IHF) modulates the expression of the pyrimidine-specific promoter of the *carAB* operons of *Escherichia coli* K12 and *Salmonella typhimurium* LT2. *Mol. Gen. Genet.* **237**:273–286.
305. **Chary, P., R. Prasad, A. K. Chopra, and J. W. Peterson.** 1993. Location of the enterotoxin gene from *Salmonella typhimurium* and characterization of the gene products. *FEMS Microbiol. Lett.* **111**:87–92.
306. **Chater, K. F.** 1970. Dominance of the wild-type of methionine regulatory genes in *Salmonella typhimurium*. *J. Gen. Microbiol.* **63**:95–109.
307. **Chater, K. F., D. A. Lawrence, R. J. Rowbury, and T. S. Gross.** 1970. Suppression of methionine transfer RNA synthetase mutants of *Salmonella typhimurium* by methionine regulatory mutations. *J. Gen. Microbiol.* **63**:121–131.
308. **Chater, K. F., and R. J. Rowbury.** 1970. A genetical study of the feedback-sensitive enzyme of methionine synthesis of *Salmonella typhimurium*. *J. Gen. Microbiol.* **63**:111–120.
309. **Chatfield, S. N., C. J. Dorman, C. Hayward, and G. Dougan.** 1991. Role of *ompR*-dependent genes in *Salmonella typhimurium* virulence: mutants deficient in both *ompC* and *ompF* are attenuated in vivo. *Infect. Immun.* **59**:449–452.
310. **Chatfield, S. N., K. Strahan, D. Pickard, I. G. Charles, C. E. Hormaeche, and G. Dougan.** 1992. Evaluation of *Salmonella typhimurium* strains harbouring defined mutations in *htrA* and *aroA* in the murine salmonellosis model. *Microb. Pathog.* **12**:145–151.
311. **Chelala, C. A., and P. Margolin.** 1974. Effects of deletions on cotransduction linkage in *Salmonella typhimurium*: evidence that bacterial chromosome deletions affect the formation of transducing DNA fragments. *Mol. Gen. Genet.* **131**:97–112.
312. **Chelsky, D., and S. M. Parsons.** 1975. Stereochemical course of the adenosine triphosphate phosphoribosyltransferase reaction in histidine biosynthesis. *J. Biol. Chem.* **250**:5669–5673.

313. **Chen, D., R. Bowater, C. J. Dorman, and D. M. Lilley.** 1992. Activity of a plasmid-borne *leu-500* promoter depends on the transcription and translation of an adjacent gene. *Proc. Natl. Acad. Sci. USA* **89**:8784–8788.
314. **Chen, J. M., G. Lee, R. B. Murphy, P. W. Brandt-Rauf, and M. R. Pincus.** 1990. Comparisons between the three-dimensional structures of the chemotactic protein CheY and the normal Gly 12-p21 protein. *Int. J. Pept. Protein Res.* **36**:1–6.
315. **Chen, P., D. I. Andersson, and J. R. Roth.** 1994. The control region of the *Salmonella pdu/cob* regulon. *J. Bacteriol.* **176**:5474–5482.
316. **Cheney, R. W., Jr., and N. M. Kredich.** 1975. Fine-structure genetic map of the *cysB* locus in *Salmonella typhimurium*. *J. Bacteriol.* **124**:1273–1281.
317. **Cheng, W., and J. R. Roth.** 1994. *Salmonella typhimurium* has two NAD kinases. *J. Bacteriol.* **176**:4260–4268.
318. **Chiariotti, L., P. Alifano, M. S. Carlomagno, and C. B. Bruni.** 1986. Nucleotide sequence of the *Escherichia coli hisD* gene of the *Escherichia coli* and *Salmonella typhimurium hisIE* region. *Mol. Gen. Genet.* **203**:382–388.
319. **Chiariotti, L., A. G. Nappo, M. S. Carlomagno, and C. B. Bruni.** 1986. Gene structure in the histidine operon of *Escherichia coli*. Identification and nucleotide sequence of the *hisB* gene. *Mol. Gen. Genet.* **202**:42–47.
320. **Child, J. D., and D. A. Smith.** 1969. New methionine structural gene in *Salmonella typhimurium*. *J. Bacteriol.* **100**:377–382.
321. **Childs, G., F. Sonnenberg, and M. Freundlich.** 1977. Detection of messenger RNA from the isoleucine-valine operons of *Salmonella typhimurium* by heterologous DNA-RNA hybridization: involvement of transfer RNA in transcriptional repression. *Mol. Gen. Genet.* **151**:121–126.
322. **Chin, A. M., D. A. Feldheim, and M. H. Saier, Jr.** 1989. Altered transcriptional patterns affecting several metabolic pathways in strains of *Salmonella typhimurium* which overexpress the fructose regulon. *J. Bacteriol.* **171**:2424–2434.
323. **Chin, A. M., B. U. Feucht, and M. H. Saier, Jr.** 1987. Evidence for regulation of gluconeogenesis by the fructose phosphotransferase system in *Salmonella typhimurium*. *J. Bacteriol.* **169**:897–899.
324. **Chin, A. M., S. Sutrina, D. A. Feldheim, and M. H. Saier, Jr.** 1987. Genetic expression of enzyme I* activity of the phosphoenolpyruvate: sugar phosphotransferase system in *ptsHI* deletion strains of *Salmonella typhimurium*. *J. Bacteriol.* **169**:894–896.
325. **Chippaux, M., F. Casse, and M.-C. Pascal.** 1972. Isolation and phenotypes of mutants from *Salmonella typhimurium* defective in formate hydrogenylase activity. *J. Bacteriol.* **110**:766–768.
326. **Chippaux, M., M.-C. Pascal, and F. Casse.** 1977. Formate hydrogenylase system in *Salmonella typhimurium*. *Eur. J. Biochem.* **72**:149–155.
327. **Cho, H., and J. E. Cronan, Jr.** 1994. “Protease I” of *Escherichia coli* functions as a thioesterase in vivo. *J. Bacteriol.* **176**:1793–1795.
328. **Chopra, A. K., C. W. Houston, J. W. Peterson, R. Prasad, and J. J. Mekalanos.** 1987. Cloning and expression of the *Salmonella* enterotoxin gene. *J. Bacteriol.* **169**:5095–5100.
329. **Chopra, A. K., J. W. Peterson, C. W. Houston, R. Pericas, and R. Prasad.** 1991. Enterotoxin-associated DNA sequence homology between *Salmonella* species and *Escherichia coli*. *FEMS Microbiol. Lett.* **61**:133–138.
330. **Chopra, A. K., J. W. Peterson, and R. Prasad.** 1991. Nucleotide sequence analysis of *purH* and *purD* genes from *Salmonella typhimurium*. *Biochim. Biophys. Acta* **1090**:351–354.
331. **Chopra, A. K., J. W. Peterson, and R. Prasad.** 1991. Cloning and sequence analysis of hydrogenase regulatory genes (*hydHG*) from *Salmonella typhimurium*. *Biochim. Biophys. Acta* **1129**:115–118.
332. **Chou, J. Y., and R. G. Martin.** 1972. Purine phosphoribosyltransferases of *Salmonella typhimurium*. *J. Bacteriol.* **112**:1010–1013.
333. **Christman, M. F., R. W. Morgan, F. S. Jacobson, and B. N. Ames.** 1985. Positive control of a regulon for defenses against oxidative stress and some heat-shock proteins in *Salmonella*

- typhimurium*. *Cell* **41**:753–762.
334. **Christman, M. F., G. Storz, and B. N. Ames.** 1989. OxyR, a positive regulator of hydrogen peroxide-inducible genes in *Escherichia coli* and *Salmonella typhimurium*, is homologous to a family of bacterial regulatory proteins. *Proc. Natl. Acad. Sci. USA* **86**:3484–3488.
335. **Chumley, F. G., and J. R. Roth.** 1980. Rearrangement of the bacterial chromosome using Tn-10 as a region of homology. *Genetics* **94**:1–14.
336. **Chumley, F. G., and J. R. Roth.** 1981. Genetic fusions that place the lactose genes under histidine operon control. *J. Mol. Biol.* **145**:697–712.
337. **Ciampi, M. S., P. Alifano, A. G. Nappo, C. B. Bruni, and M. S. Carlomagno.** 1989. Features of the rho-dependent transcription termination polar element within the *hisG* cistron of *Salmonella typhimurium*. *J. Bacteriol.* **171**:4472–4448.
338. **Ciampi, M. S., and J. R. Roth.** 1988. Polarity effects in the *hisG* gene of *Salmonella* require a site within the coding sequence. *Genetics* **118**:193–202.
339. **Ciampi, M. S., M. B. Schmid, and J. R. Roth.** 1982. Transposon Tn10 provides a promoter for transcription of adjacent sequences. *Proc. Natl. Acad. Sci. USA* **79**:5016–5020.
340. **Ciesla, F. G., M. Filutowicz, and T. Kłopotowski.** 1980. Involvement of the L-cysteine biosynthetic pathway in azide induced mutagenesis in *Salmonella typhimurium*. *Mutat. Res.* **70**:261–268.
341. **Ciesla, Z., M. Bagdasarian, W. Szczurkiewicz, M. Przygonska, and T. Kłopotowski.** 1972. Defective cell division in thermosensitive mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **116**:107–125.
342. **Ciesla, Z., K. Mardarowicz, and T. Kłopotowski.** 1974. Inhibition of DNA synthesis and cell division in *Salmonella typhimurium* by azide. *Mol. Gen. Genet.* **135**:339–348.
343. **Ciesla, Z., F. Salvatore, J. R. Broach, S. W. Artz, and B. N. Ames.** 1975. Histidine regulation in *Salmonella typhimurium*. XVI. A sensitive radiochemical assay for histidine dehydrogenase. *Anal. Biochem.* **63**:44–55.
344. **Clark, M. A., and E. L. Barrett.** 1987. The *phs* gene and hydrogen sulfide production by *Salmonella typhimurium*. *J. Bacteriol.* **169**:2391–2397.
345. **Clarke, P., J. H. Lee, K. Burke, and G. Wilcox.** 1992. Mutations in the *araC* gene of *Salmonella typhimurium* LT2 which affect both activator and auto-regulatory functions of the AraC protein. *Gene* **117**:31–37.
346. **Clarke, P., H.-C. Lin, and G. Wilcox.** 1982. The nucleotide sequence of the *araC* regulatory gene in *Salmonella typhimurium* LT2. *Gene* **18**:157–163.
347. **Clarke, S., K. Sparrow, S. Panasenko, and D. E. Koshland, Jr.** 1980. In vitro methylation of bacterial chemotaxis proteins: characterization of protein methyltransferase activity in crude extracts of *Salmonella typhimurium*. *J. Supramol. Struct.* **13**:315–328.
348. **Claverie, J. M.** 1993. Detecting frame shifts by amino acid sequence comparison. *J. Mol. Biol.* **234**:1140–1157.
349. **Clegg, S., B. K. Purcell, and J. Pruckler.** 1987. Characterization of genes encoding type 1 fimbriae of *Klebsiella pneumoniae*, *Salmonella typhimurium*, and *Serratia marcescens*. *Infect. Immun.* **55**:281–287.
350. **Coleman, M. S., W. G. Soucie, and F. B. Armstrong.** 1971. Branched chain amino acid aminotransferase of *Salmonella typhimurium*. II. Kinetic comparison with the enzyme from *Salmonella montevideo*. *J. Biol. Chem.* **246**:1310–1312.
351. **Coleman, W. G., Jr., and L. S. Williams.** 1974. First enzyme of histidine biosynthesis and repression control of histidyl-transfer ribonucleic acid synthetase of *Salmonella typhimurium*. *J. Bacteriol.* **120**:390–393.
352. **Collazo, C. M., M. K. Zierler, and J. E. Galan.** 1995. Functional analysis of the *Salmonella typhimurium* invasion genes *invI* and *invJ* and identification of a target of the protein secretion apparatus encoded in the *inv* locus. *Mol. Microbiol.* **15**:25–38.
353. **Collin-Osdoby, P., and C. G. Miller.** 1994. Mutations affecting a regulated, membrane-associated esterase in *Salmonella typhimurium* LT2. *Mol. Gen. Genet.* **243**:674–680.

354. **Collins, A. L. T., and B. A. D. Stocker.** 1976. *Salmonella typhimurium* mutants generally defective in chemotaxis. *J. Bacteriol.* **128**:754–765.
355. **Collins, A. M., and C. Colson.** 1972. Expression of *Escherichia coli* K, B, and phage P1 DNA host specificities in *Salmonella typhimurium*. *J. Gen. Microbiol.* **70**:123–128.
356. **Collins, L. V., S. Attridge, and J. Hackett.** 1991. Mutations at *rfc* or *pmi* attenuate *Salmonella typhimurium* virulence for mice. *Infect. Immun.* **59**:1079–1085.
357. **Collins, L. V., and J. Hackett.** 1991. Sequence of the phosphomannose isomerase-encoding gene of *Salmonella typhimurium*. *Gene* **103**:135–136.
358. **Collins, L. V., and J. Hackett.** 1991. Molecular cloning, characterization, and nucleotide sequence of the *rfc* gene, which encodes an O-antigen polymerase of *Salmonella typhimurium*. *J. Bacteriol.* **173**:2521–2529.
359. **Colson, A. M., C. Colson, and A. Van Pel.** 1969. Host-controlled restriction mutants of *Salmonella typhimurium*. *J. Gen. Microbiol.* **58**:57–64.
360. **Colson, C., and A. M. Colson.** 1971. A new *Salmonella typhimurium* DNA host specificity. *J. Gen. Microbiol.* **69**:345–351.
361. **Colson, C., A. M. Colson, and A. Van Pel.** 1970. Chromosomal location of host specificity in *Salmonella typhimurium*. *J. Gen. Microbiol.* **60**:265–271.
362. **Colson, C., and A. Van Pel.** 1974. DNA restriction and modification systems in *Salmonella*. I. SA and SB, two *Salmonella typhimurium* systems determined by genes with a chromosomal location comparable to that of the *Escherichia coli* *hsd* genes. *Mol. Gen. Genet.* **129**:325–337.
363. **Conlin, C. A., K. Hakensson, A. Liljas, and C. G. Miller.** 1994. Cloning and nucleotide sequence of the cyclic AMP receptor protein-regulated *Salmonella typhimurium* *pepE* gene and crystallization of its product, an alpha-aspartyl dipeptidase. *J. Bacteriol.* **176**:166–172.
364. **Conlin, C. A., and C. G. Miller.** 1992. Cloning and nucleotide sequence of *opdA*, the gene encoding oligopeptidase A in *Salmonella typhimurium*. *J. Bacteriol.* **174**:1631–1640.
365. **Conlin, C. A., N. J. Trun, T. J. Silhavy, and C. G. Miller.** 1992. *Escherichia coli* *prlC* encodes an endopeptidase and is homologous to the *Salmonella typhimurium* *opdA* gene. *J. Bacteriol.* **174**:5881–5887.
366. **Conlin, C. A., E. R. Vimr, and C. G. Miller.** 1992. Oligopeptidase A is required for normal phage P22 development. *J. Bacteriol.* **174**:5869–5880??.
367. **Contreras, A., and J. Casadesus.** 1983. Transposition of Tn10 to the *xyl-mtl* region (minute 78) of the *Salmonella typhimurium* chromosome. *Microbiol. Espan.* **36**:23–33. (In Spanish.)
368. **Cook, P. F., and R. T. Wedding.** 1976. A reaction mechanism from steady state kinetic studies for O-acetylserine sulfhydrylase from *Salmonella typhimurium*. *J. Biol. Chem.* **251**:2023–2029.
369. **Cook, W. R., T. J. MacAlister, and L. I. Rothfield.** 1986. Compartmentalization of the periplasmic space at division sites in gram-negative bacteria. *J. Bacteriol.* **168**:1430–1438.
370. **Cookson, B. T., B. M. Olivera, and J. R. Roth.** 1987. Genetic characterization and regulation of the *nadB* locus of *Salmonella typhimurium*. *J. Bacteriol.* **169**:4285–4293.
371. **Cooper, S.** 1988. Rate and topography of cell wall synthesis during the division cycle of *Salmonella typhimurium*. *J. Bacteriol.* **170**:422–430.
372. **Cooper, T. G., and B. Tyler.** 1976. Transcription of the *hut* operons of *Salmonella typhimurium*. *J. Bacteriol.* **130**:192–199.
373. **Cordaro, J. C., R. P. Anderson, E. W. Grogan, Jr., D. J. Wenzel, M. Engler, and S. Roseman.** 1974. Promoter-like mutation affecting HPr and enzyme I of the phosphoenolpyruvate:sugar phosphotransferase system in *Salmonella typhimurium*. *J. Bacteriol.* **120**:245–252.
374. **Cordaro, J. C., and E. Balbinder.** 1971. Evidence for the separability of the operator from the first structural gene in the tryptophan operon of *Salmonella typhimurium*. *Genetics* **67**:151–169.
375. **Cordaro, J. C., T. Melton, J. P. Stratis, M. Atagun, C. Gladding, P. E. Hartman, and S. Roseman.** 1976. Fosfomycin resistance: selection method for internal and extended deletions of the phosphoenolpyruvate. *J. Bacteriol.* **128**:785–793.
376. **Cordaro, J. C., and S. Roseman.** 1972. Deletion mapping of the genes coding for HPr and

- enzyme I of the phosphoenolpyruvate:sugar phosphotransferase system in *Salmonella typhimurium*. *J. Bacteriol.* **112**:17–29.
377. **Corina, D. L., and D. C. Wilton.** 1976. An apparent lack of stereospecificity in the reaction catalyzed by deoxyribose 5-phosphate aldolase due to methyl-group rotation and enolization before product release. *Biochem. J.* **157**:573–576.
378. **Cortese, R., H. O. Kammen, S. J. Spengler, and B. N. Ames.** 1974. Biosynthesis of pseudouridine in transfer ribonucleic acid. *J. Biol. Chem.* **249**:1103–1108.
379. **Cortese, R., R. Landsberg, R. A. Vonder Haar, H. E. Umberger, and B. N. Ames.** 1974. Pleiotrophy of *hisT* mutants blocked in pseudouridine synthesis in tRNA: *leucine* and *isoleucine-valine* operons. *Proc. Natl. Acad. Sci. USA* **71**:1857–1861.
380. **Corton, J. C., J. E. Ward, Jr., and J. Lutkenhaus.** 1987. Analysis of cell division gene *ftsZ* (*sulB*) from gram-negative and gram-positive bacteria. *J. Bacteriol.* **169**:1–7.
381. **Corwin, L. M., G. R. Fanning, F. Feldman, and P. Margolin.** 1966. Mutation leading to increased sensitivity to chromium in *Salmonella typhimurium*. *J. Bacteriol.* **91**:1509–1515.
382. **Cossart, P., E. A. Groisman, M.-C. Serre, M. J. Casadaban, and B. Gicquel-Sanzey.** 1986. *crp* genes of *Shigella flexneri*, *Salmonella typhimurium*, and *Escherichia coli*. *J. Bacteriol.* **167**:639–646.
383. **Costa, C. S., and D. N. Anton.** 1993. Round-cell mutants of *Salmonella typhimurium* produced by transposition mutagenesis: lethality of *rodA* and *mre* mutations. *Mol. Gen. Genet.* **236**:387–394.
384. **Cottam, A. N., and P. D. Ayling.** 1989. Genetic studies of mutants in a high-affinity methionine transport system in *Salmonella typhimurium*. *Mol. Gen. Genet.* **215**:358–363.
385. **Cottam, P. F., N.-B. He, S. W. Hui, and C. Ho.** 1986. Biochemical and morphological properties of membranes of unsaturated fatty acid auxotrophs of *Salmonella typhimurium*: effects of fluorinated myristic acids. *Biochim. Biophys. Acta* **862**:413–428.
386. **Cowan, J. M., M. L. Urbanowski, M. Talmi, and G. V. Stauffer.** 1993. Regulation of the *Salmonella typhimurium metF* gene by the MetR protein. *J. Bacteriol.* **175**:5862–5866.
387. **Coynault, C., V. Robbe-Saule, M. Y. Popoff, and F. Norel.** 1992. Growth phase and SpvR regulation of transcription of *Salmonella typhimurium spvABC* virulence genes. *Microb. Pathog.* **13**:133–143.
388. **Craven, M. G., A. E. Granston, A. T. Schauer, C. Zheng, T. A. Gray, and D. I. Friedman.** 1994. *Escherichia coli*-*Salmonella typhimurium* hybrid *nusA* genes: identification of a short motif required for action of the lambda N transcription antitermination protein. *J. Bacteriol.* **176**:1394–1404.
389. **Crawford, I. P.** 1975. Gene rearrangement in the evolution of the tryptophan synthetic pathway. *Bacteriol. Rev.* **39**:87–120.
390. **Crawford, I. P., B. P. Nichols, and C. Yanofsky.** 1980. Nucleotide sequence of the *trpB* gene in *Escherichia coli* and *Salmonella typhimurium*. *J. Mol. Biol.* **142**:489–502.
391. **Creeger, E. S., J. F. Chan, and L. I. Rothfield.** 1979. Cloning of genes for bacterial glycosyl transferases. II. Selection of a hybrid plasmid carrying the *rfaH* gene. *J. Biol. Chem.* **254**:811–815.
392. **Creeger, E. S., and L. I. Rothfield.** 1979. Cloning of genes for bacterial glycosyl transferases. I. Selection of hybrid plasmids carrying genes for two glucosyl transferases. *J. Biol. Chem.* **254**:804–810.
393. **Creeger, E. S., T. Schulte, and L. I. Rothfield.** 1984. Regulation of membrane glycosyltransferases by the *sfrB* and *rfaH* genes of *Escherichia coli* and *Salmonella typhimurium*. *J. Biol. Chem.* **259**:3064–3069.
394. **Creighton, T. E.** 1974. The functional significance of the evolutionary divergence between the tryptophan operons of *Escherichia coli* and *Salmonella typhimurium*. *J. Mol. Evol.* **4**:121–137.
395. **Crennell, S. J., E. F. Garman, W. G. Laver, E. R. Vimr, and G. L. Taylor.** 1993. Crystal structure of a bacterial sialidase (from *Salmonella typhimurium* LT2) shows the same fold as an influenza virus neuraminidase. *Proc. Natl. Acad. Sci. USA* **90**:9852–9856.
396. **Cronan, J. E., Jr., K. J. Littell, and S. Jackowski.** 1982. Genetic and biochemical analysis of pantothenate biosynthesis in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **149**:916–

397. **Csonka, L.** 1982. A third L-proline permease in *Salmonella typhimurium* which functions in media of elevated osmotic strength. *J. Bacteriol.* **151**:1433–1443.
398. **Csonka, L. N.** 1988. Regulation of cytoplasmic proline levels in *Salmonella typhimurium*: effect of osmotic stress on synthesis, degradation, and cellular retention of proline. *J. Bacteriol.* **170**:2374–2378.
399. **Csonka, L. N., M. M. Howe, J. L. Ingraham, L. S. Pierson III, and C. L. Turnbough, Jr.** 1981. Infection of *Salmonella typhimurium* with coliphage Mu d1(Apr lac): construction of *pyr::lac* gene fusions. *J. Bacteriol.* **145**:299–305.
400. **Csonka, L. N., T. P. Ikeda, S. A. Fletcher, and S. Kustu.** 1994. The accumulation of glutamate is necessary for optimal growth of *Salmonella typhimurium* in media of high osmolarity but not induction of the *proU* operon. *J. Bacteriol.* **176**:6324–6333.
401. **Dahl, M. K., W. Boos, and M. D. Manson.** 1989. Evolution of chemotactic-signal transducers in enteric bacteria. *J. Bacteriol.* **171**:2361–2371.
402. **Dahl, M. K., E. Francoz, W. Saurin, W. Boos, M. D. Manson, and M. Hofnung.** 1989. Comparison of sequences from the *malB* regions of *Salmonella typhimurium* and *Enterobacter aerogenes* with *Escherichia coli* K12: a potential new regulatory site in the interoperonic region. *Mol. Gen. Genet.* **218**:199–207.
403. **Dahlquist, F. W., P. Lovely, and D. E. Koshland, Jr.** 1972. Quantitative analysis of bacterial migration in chemotaxis. *Nature (London) New Biol.* **236**:120–123.
404. **Dailey, F. E., J. E. Cronan, Jr., and S. R. Maloy.** 1987. Acetohydroxy acid synthase I is required for isoleucine and valine biosynthesis by *Salmonella typhimurium* LT2 during growth on acetate or long-chain fatty acids. *J. Bacteriol.* **169**:917–919.
405. **Dalal, F. R., R. E. Gots, and J. S. Gots.** 1966. Mechanism of adenine inhibition in adenine-sensitive mutants of *Salmonella typhimurium*. *J. Bacteriol.* **91**:507–513.
406. **Danagulian, K. G., N. N. Sarkisian, D. B. Beglarian, and Z. A. Ktosian.** 1979. Some properties of UV-sensitive mutants of *Salmonella derby*. *Biol. Zh. Arm.* **32**:1030–1034.
407. **Dang, C. V., M. Niwano, J. Ryu, and B. L. Taylor.** 1986. Inversion of aerotactic response in *Escherichia coli* deficient in *cheB* protein methyltransferase. *J. Bacteriol.* **166**:275–280.
408. **Darekar, M. R., and H. Eyer.** 1973. The role of fimbriae in the processes of infection. Preliminary report. *Zentralbl. Bakteriologie, Mikrobiologie, Hygiene, Abt. 1 Orig. Reihe A* **225**:130–134.
409. **Dartois, V., O. De Backer, and C. Colson.** 1993. Sequence of the *Salmonella typhimurium* StyLT1 restriction-modification genes: homologies with EcoP1 and EcoP15 type-III R-M systems and presence of helicase domains. *Gene* **127**:105–110.
410. **Das, A., J. Urbanowski, H. Weissbach, J. Nestor, and C. Yanofsky.** 1983. In vitro synthesis of the tryptophan operon leader peptides of *Escherichia coli*, *Serratia marcescens*, and *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **80**:2879–2883.
411. **Dassa, E.** 1974. Localisation chromosomique du prophage N chez *Salmonella montevideo* (sous-groupe C₁). *C.R. Acad. Sci. Ser. D* **278**:385–388.
412. **Datta, D. B., C. Kramer, and U. Hemming.** 1976. Diploidy for a structural gene specifying a major protein of the outer cell envelope membrane from *Escherichia coli* K-12. *J. Bacteriol.* **128**:834–841.
413. **Daub, E., L. E. Zawadzke, D. Botstein, and C. T. Walsh.** 1988. Isolation, cloning, and sequencing of the *Salmonella typhimurium* *ddlA* gene with purification and characterization of its product, D-alanine:D-alanine ligase (ADP forming). *Biochemistry* **27**:3701–3708.
414. **Davidson, A. E., H. E. Fukimoto, C. E. Jackson, E. L. Barrett, and G. W. Chang.** 1979. Mutants of *Salmonella typhimurium* defective in the reduction of trimethylamine oxide. *FEMS Microbiol. Lett.* **6**:417–420.
415. **Davidson, J. P., and L. S. Williams.** 1979. Regulation of isoleucine and valine biosynthesis in *Salmonella typhimurium*. The effect of *hisU* on repression control. *J. Mol. Biol.* **127**:229–236.
416. **Davidson, J. P., and L. S. Williams.** 1979. Relaxed control of RNA synthesis during nutritional shiftdowns of a *hisU* mutant of *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.* **88**:682–

417. **Davidson, J. P., and D. J. Wilson.** 1991. Evidence for isoleucine as a positive effector of the *ilvBN* operon in *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.* **178**:934–939.
418. **Davidson, J. P., D. J. Wilson, and L. S. Williams.** 1982. Role of a *hisU* gene in the control of stable RNA synthesis in *Salmonella typhimurium*. *J. Mol. Biol.* **157**:237–264.
419. **Davis, L., and L. S. Williams.** 1982. Altered regulation of isoleucine-valine biosynthesis in a *hisW* mutant of *Salmonella typhimurium*. *J. Bacteriol.* **151**:860–866.
420. **Davis, L., and L. S. Williams.** 1982. Characterization of a cold-sensitive *hisW* mutant of *Salmonella typhimurium*. *J. Bacteriol.* **151**:867–887.
421. **De Backer, O., and C. Colson.** 1991. Transfer of the genes for the StyLTI restriction-modification system of *Salmonella typhimurium* to strains lacking modification ability results in death of the recipient cells and degradation of their DNA. *J. Bacteriol.* **173**:1328–1330.
422. **De Backer, O., and C. Colson.** 1991. Two-step cloning and expression in *Escherichia coli* of the DNA restriction-modification system StyLTI of *Salmonella typhimurium*. *J. Bacteriol.* **173**:1321–1327.
423. **De Backer, O., and C. Colson.** 1991. Identification of the recognition sequence for the M.StyLTI methyltransferase of *Salmonella typhimurium* LT7: an asymmetric site typical of type-III enzymes. *Gene* **97**:103–107.
424. **Dean, G. E., S.-I. Aizawa, and R. M. Macnab.** 1983. *flaAII* (*motC*, *cheV*) of *Salmonella typhimurium* is a structural gene involved in the energization and switching of the flagellar motor. *J. Bacteriol.* **154**:84–91.
425. **Decedue, C. J., J. G. Hofler, and R. O. Burns.** 1975. Threonine deaminase from *Salmonella typhimurium*. *J. Biol. Chem.* **250**:1563–1570.
426. **Deeley, R. G., R. F. Goldberger, J. S. Kovach, M. M. Meyers, and K. P. Mullinix.** 1975. Interaction between phosphoribosyltransferase and purified histidine tRNA from wild-type *Salmonella typhimurium* and a derepressed *hisT* mutant strain. *Nucleic Acids Res.* **2**:545–554.
427. **DeFranco, A. L., and D. E. Koshland, Jr.** 1980. Multiple methylation in processing of sensory signals during bacterial chemotaxis. *Proc. Natl. Acad. Sci. USA* **77**:2429–2433.
428. **DeFranco, A. L., and D. E. Koshland, Jr.** 1981. Molecular cloning of chemotaxis genes and overproduction of gene products in the bacterial sensing system. *J. Bacteriol.* **147**:390–400.
429. **DeFranco, A. L., and D. E. Koshland, Jr.** 1982. Construction and behavior of strains with mutations in two chemotaxis genes. *J. Bacteriol.* **150**:1297–1301.
430. **DeFranco, A. L., J. S. Parkinson, and D. E. Koshland, Jr.** 1979. Functional homology of chemotaxis genes in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **139**:107–114.
431. **Delavier-Klutchko, C., and M. Flavin.** 1965. Role of a bacterial cystathionine β -cleavage enzyme in disulfide decomposition. *Biochim. Biophys. Acta* **99**:375–377.
432. **DeLeo, A. B., J. Dayan, and D. B. Sprinson.** 1973. Purification and kinetics of tyrosine-sensitive 3-deoxy-D-arabino-heptulo-sonic acid 7-phosphate synthetase from *Salmonella*. *J. Biol. Chem.* **248**:2344–2353.
433. **DeLeo, A. B., and D. B. Sprinson.** 1975. 3-Deoxy-D-arabinoheptulosonic acid 7-phosphate synthase mutants of *Salmonella typhimurium*. *J. Bacteriol.* **124**:1312–1320.
434. **DeLorenzo, F., and B. N. Ames.** 1970. Histidine regulation in *Salmonella typhimurium*. VII. Purification and general properties of the histidyl transfer ribonucleic acid synthetase. *J. Biol. Chem.* **245**:1710–1716.
435. **DeLorenzo, F., P. DiNatale, and A. N. Schechter.** 1974. Chemical and physical studies on the structure of the histidyl transfer ribonucleic acid synthetase from *Salmonella typhimurium*. *J. Biol. Chem.* **249**:908–913.
436. **DeLorenzo, F., S. S. Straus, and B. N. Ames.** 1972. Histidine regulation in *Salmonella typhimurium*. X. Kinetic studies of mutant histidyl transfer ribonucleic acid synthetases. *J. Biol. Chem.* **247**:2302–2307.
437. **Demerec, M., A. E. Adelberg, A. J. Clark, and P. E. Hartman.** 1966. A proposal for a uniform nomenclature in bacterial genetics. *Genetics* **54**:61–76.

438. **Demerec, M., D. H. Gillespie, and K. Mizobuchi.** 1963. Genetic structure of the *cysC* region of the *Salmonella* genome. *Genetics* **48**:997–1009.
439. **Demerec, M., and Z. Hartman.** 1956. Tryptophan mutants in *Salmonella typhimurium*. *Carnegie Inst. Wash. Publ.* **612**:5–33.
440. **Demerec, M., E. L. Lahr, E. Balbinder, T. Miyake, C. Mack, D. MacKay, and J. Ishidsu.** 1959. Bacterial genetics. *Carnegie Inst. Wash. Year Book* **58**:433–439.
441. **den Blaauwen, J. L., and P. W. Postma.** 1985. Regulation of cyclic AMP synthase by enzyme III^{Glc} of the phosphoenolpyruvate:sugar phosphotransferase system in *crp* strains of *Salmonella typhimurium*. *J. Bacteriol.* **164**:477–478.
442. **Dendinger, S., and W. J. Brill.** 1970. Regulation of proline degradation of *Salmonella typhimurium*. *J. Bacteriol.* **103**:144–152.
443. **Dendinger, S., and W. J. Brill.** 1972. Effect of the proline analogue baikiain on proline metabolism in *Salmonella typhimurium*. *J. Bacteriol.* **112**:1134–1141.
444. **Dendinger, S. M., and J. E. Brenchley.** 1980. Temperature-sensitive glutamate dehydrogenase mutants of *Salmonella typhimurium*. *J. Bacteriol.* **144**:1043–1047.
445. **Dendinger, S. M., L. G. Patil, and J. E. Brenchley.** 1980. *Salmonella typhimurium* mutants with altered glutamate dehydrogenase and glutamate synthase activities. *J. Bacteriol.* **141**:190–198.
446. **Denk, D., and A. Bock.** 1987. L-Cysteine biosynthesis in *Escherichia coli*: nucleotide sequence and expression of the serine acetyltransferase (*cysE*) gene from the wild-type and a cysteine-excreting mutant. *J. Gen. Microbiol.* **133**:515–525.
447. **Denney, R. M., and C. Yanofsky.** 1974. Isolation and characterization of specialized $\phi 80$ transducing phages carrying regions of the *Salmonella typhimurium trp* operon. *J. Bacteriol.* **118**:505–513.
448. **Desiraju, V., W. G. Shanabruch, and A. L. Lu.** 1993. Nucleotide sequence of the *Salmonella typhimurium mutB* gene, the homolog of *Escherichia coli mutY*. *J. Bacteriol.* **175**:541–543.
449. **Desrochers, M., L. Peloquin, and A. Saarman.** 1978. Mapping of the *hemE* locus in *Salmonella typhimurium*. *J. Bacteriol.* **135**:1151–1153.
450. **diCamelli, R. F., and E. Balbinder.** 1976. The association of tryptophan synthetase subunits from *Escherichia coli* and *Salmonella typhimurium* in homologous and heterologous combinations. *Genet. Res.* **27**:323–333.
451. **Dila, D. K., and S. R. Maloy.** 1986. Proline transport in *Salmonella typhimurium*: *putP* permease mutants with altered substrate specificity. *J. Bacteriol.* **168**:590–594.
452. **DiNatale, P., F. Cimino, and F. DeLorenzo.** 1974. The pyrophosphate exchange reaction of histidyl-tRNA synthetase from *Salmonella typhimurium*: reaction parameters and inhibition by ribonucleic acid. *FEBS Lett.* **46**:175–179.
453. **DiNatale, P., A. N. Schechter, G. Castronuovo Lepore, and F. DeLorenzo.** 1976. Histidyl transfer ribonucleic acid synthetase from *Salmonella typhimurium*. Interaction with substrates and ATP analogues. *Eur. J. Biochem.* **62**:293–298.
454. **Diver, W. P., and D. G. MacPhee.** 1981. The effects of mutation in the *polA* and *recA* genes on mutagenesis by nitroguanidine in *Salmonella typhimurium*. *Mutat. Res.* **83**:349–359.
455. **Dobrogosz, W. J., G. W. Hall, D. K. Sherba, D. O. Silva, J. G. Harman, and T. Melton.** 1983. Regulatory interactions among the *cya*, *crp* and *pts* gene products in *Salmonella typhimurium*. *Mol. Gen. Genet.* **192**:477–486.
456. **Dobson, P. P., and G. C. Walker.** 1980. Plasmid pKM-101 mediated Weigle reactivation in *Escherichia coli* K-12 and *Salmonella typhimurium* LT-2. Genetic dependence kinetics of induction and effect of chloramphenicol. *Mutat. Res.* **71**:25–42.
457. **Doll, L., and G. Frankel.** 1993. *fliU* and *fliV*: two flagellar genes essential for biosynthesis of *Salmonella* and *Escherichia coli* flagella. *J. Gen. Microbiol.* **139**:2415–2422.
458. **Dombrosky, P. M., M. B. Schmid, and K. D. Young.** 1994. Sequence divergence of the *murB* and *rffB* genes from *Escherichia coli* and *Salmonella typhimurium*. *Arch. Microbiol.* **161**:501–507.
459. **Domingue, G., and E. Johnson.** 1974. Isolation of subcellular fractions containing immunogenic enterobacterial common antigens. *Z. Immunitaetsforsch. Exp. Klin. Immunol.* **148**:23–38.

460. **Dooley, M., R. Torget, and E. Balbinder.** 1979. Differences between the anthranilate-5-phosphoribosylpyrophosphate phosphoribosyltransferases of *Salmonella typhimurium* strains LT-2 and LT-7. *J. Gen. Microbiol.* **112**:171–180.
461. **Dorman, C. J., G. C. Barr, N. Ni Bhriain, and C. F. Higgins.** 1988. DNA supercoiling and the anaerobic and growth phase regulation of *tonB* gene expression. *J. Bacteriol.* **170**:2816–2826.
462. **Dorman, C. J., S. Chatfield, C. F. Higgins, C. Hayward, and G. Dougan.** 1989. Characterization of porin and *ompR* mutants of a virulent strain of *Salmonella typhimurium*: *ompR* mutants are attenuated in vivo. *Infect. Immun.* **57**:2136–2140.
463. **Downs, D., L. Waxman, A. L. Goldberg, and J. Roth.** 1986. Isolation and characterization of *lon* mutants in *Salmonella typhimurium*. *J. Bacteriol.* **165**:193–197.
464. **Downs, D. M.** 1992. Evidence for a new, oxygen-regulated biosynthetic pathway for the pyrimidine moiety of thiamine in *Salmonella typhimurium*. *J. Bacteriol.* **174**:1515–1521.
465. **Downs, D. M., and L. Petersen.** 1994. *apbA*, a new genetic locus involved in thiamine biosynthesis in *Salmonella typhimurium*. *J. Bacteriol.* **176**:4858–4864.
466. **Downs, D. M., and J. R. Roth.** 1987. A novel P22 prophage in *Salmonella typhimurium*. *Genetics* **117**:367–380.
467. **Downs, D. M., and J. R. Roth.** 1991. Synthesis of thiamine in *Salmonella typhimurium* independent of the *purF* function. *J. Bacteriol.* **173**:6597–6604.
468. **Dreyfus, G., A. W. Williams, I. Kawagishi, and R. M. Macnab.** 1993. Genetic and biochemical analysis of *Salmonella typhimurium* FliI, a flagellar protein related to the catalytic subunit of the FOF1 ATPase and to virulence proteins of mammalian and plant pathogens. *J. Bacteriol.* **175**:3131–3138.
469. **Dreyfuss, J.** 1974. The characterization of a sulfate- and thiosulfate-transporting system in *Salmonella typhimurium*. *J. Biol. Chem.* **239**:2292–2297.
470. **Dreyfuss, J., and A. B. Pardee.** 1966. Regulation of sulfate transport in *Salmonella typhimurium*. *J. Bacteriol.* **91**:2275–2280.
471. **Driks, A., and D. J. DeRosier.** 1990. Additional structures associated with bacterial flagellar basal body. *J. Mol. Biol.* **211**:669–672.
472. **Driver, R. P., and R. P. Lawther.** 1985. Restriction endonuclease analysis of the *ilvGEDA* operon of members of the family *Enterobacteriaceae*. *J. Bacteriol.* **162**:1317–1319.
473. **Droffner, M. L., and N. Yamamoto.** 1983. Anaerobic cultures of *Salmonella typhimurium* do not exhibit inducible proteolytic function of the *recA* gene and *recBC* function. *J. Bacteriol.* **156**:962–965.
474. **Droge, W., E. Ruschmann, O. Luderitz, and O. Westphal.** 1968. Biochemical studies on lipopolysaccharides of *Salmonella* R mutants. 4. Phosphate groups linked to heptose units and their absence in some lipopolysaccharides. *Eur. J. Biochem.* **4**:134–138.
475. **Druger-Liotta, J., V. J. Prange, D. G. Overdier, and L. N. Csonka.** 1986. Selection of mutations that alter the osmotic control of transcription of the *Salmonella typhimurium proU* operon. *J. Bacteriol.* **169**:2449–2459.
476. **Dubnau, E., A. B. Lenny, and P. Margolin.** 1973. Nonsense mutations of the *supX* locus: further characterization of the *supX* mutant phenotype. *Mol. Gen. Genet.* **126**:191–200.
477. **Dubnau, E., and P. Margolin.** 1972. Suppression of promoter mutations by the pleiotropic *top* mutations. *Mol. Gen. Genet.* **117**:91–112.
478. **Dugasheva, L. G., and V. S. Levashev.** 1974. Levomycetin resistance marker in *Escherichia coli* K12 and *Salmonella typhimurium*. *Zh. Mikrobiol. Epidemiol. Immunobiol.* **51**:85–90.
479. **Dunlap, V. J., and L. N. Csonka.** 1985. Osmotic regulation of L-proline transport in *Salmonella typhimurium*. *J. Bacteriol.* **163**:296–304.
480. **Dunn, S. D., and E. E. Snell.** 1979. Isolation of temperature-sensitive pantothenate kinase mutants of *Salmonella typhimurium* and mapping of the *coaA* gene. *J. Bacteriol.* **140**:805–808.
481. **Edwards, C. J., D. J. Innes, D. M. Burns, and I. R. Beacham.** 1993. UDP-sugar hydrolase isozymes in *Salmonella enterica* and *Escherichia coli*: silent alleles of *ushA* in related strains of group I *Salmonella* isolates, and of *ushB* in wild-type and K12 strains of *E. coli*, indicate recent and early silencing events, respectively. *FEMS Microbiol. Lett.* **114**:293–298.
482. **Edwards, M. F., and B. A. D. Stocker.** 1988. Construction of Δ *aroA* *his* Δ *pur* strains of

- Salmonella typhi*. *J. Bacteriol.* **170**:3991–3995.
483. **Eichelberg, K., C. C. Ginocchio, and J. E. Galan.** 1994. Molecular and functional characterization of the *Salmonella typhimurium* invasion genes *invB* and *invC*: homology of InvC to the F₀F₁ ATPase family of proteins. *J. Bacteriol.* **176**:4501–4510.
484. **Eidels, L., and M. J. Osborn.** 1971. Lipopolysaccharide and aldoheptose biosynthesis in transketolase mutants of *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **68**:1673–1677.
485. **Eidels, L., and M. J. Osborn.** 1974. Phosphoheptose isomerase, first enzyme in the biosynthesis of aldoheptose in *Salmonella typhimurium*. *J. Biol. Chem.* **249**:5642–5648.
486. **Eidels, L., P. D. Rick, N. P. Stimler, and M. J. Osborn.** 1974. Transport of D-arabinose-5-phosphate and D-sedoheptulose-7-phosphate by the hexose phosphate transport system of *Salmonella typhimurium*. *J. Bacteriol.* **119**:138–143.
487. **Eisenbach, M., A. Wolf, M. Welch, S. R. Caplan, I. R. Lapidus, R. M. Macnab, H. Aloni, and O. Asher.** 1990. Pausing, switching and speed fluctuation of the bacterial flagellar motor and their relation to motility and chemotaxis. *J. Mol. Biol.* **211**:551–563.
488. **Eisenstadt, E., M. Wolf, and I. H. Goldberg.** 1980. Mutagenesis by neocarzinostatin in *Escherichia coli* and *Salmonella typhimurium*: requirement for *umuC*⁺ or plasmid pKM101. *J. Bacteriol.* **144**:656–660.
489. **Eisenstark, A., R. Eisenstark, and S. Cunningham.** 1968. Genetic analysis of thymineless (*thy*) mutants in *Salmonella typhimurium*. *Genetics* **58**:493–506.
490. **Eisenstark, A., R. Eisenstark, J. Van Dillewijn, and A. Rorsch.** 1969. Radiation-sensitive and recombinationless mutants of *Salmonella typhimurium*. *Mutat. Res.* **8**:497–504.
491. **Ekena, K., and S. Maloy.** 1990. Regulation of proline utilization in *Salmonella typhimurium*: how do cells avoid a futile cycle? *Mol. Gen. Genet.* **220**:492–494.
492. **Elliott, C. J., and F. B. Armstrong.** 1968. Isoleucine-valine requiring mutants of *Salmonella typhimurium*. II. Strains deficient in dihydroxyacid dehydratase activity. *Genetics* **58**:171–179.
493. **Elliott, T.** 1989. Cloning, genetic characterization, and nucleotide sequence of the *hemA-prfA* operon of *Salmonella typhimurium*. *J. Bacteriol.* **171**:3948–3960.
494. **Elliott, T.** 1992. A method for constructing single-copy *lac* fusions in *Salmonella typhimurium* and its application to the *hemA-prfA* operon. *J. Bacteriol.* **174**:245–253.
495. **Elliott, T.** 1993. Transport of 5-aminolevulinic acid by the dipeptide permease in *Salmonella typhimurium*. *J. Bacteriol.* **175**:325–331.
496. **Elliott, T., Y. J. Avissar, G. E. Rhie, and S. I. Beale.** 1990. Cloning and sequence of the *Salmonella typhimurium hemL* gene and identification of the missing enzyme in *hemL* mutants as glutamate-1-semialdehyde aminotransferase. *J. Bacteriol.* **172**:7071–7084.
497. **Elliott, T., and J. R. Roth.** 1989. Heme-deficient mutants of *Salmonella typhimurium*: two genes required for ALA synthesis. *Mol. Gen. Genet.* **216**:303–314.
498. **Elliott, T., and X. Wang.** 1991. *Salmonella typhimurium prfA* mutants defective in release factor 1. *J. Bacteriol.* **173**:4144–4154.
499. **Engler, M., and M. J. Bessman.** 1977. The purification of a mutator polymerase from *Salmonella typhimurium*. *Fed. Proc.* **36**:735.
500. **Englesberg, E., and L. S. Baron.** 1959. Mutation to L-rhamnose resistance and transduction to L-rhamnose utilization in *Salmonella typhosa*. *J. Bacteriol.* **78**:675–686.
501. **Engstrom, J., J. Wong, and R. Maurer.** 1986. Interaction of DNA polymerase III γ and β subunits *in vivo* in *Salmonella typhimurium*. *Genetics* **113**:499–515.
502. **Enomoto, M.** 1966. Genetic studies of paralyzed mutants in *Salmonella*. I. Genetic fine structure of the *mot* loci in *Salmonella typhimurium*. *Genetics* **54**:715–726.
503. **Enomoto, M.** 1966. Genetic studies of paralyzed mutants in *Salmonella*. II. Mapping of three *mot* loci by linkage analysis. *Genetics* **54**:1069–1076.
504. **Enomoto, M.** 1971. Genetic analysis of non-motile mutants in *Salmonella typhimurium*: a new mapping method by abortive transduction. *Genetics* **69**:145–161.
505. **Enomoto, M.** 1972. Genetic studies of chlorate-resistant mutants of *Salmonella typhimurium*. *Jpn. J. Genet.* **47**:227–235.

506. **Enomoto, M., and B. A. D. Stocker.** 1974. Transduction by phage P1_{kc} in *Salmonella typhimurium*. *Virology* **60**:503–514.
507. **Enomoto, M., and B. A. D. Stocker.** 1975. Integration, at *hag* or elsewhere, of *H2* (phase 2 flagellin) genes transduced from *Salmonella* to *Escherichia coli*. *Genetics* **81**:595–614.
508. **Enomoto, M., and S. Yamaguchi.** 1969. Different frequencies of cotransduction of *motC* and *H1* in *Salmonella*. *Genet. Res.* **14**:45–52.
509. **Erickson, B. D., Z. F. Burton, K. K. Watanabe, and R. R. Burgess.** 1985. Nucleotide sequence of the *rpsU-dnaG-rpoD* operon from *Salmonella typhimurium* and a comparison of this sequence with the homologous operon of *Escherichia coli*. *Gene* **40**:67–78.
510. **Erickson, J. U., and G. R. Bjork.** 1986. Pleiotropic effects induced by modification deficiency next to the anticodon of tRNA from *Salmonella typhimurium* LT2. *J. Bacteriol.* **166**:1013–1021.
511. **Ernst, J. F., R. L. Bennett, and L. I. Rothfield.** 1978. Constitutive expression of the iron-enterochelin and ferrichrome uptake systems in a mutant strain of *Salmonella typhimurium*. *J. Bacteriol.* **135**:928–934.
512. **Esaki, N., and C. T. Walsh.** 1986. Biosynthetic alanine racemase of *Salmonella typhimurium*: purification and characterization of the enzyme encoded by the *alr* gene. *Biochemistry* **25**:3261–3267.
513. **Escalante-Semerena, J. C., M. G. Johnson, and J. R. Roth.** 1992. The CobII and CobIII regions of the cobalamin (vitamin B₁₂) biosynthetic operon of *Salmonella typhimurium*. *J. Bacteriol.* **174**:24–29.
514. **Escalante-Semerena, J. C., and J. R. Roth.** 1987. Regulation of cobalamin biosynthetic operons in *Salmonella typhimurium*. *J. Bacteriol.* **169**:2251–2258.
515. **Escalante-Semerena, J. C., S. J. Suh, and J. R. Roth.** 1990. *cobA* function is required for both de novo cobalamin biosynthesis and assimilation of exogenous corrinoids in *Salmonella typhimurium*. *J. Bacteriol.* **172**:273–280.
516. **Faelen, M., M. Mergeay, J. Gerits, A. Toussaint, and N. Lefebvre.** 1981. Genetic mapping of a mutation conferring sensitivity to bacteriophage Mu in *Salmonella typhimurium* LT2. *J. Bacteriol.* **146**:914–919.
517. **Falconi, M., V. McGovern, C. Gualerzi, D. Hillyard, and N. P. Higgins.** 1991. Mutations altering chromosomal protein H-NS induce mini-Mu transposition. *New Biol.* **3**:615–625.
518. **Fandl, J. P., L. K. Thorner, and S. W. Artz.** 1990. Mutations that affect transcription and cyclic AMP-CRP regulation of the adenylate cyclase gene (*cya*) of *Salmonella typhimurium*. *Genetics* **125**:719–727.
519. **Fang, F. C., S. J. Libby, N. A. Buchmeier, P. C. Loewen, J. Switala, J. Harwood, and D. G. Guiney.** 1992. The alternative sigma factor *katF* (*rpoS*) regulates *Salmonella* virulence. *Proc. Natl. Acad. Sci. USA* **89**:11978–11982.
520. **Faraci, W. S., and C. T. Walsh.** 1988. Racemization of alanine by the alanine racemases from *Salmonella typhimurium* and *Bacillus stearothermophilus*: energetic reaction profiles. *Biochemistry* **27**:3267–3276.
521. **Farewell, A., R. Brazas, E. Davie, J. Mason, and L. I. Rothfield.** 1991. Suppression of the abnormal phenotype of *Salmonella typhimurium* *rfaH* mutants by mutations in the gene for transcription termination factor Rho. *J. Bacteriol.* **173**:5188–5193.
522. **Farr, S. B., and T. Kogoma.** 1991. Oxidative stress responses in *Escherichia coli* and *Salmonella typhimurium*. *Microbiol. Rev.* **55**:561–585.
523. **Fasciano, A., and P. C. Hallenbeck.** 1991. Mutations in *trans* that affect formate dehydrogenase (*fdhF*) gene expression in *Salmonella typhimurium*. *J. Bacteriol.* **173**:5893–5900.
524. **Fasciano, A., and P. C. Hallenbeck.** 1992. The role of *ntrA* in the anaerobic metabolism of *Salmonella typhimurium*. *FEMS Microbiol. Lett.* **90**:101–104.
525. **Faust, L. P., and B. M. Babor.** 1992. Overexpression, purification, and some properties of the AdoCbl-dependent ethanolamine ammonia-lyase from *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **294**:50–54.
526. **Faust, L. R., J. A. Connor, D. M. Roof, J. A. Hoch, and B. M. Babor.** 1990. Cloning, sequencing, and expression of the genes encoding the adenosylcobalamin-dependent ethanolamine

- ammonia-lyase of *Salmonella typhimurium*. *J. Biol. Chem.* **265**:12462–12466.
527. **Feild, M. J., D. C. Nguyen, and F. B. Armstrong.** 1989. Amino acid sequence of *Salmonella typhimurium* branched-chain amino acid aminotransferase. *Biochemistry* **28**:5306–5310.
528. **Feldheim, D. A., A. M. Chin, C. T. Nierva, B. U. Feucht, Y. W. Cao, Y. F. Xu, S. L. Sutrina, and M. H. Saier, Jr.** 1990. Physiological consequences of the complete loss of phosphoryl-transfer proteins HPr and FPr of the phosphoenolpyruvate:sugar phosphotransferase system and analysis of fructose (*fru*) operon expression in *Salmonella typhimurium*. *J. Bacteriol.* **172**:5459–5469.
529. **Feng, J. A., R. C. Johnson, and R. E. Dickerson.** 1994. Hin recombinase bound to DNA: the origin of specificity in major and minor groove interactions. *Science* **263**:348–355.
530. **Fernandez, V. M., R. Martin del Rio, A. R. Tebar, M. M. Guisan, and A. O. Ballesteros.** 1975. Derepression and repression of the histidine operon: role of the feedback site of the first enzyme. *J. Bacteriol.* **124**:1366–1373.
531. **Feucht, B. U., and M. H. Saier, Jr.** 1980. Fine control of adenylate cyclase by the phosphoenolpyruvate and sugar phosphotransferase systems in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **141**:603–610.
532. **Feutrier, J., W. W. Kay, and T. J. Trust.** 1986. Purification and characterization of fimbriae from *Salmonella enteritidis*. *J. Bacteriol.* **168**:221–227.
533. **Fields, P. I., E. A. Groisman, and F. Heffron.** 1989. A *Salmonella* locus that controls resistance to microbicidal proteins from phagocytic cells. *Science* **243**:1059–1062.
534. **Fields, P. I., R. V. Swanson, C. G. Haidaris, and F. Heffron.** 1986. Mutants of *Salmonella typhimurium* that cannot survive within the macrophage are avirulent. *Proc. Natl. Acad. Sci. USA* **83**:5189–5193.
535. **Figueroa, N., N. Wills, and L. Bossi.** 1991. Common sequence determinants of the response of a prokaryotic promoter to DNA bending and supercoiling. *EMBO J.* **10**:941–949.
536. **Filutowicz, M., Z. Ciesla, and T. Klopotoski.** 1979. Interference of azide with cysteine biosynthesis in *Salmonella typhimurium*. *J. Gen. Microbiol.* **113**:45–55.
537. **Filutowicz, M., A. Wiater, and D. Hulanicka.** 1982. Delayed inducibility of sulfite reductase in *cysM* mutants of *Salmonella typhimurium* under anaerobic conditions. *J. Gen. Microbiol.* **128**:1791–1794.
538. **Finkel, S. E., and R. C. Johnson.** 1992. The Fis protein: it's not just for DNA inversion anymore. *Mol. Microbiol.* **6**:3257–3265. (Erratum, **7**:1023, 1993.)
539. **Finn, G. J., and S. Condon.** 1975. Regulation of catalase synthesis in *Salmonella typhimurium*. *J. Bacteriol.* **123**:570–579.
540. **Fira, D., B. Vasiljevic, and L. Topisirovic.** 1990. Altered translational fidelity of a *Salmonella typhimurium* LT2 mutant resistant to the aminoglycoside antibiotic neamine. *J. Gen. Microbiol.* **136**:249–253.
541. **Folterman, K. F., D. A. Beck, and J. R. Wild.** 1986. In vivo formation of hybrid aspartate transcarbamoylases from native subunits of divergent members of the family *Enterobacteriaceae*. *J. Bacteriol.* **167**:285–290.
542. **Fong, C.-L. W., N. K. Heinzinger, S. Tongklan, and E. L. Barrett.** 1993. Cloning of the *phs* genetic locus from *Salmonella typhimurium* and a role for a *phs* product in its own induction. *J. Bacteriol.* **175**:6368–6371.
543. **Ford, S. R., and R. L. Switzer.** 1975. Stimulation of derepressed enzyme synthesis in bacteria by growth on sublethal concentrations of chloramphenicol. *Antimicrob. Agents Chemother.* **7**:555–563.
544. **Ford, S. R., and R. L. Switzer.** 1975. Stimulation of enzyme synthesis by sublethal concentrations of chloramphenicol is not mediated by ribonucleotide pools. *Antimicrob. Agents Chemother.* **7**:564–570.
545. **Foster, D. L., S. L. Mowbray, B. K. Jap, and D. E. Koshland, Jr.** 1985. Purification and characterization of the aspartate chemoreceptor. *J. Biol. Chem.* **260**:11706–11710.
546. **Foster, J. W.** 1981. Pyridine nucleotide cycle of *Salmonella typhimurium*: in vitro demonstration of nicotinamide adenine dinucleotide glycohydrolase, nicotinamide mononucleotide glycohydrolase, and nicotinamide adenine dinucleotide pyrophosphatase activities. *J. Bacteriol.* **145**:1002–1009.

547. **Foster, J. W.** 1983. Identification and characterization of a *relA*-dependent starvation-inducible locus (*sin*) in *Salmonella typhimurium*. *J. Bacteriol.* **156**:424–428.
548. **Foster, J. W.** 1991. *Salmonella* acid shock proteins are required for the adaptive acid tolerance response. *J. Bacteriol.* **173**:6896–6902.
549. **Foster, J. W.** 1993. The acid tolerance response of *Salmonella typhimurium* involves transient synthesis of key acid shock proteins. *J. Bacteriol.* **175**:1981–1987.
550. **Foster, J. W., and B. Bearson.** 1994. Acid-sensitive mutants of *Salmonella typhimurium* identified through a dinitrophenol lethal screening strategy. *J. Bacteriol.* **176**:2596–2602.
551. **Foster, J. W., and D. Falconer.** 1983. Isolation of pyridine analog supersensitive (*pas*) mutants of *Salmonella typhimurium*, abstr. K52, p. 51. *Abstr. Annu. Meet. Am. Soc. Microbiol.* 1983.
552. **Foster, J. W., and H. K. Hall.** 1990. Adaptive acidification tolerance response of *Salmonella typhimurium*. *J. Bacteriol.* **172**:771–778.
553. **Foster, J. W., and H. K. Hall.** 1991. Inducible pH homeostasis and the acid tolerance response of *Salmonella typhimurium*. *J. Bacteriol.* **173**:5129–5135.
554. **Foster, J. W., and H. K. Hall.** 1992. Effect of *Salmonella typhimurium* ferric uptake regulator (*fur*) mutations on iron- and pH-regulated protein synthesis. *J. Bacteriol.* **174**:4317–4323.
555. **Foster, J. W., and E. A. Holley.** 1981. Genetic mapping of the *Salmonella typhimurium pncB* locus. *J. Bacteriol.* **148**:394–396.
556. **Foster, J. W., and E. A. Holley.** 1983. Characterization of a nicotinamide starvation-inducible locus in *Salmonella typhimurium*, abstr. K53, p. 51. *Abstr. Annu. Meet. Am. Soc. Microbiol.* 1983.
557. **Foster, J. W., E. A. Holley, and S. Mya.** 1984. NAD metabolism in *Salmonella typhimurium*: isolation of pyridine analogue supersensitive (*pas*) and *pas* suppressor mutants. *J. Gen. Microbiol.* **130**:2873–2881.
558. **Foster, J. W., E. A. Holley-Guthrie, and F. Warren.** 1987. Regulation of NAD metabolism in *Salmonella typhimurium*: genetic analysis and cloning of the *nadR* repressor locus. *Mol. Gen. Genet.* **208**:279–287.
559. **Foster, J. W., D. M. Kinney, and A. G. Moat.** 1979. Pyridine nucleotide cycle of *Salmonella typhimurium*: regulation of nicotinic acid phosphoribosyl transferase and nicotinamide deamidase. *J. Bacteriol.* **138**:957–961.
560. **Foster, J. W., D. M. Kinney, and A. G. Moat.** 1979. Pyridine nucleotide cycle of *Salmonella typhimurium*: isolation and characterization of *pncA*, *pncB*, and *pncC* mutants and utilization of exogenous nicotinamide adenine dinucleotide. *J. Bacteriol.* **137**:1165–1175.
561. **Foster, J. W., and A. G. Moat.** 1978. Mapping and characterization of the *nad* genes in *Salmonella typhimurium* LT-2. *J. Bacteriol.* **133**:775–779.
562. **Foster, J. W., Y. K. Park, I. S. Bang, K. Karem, H. Betts, H. K. Hall, and E. Shaw.** 1994. Regulatory circuits involved with pH-regulated gene expression in *Salmonella typhimurium*. *Microbiology* **140**:341–352.
563. **Foster, J. W., Y. K. Park, T. Penfound, T. Fenger, and M. P. Spector.** 1990. Regulation of NAD metabolism in *Salmonella typhimurium*: molecular sequence analysis of the bifunctional *nadR* regulator and the *nadA-pnuC* operon. *J. Bacteriol.* **172**:4187–4196.
564. **Foster, J. W., and M. P. Spector.** 1986. Phosphate starvation regulon of *Salmonella typhimurium*. *J. Bacteriol.* **166**:666–669.
565. **Fraenkel, D., M. J. Osborn, B. K. Horecker, and S. M. Smith.** 1963. Metabolism and cell wall structure of a mutant of *Salmonella typhimurium* deficient in phosphoglucose isomerase. *Biochem. Biophys. Res. Commun.* **11**:423–428.
566. **Francis, C. L., T. A. Ryan, B. D. Jones, S. J. Smith, and S. Falkow.** 1993. Ruffles induced by *Salmonella* and other stimuli direct macropinocytosis of bacteria. *Nature (London)* **364**:639–642.
567. **Francis, N. R., V. M. Irikura, S. Yamaguchi, D. J. DeRosier, and R. M. Macnab.** 1992. Localization of the *Salmonella typhimurium* flagellar switch protein FliG to the cytoplasmic M-ring face of the basal body. *Proc. Natl. Acad. Sci. USA* **89**:6304–6308.
568. **Francoz, E., A. Molla, E. Dassa, W. Saurin, and M. Hofnung.** 1990. The maltoporin of *Salmonella typhimurium*: sequence and folding model. *Res. Microbiol.* **141**:1039–1059.

569. **Francoz, E., E. Schneider, and E. Dassa.** 1990. The sequence of the *malG* gene from *Salmonella typhimurium* and its functional implications. *Res. Microbiol.* **141**:633–644.
570. **Frankhauser, D. B., and P. E. Hartman.** 1971. Direct selection for transduction of suppressor mutations and linkage of *supD* to *fla* genes in *Salmonella*. *J. Bacteriol.* **108**:1427–1430.
571. **French, S., K. Martin, T. Patterson, R. Bauerle, and O. L. Miller, Jr.** 1985. Electron microscopic visualization of *trp* operon expression in *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **82**:4638–4642.
572. **Freudl, R., G. Braun, N. Honore, and S. T. Cole.** 1987. Evolution of the enterobacterial *sulA* gene: a component of the SOS system encoding an inhibitor of cell division. *Gene* **52**:31–40.
573. **Freudl, R., and S. T. Cole.** 1983. Cloning and molecular characterization of the *ompA* gene from *Salmonella typhimurium*. *Eur. J. Biochem.* **134**:497–502.
574. **Freundlich, M., and J. M. Trela.** 1969. Control of isoleucine, valine, and leucine biosynthesis. VI. Effect of 5',5',5'-trifluoroleucine on repression in *Salmonella typhimurium*. *J. Bacteriol.* **99**:101–106.
575. **Frey, B., J. McCloskey, W. Kersten, and H. Kersten.** 1988. New function of vitamin B₁₂: cobamide-dependent reduction of epoxyqueuosine to queuosine in tRNAs of *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **170**:2078–2082.
576. **Frick, M. M., J. Neuhard, and R. A. Kelln.** 1990. Cloning, nucleotide sequence and regulation of the *Salmonella typhimurium pyrD* gene encoding dihydroorotate dehydrogenase. *Eur. J. Biochem.* **194**:573–578.
577. **Friedberg, D., T. W. Mikulka, J. Jones, and J. M. Calvo.** 1974. *flrB*, a regulatory locus controlling branched-chain amino acid biosynthesis in *Salmonella typhimurium*. *J. Bacteriol.* **118**:942–951.
578. **Friedberg, D., E. R. Rosenthal, J. W. Jones, and J. M. Calvo.** 1985. Characterization of the 3' end of the leucine operon of *Salmonella typhimurium*. *Mol. Gen. Genet.* **199**:486–494.
579. **Friedman, S. B., and P. Margolin.** 1968. Evidence for an altered operator specificity: catabolite repression control of the leucine operon in *Salmonella typhimurium*. *J. Bacteriol.* **95**:2263–2269.
580. **Friedrich, M. J., N. E. Kinsey, J. Vila, and R. J. Kadner.** 1993. Nucleotide sequence of a 13.9 kb segment of the 90 kb virulence plasmid of *Salmonella typhimurium*: the presence of fimbrial biosynthetic genes. *Mol. Microbiol.* **8**:543–558.
581. **Fuchs, R. L., M. J. Madonna, and J. E. Brenchley.** 1982. Identification of the structural genes for glutamine synthase and genetic characterization of this region of the *Salmonella typhimurium* chromosome. *J. Bacteriol.* **149**:906–915.
582. **Fujita, H., S. Yamaguchi, and T. Iino.** 1973. Studies on H-O variants in *Salmonella* in relation to phase variation. *J. Gen. Microbiol.* **76**:127–134.
583. **Fujita, H., S. Yamaguchi, T. Taira, T. Hirano, and T. Iino.** 1987. Isolation and genetic analysis of operator-constitutive mutants of the *H1* operon in *Salmonella typhimurium*. *J. Gen. Microbiol.* **133**:3071–3080.
584. **Fukasawa, T., and H. Nikaido.** 1961. Galactose mutants of *Salmonella typhimurium*. *Genetics* **46**:1295–1303.
585. **Fukuda, R., A. Ishihama, T. Saitoh, and M. Taketo.** 1977. Comparative studies of RNA polymerase subunits from various bacteria. *Mol. Gen. Genet.* **154**:135–144.
586. **Fukushi, K., H. Kudo, H. Asano, and J.-I. Sasaki.** 1977. Electron microscopy of endotoxin extracted from rough mutant of *Salmonella*. *Jpn. J. Med. Sci. Biol.* **30**:51–54.
587. **Fulcher, C. A., and R. Bauerle.** 1978. Re-initiation of tryptophan operon expression in a promoter deletion strain of *Salmonella typhimurium*. *Mol. Gen. Genet.* **158**:239–250.
588. **Fuller-Pace, F. V., and N. E. Murray.** 1986. Two DNA recognition domains of the specificity polypeptides of a family of type I restriction enzymes. *Proc. Natl. Acad. Sci. USA* **83**:9368–9372.
589. **Fultz, P. N., K. K. L. Choung, and J. Kemper.** 1980. Construction and characterization of *Salmonella typhimurium* strains that accumulate and excrete α and β isopropylmalate. *J. Bacteriol.* **142**:513–520.
590. **Fultz, P. N., and J. Kemper.** 1980. Wild-type isopropylmalate isomerase in *Salmonella*

- typhimurium* is composed of two different subunits. *J. Bacteriol.* **148**:210–219.
591. **Fultz, P. N., D. Y. Kwoh, and J. Kemper.** 1979. *Salmonella typhimurium newD* and *Escherichia coli leuC* genes code for a functional isopropyl malate isomerase in *Salmonella typhimurium*-*Escherichia coli* hybrids. *J. Bacteriol.* **137**:1253–1262.
592. **Funanage, V. L., P. D. Ayling, S. M. Dendinger, and J. E. Brenchley.** 1978. *Salmonella typhimurium* LT-2 mutants with altered glutamine synthetase levels and amino acid uptake activities. *J. Bacteriol.* **136**:588–596.
593. **Funanage, V. L., and J. Brenchley.** 1977. Characterization of *Salmonella typhimurium* mutants with altered glutamine synthetase activity. *Genetics* **86**:513–526.
594. **Fung, J., T. J. MacAlister, and L. I. Rothfield.** 1978. Role of murein lipoprotein in morphogenesis of the bacterial division septum: phenotypic similarity of *lkyD* and *lpo* mutants. *J. Bacteriol.* **133**:1467–1471.
595. **Fung, J. C., T. J. MacAlister, R. A. Weigand, and L. I. Rothfield.** 1980. Morphogenesis of the bacterial division septum: identification of potential sites of division in *lkyD* mutants of *Salmonella typhimurium*. *J. Bacteriol.* **143**:1019–1024.
596. **Furano, A. V.** 1978. Direct demonstration of duplicate *tuf* genes in enteric bacteria. *Proc. Natl. Acad. Sci. USA* **75**:3104–3108.
597. **Gaitanaris, G. A., M. McCormick, B. H. Howard, and M. E. Gottesman.** 1986. Reconstitution of an operon from overlapping fragments: use of the λ SV2, integrative cloning system. *Gene* **46**:1–11.
598. **Galakatos, N. G., E. Daub, D. Botstein, and C. T. Walsh.** 1986. Biosynthetic *alr* alanine racemase from *Salmonella typhimurium*: DNA and protein sequence determination. *Biochemistry* **25**:3255–3260.
599. **Galakatos, N. G., and C. T. Walsh.** 1987. Specific proteolysis of native alanine racemases from *Salmonella typhimurium*: identification of the cleavage site and characterization of the clipped two-domain proteins. *Biochemistry* **26**:8475–8480.
600. **Galan, J. E., and R. Curtiss.** 1989. Cloning and molecular characterization of genes whose products allow *Salmonella typhimurium* to penetrate tissue culture cells. *Proc. Natl. Acad. Sci. USA* **86**:6383–6387.
601. **Galan, J. E., and R. Curtiss.** 1989. Virulence and vaccine potential of *phoP* mutants of *Salmonella typhimurium*. *Microb. Pathog.* **6**:433–443.
602. **Galan, J. E., and R. Curtiss.** 1990. Expression of *Salmonella typhimurium* genes required for invasion is regulated by changes in DNA supercoiling. *Infect. Immun.* **58**:1879–1885.
603. **Galan, J. E., and R. Curtiss.** 1991. Distribution of the *invA*, *-B*, *-C*, and *-D* genes of *Salmonella typhimurium* among other *Salmonella* serovars: *invA* mutants of *Salmonella typhi* are deficient for entry into mammalian cells. *Infect. Immun.* **59**:2901–2908.
604. **Galan, J. E., C. Ginocchio, and P. Costeas.** 1992. Molecular and functional characterization of the *Salmonella* invasion gene *invA*: homology of InvA to members of a new protein family. *J. Bacteriol.* **174**:4338–4349.
605. **Galan, J. E., K. Nakayama, and R. Curtiss.** 1990. Cloning and characterization of the *asd* gene of *Salmonella typhimurium*: use in stable maintenance of recombinant plasmids in *Salmonella* vaccine strains. *Gene* **94**:29–35.
606. **Galinier, A., D. Negre, J. C. Cortay, S. Marcandier, S. R. Maloy, and A. J. Cozzone.** 1990. Sequence analysis of the *iclR* gene encoding the repressor of the acetate operon in *Salmonella typhimurium*. *Nucleic Acids Res.* **18**:3656.
607. **Gallagher, M. P., S. R. Pearce, and C. F. Higgins.** 1989. Identification and localization of the membrane-associated, ATP-binding subunit of the oligopeptide permease of *Salmonella typhimurium*. *Eur. J. Biochem.* **180**:133–141.
608. **Galloway, R. J., and B. L. Taylor.** 1980. Histidine starvation and adenosine 5'-triphosphate depletion in chemotaxis of *Salmonella typhimurium*. *J. Bacteriol.* **144**:1068–1075.
609. **Gan, K., S. D. Gupta, K. Sankaran, M. B. Schmid, and H. C. Wu.** 1993. Isolation and characterization of a temperature-sensitive mutant of *Salmonella typhimurium* defective in prolipoprotein modification. *J. Biol. Chem.* **268**:16544–16550.

610. **Gann, A. A., A. J. Campbell, J. F. Collins, A. F. Coulson, and N. E. Murray.** 1987. Reassortment of DNA recognition domains and the evolution of new specificities. *Mol. Microbiol.* **1**:13–22.
611. **Garber, B. B., and J. S. Gots.** 1980. Utilization of 2,6-diaminopurine by *Salmonella typhimurium*. *J. Bacteriol.* **143**:864–871.
612. **Garcia, E., S. Bancroft, S. G. Rhee, and S. Kustu.** 1977. The product of a newly identified gene, *glnF*, is required for synthesis of glutamine synthetase in *Salmonella*. *Proc. Natl. Acad. Sci. USA* **74**:1662–1666.
613. **Garcia-del Portillo, F., J. W. Foster, and B. B. Finlay.** 1993. Role of acid tolerance response genes in *Salmonella typhimurium* virulence. *Infect. Immun.* **61**:4489–4492.
614. **Garcia-del Portillo, F., J. W. Foster, M. E. Maguire, and B. B. Finlay.** 1992. Characterization of the micro-environment of *Salmonella typhimurium*-containing vacuoles within MDCK epithelial cells. *Mol. Microbiol.* **6**:3289–3297.
615. **Gardner, M. M., D. O. Hennig, and R. A. Kelln.** 1983. Control of the *arg* gene expression in *Salmonella typhimurium* by the arginine repressor from *Escherichia coli* K-12. *Mol. Gen. Genet.* **189**:458–462.
616. **Garrett, A. R., L. A. Johnson, and I. R. Beacham.** 1989. Isolation, molecular characterization and expression of the *ushB* gene of *Salmonella typhimurium* which encodes a membrane-bound UDP-sugar hydrolase. *Mol. Microbiol.* **3**:177–186.
617. **Garrido-Pertierra, A.** 1980. Isolation and properties of *Salmonella typhimurium* mutants defective in enolase. *Rev. Esp. Fisiol.* **36**:33–40.
618. **Garriga, X., S. Calero, and J. Barbe.** 1992. Nucleotide sequence analysis and comparison of the *lexA* genes from *Salmonella typhimurium*, *Erwinia carotovora*, *Pseudomonas aeruginosa* and *Pseudomonas putida*. *Mol. Gen. Genet.* **236**:125–134.
619. **Geerse, R. H., F. Izzo, and P. W. Postma.** 1989. The PEP:fructose phosphotransferase system in *Salmonella typhimurium*: FPr combines enzyme III_{Fru} and pseudo-HPr activities. *Mol. Gen. Genet.* **216**:517–525.
620. **Geerse, R. H., C. R. J. Ruig, A. R. J. Schuitema, and P. W. Postma.** 1986. Relationship between pseudo-HPr and the PEP: fructose phosphotransferase system in *Salmonella typhimurium* and *Escherichia coli*. *Mol. Gen. Genet.* **203**:435–444.
621. **Gemmill, R. M., J. W. Jones, G. W. Haughn, and J. M. Calvo.** 1983. Transcription initiation sites of the leucine operons of *Salmonella typhimurium* and *Escherichia coli*. *J. Mol. Biol.* **170**:39–59.
622. **Gemmill, R. M., M. Tripp, S. B. Friedman, and J. M. Calvo.** 1984. Promoter mutation causing catabolite repression of the *Salmonella typhimurium* leucine operon. *J. Bacteriol.* **158**:948–953.
623. **Gemmill, R. M., S. R. Wessler, E. B. Keller, and J. M. Calvo.** 1979. *Leu* operon of *Salmonella typhimurium* is controlled by an attenuation mechanism. *Proc. Natl. Acad. Sci. USA* **76**:4941–4945.
624. **Gemski, P., Jr., and B. A. D. Stocker.** 1967. Transduction by bacteriophage P22 in non-smooth mutants of *Salmonella typhimurium*. *J. Bacteriol.* **93**:1588–1597.
625. **Gerson, S. L., and B. Magasanik.** 1975. Regulation of the *hut* operons of *Salmonella typhimurium* and *Klebsiella aerogenes* by the heterologous *hut* repressors. *J. Bacteriol.* **124**:1269–1272.
626. **Ghangas, G. S., and D. B. Wilson.** 1984. Isolation and characterization of the *Salmonella typhimurium* LT2 xylose regulon. *J. Bacteriol.* **157**:158–164.
627. **Gibert, I., J. Barbe, and J. Casadesus.** 1990. Distribution of insertion sequence IS200 in *Salmonella* and *Shigella*. *J. Gen. Microbiol.* **136**:2555–2560.
628. **Gibert, I., and J. Casadesus.** 1990. *sulA*-independent division inhibition in *his*-constitutive strains of *Salmonella typhimurium*. *FEMS Microbiol. Lett.* **57**:205–210.
629. **Gibson, B. W., W. Melaugh, N. J. Phillips, M. A. Apicella, A. A. Campagnari, and J. M. Griffiss.** 1993. Investigation of the structural heterogeneity of lipooligosaccharides from pathogenic *Haemophilus* and *Neisseria* species and of R-type lipopolysaccharides from *Salmonella typhimurium* by electrospray mass spectrometry. *J. Bacteriol.* **175**:2702–2712.
630. **Gibson, M. M., D. A. Bagga, C. G. Miller, and M. E. Maguire.** 1991. Magnesium transport in

- Salmonella typhimurium*: the influence of new mutations conferring Co₂⁺ resistance on the CorA Mg²⁺ transport system. *Mol. Microbiol.* **5**:2753–2762.
631. **Gibson, M. M., E. M. Ellis, K. A. Graeme-Cook, and C. F. Higgins.** 1987. OmpR and EnvZ are pleiotropic regulatory proteins: positive regulation of the tripeptide permease (*tppB*) of *Salmonella typhimurium*. *Mol. Gen. Genet.* **207**:120–129.
632. **Gibson, M. M., M. Price, and C. F. Higgins.** 1984. Genetic characterization and molecular cloning of the tripeptide permease (*tpp*) genes of *Salmonella typhimurium*. *J. Bacteriol.* **160**:122–130.
633. **Gillen, K. L., and K. T. Hughes.** 1991. Molecular characterization of *flgM*, a gene encoding a negative regulator of flagellin synthesis in *Salmonella typhimurium*. *J. Bacteriol.* **173**:6453–6459.
634. **Gillen, K. L., and K. T. Hughes.** 1991. Negative regulatory loci coupling flagellin synthesis to flagellar assembly in *Salmonella typhimurium*. *J. Bacteriol.* **173**:2301–2310.
635. **Gillen, K. L., and K. T. Hughes.** 1993. Transcription from two promoters and autoregulation contribute to the control of expression of the *Salmonella typhimurium* flagellar regulatory gene *flgM*. *J. Bacteriol.* **175**:7006–7015.
636. **Gilman, R. H., R. B. Hornick, W. E. Woodward, H. L. Dupont, M. J. Snyder, M. M. Levine, and J. P. Libonti.** 1977. Evaluation of a UDP glucose-4-epimeraseless mutant of *Salmonella typhi* as a live oral vaccine. *J. Infect. Dis.* **136**:717–723.
637. **Gilson, E., C. F. Higgins, M. Hofnung, G. Ferro-Luzzi Ames, and H. Nikaido.** 1982. Extensive homology between membrane-associated components of histidine and maltose transport systems of *Salmonella typhimurium* and *Escherichia coli*. *J. Biol. Chem.* **257**:9915–9918.
638. **Ginocchio, C., J. Pace, and J. E. Galan.** 1992. Identification and molecular characterization of a *Salmonella typhimurium* gene involved in triggering the internalization of salmonellae into cultured epithelial cells. *Proc. Natl. Acad. Sci. USA* **89**:5976–5980.
639. **Ginocchio, C. C., S. B. Olmsted, C. L. Wells, and J. E. Galan.** 1994. Contact with epithelial cells induces the formation of surface appendages on *Salmonella typhimurium*. *Cell* **76**:717–724.
640. **Ginther, C. L., and J. L. Ingraham.** 1974. Nucleoside diphosphokinase of *Salmonella typhimurium*. *J. Biol. Chem.* **249**:3406–3411.
641. **Ginther, C. L., and J. L. Ingraham.** 1974. Cold-sensitive mutant of *Salmonella typhimurium* defective in nucleosidediphosphokinase. *J. Bacteriol.* **118**:1020–1026.
642. **Glanville, E. V., and M. Demerec.** 1960. Threonine, isoleucine and isoleucine-valine mutants of *Salmonella typhimurium*. *Genetics* **45**:1359–1374.
643. **Glasgow, A. C., M. F. Bruist, and M. I. Simon.** 1989. DNA-binding properties of the Hin recombinase. *J. Biol. Chem.* **264**:10072–10082.
644. **Gmeiner, J., and S. Schlecht.** 1979. Molecular organization of the outer membrane of *Salmonella typhimurium*. *Eur. J. Biochem.* **93**:609–620.
645. **Goitein, R. K., and S. M. Parsons.** 1980. Possible regulation of the *Salmonella typhimurium* histidine operon by adenosine triphosphate phosphoribosyltransferase: large metabolic effects. *J. Bacteriol.* **144**:337–345.
646. **Goldberger, R. F.** 1974. Autogenous regulation of gene expression. *Science* **183**:810–816.
647. **Goldberger, R. F., and J. S. Kovach.** 1972. Regulation of histidine biosynthesis in *Salmonella typhimurium*. *Curr. Top. Cell. Regul.* **5**:285–308.
648. **Goldman, B. S., and J. R. Roth.** 1993. Genetic structure and regulation of the *cysG* gene in *Salmonella typhimurium*. *J. Bacteriol.* **175**:1457–1466.
649. **Goldman, R., W. Kohlbrenner, P. Lartey, and A. Pernet.** 1987. Antibacterial agents specifically inhibiting lipopolysaccharide synthesis. *Nature (London)* **329**:162–164.
650. **Goldman, R. C., and E. M. Devine.** 1987. Isolation of *Salmonella typhimurium* strains that utilize exogenous 3-deoxy-D-manno-octulosonate for synthesis of lipopolysaccharide. *J. Bacteriol.* **169**:5060–5065.
651. **Goldman, R. C., C. C. Doran, and J. O. Capobianco.** 1988. Analysis of lipopolysaccharide biosynthesis in *Salmonella typhimurium* and *Escherichia coli* by using agents which specifically block incorporation of 3-deoxy-D-manno-octulosonate. *J. Bacteriol.* **170**:2185–2191.
652. **Goldman, R. C., and F. Hunt.** 1990. Mechanism of O-antigen distribution in lipopolysaccharide.

- J. Bacteriol.* **172**:5352–5359.
653. **Goldman, R. C., and L. Leive.** 1980. Heterogeneity of antigenic-side-chain length in lipopolysaccharide from *Escherichia coli* O111 and *Salmonella typhimurium* LT2. *Eur. J. Biochem.* **107**:145–153.
654. **Goldrick, D., G.-Q. Yu, S.-Q. Jiang, and J.-S. Hong.** 1988. Nucleotide sequence and transcription start point of the phosphoglycerate transporter gene of *Salmonella typhimurium*. *J. Bacteriol.* **170**:3421–3426.
655. **Gollub, E., H. Zalkin, and D. B. Sprinson.** 1966. Correlation of genes and enzymes, and studies on regulation of the aromatic pathway in *Salmonella*. *J. Biol. Chem.* **242**:5323–5328.
656. **Gollub, E. G., and J. S. Gots.** 1959. Purine metabolism in bacteria. VI. Accumulations by mutants lacking adenylosuccinase. *J. Bacteriol.* **78**:320–325.
657. **Gollub, E. G., K. P. Liu, and D. B. Sprinson.** 1973. A regulatory gene of phenylalanine biosynthesis (*pheR*) in *Salmonella typhimurium*. *J. Bacteriol.* **115**:121–128.
658. **Gollub, E. G., K. P. Liu, and D. B. Sprinson.** 1973. *tyrR*, a regulatory gene of tyrosine biosynthesis in *Salmonella typhimurium*. *J. Bacteriol.* **115**:1094–1102.
659. **Gomez-Eichelmann, M. C.** 1979. Deoxyribonucleic acid adenine and cytosine methylation in *Salmonella typhimurium* and *Salmonella typhi*. *J. Bacteriol.* **140**:574–579.
660. **Gomez-Eichelmann, M. C., and H. K. Torres.** 1983. Stability of plasmids R1–19 and R100 in hyper-recombinant *Escherichia coli* strains and in *Salmonella typhimurium* strains. *J. Bacteriol.* **154**:1493–1497.
661. **Goncharoff, P., and B. P. Nichols.** 1988. Evolution of aminobenzoate synthases: nucleotide sequences of *Salmonella typhimurium* and *Klebsiella aerogenes pabB*. *Mol. Biol. Evol.* **5**:531–548.
662. **Goodell, E. W., and C. F. Higgins.** 1987. Uptake of cell wall peptides by *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **169**:3861–3865.
663. **Gopinathan, K. P., and A. Garen.** 1970. A leucyl-transfer RNA specified by the amber suppressor gene *Su6*⁺. *J. Mol. Biol.* **47**:393–401.
664. **Gots, J. S.** 1971. Regulation of purine and pyrimidine metabolism, p. 225–255. In H. J. Vogel (ed.), *Metabolic Regulation*, vol. 5 in D. Greenberg (ed.), *Metabolic Pathways*. Academic Press, Inc., New York.
665. **Gots, J. S., and C. E. Benson.** 1974. Genetic control of bacterial purine phosphoribosyltransferases and an approach to gene enrichment, p. 33–39. In O. Sperling, A. de Vries, and J. B. Wyngaarden (ed.), *Purine Metabolism in Man*. Plenum Publishing Corp, New York.
666. **Gots, J. S., C. E. Benson, and S. R. Shumas.** 1972. Genetic separation of hypoxanthine and guanine-xanthine phosphoribosyltransferase activities by deletion mutations in *Salmonella typhimurium*. *J. Bacteriol.* **112**:910–916.
667. **Gots, J. S., F. R. Dalal, and S. R. Shumas.** 1969. Genetic separation of the inosinic acid cyclohydrolase-transformylase complex of *Salmonella typhimurium*. *J. Bacteriol.* **99**:441–449.
668. **Gots, J. S., and E. G. Gollub.** 1957. Sequential blockade in adenine biosynthesis by genetic loss of an apparent bifunctional deacylase. *Proc. Natl. Acad. Sci. USA* **43**:826–834.
669. **Grabau, C., and J. R. Roth.** 1992. A *Salmonella typhimurium* cobalamin-deficient mutant blocked in 1-amino-2-propanol synthesis. *J. Bacteriol.* **174**:2138–2144.
670. **Graeme-Cook, K. A., G. May, E. Bremer, and C. F. Higgins.** 1989. Osmotic regulation of porin expression: a role for DNA supercoiling. *Mol. Microbiol.* **3**:1287–1294.
671. **Graf, L. H., Jr., and R. O. Burns.** 1973. The *supX/leu-500* mutations and expression of the leucine operon. *Mol. Gen. Genet.* **126**:291–301.
672. **Graf, L. H., Jr., R. Kim, and R. O. Burns.** 1974. New class of streptomycin-resistant mutants incompatible with *supX* suppressor mutations in *Salmonella typhimurium*. *J. Bacteriol.* **120**:1315–1321.
673. **Graham, A. C., and B. A. D. Stocker.** 1977. Genetics of sensitivity of *Salmonella* species to colicin M and bacteriophages T5, T1 and ES18. *J. Bacteriol.* **130**:1214–1223.
674. **Greeb, J., J. F. Atkins, and J. C. Loper.** 1971. Histidinol dehydrogenase (*hisD*) mutants of *Salmonella typhimurium*. *J. Bacteriol.* **106**:421–431.

675. **Green, L., and C. G. Miller.** 1980. Genetic mapping of the *Salmonella typhimurium pepB* locus. *J. Bacteriol.* **143**:1524–1526.
676. **Grenier, F. C., E. B. Waygood, and M. H. Saier, Jr.** 1986. The bacterial phosphotransferase system: kinetic characterization of the glucose, mannitol, glucitol, and N-acetylglucosamine systems. *J. Cell. Biochem.* **31**:97–105.
677. **Grieshaber, M.** 1978. On the evolution of an oligocephalic enzyme. Glutamine chorismate amidotransferase-free anthranilate phosphoribosyl transferases from mutant strains of *Salmonella typhimurium*. *Z. Naturforsch. Teil C Biosci.* **33**:235–244.
678. **Grieshaber, M., and R. Bauerle.** 1972. Structure and evolution of a bifunctional enzyme of the tryptophan operon. *Nature (London) New Biol.* **236**:232–235.
679. **Grieshaber, M., and R. Bauerle.** 1974. Monomeric and dimeric forms of component II of the anthranilate synthetase-anthranilate 5-phosphoribosylpyrophosphate phosphoribosyltransferase complex of *Salmonella typhimurium*. Implications concerning the mode of assembly of the complex. *Biochemistry* **13**:232–235.
680. **Griffin, H. G.** 1990. Nucleotide sequence of the *Salmonella serC* gene. *Nucleic Acids Res.* **18**:4260.
681. **Grill, H., N. Weigel, B. J. Gaffney, and S. Roseman.** 1982. Sugar transport by bacterial phosphotransferase system. Radioactive and electron paramagnetic resonance labelling of the *Salmonella typhimurium* phosphocarrier protein (HPr) at the NH₂-terminal methionine. *J. Biol. Chem.* **257**:24510–24517.
682. **Gritzmacher, C. A., and M. Levinthal.** 1976. A mutation amplifying the genes carried by the pi histidine plasmid. *ICN-UCLA Symp. Mol. Cell. Biol.* **5**:479–485.
683. **Grodberg, J., and J. J. Dunn.** 1989. Comparison of *Escherichia coli* K-12 outer membrane protease OmpT and *Salmonella typhimurium* E protein. *J. Bacteriol.* **171**:2903–2905.
684. **Groisman, E. A., E. Chiao, C. J. Lipps, and F. Heffron.** 1989. *Salmonella typhimurium phoP* virulence gene is a transcriptional regulator. *Proc. Natl. Acad. Sci. USA* **86**:7077–7081.
685. **Groisman, E. A., and H. Ochman.** 1993. Cognate gene clusters govern invasion of host epithelial cells by *Salmonella typhimurium* and *Shigella flexneri*. *EMBO J.* **12**:3779–3787.
686. **Groisman, E. A., C. Parra-Lopez, M. Salcedo, C. J. Lipps, and F. Heffron.** 1992. Resistance to host antimicrobial peptides is necessary for *Salmonella* virulence. *Proc. Natl. Acad. Sci. USA* **89**:11939–11943.
687. **Groisman, E. A., M. H. Saier, Jr., and H. Ochman.** 1992. Horizontal transfer of a phosphatase gene as evidence for mosaic structure of the *Salmonella* genome. *EMBO J.* **11**:1309–1316.
688. **Groisman, E. A., M. A. Sturmoski, F. R. Solomon, R. Lin, and H. Ochman.** 1993. Molecular, functional, and evolutionary analysis of sequences specific to *Salmonella*. *Proc. Natl. Acad. Sci. USA* **90**:1033–1037.
689. **Gross, S. R., R. O. Burns, and H. E. Umbarger.** 1963. The biosynthesis of leucine. II. The enzymic isomerization of α -carboxy- β -hydroxyisocaproate and α -hydroxy- β -carboxyisocaproate. *Biochemistry* **2**:1046–1052.
690. **Gross, T. S., and R. J. Rowbury.** 1969. Methionyl transfer RNA synthetase mutants of *Salmonella typhimurium* which have normal control of the methionine biosynthetic enzymes. *Biochim. Biophys. Acta* **184**:233–236.
691. **Gross, T. S., and R. J. Rowbury.** 1971. Biochemical and physiological properties of methionyl-sRNA synthetase mutants of *Salmonella typhimurium*. *J. Gen. Microbiol.* **65**:5–21.
692. **Grossman, N., M. A. Schmetz, J. Foulds, E. N. Klima, V. Jiminez, L. L. Leive, and K. K. Joiner.** 1987. Lipopolysaccharide size and distribution determine serum resistance in *Salmonella montevideo*. *J. Bacteriol.* **169**:856–863.
693. **Grove, T. H., and H. R. Levy.** 1975. Anthranilate synthetase-anthranilate 5-phosphoribosylpyrophosphate phosphoribosyltransferase from *Salmonella typhimurium*. Inactivation of glutamine-dependent anthranilate synthetase by agarose-bound anthranilate. *Biochim. Biophys. Acta* **397**:80–93.
694. **Grove, T. H., and H. R. Levy.** 1976. Anthranilate synthase-anthranilate 5-

- phosphoribosylpyrophosphate phosphoribosyltransferase from *Salmonella typhimurium*. Purification of the enzyme complex and analysis of multiple forms. *Biochim. Biophys. Acta* **445**:464–474.
695. **Grubmeyer, C. T., and W. R. Gray.** 1986. A cysteine residue (cysteine-116) in the histidinol binding site of histidinol dehydrogenase. *Biochemistry* **25**:4778–4784.
696. **Grubmeyer, C. T., S. Insinga, M. Bhatia, and N. Moazami.** 1989. *Salmonella typhimurium* histidinol dehydrogenase: complete reaction stereochemistry and active site mapping. *Biochemistry* **28**:8174–8180.
697. **Grundy, C. E., and P. D. Ayling.** 1992. Fine structure mapping and complementation studies of the *metD* methionine transport system in *Salmonella typhimurium*. *Genet. Res.* **60**:1–6.
698. **Guerrero, R., and J. Barbe.** 1982. Expression of *recA*-gene dependent SOS functions in *Salmonella typhimurium*. *Antonie Van Leeuwenhoek J. Microbiol. Serol.* **48**:159–167.
699. **Guggenheim, S., and M. Flavin.** 1969. Cystathionine α -synthase from *Salmonella*. β Elimination and replacement reactions and inhibition by *O*-succinylserine. *J. Biol. Chem.* **244**:3722–3727.
700. **Gulig, P. A., and V. A. Chiodo.** 1990. Genetic and DNA sequence analysis of the *Salmonella typhimurium* virulence plasmid gene encoding the 28,000-molecular-weight protein. *Infect. Immun.* **58**:2651–2658.
701. **Gulig, P. A., and R. Curtiss.** 1988. Cloning and transposon insertion mutagenesis of virulence genes of the 100-kilobase plasmid of *Salmonella typhimurium*. *Infect. Immun.* **56**:3262–3271.
702. **Gulig, P. A., H. Danbara, D. G. Guiney, A. J. Lax, F. Norel, and M. Rhen.** 1993. Molecular analysis of *spv* virulence genes of the *Salmonella* virulence plasmids. *Mol. Microbiol.* **7**:825–830.
703. **Gupta, S. D., K. Gan, M. B. Schmid, and H. C. Wu.** 1993. Characterization of a temperature-sensitive mutant of *Salmonella typhimurium* defective in apolipoprotein N-acyltransferase. *J. Biol. Chem.* **268**:16551–16556.
704. **Gustafsson, C., P. H. R. Lindstrom, T. G. Hagervall, K. B. Esberg, and G. R. Bjork.** 1991. The *trmA* promoter has regulatory features and sequence elements in common with the rRNA P1 promoter family of *Escherichia coli*. *J. Bacteriol.* **173**:1757–1764.
705. **Guterman, S. K., and A. Wright.** 1974. Effect of mutator mutation of *Salmonella typhimurium* on P22 and R factor genes. *J. Bacteriol.* **119**:638–639.
706. **Guterman, S. K., A. Wright, and D. H. Boyd.** 1975. Genes affecting coliphage BF23 and E colicin sensitivity in *Salmonella typhimurium*. *J. Bacteriol.* **124**:1351–1358.
707. **Gutierrez, J. A., and L. N. Csonka.** 1995. Isolation and characterization of adenylate kinase (*adk*) mutations in *Salmonella typhimurium* which block the ability of glycine betaine to function as an osmoprotectant. *J. Bacteriol.* **177**:390–400.
708. **Gutterson, N. I., and D. E. Koshland, Jr.** 1983. Replacement and amplification of bacterial genes with sequences altered *in vitro*. *Proc. Natl. Acad. Sci. USA* **80**:4894–4898.
709. **Haber, L. T., P. P. Pang, D. I. Sobell, J. A. Mankovich, and G. C. Walker.** 1988. Nucleotide sequence of the *Salmonella typhimurium mutS* gene required for mismatch repair: homology of MutS and HexA of *Streptococcus pneumoniae*. *J. Bacteriol.* **170**:197–202.
710. **Haber, L. T., and G. C. Walker.** 1991. Altering the conserved nucleotide binding motif in the *Salmonella typhimurium* MutS mismatch repair protein affects both its ATPase and mismatch binding activities. *EMBO J.* **10**:2707–2715.
711. **Hackett, J., P. Wyk, P. Reeves, and V. Mathan.** 1987. Mediation of serum resistance in *Salmonella typhimurium* by an 11-kilodalton polypeptide encoded by the cryptic plasmid. *J. Infect. Dis.* **155**:540–549.
712. **Haefner-Gormley, L., Z. D. Chen, H. Zalkin, and R. F. Colman.** 1991. Evaluation of cysteine 283 and glutamic acid 284 in the coenzyme binding site of *Salmonella typhimurium* glutamate dehydrogenase by site-directed mutagenesis and reaction with the nucleotide analogue 2-((4-bromo-2,3-dioxobutyl)thio)-1, N^6 -ethenoadenosine 2',5'-bisphosphate. *J. Biol. Chem.* **266**:5388–5394.
713. **Hafner, L. M., and D. G. MacPhee.** 1991. Precise excision of Tn10 in *Salmonella typhimurium*: effects of mutations in the *polA*, *dam*, *mutH*, and *mutB* genes and of methionine or ethionine in the plating medium. *Mutat. Res.* **263**:179–184.
714. **Hagen, D. C., S. L. Gerson, and B. Magasanik.** 1975. Isolation of super-repressor mutants in the

- histidine utilization system of *Salmonella typhimurium*. *J. Bacteriol.* **121**:583–593.
715. **Hagen, D. C., P. J. Lipton, and B. Magasanik.** 1974. Isolation of a *trans*-dominant histidase-negative mutant of *Salmonella typhimurium*. *J. Bacteriol.* **120**:906–916.
716. **Hagen, D. C., and B. Magasanik.** 1973. Isolation of the self-regulated repressor protein of the *hut* operons of *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **70**:808–812.
717. **Hagen, D. C., and B. Magasanik.** 1976. Deoxyribonucleic acid-binding studies on the *hut* repressor and mutant forms of the *hut* repressor on *Salmonella typhimurium*. *J. Bacteriol.* **127**:837–847.
718. **Hahn, D. R., and S. R. Maloy.** 1986. Regulation of the *put* operon in *Salmonella typhimurium*: characterization of promoter and operator mutations. *Genetics* **114**:687–703.
719. **Hahn, D. R., R. S. Myers, C. R. Kent, and S. R. Maloy.** 1988. Regulation of proline utilization in *Salmonella typhimurium*: molecular characterization of the *put* operon, and DNA sequence of the *put* control region. *Mol. Gen. Genet.* **213**:125–133.
720. **Hakura, A., K. Morimoto, T. Sofuni, and T. Nohmi.** 1991. Cloning and characterization of the *Salmonella typhimurium ada* gene, which encodes O⁶-methylguanine-DNA methyltransferase. *J. Bacteriol.* **173**:3663–3672.
721. **Hall, B. G.** 1993. The role of single-mutant intermediates in the generation of *trpAB* double revertants during prolonged selection. *J. Bacteriol.* **175**:6411–6414.
722. **Hall, G. W., D. O. Silva, T. Melton, and W. J. Dobrogosz.** 1980. Catabolite repression and inducer exclusion in *Salmonella typhimurium* mutants possessing deletions in the *pts* locus, abstr. K94, p. 142. *Abstr. Annu. Meet. Am. Soc. Microbiol., 1980.*
723. **Hallenbeck, P. C., M. A. Clark, and E. L. Barrett.** 1989. Characterization of anaerobic sulfite reduction by *Salmonella typhimurium* and purification of the anaerobically induced sulfite reductase. *J. Bacteriol.* **171**:3008–3015.
724. **Hamilton, S., and C. G. Miller.** 1992. Cloning and nucleotide sequence of the *Salmonella typhimurium dcp* gene encoding dipeptidyl carboxypeptidase. *J. Bacteriol.* **174**:1626–1630.
725. **Hammerling, G., V. Lehmann, and O. Luderitz.** 1973. Structural studies on the heptose region of *Salmonella* lipopolysaccharides. *Eur. J. Biochem.* **38**:453–458.
726. **Hammond, S. M., A. Claesson, A. M. Jansson, L.-G. Larsson, B. G. Pring, C. M. Town, and B. Ekstrom.** 1987. A new class of synthetic antibacterials acting on lipopolysaccharide biosynthesis. *Nature (London)* **327**:730–732.
727. **Hampton, M. J., R. A. Floyd, J. B. Clark, and J. H. Lancaster.** 1980. Studies of the fatty acid composition and membrane microviscosity in *Salmonella typhimurium* TA98. *Chem. Phys. Lipids* **27**:177–183.
728. **Han, B. D., W. G. Nolan, H. P. Hopkins, R. T. Jones, J. L. Ingraham, and A. T. Abdelal.** 1990. Effect of growth temperature on folding of carbamoylphosphate synthetases of *Salmonella typhimurium* and a cold-sensitive derivative. *J. Bacteriol.* **172**:5089–5096.
729. **Hanau, R., R. K. Koduri, N. Ho, and J. E. Brenchley.** 1983. Nucleotide sequence of the control regions for the *glnA* and *glnL* genes of *Salmonella typhimurium*. *J. Bacteriol.* **155**:82–89.
730. **Hannavy, K., G. C. Barr, C. J. Dorman, J. Adamson, L. R. Mazengera, M. P. Gallagher, J. S. Evans, B. A. Levine, I. P. Trayer, and C. F. Higgins.** 1990. TonB protein of *Salmonella typhimurium*. A model for signal transduction between membranes. *J. Mol. Biol.* **216**:897–910.
731. **Hansen, F. G., T. Atlung, R. E. Braun, A. Wright, P. Hughes, and M. Kohiyama.** 1991. Initiator (DnaA) protein concentration as a function of growth rate in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **173**:5194–5199.
732. **Hansen-Hagge, T., V. Lehmann, U. Seydel, B. Linder, and U. Zahringer.** 1985. Isolation and structural analysis of two lipid A precursors from a KDO deficient mutant of *Salmonella typhimurium* differing in their hexadecanoic acid content. *Arch. Microbiol.* **141**:353–358.
733. **Harlow, K. W., and R. L. Switzer.** 1990. Chemical modification of *Salmonella typhimurium* phosphoribosylpyrophosphate synthetase with 5′-(p-fluorosulfonylbenzoyl)adenosine. Identification of an active site histidine. *J. Biol. Chem.* **265**:5487–5493.
734. **Harlow, K. W., and R. L. Switzer.** 1990. Sulfhydryl chemistry of *Salmonella typhimurium*

- phosphoribosylpyrophosphate synthetase: identification of two classes of cysteinyl residues. *Arch. Biochem. Biophys.* **276**:466–472.
735. **Harms, E., J.-H. Hsu, C. S. Subrahmanyam, and H. E. Umbarger.** 1985. Comparison of the regulatory regions of *ilvGEDA* operons from several enteric organisms. *J. Bacteriol.* **164**:207–216.
736. **Hartman, P. E., Z. Hartman, and D. Serman.** 1970. Complementation mapping by abortive transduction of histidine-requiring *Salmonella* mutants. *J. Gen. Microbiol.* **22**:354–368.
737. **Hartman, P. E., Z. Hartman, R. C. Stahl, and B. N. Ames.** 1971. Classification and mapping of spontaneous and induced mutations in the histidine operon of *Salmonella*. *Adv. Genet.* **17**:1–34.
738. **Hartman, P. E., J. C. Loper, and D. Serman.** 1960. Fine structure mapping by complete transduction between histidine-requiring *Salmonella* mutants. *J. Gen. Microbiol.* **22**:323–353.
739. **Hatfield, G. W., and R. O. Burns.** 1970. Specific binding of leucyl transfer RNA to an immature form of L-threonine deaminase: its implications in repression. *Proc. Natl. Acad. Sci. USA* **66**:1027–1035.
740. **Hattman, S.** 1971. Variation of 6-methylaminopurine content in bacteriophage P22 deoxyribonucleic acid as a function of host specificity. *J. Virol.* **7**:690–691.
741. **Hattman, S., S. Schlagman, L. Goldstein, and M. Frohlich.** 1976. *Salmonella typhimurium* SA host specificity system is based on deoxyribonucleic acid-adenine methylation. *J. Bacteriol.* **127**:211–217.
742. **Haughn, G. W., S. R. Wessler, R. M. Gemmill, and J. M. Calvo.** 1986. High A+T content conserved in DNA sequences upstream of *leuABCD* in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **166**:1113–1117.
743. **He, X.-S., M. Rivkina, B. A. D. Stocker, and W. S. Robinson.** 1994. Hypervariable region IV of *Salmonella* gene *fliC^d* encodes a dominant surface epitope and a stabilizing factor for functional flagella. *J. Bacteriol.* **176**:2406–2414.
744. **Heasley, F. A.** 1981. Reducing terminus of *O*-haptene accumulated in a *Salmonella montevideo galE* mutant. *J. Bacteriol.* **145**:624–627.
745. **Heffernan, E. J., J. Harwood, J. Fierer, and D. Guiney.** 1992. The *Salmonella typhimurium* virulence plasmid complement resistance gene *rck* is homologous to a family of virulence-related outer membrane protein genes, including *pagC* and *ail*. *J. Bacteriol.* **174**:84–91.
746. **Heffernan, E. J., S. Reed, J. Hackett, J. Fierer, C. Roudier, and D. Guiney.** 1992. Mechanism of resistance to complement-mediated killing of bacteria encoded by the *Salmonella typhimurium* virulence plasmid gene *rck*. *J. Clin. Invest.* **90**:953–964.
747. **Heichman, K. A., and R. C. Johnson.** 1990. The *Hin* invertasome: protein-mediated joining of distant recombination sites at the enhancer. *Science* **249**:511–517.
748. **Heiman, C., and C. G. Miller.** 1978. *Salmonella typhimurium* mutants lacking protease II. *J. Bacteriol.* **135**:588–594.
749. **Heiman, C., and C. G. Miller.** 1978. Acylamino acid esterase mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **164**:57–62.
750. **Helander, I. M., L. Hirvas, J. Tuominen, and M. Vaara.** 1992. Preferential synthesis of heptaacyl lipopolysaccharide by the *ssc* permeability mutant of *Salmonella typhimurium*. *Eur. J. Biochem.* **204**:1101–1106.
751. **Helander, I. M., M. Vaara, S. Sukupolvi, M. Rhen, S. Saarela, U. Zahringer, and P. H. Makela.** 1989. *rfaP* mutants of *Salmonella typhimurium*. *Eur. J. Biochem.* **185**:541–546.
752. **Hellerqvist, C. G.** 1971. Structural studies of the common-core polysaccharide of the cell-wall lipopolysaccharide from *Salmonella typhimurium*. *Carbohydr. Res.* **16**:39–48.
753. **Helmann, J. D., and M. J. Chamberlin.** 1987. DNA sequence analysis suggests that expression of flagellar and chemotaxis genes in *Escherichia coli* and *Salmonella typhimurium* is controlled by an alternative σ factor. *Proc. Natl. Acad. Sci. USA* **84**:6422–6424.
754. **Henderson, G. B., S. Shaltiel, and E. E. Snell.** 1974. ω -Aminoalkylagaroses in the purification of the L-histidinolphosphate aminotransferase. *Biochemistry* **13**:4335–4338.
755. **Henderson, G. B., and E. E. Snell.** 1973. Crystalline L-histidinolphosphate aminotransferase from *Salmonella typhimurium*. *J. Biol. Chem.* **248**:1906–1911.

756. **Hengge, R., and W. Boos.** 1985. Defective secretion of maltose- and ribose-binding proteins caused by a truncated periplasmic protein in *Escherichia coli*. *J. Bacteriol.* **162**:972–978.
757. **Hengge, R., T. J. Larson, and W. Boos.** 1983. *sn*-Glycerol-3-phosphate transport in *Salmonella typhimurium*. *J. Bacteriol.* **155**:186–195.
758. **Henikoff, S., G. W. Haughn, J. M. Calvo, and J. C. Wallace.** 1988. A large family of bacterial activator proteins. *Proc. Natl. Acad. Sci. USA* **85**:6602–6606.
759. **Herrera, G., A. Urios, V. Aleixandre, and M. Blanco.** 1988. UV light-induced mutability in *Salmonella* strains containing the *umuDC* or the *mucAB* operon: evidence for a *umuC* function. *Mutat. Res.* **198**:9–13.
760. **Hertzberg, K. M., R. Gemmill, J. Jones, and J. M. Calvo.** 1979. Cloning of an *EcoRI* generated fragment of the leucine operon of *Salmonella typhimurium*. *Gene* **8**:135–152.
761. **Hess, J. F., K. Oosawa, N. Kaplan, and M. I. Simon.** 1988. Phosphorylation of three proteins in the signaling pathway of bacterial chemotaxis. *Cell* **53**:78–87.
762. **Higgins, C. F., and G. F.-L. Ames.** 1981. Two periplasmic transport proteins which interact with a common membrane receptor show extensive homology: complete nucleotide sequences. *Proc. Natl. Acad. Sci. USA* **78**:6038–6042.
763. **Higgins, C. F., and G. F.-L. Ames.** 1982. Regulatory regions of two transport operons under nitrogen control: nucleotide sequences. *Proc. Natl. Acad. Sci. USA* **79**:1083–1087.
764. **Higgins, C. F., C. J. Dorman, D. A. Stirling, L. Waddell, I. R. Booth, G. May, and E. Bremer.** 1988. A physiological role for DNA supercoiling in the osmotic regulation of gene expression in *S. typhimurium* and *E. coli*. *Cell* **52**:569–584.
765. **Higgins, C. F., and M. M. Gibson.** 1984. Peptide transport in bacteria. *Methods Enzymol.* **125**:365–377.
766. **Higgins, C. F., P. D. Haag, K. Nikaido, F. Ardeshir, G. Garcia, and G. F.-L. Ames.** 1982. Complete nucleotide sequence and identification of membrane components of the histidine transport operon of *S. typhimurium*. *Nature (London)* **298**:723–727.
767. **Higgins, C. F., and M. M. Hardie.** 1983. Periplasmic protein associated with the oligopeptide permeases of *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **155**:1434–1438.
768. **Higgins, C. F., M. M. Hardie, D. Jamieson, and L. M. Powell.** 1983. Genetic map of the *opp* (oligopeptide permease) locus of *Salmonella typhimurium*. *J. Bacteriol.* **153**:830–836.
769. **Higgins, C. F., I. D. Hiles, K. Whalley, and D. J. Jamieson.** 1985. Nucleotide binding by membrane components of bacterial periplasmic binding protein-dependent transport systems. *EMBO J.* **4**:1033–1039.
770. **Higgins, C. F., J. C. D. Hinton, C. S. J. Hulton, T. Owen-Hughes, and A. Serirafi.** 1990. Protein H1: a role for chromatin structure in the regulation of bacterial gene expression and virulence? *Mol. Microbiol.* **4**:2007–2012.
771. **Higgins, C. F., R. S. McLaren, and S. F. Newbury.** 1988. Repetitive extragenic palindromic sequences, mRNA stability and gene expression: evolution by gene conversion? A review. *Gene* **72**:3–14.
772. **Higgins, C. F., L. Sutherland, J. Cairney, and I. R. Booth.** 1987. The osmotically regulated *proU* locus of *Salmonella typhimurium* encodes a periplasmic betaine-binding protein. *J. Gen. Microbiol.* **133**:305–310.
773. **Higgins, N. P., and D. Hillyard.** 1988. Primary structure and mapping of the *hupA* gene of *Salmonella typhimurium*. *J. Bacteriol.* **170**:5751–5758.
774. **Hildenbrand, K., L. Brand, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Nanosecond fluorescence studies of the phosphocarrier protein (HPr) labelled at the NH₂-terminal methionine. *J. Biol. Chem.* **257**:14518–14525.
775. **Hiles, I. D., M. P. Gallagher, D. J. Jamieson, and C. F. Higgins.** 1987. Molecular characterization of the oligopeptide permease of *Salmonella typhimurium*. *J. Mol. Biol.* **195**:125–142.
776. **Hiles, I. D., and C. F. Higgins.** 1986. Peptide uptake by *Salmonella typhimurium*. The periplasmic oligopeptide-binding protein. *Eur. J. Biochem.* **158**:561–567.
777. **Hiles, I. D., L. M. Powell, and C. F. Higgins.** 1987. Peptide transport in *Salmonella*

- typhimurium*: molecular cloning and characterization of the oligopeptide permease genes. *Mol. Gen. Genet.* **206**:101–109.
778. **Hill-Chappell, J. M., M. P. Spector, and J. W. Foster.** 1986. The pyridine nucleotide cycle of *Salmonella typhimurium*: genetic characterization of the *pncXA* operon. *Mol. Gen. Genet.* **205**:507–514.
779. **Hillyard, D. R., M. Edlund, K. T. Hughes, M. Marsh, and N. P. Higgins.** 1990. Subunit-specific phenotypes of *Salmonella typhimurium* HU mutants. *J. Bacteriol.* **172**:5402–5407.
780. **Hinton, J. C., D. S. Santos, A. Seirafi, C. S. Hulton, G. D. Pavitt, and C. F. Higgins.** 1992. Expression and mutational analysis of the nucleoid-associated protein H-NS of *Salmonella typhimurium*. *Mol. Microbiol.* **6**:2327–2337.
781. **Hirano, T., S. Yamaguchi, K. Oosawa, and S.-I. Aizawa.** 1994. Roles of FliK and FlhB in determination of flagellar hook length in *Salmonella typhimurium*. *J. Bacteriol.* **176**:5439–5449.
782. **Hirvas, L., J. Coleman, P. Koski, and M. Vaara.** 1990. Bacterial “histone-like protein I” (HLP-I) is an outer membrane constituent? *FEBS Lett.* **262**:123–126.
783. **Hirvas, L., P. Koski, and M. Vaara.** 1990. Primary structure and expression of the Ssc-protein of *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.* **173**:53–59.
784. **Hirvas, L., P. Koski, and M. Vaara.** 1991. Identification and sequence analysis of the gene mutated in the conditionally lethal outer membrane permeability mutant SS-C of *Salmonella typhimurium*. *EMBO J.* **10**:1017–1023.
785. **Hirvas, L., and M. Vaara.** 1992. Effect of Ssc protein mutations on the outer membrane permeability barrier function in *Salmonella typhimurium*: a study using *ssc* mutant alleles made by site-directed mutagenesis. *FEMS Microbiol. Lett.* **69**:289–294.
786. **Hitchcock, P. J., and T. M. Brown.** 1983. Morphological heterogeneity among *Salmonella* lipopolysaccharide chemotypes in silver-stained polyacrylamide gels. *J. Bacteriol.* **154**:269–277.
787. **Hmiel, S. P., M. D. Snavely, J. B. Florer, M. E. Maguire, and C. G. Miller.** 1989. Magnesium transport in *Salmonella typhimurium*: genetic characterization and cloning of three magnesium transport loci. *J. Bacteriol.* **171**:4742–4751.
788. **Hmiel, S. P., M. D. Snavely, C. G. Miller, and M. E. Maguire.** 1986. Magnesium transport in *Salmonella typhimurium*: characterization of magnesium influx and cloning of a transport gene. *J. Bacteriol.* **168**:1444–1450.
789. **Ho, C., Y.-H. Giza, S. Takahashi, K. E. Ugen, P. F. Cottam, and S. R. Dowd.** 1981. A proton nuclear magnetic resonance investigation of histidine-binding protein J of *Salmonella typhimurium*: a model for transport of L-histidine across cytoplasmic membrane. *J. Supramol. Struct.* **13**:131–145.
790. **Hobson, A. C.** 1974. A norleucine-resistant mutant of *Salmonella typhimurium* with a possible defect in valine uptake or regulation. *J. Gen. Microbiol.* **82**:425–429.
791. **Hobson, A. C.** 1974. The regulation of methionine and S-adenosylmethionine biosynthesis and utilization in mutants of *Salmonella typhimurium* with defects in S-adenosylmethionine synthetase. *Mol. Gen. Genet.* **131**:263–273.
792. **Hobson, A. C.** 1976. The synthesis of S-adenosylmethionine by mutants with defects in S-adenosylmethionine synthetase. *Mol. Gen. Genet.* **144**:87–95.
793. **Hobson, A. C., and D. A. Smith.** 1973. S-Adenosylmethionine synthetase in methionine regulatory mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **126**:7–18.
794. **Hoeksma, W. D., and D. E. Schoenhard.** 1971. Characterization of a thermolabile sulfite reductase from *Salmonella pullorum*. *J. Bacteriol.* **108**:154–158.
795. **Hof, H., J. Stroder, J. P. Buisson, and R. Royer.** 1986. Effect of different nitroheterocyclic compounds on aerobic, microaerophilic, and anaerobic bacteria. *Antimicrob. Agents Chemother.* **30**:679–683.
796. **Hoffee, P., and B. C. Robertson.** 1969. 2-Deoxyribose gene-enzyme complex in *Salmonella typhimurium*: regulation of phosphodeoxyribomutase. *J. Bacteriol.* **97**:1386–1396.
797. **Hoffee, P., R. Snyder, C. Sushak, and P. Jargiello.** 1974. Deoxyribose-5-P aldolase: subunit structure and composition of active site lysine region. *Arch. Biochem. Biophys.* **164**:736–742.
798. **Hoffee, P. A.** 1968. 2-Deoxyribose gene-enzyme complex in *Salmonella typhimurium*. I. Isolation

- and enzymatic characterization of 2-deoxyribose-negative mutants. *J. Bacteriol.* **95**:449–457.
799. **Hoffee, P. A.** 1968. 2-Deoxyribose-5-phosphate aldolase of *Salmonella typhimurium*: purification and properties. *Arch. Biochem. Biophys.* **126**:795–802.
800. **Hoffman, G. R., M. J. Walkowicz, J. M. Mason, and J. F. Atkins.** 1983. Genetic instability associated with the *aroC321* allele in *Salmonella typhimurium* involves genetic duplication. *Mol. Gen. Genet.* **190**:183–188.
801. **Hoffman, J., B. Lindberg, M. Glowacka, M. Derylo, and Z. Lorkiewicz.** 1980. Structural studies of the lipopolysaccharide from *Salmonella typhimurium* 902 (ColIb *drd2*). *Eur. J. Biochem.* **105**:103–107.
802. **Hofler, J. G., and R. O. Burns.** 1978. Threonine deaminase from *Salmonella typhimurium*. *J. Biol. Chem.* **253**:1245–1251.
803. **Hofler, J. G., D. J. Decedue, G. H. Luginbuhl, J. A. Reynolds, and R. O. Burns.** 1975. The subunit structure of α -acetohydroxyacid isomerase from *Salmonella typhimurium*. *J. Biol. Chem.* **250**:877–882.
804. **Hogarth, B. C., and C. F. Higgins.** 1983. Genetic organization of the oligopeptide permease (*opp*) locus of *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **153**:1548–1551.
805. **Hogg, R. W.** 1981. The amino acid sequence of the histidine binding protein of *Salmonella typhimurium*. *J. Biol. Chem.* **256**:1935–1939.
806. **Hoiseth, S. K.** 1982. Aromatic-deficient mutants as live *Salmonella* vaccines. Ph.D. thesis. Stanford University, Stanford, Calif.
807. **Hoiseth, S. K., and B. A. D. Stocker.** 1981. Aromatic-dependent *Salmonella typhimurium* are non-virulent and effective as vaccines. *Nature* (London) **291**:238–239.
808. **Hoiseth, S. K., and B. A. D. Stocker.** 1985. Genes *aroA* and *serC* of *Salmonella typhimurium* constitute an operon. *J. Bacteriol.* **163**:355–361.
809. **Holland, M. M., T. K. Leib, and J. A. Gerlt.** 1988. Isolation and characterization of a small catalytic domain released from adenylate cyclase from *Escherichia coli* by digestion with trypsin. *J. Biol. Chem.* **263**:14661–14668.
810. **Holley, E. A., and J. W. Foster.** 1982. Bacteriophage P22 as a vector for Mu mutagenesis in *Salmonella typhimurium*: isolation of *nad-lac* and *pnc-lac* gene fusions. *J. Bacteriol.* **152**:959–962.
811. **Holley, E. A., M. P. Spector, and J. W. Foster.** 1985. Regulation of NAD biosynthesis in *Salmonella typhimurium*: expression of *nad-lac* gene fusions and identification of a *nad* regulatory focus. *J. Gen. Microbiol.* **131**:2759–2770.
812. **Homma, M., D. J. DeRosier, and R. M. Macnab.** 1990. Flagellar hook and hook-associated proteins of *Salmonella typhimurium* and their relationship to other axial components of the flagellum. *J. Mol. Biol.* **213**:819–832.
813. **Homma, M., H. Fujita, S. Yamaguchi, and T. Iino.** 1984. Excretion of unassembled flagellin by *Salmonella typhimurium* mutants deficient in hook-associated proteins. *J. Bacteriol.* **159**:1056–1059.
814. **Homma, M., H. Fujita, S. Yamaguchi, and T. Iino.** 1987. Regions of *Salmonella typhimurium* flagellin essential for its polymerization and excretion. *J. Bacteriol.* **169**:291–296.
815. **Homma, M., and T. Iino.** 1985. Locations of hook-associated proteins in flagellar structures of *Salmonella typhimurium*. *J. Bacteriol.* **162**:183–189.
816. **Homma, M., and T. Iino.** 1985. Excretion of unassembled hook-associated proteins by *Salmonella typhimurium*. *J. Bacteriol.* **164**:1370–1372.
817. **Homma, M., T. Iino, K. Kutsukake, and S. Yamaguchi.** 1986. *In vitro* reconstitution of flagellar filaments onto hooks of filamentless mutants of *Salmonella typhimurium* by addition of hook-associated proteins. *Proc. Natl. Acad. Sci. USA* **83**:6169–6173.
818. **Homma, M., T. Iino, and R. M. Macnab.** 1988. Identification and characterization of the products of six region III flagellar genes (*flaAII.3* through *flaQII*) of *Salmonella typhimurium*. *J. Bacteriol.* **170**:2221–2228.
819. **Homma, M., Y. Komeda, T. Iino, and R. M. Macnab.** 1987. The *flaFIX* gene product of *Salmonella typhimurium* is a flagellar basal body component with a signal peptide for export. *J. Bacteriol.* **169**:1493–1498.

820. **Homma, M., K. Kutsukake, M. Hasebe, T. Iino, and R. M. Macnab.** 1990. FlgB, FlgC, FlgF and FlgG. A family of structurally related proteins in the flagellar basal body of *Salmonella typhimurium*. *J. Mol. Biol.* **211**:465–477.
821. **Homma, M., K. Kutsukake, and T. Iino.** 1985. Structural genes for flagellar hook-associated proteins in *Salmonella typhimurium*. *J. Bacteriol.* **163**:464–471.
822. **Homma, M., K. Kutsukake, T. Iino, and S. Yamaguchi.** 1984. Hook-associated proteins essential for flagellar filament formation in *Salmonella typhimurium*. *J. Bacteriol.* **157**:100–108.
823. **Homma, M., K. Ohnishi, T. Iino, and R. M. Macnab.** 1987. Identification of flagellar hook and basal body gene products (FlaFV, FlaFVI, FlaFVII, and FlaFVIII) in *Salmonella typhimurium*. *J. Bacteriol.* **169**:3617–3624.
824. **Hong, J.-S., and B. N. Ames.** 1971. Localized mutagenesis of any specific small region of the bacterial chromosome. *Proc. Natl. Acad. Sci. USA* **68**:3158–3162.
825. **Hong, J.-S., G. R. Smith, and B. N. Ames.** 1971. Adenosine 3'5'-cyclic monophosphate concentration in the bacterial host regulates the viral decision between lysogeny and lysis. *Proc. Natl. Acad. Sci. USA* **68**:2258–2262.
826. **Hongo, E., M. Morimyo, K. Mita, I. Machida, H. Hama-Inaba, H. Tsuji, S. Ichimura, and Y. Noda.** 1994. The methyl viologen-resistance-encoding gene *smvA* of *Salmonella typhimurium*. *Gene* **148**:173–174.
827. **Hoppe, I., H. M. Johnston, D. Biek, and J. R. Roth.** 1979. A refined map of the *hisG* gene of *Salmonella typhimurium*. *Genetics* **92**:17–26.
828. **Hoppe, I., and J. Roth.** 1974. Specialized transducing phages derived from *Salmonella* phage P22. *Genetics* **76**:633–654.
829. **Horiguchi, T., S. Yamaguchi, K. Yao, T. Tairo, and T. Iino.** 1975. Genetic analysis of *H1*, the structural gene for phase-1 flagellin in *Salmonella*. *J. Gen. Microbiol.* **91**:139–149.
830. **Horowitz, H., J. Van Arsdell, and T. Platt.** 1983. Nucleotide sequence of the *trpD* and *trpC* genes of *Salmonella typhimurium*. *J. Mol. Biol.* **169**:775–797.
831. **Horwitz, A. H., L. Heffernan, C. Morandi, J.-H. Lee, J. Timko, and G. Wilcox.** 1981. DNA sequence of the *araBAD-araC* controlling region in *Salmonella typhimurium* LT2. *Gene* **14**:309–319.
832. **Hotani, H.** 1976. Light microscope study of mixed helices in reconstituted *Salmonella* flagella. *J. Mol. Biol.* **106**:151–166.
833. **Houlberg, U., and K. J. Jensen.** 1983. Role of hypoxanthine and guanine in regulation of *Salmonella typhimurium pur* gene expression. *J. Bacteriol.* **153**:837–845.
834. **Houng, H. S., D. J. Kopecko, and L. S. Baron.** 1990. Molecular cloning and physical and functional characterization of the *Salmonella typhimurium* and *Salmonella typhi* galactose utilization operons. *J. Bacteriol.* **172**:4392–4398.
835. **Housley, P. R., A. D. Leavitt, and H. J. Whitfield.** 1981. Genetic analysis of a temperature-sensitive *Salmonella typhimurium rho* mutant with an altered rho-associated polycytidylate-dependent adenosine triphosphatase activity. *J. Bacteriol.* **147**:13–24.
836. **Housley, P. R., and H. J. Whitfield.** 1982. Transcription termination factor ρ from wildtype and ρ -111 strains of *Salmonella typhimurium*. *J. Biol. Chem.* **257**:2569–2577.
837. **Houston, L. L.** 1973. Specialized subregions of the bifunctional *hisB* gene of *Salmonella typhimurium*. *J. Bacteriol.* **113**:82–87.
838. **Houston, L. L.** 1973. Purification and properties of a mutant bifunctional enzyme from the *hisB* gene of *Salmonella typhimurium*. *J. Biol. Chem.* **248**:4144–4149.
839. **Houston, L. L.** 1973. Evidence for proteolytic degradation of histidinol phosphate phosphatase specified by nonsense mutants of the *hisB* gene of *Salmonella typhimurium*. *J. Bacteriol.* **116**:88–97.
840. **Houston, L. L., and M. E. Graham.** 1974. Divalent metal ion effects on a mutant histidinol phosphate phosphatase from *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **162**:513–522.
841. **Houston, L. L., and R. H. Millay, Jr.** 1974. Effect of sulfhydryl reagents on the activity of histidinolphosphatase from *Salmonella typhimurium* and baker's yeast. *Biochim. Biophys. Acta* **370**:216–226.
842. **Howlett, B. J., and J. Bar-Tana.** 1980. Polyprenyl *p*-hydroxybenzoate carboxylase in

- flagellation of *Salmonella typhimurium*. *J. Bacteriol.* **143**:644–651.
843. **Hoyer, L. L., A. C. Hamilton, S. M. Steenbergen, and E. R. Vimr.** 1992. Cloning, sequencing and distribution of the *Salmonella typhimurium* LT2 sialidase gene, *nanH*, provides evidence for interspecies gene transfer. *Mol. Microbiol.* **6**:873–884.
844. **Hoyer, L. L., P. Roggentin, R. Schauer, and E. R. Vimr.** 1991. Purification and properties of cloned *Salmonella typhimurium* LT2 sialidase with virus-typical kinetic preference for sialyl α 2-3 linkages. *J. Biochem. (Tokyo)* **110**:462–467.
845. **Hryniewicz, M., M. Bagdasarian, and M. Bagdasarian.** 1979. Integration of F factor and cryptic LT-2 plasmid into a specific site of the *Salmonella typhimurium* chromosome. *Acta Biochim. Pol.* **26**:73–82.
846. **Hryniewicz, M., A. Sirko, A. Palucha, A. Bock, and D. Hulanicka.** 1990. Sulfate and thiosulfate transport in *Escherichia coli* K-12: identification of a gene encoding a novel protein involved in thiosulfate binding. *J. Bacteriol.* **172**:3358–3366.
847. **Hryniewicz, M. M., and N. M. Kredich.** 1991. The *cysP* promoter of *Salmonella typhimurium*: characterization of two binding sites for CysB protein, studies of *in vivo* transcription initiation, and demonstration of the anti-inducer effects of thiosulfate. *J. Bacteriol.* **173**:5876–5886.
848. **Hryniewicz, M. M., and N. M. Kredich.** 1994. Stoichiometry of binding of CysB to the *cysJIIH*, *cysK*, and *cysP* promoter regions of *Salmonella typhimurium*. *J. Bacteriol.* **176**:3673–3682.
849. **Hu, C.-Y., and D. B. Sprinson.** 1977. Properties of tyrosine-inhibitable 3-deoxy-D-arabinoheptulosonic acid-7-phosphate synthase from *Salmonella*. *J. Bacteriol.* **129**:177–183.
850. **Huang, C. J., and E. L. Barrett.** 1990. Identification and cloning of genes involved in anaerobic sulfite reduction by *Salmonella typhimurium*. *J. Bacteriol.* **172**:4100–4102.
851. **Huang, C. J., and E. L. Barrett.** 1991. Sequence analysis and expression of the *Salmonella typhimurium* *asr* operon encoding production of hydrogen sulfide from sulfite. *J. Bacteriol.* **173**:1544–1553.
852. **Hudson, H. P., A. A. Lindberg, and B. A. D. Stocker.** 1978. Lipopolysaccharide core defects in *Salmonella typhimurium* mutants which are resistant to Felix O phage but retain smooth character. *J. Gen. Microbiol.* **109**:97–112.
853. **Huffman, G. A., and R. H. Rownd.** 1984. Transition of deletion mutants of the composite resistance plasmid NR1 in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **159**:488–498.
854. **Hughes, D.** 1986. The isolation and mapping of EF-Tu mutations in *Salmonella typhimurium*. *Mol. Gen. Genet.* **202**:108–111.
855. **Hughes, D.** 1987. Mutant forms of *tufA* and *tufB* independently suppress nonsense mutations. *J. Mol. Biol.* **197**:611–615.
856. **Hughes, D.** 1990. Both genes for EF-Tu in *Salmonella typhimurium* are individually dispensable for growth. *J. Mol. Biol.* **215**:41–51.
857. **Hughes, D.** 1991. Error-prone EF-Tu reduces *in vivo* enzyme activity and cellular growth rate. *Mol. Microbiol.* **5**:623–630.
858. **Hughes, D., J. F. Atkins, and S. Thompson.** 1987. Mutants of elongation factor Tu promote ribosomal frameshifting and nonsense readthrough. *EMBO J.* **6**:4235–4239.
859. **Hughes, D., and R. H. Buckingham.** 1991. The nucleotide sequence of *rpsL* and its flanking regions in *Salmonella typhimurium*. *Gene* **104**:123–124.
860. **Hughes, K. T., B. T. Cookson, D. Ladika, B. M. Olivera, and J. R. Roth.** 1983. 6-Aminonicotinamide-resistant mutants of *Salmonella typhimurium*. *J. Bacteriol.* **154**:1126–1136.
861. **Hughes, K. T., A. Dessen, J. P. Gray, and C. Grubmeyer.** 1993. The *Salmonella typhimurium* *nadC* gene: sequence determination by use of Mud-P22 and purification of quinolinate phosphoribosyltransferase. *J. Bacteriol.* **175**:479–486.
862. **Hughes, K. T., D. Ladika, J. R. Roth, and B. M. Olivera.** 1983. An indispensable gene for NAD biosynthesis in *Salmonella typhimurium*. *J. Bacteriol.* **155**:213–221.
863. **Hughes, K. T., B. M. Olivera, and J. R. Roth.** 1983. *nadD*: novel mutants in an essential step in NAD biosynthesis in *Salmonella typhimurium*, abstr. K189, p. 208. *Abstr. Annu. Meet. Am. Soc. Microbiol.*, 1983.

864. **Hughes, K. T., B. M. Olivera, and J. R. Roth.** 1987. Rec dependence of Mu transposition from P22-transduced fragments. *J. Bacteriol.* **169**:403–409.
865. **Hughes, K. T., B. M. Olivera, and J. R. Roth.** 1988. Structural gene for NAD synthetase in *Salmonella typhimurium*. *J. Bacteriol.* **170**:2113–2120.
866. **Hughes, K. T., and J. R. Roth.** 1984. Conditionally transposition-defective derivative of Mu d1(Amp Lac). *J. Bacteriol.* **159**:130–137.
867. **Hughes, K. T., and J. R. Roth.** 1988. Transitory *cis* complementation: a method for providing transposition functions to defective transposons. *Genetics* **119**:9–12.
868. **Hughes, K. T., J. R. Roth, and B. M. Olivera.** 1991. A genetic characterization of the *nadC* gene of *Salmonella typhimurium*. *Genetics* **127**:657–670.
869. **Hughes, K. T., P. Youderian, and M. I. Simon.** 1988. Phase variation in *Salmonella*: analysis of Hin recombinase and *hix* recombination site interaction *in vivo*. *Genes Dev.* **2**:937–948.
870. **Hughes, V., and G. G. Meynell.** 1977. The contribution of plasmid and host genes to plasmid mediated interference with phage growth. *Genet. Res.* **30**:179–186.
871. **Hulanicka, D., and T. Klopotoski.** 1972. Mutants of *Salmonella typhimurium* resistant to triazole. *Acta Biochim. Pol.* **19**:251–260.
872. **Hulanicka, D., T. Klopotoski, and D. A. Smith.** 1972. The effect of triazole on cysteine biosynthesis in *Salmonella typhimurium*. *J. Gen. Microbiol.* **72**:291–301.
873. **Hulanicka, M. D., C. Garrett, G. Jagura-Burdzy, and N. M. Kredich.** 1986. Cloning and characterization of the *cysAMK* region of *Salmonella typhimurium*. *J. Bacteriol.* **168**:322–327.
874. **Hulanicka, M. D., S. G. Hallquist, N. M. Kredich, and T. Mojica-a.** 1979. Regulation of *O*-acetylserine sulfhydrylase B by L-cysteine in *Salmonella typhimurium*. *J. Bacteriol.* **140**:141–146.
875. **Hulanicka, M. D., and N. M. Kredich.** 1976. A mutation affecting expression of the gene coding for serine transacetylase in *Salmonella typhimurium*. *Mol. Gen. Genet.* **148**:143–148.
876. **Hulanicka, M. D., N. M. Kredich, and D. M. Treiman.** 1974. The structural gene of *O*-acetylserine sulfhydrylase A in *Salmonella typhimurium*. Identity with the *trzA* locus. *J. Biol. Chem.* **249**:867–872.
877. **Hulton, C. S., A. Seirafi, J. C. Hinton, J. M. Sidebotham, L. Waddell, G. D. Pavitt, T. Owen-Hughes, A. Spassky, H. Buc, and C. F. Higgins.** 1990. Histone-like protein H1 (H-NS), DNA supercoiling, and gene expression in bacteria. *Cell* **63**:631–642.
878. **Hurme, R., E. Namork, E. L. Nurmiaho-Lassila, and M. Rhen.** 1994. Intermediate filament-like network formed *in vitro* by a bacterial coiled coil protein. *J. Biol. Chem.* **269**:10675–10682.
879. **Hwang, L. H., and H. Zalkin.** 1971. Multiple forms of anthranilate synthetase-anthranilate 5-phosphoribosylpyrophosphate phosphoribosyl-transferase from *Salmonella typhimurium*. *J. Biol. Chem.* **246**:2338–2345.
880. **Hyde, C. C., S. A. Ahmed, E. A. Padlan, E. W. Miles, and D. R. Davies.** 1988. Three-dimensional structure of the tryptophan synthase alpha 2 beta 2 multienzyme complex from *Salmonella typhimurium*. *J. Biol. Chem.* **263**:17857–17871.
881. **Hyman, H. C., and S. Trachtenberg.** 1991. Point mutations that lock *Salmonella typhimurium* flagellar filaments in the straight right-handed and left-handed forms and their relation to filament superhelicity. *J. Mol. Biol.* **220**:79–88.
882. **Ibe, S. N., A. J. Sinskey, and D. Botstein.** 1982. Genetic mapping of mutations in a highly radiation-resistant mutant of *Salmonella typhimurium* LT2. *J. Bacteriol.* **152**:260–268.
883. **Iijima, T., and K. Imai.** 1975. Genetic locus of *tct* (tricarboxylic acid transport) gene in *Salmonella typhimurium*. *Inst. Ferment. Res. Commun.* **7**:61–64.
884. **Iino, T.** 1961. A stabilizer of antigenic phases in *Salmonella abortus-equi*. *Genetics* **46**:1465–1469.
885. **Iino, T.** 1961. Genetic analysis of O-H variation in *Salmonella*. *Jpn. J. Genet.* **36**:268–275.
886. **Iino, T.** 1969. Phase specific regulator of flagellar genes (H1 and H2) in *Salmonella*. *Nat. Inst. Genet. (Mishima) Annu. Rep.* **13**:72–73.
887. **Iino, T.** 1969. Genetics and chemistry of bacterial flagella. *Bacteriol. Rev.* **33**:454–475.
888. **Iino, T.** 1974. Assembly of *Salmonella* flagellin *in vitro* and *in vivo*. *J. Supramol. Struct.* **2**:372–

889. **Iino, T.** 1977. Genetics of structure and function of bacterial flagella. *Annu. Rev. Genet.* **11**:161–182.
890. **Iino, T., and M. Enomoto.** 1966. Genetical studies of nonflagellate mutants of *Salmonella*. *J. Gen. Microbiol.* **43**:315–327.
891. **Iino, T., Y. Komeda, K. Kutsukake, R. Macnab, P. Matsumura, J. S. Parkinson, M. I. Simon, and S. Yamaguchi.** 1988. New unified nomenclature for the flagellar genes of *Escherichia coli* and *Salmonella typhimurium*. *Microbiol. Rev.* **52**:533–535.
892. **Iino, T., and T. Oguchi.** 1972. A non-chemotactic mutant in *Salmonella*. *Annu. Rep. Natl. Inst. Genet.* **22**:13–14.
893. **Iino, T., T. Oguchi, and T. Hirano.** 1975. Temporary expression of flagellar phase-1 phase-2 clones of diphasic *Salmonella*. *J. Gen. Microbiol.* **89**:265–276.
894. **Iino, T., T. Oguchi, and T. Kuroiwa.** 1974. Polymorphism in a flagellar-shape mutant of *Salmonella typhimurium*. *J. Gen. Microbiol.* **81**:37–45.
895. **Ikeda, T., M. Homma, T. Iino, S. Asakura, and R. Kamiya.** 1987. Localization and stoichiometry of hook-associated proteins within *Salmonella typhimurium* flagella. *J. Bacteriol.* **169**:1168–1173.
896. **Ikeda, T., R. Kamiya, and S. Yamaguchi.** 1983. Excretion of flagellin by a short-flagella mutant of *Salmonella typhimurium*. *J. Bacteriol.* **153**:506–510.
897. **Ikeda, T., R. Kamiya, and S. Yamaguchi.** 1984. In vitro polymerization of flagellin excreted by a short-flagellum *Salmonella typhimurium* mutant. *J. Bacteriol.* **159**:787–789.
898. **Imai, K.** 1975. Isolation of tricarboxylic acid transport-negative mutants of *Salmonella typhimurium*. *J. Gen. Appl. Microbiol.* **21**:127–134.
899. **Imai, K.** 1975. Transport system for the C₄-dicarboxylic acids in *Salmonella typhimurium*. *Inst. Ferment. Res. Commun.* **7**:53–60.
900. **Imai, K., T. Iijima, and I. Banno.** 1977. Location of *tct* (tricarboxylic acid transport) genes on the chromosome of *Salmonella typhimurium*. *Inst. Ferment. Res. Commun.* **8**:63–68.
901. **Imai, K., T. Iijima, and T. Hasegawa.** 1973. Transport of tricarboxylic acids in *Salmonella typhimurium*. *J. Bacteriol.* **114**:961–965.
902. **Imray, F. P., and D. G. MacPhee.** 1975. Induction of base-pair substitution and frameshift mutations in wild-type and repair-deficient strains of *Salmonella typhimurium* by the photodynamic action of methylene blue. *Mutat. Res.* **27**:299–306.
903. **Imray, F. P., and D. G. MacPhee.** 1976. Spontaneous and induced mutability of frameshift strains of *Salmonella typhimurium* carrying *uvrB* and *polA* mutations. *Mutat. Res.* **34**:35–42.
904. **Ingraham, J. L., and J. Neuhard.** 1972. Cold-sensitive mutants of *Salmonella typhimurium* defective in UMP kinase (*pyrH*). *J. Biol. Chem.* **247**:6259–6265.
905. **Ino, I., P. E. Hartman, Z. Hartman, and J. Yourno.** 1975. Deletions fusing the *hisG* genes in *Salmonella typhimurium*. *J. Bacteriol.* **123**:1254–1264.
906. **Inoue, Y. H., K. Kutsukake, T. Iino, and S. Yamaguchi.** 1989. Sequence analysis of operator mutants of the phase-1 flagellin-encoding gene, *fliC*, in *Salmonella typhimurium*. *Gene* **85**:221–226.
907. **Irikura, V. M., M. Kihara, S. Yamaguchi, H. Sockett, and R. M. Macnab.** 1993. *Salmonella typhimurium* *fliG* and *fliN* mutations causing defects in assembly, rotation, and switching of the flagellar motor. *J. Bacteriol.* **175**:802–810.
908. **Isaki, L. S., and M. J. Voll.** 1976. Genetic characterization of a ϕ 80 transducing bacteriophage carrying the histidine operon of *Salmonella typhimurium*. *J. Virol.* **19**:313–317.
909. **Ishido, M., T. Hase, F. Ito, and Y. Masamune.** 1980. Comparative studies of DNA polymerase I of enteric bacteria. *J. Gen. Appl. Microbiol.* **26**:183–202.
910. **Ishidsu, J.** 1975. Physiological properties of arginine sensitive mutants of *Salmonella typhimurium*. *Jpn. J. Genet.* **50**:99–113.
911. **Ishiguro, E. E., D. Vanderwel, and W. Kusser.** 1986. Control of lipopolysaccharide biosynthesis and release by *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **168**:328–333.
912. **Ishihara, A., S. Yamaguchi, and H. Hotani.** 1981. Passive rotation of flagella on paralyzed

- Salmonella typhimurium* (*mot*) mutants by external rotatory driving force. *J. Bacteriol.* **145**:1082–1084.
913. **Ishima, R., K. Akasaka, S. Aizawa, and F. Vonderviszt.** 1991. Mobility of the terminal regions of flagellin in solution. *J. Biol. Chem.* **266**:23682–23688.
914. **Isihara, H., and R. W. Hogg.** 1980. Amino acid sequence of the sulfate-binding protein from *Salmonella typhimurium* LT2. *J. Biol. Chem.* **255**:4614–4618.
915. **Island, M. D., B. Y. Wei, and R. J. Kadner.** 1992. Structure and function of the *uhp* genes for the sugar phosphate transport system in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **174**:2754–2762.
916. **Isono, K., and J. Yourno.** 1973. Mutation leading to gene fusion in the histidine operon of *Salmonella typhimurium*. *J. Mol. Biol.* **76**:455–461.
917. **Isono, K., and J. Yourno.** 1974. Chemical carcinogens as frameshift mutagens: *Salmonella* DNA sequence sensitive to mutagenesis by polycyclic carcinogens. *Proc. Natl. Acad. Sci. USA* **71**:1612–1617.
918. **Itaya, M., D. McKelvin, S. K. Chatterjie, and R. J. Crouch.** 1991. Selective cloning of genes encoding RNase H from *Salmonella typhimurium*, *Saccharomyces cerevisiae* and *Escherichia coli* *rnh* mutant. *Mol. Gen. Genet.* **227**:438–445.
919. **Itikawa, H., and M. Demerec.** 1967. Ditto deletions in the *cysC* region of the *Salmonella* chromosome. *Genetics* **55**:63–68.
920. **Itikawa, H., and M. Demerec.** 1968. *Salmonella typhimurium* proline mutants. *J. Bacteriol.* **95**:1189–1190.
921. **Jackson, M. B., J. M. Becker, A. S. Steinfield, and F. Naider.** 1976. Oligopeptide transport in proline peptidase mutants of *Salmonella typhimurium*. *J. Biol. Chem.* **251**:5300–5309.
922. **Jacobson, F. S., R. W. Morgan, M. F. Christman, and B. N. Ames.** 1989. An alkyl hydroperoxide reductase from *Salmonella typhimurium* involved in the defense of DNA against oxidative damage. Purification and properties. *J. Biol. Chem.* **264**:1488–1496.
923. **Jagura, G., D. Hulanicka, and N. M. Kredich.** 1978. Analysis of merodiploids of the *cysB* region in *Salmonella typhimurium*. *Mol. Gen. Genet.* **165**:31–38.
924. **Jagura-Burdzy, G., and D. Hulanicka.** 1987. Cloning of *cysB* mutant alleles of *S. typhimurium*. *Acta Biochim. Pol.* **34**:35–44.
925. **Jagura-Burdzy, G., and N. M. Kredich.** 1983. Cloning and physical mapping of the *cysB* region of *Salmonella typhimurium*. *J. Bacteriol.* **155**:578–585.
926. **Jahreis, K., P. W. Postma, and J. W. Lengeler.** 1991. Nucleotide sequence of the *ilvH-fruR* gene region of *Escherichia coli* K12 and *Salmonella typhimurium* LT2. *Mol. Gen. Genet.* **226**:332–336.
927. **Jamieson, D. J., and C. F. Higgins.** 1984. Anaerobic and leucine-dependent expression of a peptide transport gene in *Salmonella typhimurium*. *J. Bacteriol.* **160**:131–136.
928. **Jamieson, D. J., and C. F. Higgins.** 1986. Two genetically distinct pathways for transcriptional regulation of anaerobic gene expression in *Salmonella typhimurium*. *J. Bacteriol.* **168**:389–397.
929. **Jamieson, D. J., R. G. Sawers, P. A. Rugman, D. H. Boxer, and C. F. Higgins.** 1986. Effects of anaerobic regulatory mutations and catabolite repression on regulation of hydrogen metabolism and hydrogenase isoenzyme composition in *Salmonella typhimurium*. *J. Bacteriol.* **168**:405–411.
930. **Janion, C.** 1977. On the ability of *Salmonella typhimurium* cells to form deoxycytidine nucleotides. *Mol. Gen. Genet.* **153**:179–183.
931. **Janion, C., and E. Popowska.** 1975. The reduction of N₄-hydroxycytidine to cytidine by *Salmonella typhimurium* cells. *Nucleic Acids Res.* **2**(Suppl.):s159-s163.
932. **Jann, K. S., S. Kanegasaki, G. Goldemann, and P. H. Makela.** 1979. On the effect of *rfe* mutation on the biosynthesis of the O-8 and O-9 antigens of *Escherichia coli*. *Biochem. Biophys. Res. Commun.* **86**:1185–1191.
933. **Janson, C. A., P. S. Kayne, R. J. Almassy, M. Grunstein, and D. Eisenberg.** 1986. Sequence of glutamine synthetase from *Salmonella typhimurium* and implications for the protein structure. *Gene* **46**:297–300.

934. **Janzer, J., H. Stan-Lotter, and K. E. Sanderson.** 1981. Isolation and characterization of hemin-permeable, envelope-defective mutants of *Salmonella typhimurium*. *Can. J. Microbiol.* **27**:226–237.
935. **Jargiello, P.** 1976. Simultaneous selection of mutants in gluconeogenesis and nucleoside catabolism in *Salmonella typhimurium*. *Biochim. Biophys. Acta* **444**:321–325.
936. **Jargiello, P., and P. Hoffee.** 1972. Orientation of the *deo* genes and the *serB* locus in *Salmonella typhimurium*. *J. Bacteriol.* **111**:296–297.
937. **Jargiello, P., M. D. Stern, and P. Hoffee.** 1974. 2-Deoxyribose 5-phosphate aldolase: genetic analyses of structure. *J. Mol. Biol.* **88**:671–691.
938. **Jargiello, P., C. Sushak, and P. Hoffee.** 1976. 2-Deoxyribose 5-phosphate aldolase: isolation and characterization of proteins genetically modified in the active site region. *Arch. Biochem. Biophys.* **177**:630–641.
939. **Jegade, V. A., F. Spencer, and J. E. Brenchley.** 1976. Thialysine-resistant mutant of *Salmonella typhimurium* with a lesion in the *thrA* gene. *Genetics* **83**:619–632.
940. **Jenness, D. D., and H. K. Schachman.** 1980. *pyrB* mutations as suppressors of arginine auxotrophy in *Salmonella typhimurium*. *J. Bacteriol.* **141**:33–40.
941. **Jenness, D. D., and H. K. Schachman.** 1983. Genetic characterization of the folding domains of the catalytic chains in aspartate transcarbamoylase. *J. Biol. Chem.* **258**:3266–3279.
942. **Jennings, M. P., S. P. Scott, and I. R. Beacham.** 1993. Regulation of the *ansB* gene of *Salmonella enterica*. *Mol. Microbiol.* **9**:165–172.
943. **Jensen, K. F.** 1979. Apparent involvement of purines in the control of expression of *Salmonella typhimurium pyr* genes: analysis of a leaky *guaB* mutant resistant to pyrimidine analogs. *J. Bacteriol.* **138**:731–738.
944. **Jensen, K. F.** 1989. Regulation of *Salmonella typhimurium pyr* gene expression: effect of changing both purine and pyrimidine nucleotide pools. *J. Gen. Microbiol.* **135**:805–815.
945. **Jensen, K. F., R. Fast, O. Karlstrom, and J. N. Larsen.** 1986. Association of RNA polymerase having increased K_m for ATP and UTP with hyperexpression of the *pyrB* and *pyrE* genes of *Salmonella typhimurium*. *J. Bacteriol.* **166**:857–865.
946. **Jensen, K. F., J. Neuhard, and L. Shack.** 1982. RNA polymerase involvement in the control of *Salmonella typhimurium pyr* gene expression. Isolation and characterization of a fluorouracil resistant mutant with high constitutive expression of *pyrB* and *pyrE* due to a mutation in *rpoBC*. *EMBO J.* **1**:69–74.
947. **Jenson, P., C. Parkes, and D. Berkowitz.** 1972. Mannitol sensitivity. *J. Bacteriol.* **111**:351–355.
948. **Jessop, A. P.** 1972. A specialized transducing phage of P22 for which the ability to form plaques is associated with transduction of the *proAB* region. *Mol. Gen. Genet.* **114**:214–222.
949. **Jessop, A. P.** 1976. Specialized transducing phages derived from phage P22 that carry the *proAB* region of the host, *Salmonella typhimurium*: genetic evidence for their structure and mode of transduction. *Genetics* **83**:459–475.
950. **Jeter, R. M.** 1990. Cobalamin-dependent 1,2-propanediol utilization by *Salmonella typhimurium*. *J. Gen. Microbiol.* **136**:887–896.
951. **Jeter, R. M., B. M. Olivera, and J. R. Roth.** 1984. *Salmonella typhimurium* synthesizes cobalamin (vitamin B₁₂) de novo under anaerobic growth conditions. *J. Bacteriol.* **159**:206–213.
952. **Jeter, R. M., and J. R. Roth.** 1987. Cobalamin (vitamin B₁₂) biosynthetic genes of *Salmonella typhimurium*. *J. Bacteriol.* **169**:3189–3198.
953. **Jiang, S.-Q., G.-Q. Yu, Z.-G. Li, and J.-S. Hong.** 1988. Genetic evidence for modulation of the activator by two regulatory proteins involved in the exogenous induction of phosphoglycerate transport in *Salmonella typhimurium*. *J. Bacteriol.* **170**:4304–4308.
954. **Jiang, X. M., B. Neal, F. Santiago, S. J. Lee, L. K. Romana, and P. R. Reeves.** 1991. Structure and sequence of the *rfb* (O antigen) gene cluster of *Salmonella* serovar *typhimurium* (strain LT2). *Mol. Microbiol.* **5**:695–713.
955. **Jochimsen, B., B. Garber, and J. S. Gots.** 1980. Phosphoribosylpyrophosphate (PRPP) synthetase mutant in *Salmonella typhimurium*. *Adv. Exp. Med. Biol.* **122B**:131–136.
956. **Jochimsen, B. U., B. Hove-Jensen, B. B. Garber, and J. S. Gots.** 1985. Characterization of a

- Salmonella typhimurium* mutant defective in phosphoribosylpyrophosphate synthetase. *J. Gen. Microbiol.* **131**:245–252.
957. **Joh, K., and S. Hiraga.** 1979. Genetic mapping of the chromosomal replication origin of *Salmonella typhimurium*. *J. Bacteriol.* **138**:297–304.
958. **Johanson, U., and D. Hughes.** 1992. Comparison of the complete sequence of the *str* operon in *Salmonella typhimurium* and *Escherichia coli*. *Gene* **120**:93–98.
959. **Johansson, V., A. Aarti, M. Nurminen, and P. H. Makela.** 1978. Outer membrane protein-specific bacteriophage of *Salmonella typhimurium*. *J. Bacteriol.* **107**:183–187.
960. **Johnson, B. N., A. Weintraub, A. A. Lindberg, and B. A. Stocker.** 1992. Construction of *Salmonella* strains with both antigen O4 (of group B) and antigen O9 (of group D). *J. Bacteriol.* **174**:1911–1915.
961. **Johnson, E. M., and L. S. Baron.** 1969. Genetic transfer of the Vi antigen from *Salmonella typhosa* to *Escherichia coli*. *J. Bacteriol.* **99**:358–359.
962. **Johnson, E. M., B. Krauskopf, and L. S. Baron.** 1965. Genetic mapping of Vi and somatic antigenic determinants in *Salmonella*. *J. Bacteriol.* **90**:302–308.
963. **Johnson, E. M., B. Krauskopf, and L. S. Baron.** 1966. Genetic analysis of the ViA-*his* chromosomal region in *Salmonella*. *J. Bacteriol.* **92**:1457–1463.
964. **Johnson, K., I. Charles, G. Dougan, D. Pickard, P. O’Gaora, G. Costa, T. Ali, I. Miller, and C. Hormaeche.** 1991. The role of a stress-response protein in *Salmonella typhimurium* virulence. *Mol. Microbiol.* **5**:401–407.
965. **Johnson, M. G., and J. C. Escalante-Semerena.** 1992. Identification of 5,6-dimethylbenzimidazole as the Co alpha ligand of the cobamide synthesized by *Salmonella typhimurium*. Nutritional characterization of mutants defective in biosynthesis of the imidazole ring. *J. Biol. Chem.* **267**:13302–13305.
966. **Johnston, H. M., W. M. Barnes, F. G. Chumley, L. Bossi, and J. R. Roth.** 1980. Model for regulation of the histidine operon of *Salmonella*. *Proc. Natl. Acad. Sci. USA* **77**:508–512.
967. **Johnston, H. M., and J. R. Roth.** 1979. Histidine mutants requiring adenine: selection of mutants with reduced *hisG* expression in *Salmonella typhimurium*. *Genetics* **92**:1–16.
968. **Johnston, H. M., and J. R. Roth.** 1980. UGA suppressor that maps within a cluster of ribosomal protein genes. *J. Bacteriol.* **144**:300–305.
969. **Jones, B. D., and S. Falkow.** 1994. Identification and characterization of a *Salmonella typhimurium* oxygen-regulated gene required for bacterial internalization. *Infect. Immun.* **62**:3745–3752.
970. **Jones, B. D., N. Ghori, and S. Falkow.** 1994. *Salmonella typhimurium* initiates murine infection by penetrating and destroying the specialized epithelial M cells of the Peyer’s patches. *J. Exp. Med.* **180**:15–23.
971. **Jones, C. J., M. Homma, and R. M. Macnab.** 1989. L-, P-, and M-ring proteins of the flagellar basal body of *Salmonella typhimurium*: gene sequences and deduced protein sequences. *J. Bacteriol.* **171**:3890–3900.
972. **Jones, C. J., and R. M. Macnab.** 1990. Flagellar assembly in *Salmonella typhimurium*: analysis with temperature-sensitive mutants. *J. Bacteriol.* **172**:1327–1339.
973. **Jones, C. J., R. M. Macnab, H. Okino, and S. Aizawa.** 1990. Stoichiometric analysis of the flagellar hook-(basal-body) complex of *Salmonella typhimurium*. *J. Mol. Biol.* **212**:377–387.
974. **Jones, R. T., D. E. Keltzow, and B. A. D. Stocker.** 1972. Genetic transfer of *Salmonella typhimurium* and *Escherichia coli* lipopolysaccharide antigens to *Escherichia coli* K-12. *J. Bacteriol.* **111**:758–770.
975. **Jones, W. R., G. J. Barcak, and R. E. Wolf, Jr.** 1990. Altered growth-rate-dependent regulation of 6-phosphogluconate dehydrogenase level in *hisT* mutants of *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **172**:1197–1205.
976. **Jones-Mortimer, M. C.** 1973. Mapping of structural genes for the enzymes of cysteine biosynthesis in *Escherichia coli* K12 and *Salmonella typhimurium* LT2. *Heredity* **31**:213–221.
977. **Jordan, A., I. Gibert, and J. Barbe.** 1994. Cloning and sequencing of the genes from *Salmonella*

- typhimurium* encoding a new bacterial ribonucleotide reductase. *J. Bacteriol.* **176**:3420–3427.
978. **Joshi, A., J. Z. Siddiqui, M. Verma, and M. Chakravorty.** 1982. Participation of the host protein(s) in the morphogenesis of bacteriophage P22. *Mol. Gen. Genet.* **186**:44–49.
979. **Joshi, A., M. Verma, and M. Chakravorty.** 1982. Thiolutin-resistant mutants of *Salmonella typhimurium*. *Antimicrob. Agents Chemother.* **22**:541–547.
980. **Joshi, A. R., and M. Chakravorty.** 1979. Bacteriophage P-22 development is temperature sensitive in thiolutin resistant mutants of *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.* **89**:1–6.
981. **Jousimies, H., and P. H. Makela.** 1974. Genetic analysis of *Salmonella minnesota* R mutants with defects in the biosynthesis of the lipopolysaccharide core. *J. Bacteriol.* **119**:753–759.
982. **Jovanovich, S. B.** 1985. Regulation of a *cya-lac* fusion by cyclic AMP in *Salmonella typhimurium*. *J. Bacteriol.* **161**:641–649.
983. **Jovanovich, S. B., and J. Lebowitz.** 1987. Estimation of the effect of coumermycin A₁ on *Salmonella typhimurium* promoters by using random operon fusions. *J. Bacteriol.* **169**:4431–4435.
984. **Jovanovich, S. B., M. Martinell, M. T. Record, Jr., and R. R. Burgess.** 1988. Rapid response to osmotic upshift by osmoregulated genes in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **170**:234–539.
985. **Joys, T. M.** 1976. Identification of the antibody binding site in the phase-1 flagellar protein of *Salmonella typhimurium*. *Microbios* **15**:221–228.
986. **Joys, T. M.** 1985. The covalent structure of the phase-1 flagellar filament protein of *Salmonella typhimurium* and its comparison with other flagellins. *J. Biol. Chem.* **260**:15758–15761.
987. **Joys, T. M., J. F. Martin, H. L. Wilson, and V. Rankis.** 1974. Differences in the primary structure of the phase-1 flagellins of two strains of *Salmonella typhimurium*. *Biochim. Biophys. Acta* **351**:301–305.
988. **Joys, T. M., and V. Rankis.** 1972. The primary structure of the phase-1 flagellar protein of *Salmonella typhimurium*. I. The tryptic peptides. *J. Biol. Chem.* **247**:5180–5193.
989. **Joys, T. M., and B. A. D. Stocker.** 1969. Recombination of *H1*, the gene determining the flagellar antigen-*i* of *Salmonella typhimurium*: mapping of *H1* and *fla* mutations. *J. Gen. Microbiol.* **58**:267–276.
990. **Jungwirth, C., S. R. Gross, P. Margolin, and H. E. Umbarger.** 1963. The biosynthesis of leucine. I. The accumulation of β -carboxy- β -hydroxyisocaproate by leucine auxotrophs of *Salmonella typhimurium* and *Neurospora crassa*. *Biochemistry* **2**:1–6.
991. **Kadam, S. K., M. S. Pepler, and K. E. Sanderson.** 1985. Temperature-sensitive mutants in *rfaI* and *rfaJ*, genes for galactosyltransferase I and glucosyltransferase II, for synthesis of lipopolysaccharide in *Salmonella typhimurium*. *Can. J. Microbiol.* **31**:861–869.
992. **Kadam, S. K., A. Rehemtulla, and K. E. Sanderson.** 1985. Cloning of *rfaG*, *B*, *I*, and *J* genes for glycosyltransferase enzymes for synthesis of the lipopolysaccharide core of *Salmonella typhimurium*. *J. Bacteriol.* **161**:277–284.
993. **Kagawa, H., T. Nishiyama, and S. Yamaguchi.** 1983. Motility development of *Salmonella typhimurium* cells with *flaV* mutations after addition of exogenous flagellin. *J. Bacteriol.* **155**: 435–437.
994. **Kagawa, H., N. Ono, M. Enomoto, and Y. Komeda.** 1984. Bacteriophage Chi sensitivity and motility of *Escherichia coli* K-12 and *Salmonella typhimurium* Fla⁻ mutants possessing the hook structure. *J. Bacteriol.* **157**:649–654.
995. **Kagawa, H., K. Owaribe, S. Asakura, and N. Takahashi.** 1976. Flagellar hook protein from *Salmonella* SJ25. *J. Bacteriol.* **125**:68–73.
996. **Kamiya, R., and S. Asakura.** 1974. Formation of a flagella-like but straight polymer of *Salmonella* flagellin. *J. Mol. Biol.* **87**:55–62.
997. **Kamiya, R., and S. Asakura.** 1976. Helical transformations of *Salmonella* flagella *in vitro*. *J. Mol. Biol.* **106**:167–186.
998. **Kamp, D., and R. Kahmann.** 1981. The relationship of two invertible segments in bacteriophage Mu and *Salmonella typhimurium* DNA. *Mol. Gen. Genet.* **184**:564–566.

999. **Kang, C. H., W. C. Shin, Y. Yamagata, S. Gokcen, G. F. Ames, and S. H. Kim.** 1991. Crystal structure of the lysine-, arginine-, ornithine-binding protein (LAO) from *Salmonella typhimurium* at 2.7-Å resolution. *J. Biol. Chem.* **266**:23893–23899.
1000. **Kaniga, K., J. C. Bossio, and J. E. Galan.** 1994. The *Salmonella typhimurium* invasion genes *invF* and *invG* encode homologues of the AraC and PulD family of proteins. *Mol. Microbiol.* **13**:555–568.
1001. **Kanto, S., H. Okino, S. Aizawa, and S. Yamaguchi.** 1991. Amino acids responsible for flagellar shape are distributed in terminal regions of flagellin. *J. Mol. Biol.* **219**:471–480.
1002. **Kanzaki, H., P. McPhie, and E. W. Miles.** 1991. Effect of single amino acid substitutions at positions 49 and 60 on the thermal unfolding of the tryptophan synthase alpha subunit from *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **284**:174–180.
1003. **Kaplan, J. B., W. K. Merkel, and B. P. Nichols.** 1985. Evolution of glutamine amidotransferase genes. Nucleotide sequences of the *pabA* genes from *Salmonella typhimurium*, *Klebsiella aerogenes* and *Serratia marcescens*. *J. Mol. Biol.* **183**:327–340.
1004. **Kaplan, M. M., and M. Flavin.** 1966. Cystathionine γ -synthetase of *Salmonella*: structural properties of a new enzyme in bacterial methionine biosynthesis. *J. Biol. Chem.* **241**:5781–5789.
1005. **Karbonowska, H., A. Wiater, and D. Hulanicka.** 1977. Sulfate permease of *Escherichia coli* K12. *Acta Biochim. Pol.* **24**:329–334.
1006. **Karlsson, M., K. Hannavy, and C. F. Higgins.** 1993. A sequence-specific function for the N-terminal signal-like sequence of the TonB protein. *Mol. Microbiol.* **8**:379–388.
1007. **Kasahara, M., A. Nakata, and H. Shinagawa.** 1991. Molecular analysis of the *Salmonella typhimurium* *phoN* gene, which encodes nonspecific acid phosphatase. *J. Bacteriol.* **173**:6760–6765.
1008. **Kawagishi, I., V. Muller, A. W. Williams, V. M. Irikura, and R. M. Macnab.** 1992. Subdivision of flagellar region III of the *Escherichia coli* and *Salmonella typhimurium* chromosomes and identification of two additional flagellar genes. *J. Gen. Microbiol.* **138**:1051–1065.
1009. **Kawakami, K., and Y. Nakamura.** 1990. Autogenous suppression of an opal mutation in the gene encoding peptide chain release factor 2. *Proc. Natl. Acad. Sci. USA* **87**:8432–8436.
1010. **Kay, W. W., and M. Cameron.** 1978. Citrate transport in *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **190**:270–280.
1011. **Kay, W. W., and M. J. Cameron.** 1978. Transport of C₄ dicarboxylic acids in *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **190**:281–289.
1012. **Kayastha, A. M., Y. Sawa, S. Nagata, and E. W. Miles.** 1991. Site-directed mutagenesis of the beta subunit of tryptophan synthase from *Salmonella typhimurium*. Role of active site glutamic acid 350. *J. Biol. Chem.* **266**:7618–7625.
1013. **Kaye, R., J. Barravecchio, and J. Roth.** 1974. Isolation of P22 specialized transducing phage following F'-episome fusion. *Genetics* **76**:655–667.
1014. **Kelln, R. A.** 1984. Evidence for involvement of *pyrH*⁺ of an *Escherichia coli* K-12 F-prime factor in inhibiting construction of hybrid merodiploids with *Salmonella typhimurium*. *Can. J. Microbiol.* **30**:991–996.
1015. **Kelln, R. A., K. F. Foltermann, and G. A. O'Donovan.** 1975. Location of the *argR* gene on the chromosome of *Salmonella typhimurium*. *Mol. Gen. Genet.* **139**:279–284.
1016. **Kelln, R. A., J. J. Kinahan, K. F. Foltermann, and G. A. O'Donovan.** 1975. Pyrimidine biosynthetic enzymes of *Salmonella typhimurium*, repressed specifically by growth in the presence of cytidine. *J. Bacteriol.* **124**:764–774.
1017. **Kelln, R. A., and J. Neuhard.** 1988. Regulation of *pyrC* expression in *Salmonella typhimurium*: identification of a regulatory region. *Mol. Gen. Genet.* **212**:287–294.
1018. **Kelln, R. A., J. Neuhard, and L. Stauning.** 1985. Isolation and characterization of pyrimidine mutants of *Salmonella typhimurium* altered in expression of *pyrC*, *pyrD*, and *pyrE*. *Can. J. Microbiol.* **31**:981–987.
1019. **Kelln, R. A., and G. A. O'Donovan.** 1976. Isolation and partial characterization of an *argR* mutant of *Salmonella typhimurium*. *J. Bacteriol.* **128**:528–535.
1020. **Kelln, R. A., and V. L. Zak.** 1978. Arginine regulon control in a *Salmonella typhimurium*-

- Escherichia coli* hybrid merodiploid. *Mol. Gen. Genet.* **161**:333–336.
1021. **Kelln, R. A., and V. L. Zak.** 1980. A mutation in *Salmonella typhimurium* imparting conditional resistance to 5-fluorouracil and a bio-energetic defect: mapping of *cad*. *Mol. Gen. Genet.* **179**:678–682.
1022. **Kemper, J.** 1974. Evolution of a new gene substituting for the *leuD* gene of *Salmonella typhimurium*: characterization of *supQ* mutations. *J. Bacteriol.* **119**:937–951.
1023. **Kemper, J.** 1974. Gene order and co-transduction in the *leu-ara-fol-pyrA* region of the *Salmonella typhimurium* linkage map. *J. Bacteriol.* **117**:94–99.
1024. **Kemper, J.** 1974. Evolution of a new gene substituting for the *leuD* gene of *Salmonella typhimurium*: origin and nature of *supQ* and *newD* mutations. *J. Bacteriol.* **120**:1176–1185.
1025. **Kemper, J., and P. Margolin.** 1970. Suppression by gene substitution for the *leuD* gene of *Salmonella typhimurium*. *Genetics* **63**:263–279.
1026. **Kerridge, D.** 1966. Flagellar synthesis in *Salmonella typhimurium*: factors affecting the formation of the flagellar epsilon-*N*-methyllysine. *J. Gen. Microbiol.* **42**:71–82.
1027. **Khan, I. H., T. S. Reese, and S. Khan.** 1992. The cytoplasmic component of the bacterial flagellar motor. *Proc. Natl. Acad. Sci. USA* **89**:5956–5960.
1028. **Khan, S., and R. M. Macnab.** 1980. The steady state counterclockwise-clockwise ratio of bacterial flagellar motors is regulated by protonmotive force. *J. Mol. Biol.* **138**:563–597.
1029. **Khan, S., R. M. Macnab, A. L. DeFranco, and D. E. Koshland, Jr.** 1978. Inversion of a behavioral response in bacterial chemotaxis: explanation at the molecular level. *Proc. Natl. Acad. Sci. USA* **75**:4150–4154.
1030. **Kiefer, V., G. Schmidt, B. Jann, and K. Jann.** 1976. Genetic transfer of *Salmonella* O antigens to *Escherichia coli* O8. *J. Gen. Microbiol.* **92**:311–324.
1031. **Kier, L. D., R. Weppelman, and B. N. Ames.** 1977. Resolution and purification of three periplasmic phosphatases of *Salmonella typhimurium*. *J. Bacteriol.* **130**:399–410.
1032. **Kier, L. D., R. Weppelman, and B. N. Ames.** 1977. Regulation of two phosphatases and a cyclic phosphodiesterase of *Salmonella typhimurium*. *J. Bacteriol.* **130**:420–428.
1033. **Kier, L. D., R. M. Weppelman, and B. N. Ames.** 1979. Regulation of nonspecific acid phosphatase in *Salmonella*: *phoN* and *phoP* genes. *J. Bacteriol.* **138**:155–161.
1034. **Kihara, M., M. Homma, K. Kutsukake, and R. M. Macnab.** 1989. Flagellar switch of *Salmonella typhimurium*: gene sequences and deduced protein sequences. *J. Bacteriol.* **171**:3247–3257.
1035. **Kilstrup, M., C. D. Lu, A. Abdelal, and J. Neuhard.** 1988. Nucleotide sequence of the *carA* gene and regulation of the *carAB* operon in *Salmonella typhimurium*. *Eur. J. Biochem.* **176**:421–429.
1036. **Kim, S. S., and P. Datta.** 1982. Chemical characterization of biodegradative threonine dehydratases from two enteric bacteria. *Biochim. Biophys. Acta* **706**:27–35.
1037. **Kingsman, A. J.** 1977. The structure of the *cysCDHIJ* region in unstable cysteine or methionine requiring mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **156**:327–332.
1038. **Kingsman, A. J., and D. A. Smith.** 1978. The nature of genetic instability in auxotrophs of *Salmonella typhimurium* requiring cysteine or methionine and resistant to inhibition by 1,2,4-triazole. *Genetics* **89**:439–452.
1039. **Kingsman, A. J., D. A. Smith, and M. D. Hulanicka.** 1978. Genetic instability in auxotrophs of *Salmonella typhimurium* requiring cysteine or methionine and resistant to inhibition by 1,2,4-triazole. *Genetics* **89**:419–438.
1040. **Kinkeldey, U., D. Von Lieres, and H. Schmieger.** 1978. Bacterial donor mutants affecting the efficiency of generalized transduction by *Salmonella typhimurium* phage P-22. *J. Gen. Microbiol.* **108**:227–238.
1041. **Kinney, D. M., and J. W. Foster.** 1985. Identification of a *cis*-acting regulatory region in the *pncB* locus of *Salmonella typhimurium*. *Mol. Gen. Genet.* **199**:512–517.
1042. **Kinney, D. M., J. W. Foster, and A. G. Moat.** 1979. Pyridine nucleotide cycle of *Salmonella typhimurium*: in vitro demonstration of nicotinamide mononucleotide deamidase and characterization of *pnuA* mutants defective in nicotinamide mononucleotide transport. *J. Bacteriol.* **140**:607–611.

1043. **Kirchner, C. E. J., and M. J. Rudden.** 1966. Location of a mutator gene in *Salmonella typhimurium* by cotransduction. *J. Bacteriol.* **92**:1453–1456.
1044. **Kiritani, K.** 1972. Mutants deficient or altered in branched-chain-amino-acid transferase in *Salmonella typhimurium*. *Jpn. J. Genet.* **47**:91–102.
1045. **Kiritani, K.** 1974. Mutants of *Salmonella typhimurium* defective in transport of branched-chain amino acids. *J. Bacteriol.* **120**:1093–1101.
1046. **Kiritani, K., and N. Inuzuka.** 1970. Mutations affecting the branched-chain-amino-acid aminotransferase in *Salmonella typhimurium*. *Jpn. J. Genet.* **45**:293–304.
1047. **Kiritani, K., and K. Ohnishi.** 1977. Repression and inhibition of transport systems for branched-chain amino acids in *Salmonella typhimurium*. *J. Bacteriol.* **129**:589–598.
1048. **Kiritani, K., and K. Ohnishi.** 1978. Multiple transport systems for branched-chain amino acids as studied by mutants of *Salmonella typhimurium*. *Jpn. J. Genet.* **53**:265–274.
1049. **Kirsh, M., D. R. Dembinski, P. E. Hartman, and C. G. Miller.** 1978. *Salmonella typhimurium* peptidase active on carnosine. *J. Bacteriol.* **134**:361–374.
1050. **Kishi, K., and S. Iseki.** 1973. Genetic analysis of the O antigens in *Salmonella*. III. Inheritance of O antigens 3, 10, and 15 of *Salmonella* group E. *Jpn. J. Genet.* **48**:255–262.
1051. **Kishi, K., and S. Iseki.** 1973. Genetic analysis of the O antigens in *Salmonella*. I. Heredity of blood group-active O antigens in *Salmonella* groups G, R, and U. *Jpn. J. Genet.* **48**:89–97.
1052. **Kishi, K., and S. Iseki.** 1973. Genetic analysis of the O antigens in *Salmonella*. II. Heredity of the O antigens 4, 5, and 9 of *Salmonella*. *Jpn. J. Genet.* **48**:133–136.
1053. **Kishi, K., and S. Iseki.** 1974. Genetic analysis of the O antigens in *Salmonella*. IV. Inheritance of O antigens 1, 3, 19, and 34 of *Salmonella* group E. *Jpn. J. Genet.* **49**:125–129.
1054. **Kita, H., and H. Nikaido.** 1973. Structure of cell wall lipopolysaccharide of *Salmonella typhimurium*. IV. Anomeric configuration of L-rhamnose residues and its taxonomic implications. *J. Bacteriol.* **113**:672–679.
1055. **Kleckner, N., K. Reichardt, and D. Botstein.** 1979. Inversions and deletions of the *Salmonella typhimurium* chromosome generated by the translocatable tetracycline resistance element Tn-10. *J. Mol. Biol.* **127**:89–116.
1056. **Kleckner, N., J. Roth, and D. Botstein.** 1977. Genetic engineering *in vivo* using translocatable drug-resistance elements: new methods in bacterial genetics. *J. Mol. Biol.* **116**:125–159.
1057. **Kleckner, N., D. A. Steele, K. Reichardt, and D. Botstein.** 1979. Specificity of insertion by the translocatable tetracycline resistance element Tn-10. *Genetics* **92**:1023–1040.
1058. **Kleeman, J. E., and S. M. Parsons.** 1975. A sensitive assay for the reverse reaction of the first histidine biosynthetic enzyme. *Anal. Biochem.* **68**:236–241.
1059. **Kleeman, J. E., and S. M. Parsons.** 1977. Inhibition of histidyl-tRNA-adenosine triphosphate phosphoribosyltransferase complex formation by histidine and by guanosine tetraphosphate. *Proc. Natl. Acad. Sci. USA* **74**:1535–1537.
1060. **Klena, J. D., E. Pradel, and C. A. Schnaitman.** 1992. Comparison of lipopolysaccharide biosynthesis genes *rfaK*, *rfaL*, *rfaY*, and *rfaZ* of *Escherichia coli* K-12 and *Salmonella typhimurium*. *J. Bacteriol.* **174**:4746–4752.
1061. **Klena, J. D., E. Pradel, and C. A. Schnaitman.** 1993. The *rfaS* gene, which is involved in production of a rough form of lipopolysaccharide core in *Escherichia coli* K-12, is not present in the *rfa* cluster of *Salmonella typhimurium* LT2. *J. Bacteriol.* **175**:1524–1527.
1062. **Knox, J. R., H. S. Liu, C. T. Walsh, and L. E. Zawadzke.** 1989. D-Alanine-D-alanine ligase (ADP) from *Salmonella typhimurium*. Overproduction, purification, crystallization and preliminary X-ray analysis. *J. Mol. Biol.* **205**:461–463.
1063. **Kobori, J. A., and A. Kornberg.** 1982. The *Escherichia coli dnaC* gene product. I. Overproduction of the *dnaC* proteins of *Escherichia coli* and *Salmonella typhimurium* by cloning into a high copy number plasmid. *J. Biol. Chem.* **257**:13757–13762.
1064. **Koch, W. H., T. A. Cebula, P. L. Foster, and E. Eisenstadt.** 1992. UV mutagenesis in *Salmonella typhimurium* is *umuDC* dependent despite the presence of *samAB*. *J. Bacteriol.* **174**:2809–2815.

1065. **Koduri, R., C. E. Benson, and J. S. Gots.** 1978. A DNA binding protein with specificity for *pur* genes in enteric bacteria. *Fed. Proc.* **37**:1875.
1066. **Koduri, R. K., D. M. Bedwell, and J. E. Brenchley.** 1980. Characterization of a *Hind*III-generated DNA fragment carrying the glutamine synthetase gene of *Salmonella typhimurium*. *Gene* **11**:227–237.
1067. **Koebnik, R., K. Hantke, and V. Braun.** 1993. The TonB-dependent ferrichrome receptor FcuA of *Yersinia enterocolitica*: evidence against a strict co-evolution of receptor structure and substrate specificity. *Mol. Microbiol.* **7**:383–393.
1068. **Kohno, T., L. Bossi, and J. R. Roth.** 1983. Genetic characterization of the *sufJ* frameshift suppressor in *Salmonella typhimurium*. *Genetics* **103**:31–42.
1069. **Kohno, T., L. Bossi, and J. R. Roth.** 1983. New suppressors of frameshift mutations in *Salmonella typhimurium*. *Genetics* **103**:23–29.
1070. **Kohno, T., and W. R. Gray.** 1981. Chemical and genetic studies of L-histidinol dehydrogenase of *Salmonella typhimurium*. Isolation and structure of tryptic peptides. *J. Mol. Biol.* **147**:451–464.
1071. **Kohno, T., and J. Roth.** 1979. Electrolyte effects on the activity of mutant enzymes *in vivo* and *in vitro*. *Biochemistry* **18**:1386–1392.
1072. **Kohno, T., and J. R. Roth.** 1978. A *Salmonella* frameshift suppressor that acts at runs of adenylic acid residues in the messenger RNA. *J. Mol. Biol.* **126**:37–52.
1073. **Kohno, T., M. Schmid, and J. R. Roth.** 1980. Effect of electrolytes on growth of mutant bacteria, p. 53–57. In D. W. Rains, R. C. Valentine, and A. Hollaender (ed.), *Genetic Engineering of Osmoregulation*. Plenum Publishing Corp., New York.
1074. **Komeda, Y., H. Suzuki, J. Ishidsu, and T. Iino.** 1975. The role of cAMP in flagellation of *Salmonella typhimurium*. *Mol. Gen. Genet.* **142**:289–298.
1075. **Kondratiev, Y. S., G. V. Brukhansky, I. V. Andreeva, and A. G. Skavronskaya.** 1977. UV sensitivity and repair of UV damages in *Salmonella* of wild type. *Mol. Gen. Genet.* **158**:211–214.
1076. **Konno, R., H. Fujita, T. Horiguchi, and S. Yamaguchi.** 1976. Precise position of the *nml* locus on the genetic map of *Salmonella*. *J. Gen. Microbiol.* **93**:182–183.
1077. **Korenevskaya, N. F., I. V. Andreeva, A. A. Kiryushkina, L. Y. Lichoded, Y. S. Kondratiev, and A. G. Skavronskaya.** 1977. Intergeneric mating transfer of *polA* gene from *Escherichia coli* to *Salmonella typhimurium*. *Mutat. Res.* **45**:351–354.
1078. **Kornberg, H. L., and M. C. James-Mortimer.** 1977. The phosphotransferase system as a site of cellular control. *Symp. Soc. Gen. Microbiol.* **27**:217–240.
1079. **Koshland, D. E., Jr.** 1977. Bacterial chemotaxis and some enzymes in energy metabolism. *Symp. Soc. Gen. Microbiol.* **27**:317–331.
1080. **Koski, P., L. Hirvas, and M. Vaara.** 1990. Complete sequence of the *ompH* gene encoding the 16-kDa cationic outer membrane protein of *Salmonella typhimurium*. *Gene* **88**:117–120.
1081. **Koski, P., M. Rhen, J. Kantele, and M. Vaara.** 1989. Isolation, cloning, and primary structure of a cationic 16-kDa outer membrane protein of *Salmonella typhimurium*. *J. Biol. Chem.* **264**:18973–18980.
1082. **Koski, P., H. Saarilahti, S. Sukupolvi, S. Taira, P. Riikonen, K. Osterlund, R. Hurme, and M. Rhen.** 1992. A new alpha-helical coiled coil protein encoded by the *Salmonella typhimurium* virulence plasmid. *J. Biol. Chem.* **267**:12258–12265.
1083. **Kotani, H., and K. Nakajima.** 1992. Cloning and sequence of thioredoxin gene of *Salmonella typhimurium* LT2. *Nucleic Acids Res.* **20**:1424.
1084. **Kovach, J. S., A. O. Ballesteros, M. Meyers, M. Soria, and R. F. Goldberger.** 1973. A *cis/trans* test of the effect on the first enzymes for histidine biosynthesis on regulation of the histidine operon. *J. Bacteriol.* **114**:351–356.
1085. **Kowarz, L., C. Coynault, V. Robbe-Saule, and F. Norel.** 1994. The *Salmonella typhimurium* *katF* (*rpoS*) gene: cloning, nucleotide sequence, and regulation of *spvR* and *spvABCD* virulence plasmid genes. *J. Bacteriol.* **176**:6852–6860.
1086. **Krajewska, E., and D. Shugar.** 1975. Pyrimidine nucleoside analogues as inducers of pyrimidine nucleoside catabolizing enzymes in *Salmonella typhimurium*. *Mol. Biol. Rep.* **2**:295–301.

1087. **Krajewska-Grynkiewicz, K., and T. Klopotoski.** 1979. Altered linkage values in phage P22-mediated transduction caused by distant deletions or insertions in donor chromosomes. *Mol. Gen. Genet.* **176**:87–94.
1088. **Krajewska-Grynkiewicz, K., and S. Kustu.** 1983. Regulation of transcription of *glnA*, the structural gene encoding glutamine synthetase, in *glnA::Mud1(Ap^R, lac)* fusion strains of *Salmonella typhimurium*. *Mol. Gen. Genet.* **192**:187–197.
1089. **Krajewska-Grynkiewicz, K., and S. Kustu.** 1983. Operon organization of the *glnA*, *ntxB*, and *ntxC* genes of *Salmonella typhimurium*, abstr. H153, p. 131. *Abstr. Annu. Meet. Am. Soc. Microbiol.* 1983.
1090. **Krajewska-Grynkiewicz, K., and S. Kustu.** 1984. Evidence that nitrogen regulatory gene *ntxC* of *Salmonella typhimurium* is transcribed from the *glnA* promoter as well as from a separate *ntx* promoter. *Mol. Gen. Genet.* **193**:135–142.
1091. **Krajewska-Grynkiewicz, K., W. Walczak, and T. Klopotoski.** 1971. Mutants of *Salmonella typhimurium* able to utilize D-histidine as a source of L-histidine. *J. Bacteriol.* **105**:28–37.
1092. **Kramer, G. F., and B. N. Ames.** 1988. Isolation and characterization of a selenium metabolism mutant of *Salmonella typhimurium*. *J. Bacteriol.* **170**:736–743.
1093. **Kramer, G. F., J. C. Baker, and B. N. Ames.** 1988. Near-UV stress in *Salmonella typhimurium*: 4-thiouridine in tRNA, ppGpp, and ApppGpp as components of an adaptive response. *J. Bacteriol.* **170**:2344–2351.
1094. **Krause, M., F. C. Fang, and D. G. Guiney.** 1992. Regulation of plasmid virulence gene expression in *Salmonella dublin* involves an unusual operon structure. *J. Bacteriol.* **174**:4482–4489.
1095. **Kredich, N. M., M. A. Becker, and G. M. Tomkins.** 1969. Purification and characterization of cysteine synthetase, a bifunctional protein complex, from *Salmonella typhimurium*. *J. Biol. Chem.* **244**:2428–2439.
1096. **Kredich, N. M., L. J. Foote, and J. D. Hulanicka.** 1975. Studies on the mechanism of inhibition of *Salmonella typhimurium* by 1,2,4-triazole. *J. Biol. Chem.* **250**:7324–7331.
1097. **Kredich, N. M., and G. M. Tomkins.** 1966. The enzymic synthesis of L-cysteine in *Escherichia coli* and *Salmonella typhimurium*. *J. Biol. Chem.* **241**:4955–4965.
1098. **Krone, F. A., G. Westphal, and J. D. Schwenn.** 1991. Characterisation of the gene *cysH* and of its product phospho-adenylylsulphate reductase from *Escherichia coli*. *Mol. Gen. Genet.* **225**:314–319.
1099. **Kronenberg, H. M., T. Vogel, and R. F. Goldberger.** 1975. A new and highly sensitive assay for the ATP phosphoribosyltransferase that catalyzes the first step in histidine biosynthesis. *Anal. Biochem.* **65**:380–388.
1100. **Kruger, D. H., S. Hansen, and M. Reuter.** 1983. The *ocr⁺* gene function of bacteriophages T3 and T7 counteracts the *Salmonella typhimurium* DNA restriction systems SA and SB. *J. Virol.* **45**:1147–1149.
1101. **Ktsoyan, Z. A., and N. N. Sarkisyan.** 1979. Transfection of phage DP-8 DNA in *Salmonella derby* and radio-sensitive mutants. *Biol. Zh. Arm.* **32**:352–356.
1102. **Kubori, T., N. Shimamoto, S. Yamaguchi, K. Namba, and S.-I. Aizawa.** 1992. Morphological pathway of flagellar assembly in *Salmonella typhimurium*. *J. Mol. Biol.* **226**:433–446.
1103. **Kuchino, Y., Y. Yabusaki, F. Mori, and S. Nishimura.** 1984. Nucleotide sequences of three proline tRNAs from *Salmonella typhimurium*. *Nucleic Acids Res.* **12**:1559–1562.
1104. **Kukuruzinska, M. A., W. F. Harrington, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Studies on the molecular weight and association of enzyme I. *J. Biol. Chem.* **257**:14470–14476.
1105. **Kulla, H. G.** 1983. Regulatory citrate lyase mutants of *Salmonella typhimurium*. *J. Bacteriol.* **153**:546–549.
1106. **Kuo, T.-T., and B. A. D. Stocker.** 1969. Suppressor of proline requirement of *proA* and *proAB* deletion mutants in *Salmonella typhimurium* by mutation to arginine requirement. *J. Bacteriol.* **98**:593–598.
1107. **Kuo, T.-T., and B. A. D. Stocker.** 1972. Mapping of *rfa* genes in *Salmonella typhimurium* by

- ES18 and P22 transduction by conjugation. *J. Bacteriol.* **112**:48–63.
1108. **Kuroda, M., S. de Waard, K. Mizushima, M. Tsuda, P. Postma, and T. Tsuchiya.** 1992. Resistance of the melibiose carrier to inhibition by the phosphotransferase system due to substitutions of amino acid residues in the carrier of *Salmonella typhimurium*. *J. Biol. Chem.* **267**:18336–18341.
1109. **Kustu, S., J. Hirschman, D. Burton, J. Jelesko, and J. C. Meeks.** 1984. Covalent modification of bacterial glutamine synthetase: physiological significance. *Mol. Gen. Genet.* **197**:309–317.
1110. **Kustu, S. G., and G. F. Ames.** 1973. The *hisP* protein, a known histidine transport component in *Salmonella typhimurium*, is also an arginine transport component. *J. Bacteriol.* **116**:107–113.
1111. **Kustu, S. G., and G. F. Ames.** 1974. The histidine-binding protein J, a histidine transport component, has two different functional sites. *J. Biol. Chem.* **249**:6976–6983.
1112. **Kustu, S. G., D. Burton, E. Garcia, L. McCarter, and N. McFarland.** 1979. Nitrogen control in *Salmonella*: regulation by the *glnR* and *glnF* gene products. *Proc. Natl. Acad. Sci. USA* **76**:4576–4580.
1113. **Kustu, S. G., N. C. McFarland, S. P. Hui, B. Esmon, and G. F.-L. Ames.** 1979. Nitrogen control in *Salmonella typhimurium*: co-regulation of synthesis of glutamine synthetase and amino acid transport systems. *J. Bacteriol.* **138**:218–234.
1114. **Kustu, S. G., and K. McKereghan.** 1975. Mutations affecting glutamine synthetase activity in *Salmonella typhimurium*. *J. Bacteriol.* **122**:1006–1016.
1115. **Kutsukake, K., and H. Doi.** 1994. Nucleotide sequence of the *flgD* gene of *Salmonella typhimurium* which is essential for flagellar hook formation. *Biochim. Biophys. Acta* **1218**:443–446.
1116. **Kutsukake, K., and T. Iino.** 1980. A *trans*-acting factor mediates inversion of a specific DNA segment in flagellar phase variation of a *Salmonella*. *Nature (London)* **284**:479–481.
1117. **Kutsukake, K., and T. Iino.** 1980. Inversions of specific DNA segments in flagellar phase variation of *Salmonella* and inversion systems of bacteriophages P1 and Mu. *Proc. Natl. Acad. Sci. USA* **77**:7338–7341.
1118. **Kutsukake, K., and T. Iino.** 1985. Refined genetic analysis of the region II *che* mutants in *Salmonella typhimurium*. *Mol. Gen. Genet.* **199**:406–409.
1119. **Kutsukake, K., and T. Iino.** 1994. Role of the FliA-FlgM regulatory system on the transcriptional control of the flagellar regulon and flagellar formation in *Salmonella typhimurium*. *J. Bacteriol.* **176**:3598–3605.
1120. **Kutsukake, K., T. Iino, Y. Komeda, and S. Yamaguchi.** 1980. Functional homology of *fla* genes between *Salmonella typhimurium* and *Escherichia coli*. *Mol. Gen. Genet.* **178**:59–67.
1121. **Kutsukake, K., T. Minamino, and T. Yokoseki.** 1994. Isolation and characterization of FliK-dependent flagellation mutants from *Salmonella typhimurium*. *J. Bacteriol.* **176**:7625–7629.
1122. **Kutsukake, K., Y. Ohya, and T. Iino.** 1990. Transcriptional analysis of the flagellar regulon of *Salmonella typhimurium*. *J. Bacteriol.* **172**:741–747.
1123. **Kutsukake, K., Y. Ohya, S. Yamaguchi, and T. Iino.** 1988. Operon structure of flagellar genes in *Salmonella typhimurium*. *Mol. Gen. Genet.* **214**:11–15.
1124. **Kutsukake, K., T. Okada, T. Yokoseki, and T. Iino.** 1994. Sequence analysis of the *flgA* gene and its adjacent region in *Salmonella typhimurium*, and identification of another flagellar gene, *flgN*. *Gene* **143**:49–54.
1125. **Kutsukake, K., T. Suzuki, S. Yamaguchi, and T. Iino.** 1979. Role of gene *flaFV* on flagellar hook formation in *Salmonella typhimurium*. *J. Bacteriol.* **140**:267–275.
1126. **Kwan, H. S., and E. L. Barrett.** 1983. Roles for menaquinone and the two trimethylamine oxide (TMAO) reductases in TMAO respiration in *Salmonella typhimurium*: Mud(Ap^r lac) insertion mutations in *men* and *tor*. *J. Bacteriol.* **155**:1147–1155.
1127. **Kwan, H. S., and E. L. Barrett.** 1983. Mutants of *Salmonella typhimurium* defective in trimethylamine oxide reduction, abstr. K46, p. 51. *Abstr. Annu. Meet. Am. Soc. Microbiol., 1983.*
1128. **Kwan, H. S., and E. L. Barrett.** 1983. Purification and properties of trimethylamine oxide reductase from *Salmonella typhimurium*. *J. Bacteriol.* **155**:1455–1458.
1129. **Kwan, H. S., and E. L. Barrett.** 1984. Map locations and functions of *Salmonella typhimurium* *men* genes. *J. Bacteriol.* **159**:1090–1092.

1130. **Kwan, H. S., H. W. Chui, and K. K. Wong.** 1988. *ack::Mu d1–8 (Ap^r lac)* operon fusions of *Salmonella typhimurium* LT2. *Mol. Gen. Genet.* **211**:183–185.
1131. **Kwan, H. S., and K. K. Wong.** 1986. A general method for isolation of *Mu d 1–8 (Ap^r lac)* operon fusions in *Salmonella typhimurium* LT2 from *Tn10* insertion strains: *chlC::Mud1–8*. *Mol. Gen. Genet.* **205**:221–224.
1132. **Kwoh, D. Y., and J. Kemper.** 1978. Bacteriophage P22-mediated specialized transduction in *Salmonella typhimurium*: high frequency of aberrant prophage excision. *J. Virol.* **27**:519–534.
1133. **Kwoh, D. Y., and J. Kemper.** 1978. Bacteriophage P22-mediated specialized transduction in *Salmonella typhimurium*: identification of different types of specialized transducing particles. *J. Virol.* **27**:535–550.
1134. **Lam, S., and J. R. Roth.** 1983. Genetic mapping of IS200 copies in *Salmonella typhimurium* strain LT2. *Genetics* **105**:801–811.
1135. **Lam, S., and J. R. Roth.** 1983. IS200: a *Salmonella*-specific insertion sequence. *Cell* **34**:951–960.
1136. **Lam, S., and J. R. Roth.** 1986. Structural and functional studies of insertion element IS200. *J. Mol. Biol.* **187**:157–167.
1137. **Lampel, K. A., and M. Riley.** 1982. Discontinuity of homology of *Escherichia coli* and *Salmonella typhimurium* DNA in the *lac* region. *Mol. Gen. Genet.* **186**:82–86.
1138. **Lancy, E. D., M. R. Lifics, D. G. Kehres, and R. Maurer.** 1989. Isolation and characterization of mutants with deletions in *dnaQ*, the gene for the editing subunit of DNA polymerase III in *Salmonella typhimurium*. *J. Bacteriol.* **171**:5572–5580.
1139. **Lancy, E. D., M. R. Lifics, P. Munson, and R. Maurer.** 1989. Nucleotide sequences of *dnaE*, the gene for the polymerase subunit of DNA polymerase III in *Salmonella typhimurium*, and a variant that facilitates growth in the absence of another polymerase subunit. *J. Bacteriol.* **171**:5581–5586.
1140. **Langley, D., and J. R. Guest.** 1974. Biochemical and genetic characteristics of deletion and other mutant strains of *Salmonella typhimurium* LT2 lacking α -keto acid dehydrogenase complex activities. *J. Gen. Microbiol.* **82**:319–335.
1141. **Lapidus, I. R., M. Welch, and M. Eisenbach.** 1988. Pausing of flagellar rotation is a component of bacterial motility and chemotaxis. *J. Bacteriol.* **170**:3627–3632.
1142. **LaRossa, R. A., and J. V. Schloss.** 1984. The sulfonylurea herbicide sulfometuron methyl is an extremely potent and selective inhibitor of acetolactate synthase in *Salmonella typhimurium*. *J. Biol. Chem.* **259**:8753–8757.
1143. **LaRossa, R. A., and D. R. Smulski.** 1984. *ilvB*-encoded acetolactate synthase is resistant to the herbicide sulfometuron methyl. *J. Bacteriol.* **160**:391–394.
1144. **LaRossa, R. A., and T. K. Van Dyk.** 1989. Leaky pantothenate and thiamin mutations of *Salmonella typhimurium* conferring sulphometuron methyl sensitivity. *J. Gen. Microbiol.* **135**:2209–2222.
1145. **LaRossa, R. A., T. K. VanDyk, and D. R. Smulski.** 1987. Toxic accumulation of α -ketobutyrate caused by inhibition of the branched-chain amino acid biosynthetic enzyme acetolactate synthase in *Salmonella typhimurium*. *J. Bacteriol.* **169**:1372–1378.
1146. **LaScolea, L. J., Jr., and E. Balbinder.** 1972. Restoration of phosphoribosyl transferase activity by partially deleting the *trpB* gene in the tryptophan operon of *Salmonella typhimurium*. *J. Bacteriol.* **112**:877–885.
1147. **LaScolea, L. J., Jr., M. M. Dooley, R. Torget, and E. Balbinder.** 1978. A mutation to 5-methyl tryptophan dependence in the *trp* operon of *Salmonella typhimurium*. III. Correlation between phenotype and the properties of the second enzyme for tryptophan biosynthesis in a 5-methyl tryptophan dependent mutant and several 5-methyl tryptophan independent revertants. *Mol. Gen. Genet.* **165**:145–153.
1148. **Laszlo, D. J., and B. L. Taylor.** 1981. Aerotaxis in *Salmonella typhimurium*: role of electron transport. *J. Bacteriol.* **145**:990–1001.
1149. **Lauble, H., Y. Georgalis, and U. Heinemann.** 1989. Studies on the domain structure of the *Salmonella typhimurium* AraC protein. *Eur. J. Biochem.* **185**:319–325.

1150. **Lawrence, D. A.** 1972. Regulation of the methionine feedback sensitive enzyme in mutants of *Salmonella typhimurium*. *J. Bacteriol.* **109**:8–11.
1151. **Lawrence, D. A., D. A. Smith, and R. J. Rowbury.** 1968. Regulation of methionine synthesis in *Salmonella typhimurium*: mutants resistant to inhibition by analogues of methionine. *Genetics* **58**:473–492.
1152. **Lawrence, J. G., H. Ochman, and D. L. Hartl.** 1991. Molecular and evolutionary relationships among enteric bacteria. *J. Gen. Microbiol.* **137**(Pt. 8):1911–1921.
1153. **Lawther, R. P., R. C. Wek, J. M. Lopes, R. Pereira, B. E. Taillon, and G. W. Hatfield.** 1987. The complete nucleotide sequence of the *ilvGMEDA* operon of *Escherichia coli* K-12. *Nucleic Acids Res.* **15**:2137–2155. (Errata, **15**:9108, 1987, **16**:3602, 1988.)
1154. **Lawton, K. G., and H. W. Taber.** 1980. Isolation of an F' carrying a portion of the histidine transport operon of *Salmonella typhimurium*, abstr. H106, p. 126. *Abstr. Annu. Meet. Am. Soc. Microbiol.*, 1980.
1155. **Lawton, K. G., and H. W. Taber.** 1984. Isolation of F' plasmids carrying a portion of the *Salmonella typhimurium* histidine transport operon. *J. Bacteriol.* **157**:697–702.
1156. **Leary, T. R., and G. B. Kohlhaw.** 1974. α -Isopropylmalate synthase from *Salmonella typhimurium*. *J. Biol. Chem.* **247**:1089–1095.
1157. **Lederberg, J., and T. Iino.** 1956. Phase variation in *Salmonella*. *Genetics* **41**:743–757.
1158. **Lee, C. A., B. D. Jones, and S. Falkow.** 1992. Identification of a *Salmonella typhimurium* invasion locus by selection for hyperinvasive mutants. *Proc. Natl. Acad. Sci. USA* **89**:1847–1851.
1159. **Lee, F., K. Bertrand, G. Bennett, and C. Yanofsky.** 1978. Comparison of the nucleotide sequences of the initial transcribed regions of the tryptophan operons of *Escherichia coli* and *Salmonella typhimurium*. *J. Mol. Biol.* **121**:193–217.
1160. **Lee, G. S., and G. F.-L. Ames.** 1984. Analysis of promoter mutations in the histidine transport operon of *Salmonella typhimurium*: use of hybrid M13 bacteriophages for cloning, transformation, and sequencing. *J. Bacteriol.* **159**:1000–1005.
1161. **Lee, J.-H., K. Burke, and G. Wilcox.** 1986. Mutations resulting in promoter-like sequences which enhance the expression of *araC* in *Salmonella typhimurium*. *Gene* **46**:113–121.
1162. **Lee, J.-H., L. Heffernan, and G. Wilcox.** 1980. Isolation of *ara-lac* gene fusions in *Salmonella typhimurium* LT-2 by using transducing bacteriophage Mu *d*(Ap^r *lac*). *J. Bacteriol.* **143**:1325–1331.
1163. **Lee, J.-H., J. Nishitani, and G. Wilcox.** 1984. Genetic characterization of *Salmonella typhimurium* LT2 *ara* mutations. *J. Bacteriol.* **158**:344–346.
1164. **Lee, P. C., B. R. Bochner, and B. N. Ames.** 1983. AppppA, heat-shock stress, and cell oxidation. *Proc. Natl. Acad. Sci. USA* **80**:7496–7500.
1165. **Lee, S. Y., and C. T. Grubmeyer.** 1987. Purification and in vitro complementation of mutant histidinol dehydrogenases. *J. Bacteriol.* **169**:3938–3944.
1166. **Lee-Peng, F.-C., M. A. Hermodson, and G. B. Kohlhaw.** 1979. Transaminase B from *Escherichia coli*: quaternary structure, amino-terminal sequence, substrate specificity, and absence of a separate valine- α -ketoglutarate activity. *J. Bacteriol.* **139**:339–345.
1167. **Lehman, V., J. Redmond, A. Egan, and I. Minner.** 1978. The acceptor for polar head groups of the lipid A component of *Salmonella* lipopolysaccharides. *Eur. J. Biochem.* **86**:487–496.
1168. **Lehman, V., and E. Rupprecht.** 1977. Micro-heterogeneity in lipid A demonstrated by a new intermediate in the biosynthesis of 3-deoxy-D-manno-octulosonic acid lipid A. *Eur. J. Biochem.* **81**:443–452.
1169. **Lehman, V., E. Rupprecht, and M. J. Osborn.** 1977. Isolation of mutants conditionally blocked in the biosynthesis of the 3-deoxy-D-manno-octulosonic acid lipid A part of lipopolysaccharides derived from *Salmonella typhimurium*. *Eur. J. Biochem.* **76**:41–49.
1170. **Lehmann, V., G. Hammerling, M. Nurminen, I. Minner, E. Ruschmann, O. Luderitz, T. Kuo, and B. A. D. Stocker.** 1973. A new class of heptose-defective mutants of *Salmonella typhimurium*. *Eur. J. Biochem.* **32**:268–275.
1171. **Lehner, A. F., S. Harvey, and C. W. Hill.** 1984. Mapping and spacer identification of rRNA operons of *Salmonella typhimurium*. *J. Bacteriol.* **160**:682–686.

1172. **Lehner, A. F., and C. W. Hill.** 1980. Involvement of ribosomal ribonucleic acid operons in *Salmonella typhimurium* chromosomal rearrangements. *J. Bacteriol.* **143**:492–498.
1173. **Lehner, A. F., and C. W. Hill.** 1985. Merodiploidy in *Escherichia coli*-*Salmonella typhimurium* crosses: the role of unequal recombination between ribosomal RNA genes. *Genetics* **110**:365–380.
1174. **Lemoine, V. R., and R. J. Rowbury.** 1977. An effect of F-like plasmids on the maintenance of *Flac* in a *dnaC* mutant of *Salmonella typhimurium*. *Mol. Gen. Genet.* **156**:313–318.
1175. **Lenny, A. B., and P. Margolin.** 1980. Locations of the *opp* and *supX* genes of *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **143**:747–752.
1176. **Leonard, J. E., and M. H. Saier, Jr.** 1981. Genetic dissection of catalytic activities of the *Salmonella typhimurium* mannitol enzyme II. *J. Bacteriol.* **145**:1106–1109.
1177. **Leong, J., and J. B. Neilands.** 1976. Mechanisms of siderophore iron transport in enteric bacteria. *J. Bacteriol.* **126**:823–830.
1178. **Leong, J. M., S. Nunes-Duenby, C. F. Lesser, P. Youderian, M. M. Susskind, and A. Landy.** 1985. The (phi)80 and P22 attachment sites: primary structure and interaction with *Escherichia coli* integration host factor. *J. Biol. Chem.* **260**:4468–4477.
1179. **Lepore, G. C., P. DiNatale, L. Guarini, and F. DeLorenzo.** 1975. Histidyl-tRNA synthetase from *Salmonella typhimurium*: specificity in the binding of histidine analogues. *Eur. J. Biochem.* **56**:369–374.
1180. **Leung, P. S. C., and J. Preiss.** 1987. Cloning of the ADPglucose pyrophosphorylase (*glgC*) and glycogen synthase (*glgA*) structural genes from *Salmonella typhimurium* LT2. *J. Bacteriol.* **169**:4349–4354.
1181. **Leung, P. S. C., and J. Preiss.** 1987. Biosynthesis of bacterial glycogen: primary structure of *Salmonella typhimurium* ADP-glucose synthetase as deduced from the nucleotide sequence of the *glgC* gene. *J. Bacteriol.* **169**:4355–4360.
1182. **Lever, J. E.** 1972. Purification and properties of a component of histidine transport in *Salmonella typhimurium*. *J. Biol. Chem.* **247**:4317–4326.
1183. **Levine, S. M., F. Ardeshir, and G. F.-L. Ames.** 1980. Isolation and characterization of acetatekinase and phosphotransacetylase mutants of *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **143**:1081–1085.
1184. **Levinthal, M., and H. Nikaido.** 1969. Consequences of deletion mutations joining two operons of opposite polarity. *J. Mol. Biol.* **42**:511–520.
1185. **Levinthal, M., L. S. Williams, and H. E. Umbarger.** 1973. Role of threonine deaminase in the regulation of isoleucine and valine biosynthesis. *Nature (London) New Biol.* **246**:65–68.
1186. **Levy, M. S., P. Pomposiello, and R. Nagel.** 1991. *RecA*-dependent increased precise excision of Tn10 in *Salmonella typhimurium*. *Mutat. Res.* **255**:95–100.
1187. **Lew, H. C., P. H. Makela, H.-M. Kuhn, H. Mayer, and H. Nikaido.** 1986. Biosynthesis of enterobacterial common antigen requires dTDPglucose pyrophosphorylase determined by a *Salmonella typhimurium rfb* gene and a *Salmonella montevideo rfe* gene. *J. Bacteriol.* **168**:715–721.
1188. **Lew, H. C., H. Nikaido, and P. H. Makela.** 1978. Biosynthesis of uridine diphosphate *N*-acetylmannosaminuronic acid in *rff* mutants of *Salmonella typhimurium*. *J. Bacteriol.* **136**:227–233.
1189. **Lewis, J. A., and B. N. Ames.** 1972. Histidine regulation in *Salmonella typhimurium*. XI. The percentage of transfer RNA^{his} charged *in vivo* and its relation to the repression of the histidine operon. *J. Mol. Biol.* **66**:131–142.
1190. **Li, S.-L., J. Hanlon, and C. Yanofsky.** 1974. Structural homology of the glutamine amidotransferase subunits of the anthranilate synthetases of *Escherichia coli*, *Salmonella typhimurium*, and *Serratia marcescens*. *Nature (London)* **248**:48–50.
1191. **Li, S.-L., J. Hanlon, and C. Yanofsky.** 1974. Separation of anthranilate synthesis components I and II of *Escherichia coli*, *Salmonella typhimurium*, and *Serratia marcescens* and determination of their amino-terminal sequences by Edman degradation. *Biochemistry* **13**:1736–1744.
1192. **Li, S.-L., J. Hanlon, and C. Yanofsky.** 1975. Amino-terminal sequences of indoleglycerol phosphate synthetase of *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **123**:761–764.
1193. **Li, S.-L., and C. Yanofsky.** 1972. Amino acid sequences of fifty residues from the amino

- termini of the tryptophan synthetase α chains of several Enterobacteria. *J. Biol. Chem.* **247**:1031–1037.
1194. **Li, S.-L., and C. Yanofsky.** 1973. Amino acid sequence studies with the tryptophan synthetase α chain of *Salmonella typhimurium*. *J. Biol. Chem.* **248**:1830–1836.
1195. **Li, Y. F., and A. Sancar.** 1991. Cloning, sequencing, expression and characterization of DNA photolyase from *Salmonella typhimurium*. *Nucleic Acids Res.* **19**:4885–4890.
1196. **Li, Z. J., D. Hillyard, and P. Higgins.** 1989. Nucleotide sequence of the *Salmonella typhimurium* *himA* gene. *Nucleic Acids Res.* **17**:8880.
1197. **Libby, S. J., W. Goebel, A. Ludwig, N. Buchmeier, F. Bowe, F. C. Fang, D. G. Guiney, J. G. Songer, and F. Heffron.** 1994. A cytolysin encoded by *Salmonella* is required for survival within macrophages. *Proc. Natl. Acad. Sci. USA* **91**:489–493.
1198. **Libby, S. J., W. Goebel, S. Muir, G. Songer, and F. Heffron.** 1990. Cloning and characterization of a cytotoxin gene from *Salmonella typhimurium*. *Res. Microbiol.* **141**:775–783.
1199. **LiCalsi, C., T. S. Croceni, E. Freire, and S. Roseman.** 1991. Sugar transport by the bacterial phosphotransferase system. Structural and thermodynamic domains of enzyme I of *Salmonella typhimurium*. *J. Biol. Chem.* **266**:19519–19527.
1200. **Lifsics, M. R., E. D. Lancy, Jr., and R. Maurer.** 1992. DNA replication defect in *Salmonella typhimurium* mutants lacking the editing (epsilon) subunit of DNA polymerase III. *J. Bacteriol.* **174**:6965–6973.
1201. **Liljestrom, P., I. Laamanen, and E. T. Palva.** 1988. Structure and expression of the *ompB* operon, the regulatory locus for the outer membrane porin regulon in *Salmonella typhimurium* LT-2. *J. Mol. Biol.* **201**:663–673.
1202. **Liljestrom, P., M. Luokkamaki, and E. T. Palva.** 1987. Isolation and characterization of a substitution mutation in the *ompR* gene of *Salmonella typhimurium* LT2. *J. Bacteriol.* **169**:438–441.
1203. **Liljestrom, P., P. L. Maattanen, and E. T. Palva.** 1982. Cloning of the regulatory locus *ompB* of *Salmonella typhimurium* LT-2. I. Isolation of the *ompR* gene and identification of its gene product. *Mol. Gen. Genet.* **188**:184–189.
1204. **Liljestrom, P., P. L. Maattanen, and E. T. Palva.** 1982. Cloning of the regulatory locus *ompB* of *Salmonella typhimurium* LT-2. II. Identification of the *envZ* gene product, a protein involved in the expression of the porin proteins. *J. Bacteriol.* **188**:190–194.
1205. **Lilleengen, K.** 1948. Typing *Salmonella typhimurium* by means of bacteriophage. *Acta Pathol. Microbiol. Scand. Suppl.* **77**:11–125.
1206. **Lilley, D. M., and C. F. Higgins.** 1991. Local DNA topology and gene expression: the case of the *leu-500* promoter. *Mol. Microbiol.* **5**:779–783.
1207. **Lin, H.-C., S.-P. Lei, G. Studnicka, and G. Wilcox.** 1985. The *araBAD* operon of *Salmonella typhimurium* LT2. III. Nucleotide sequence of *araD* and its flanking regions, and primary structure of its product, L-ribulose-5-phosphate 4-epimerase. *Gene* **34**:129–134.
1208. **Lin, H.-C., S.-P. Lei, and G. Wilcox.** 1985. The *araBAD* operon of *Salmonella typhimurium* LT2. I. Nucleotide sequence of *araB* and primary structure of its product, ribulokinase. *Gene* **34**:111–122.
1209. **Lin, H.-C., S.-P. Lei, and G. Wilcox.** 1985. The *araBAD* operon of *Salmonella typhimurium* LT2. II. Nucleotide sequence of *araA* and primary structure of its product, L-arabinose isomerase. *Gene* **34**:123–128.
1210. **Lin, J. J.-C., and H. C. P. Wu.** 1976. Biosynthesis and assembly of envelope lipoprotein in a glycerol-requiring mutant of *Salmonella typhimurium*. *J. Bacteriol.* **125**:892–904.
1211. **Lindberg, A. A., and C.-G. Hellerqvist.** 1980. Rough mutants of *Salmonella typhimurium*. Immunochemical and structural analysis of lipopolysaccharides from *rfaH* mutants. *J. Gen. Microbiol.* **116**:25–32.
1212. **Lindberg, A. A., C. G. Hellerqvist, G. Bagdian-Motta, and P. H. Makela.** 1978. Lipopolysaccharide modification accompanying antigenic conversion by phage P27. *J. Gen. Microbiol.* **107**:279–287.
1213. **Lindberg, A. A., and S. Svensson.** 1975. *Salmonella typhimurium* mutations conferring

- resistance to Felix O phage without loss of smooth character: phage attachment and immunochemical and structural analyses of lipopolysaccharides. *J. Gen. Microbiol.* **87**:11–19.
1214. **Lindqvist, L., R. Kaiser, P. R. Reeves, and A. A. Lindberg.** 1993. Purification, characterization and HPLC assay of *Salmonella* glucose-1-phosphate thymidyltransferase from the cloned *rfaA* gene. *Eur. J. Biochem.* **211**:763–770.
1215. **Lindqvist, L., R. Kaiser, P. R. Reeves, and A. A. Lindberg.** 1994. Purification, characterization, and high performance liquid chromatography assay of *Salmonella* glucose-1-phosphate cytidyltransferase from the cloned *rfaF* gene. *J. Biol. Chem.* **269**:122–126.
1216. **Lindqvist, L., E. K. H. Schweda, P. R. Reeves, and A. A. Lindberg.** 1994. *In vitro* synthesis of CDP-D-abequose using *Salmonella* enzymes of cloned *rfa* genes: production of CDP-6-deoxy-D-xylo-4-hexulose, CDP-3,6-dideoxy-D-xylo-hexulose and CDP-3,6-dideoxy-D-galactose, and isolation by HPLC. *Eur. J. Biochem.* **225**:863–872.
1217. **Lisitsyn, N. A., G. S. Monastyrskaya, and E. D. Sverdlov.** 1988. Genes coding for RNA polymerase beta subunit in bacteria. Structure/function analysis. *Eur. J. Biochem.* **177**:363–369.
1218. **Liu, D., A. M. Haase, L. Lindqvist, A. A. Lindberg, and P. R. Reeves.** 1994. Glycosyl transferases of O-antigen biosynthesis in *Salmonella enterica*: identification and characterization of transferase genes of groups B, C2, and E1. *J. Bacteriol.* **175**:3408–3413.
1219. **Liu, D., N. K. Verma, L. K. Romana, and P. R. Reeves.** 1991. Relationships among the *rfa* regions of *Salmonella* serovars A, B, and D. *J. Bacteriol.* **173**:4814–4819.
1220. **Liu, G., J. Foster, P. Manlapaz-Ramos, and B. M. Olivera.** 1982. Nucleoside salvage pathway for NAD biosynthesis in *Salmonella typhimurium*. *J. Bacteriol.* **152**:1111–1116.
1221. **Liu, J., and I. R. Beacham.** 1990. Transcription and regulation of the *cpdB* gene in *Escherichia coli* K12 and *Salmonella typhimurium* LT2: evidence for modulation of constitutive promoters by cyclic AMP-CRP complex. *Mol. Gen. Genet.* **222**:161–165.
1222. **Liu, S.-L., A. Hessel, and K. E. Sanderson.** 1993. The *XbaI-BlnI-CeuI* genomic cleavage map of *Salmonella typhimurium* LT2 determined by double digestion, end labelling, and pulsed-field gel electrophoresis. *J. Bacteriol.* **175**:4104–4120.
1223. **Liu, S.-L., A. Hessel, and K. E. Sanderson.** 1994. Genomic mapping with I-*CeuI*, an intron-encoded endonuclease specific for genes for ribosomal RNA, in *Salmonella* spp., *Escherichia coli*, and other bacteria. *Proc. Natl. Acad. Sci. USA* **90**:6874–6878.
1224. **Liu, S.-L., and K. E. Sanderson.** 1992. A physical map of the *Salmonella typhimurium* LT2 genome made by using *XbaI* analysis. *J. Bacteriol.* **174**:1662–1672.
1225. **Liveris, D., J. J. Schwartz, R. Geertman, and I. Schwartz.** 1993. Molecular cloning and sequencing of *infC*, the gene encoding translation initiation factor IF3, from four enterobacterial species. *FEMS Microbiol. Lett.* **112**:211–216.
1226. **Lockman, H. A., and R. Curtiss.** 1990. *Salmonella typhimurium* mutants lacking flagella or motility remain virulent in BALB/c mice. *Infect. Immun.* **58**:137–143.
1227. **Lockman, H. A., and R. Curtiss.** 1992. Isolation and characterization of conditional adherent and non-type 1 fimbriated *Salmonella typhimurium* mutants. *Mol. Microbiol.* **6**:933–945.
1228. **Lockman, H. A., and R. Curtiss.** 1992. Virulence of non-type 1-fimbriated and nonfimbriated nonflagellated *Salmonella typhimurium* mutants in murine typhoid fever. *Infect. Immun.* **60**:491–496.
1229. **Loewen, P. C., and G. V. Stauffer.** 1990. Nucleotide sequence of *katG* of *Salmonella typhimurium* LT2 and characterization of its product, hydroperoxidase I. *Mol. Gen. Genet.* **224**:147–151.
1230. **Lombardo, M. J., D. Bagga, and C. G. Miller.** 1991. Mutations in *rpoA* affect expression of anaerobically regulated genes in *Salmonella typhimurium*. *J. Bacteriol.* **173**:7511–7518.
1231. **Loper, J. C., M. Grabnar, R. C. Stahl, Z. Hartman, and P. E. Hartman.** 1964. Genes and proteins involved in histidine biosynthesis in *Salmonella*. *Brookhaven Symp. Biol.* **17**:15–52.
1232. **Lopes, J. M., and R. P. Lawther.** 1986. Analysis and comparison of the internal promoter, pE, of the *ilvGMEDA* operons from *Escherichia coli* K-12 and *Salmonella typhimurium*. *Nucleic Acids Res.* **14**:2779–2798.
1233. **Lopes, J. M., and R. P. Lawther.** 1989. Physical identification of an internal promoter, *ilvAp*, in

- the distal portion of the *ilvGMEDA* operon. *Gene* **76**:255–269.
1234. **Lorenzo, C., E. Howard, and R. Nagel.** 1990. Studies on Tn10 transposition and excision in DNA-repair mutants of *Salmonella typhimurium*. *Mutat. Res.* **232**:99–104.
1235. **Loughlin, R. E.** 1975. Polarity of the *cysJIH* operon of *Salmonella typhimurium*. *J. Gen. Microbiol.* **86**:275–282.
1236. **Loughlin, R. E.** 1976. Identification of nonsense mutations in the *cysJ* gene of *Salmonella typhimurium*. *J. Gen. Microbiol.* **95**:186–187.
1237. **Lounatmaa, K.** 1979. Ultrastructure of the outer membrane of *Salmonella typhimurium* bacteriocin-resistant mutants deficient in the 33K protein. *J. Bacteriol.* **139**:646–651.
1238. **Lounatmaa, K., P. H. Makela, and M. Sarvas.** 1976. Effect of polymyxin on the ultrastructure of the outer membrane of wild-type and polymyxin-resistant strains of *Salmonella*. *J. Bacteriol.* **127**:1400–1407.
1239. **Lu, A. L., M. J. Cuipa, M. S. Ip, and W. G. Shanabruch.** 1990. Specific A/G-to-C/G mismatch repair in *Salmonella typhimurium* LT2 requires the *mutB* gene product. *J. Bacteriol.* **172**:1232–1240.
1240. **Lu, C. D., and A. T. Abdelal.** 1993. Complete sequence of the *Salmonella typhimurium* gene encoding malate dehydrogenase. *Gene* **123**:143–144.
1241. **Lu, C. D., and A. T. Abdelal.** 1993. The *Salmonella typhimurium* uracil-sensitive mutation use is in *argU* and encodes a minor arginine tRNA. *J. Bacteriol.* **175**:3897–3899.
1242. **Lu, C. D., J. E. Houghton, and A. T. Abdelal.** 1992. Characterization of the arginine repressor from *Salmonella typhimurium* and its interactions with the *carAB* operator. *J. Mol. Biol.* **225**:11–24.
1243. **Lu, C. D., M. Kilstrup, J. Neuhard, and A. Abdelal.** 1989. Pyrimidine regulation of tandem promoters for *carAB* in *Salmonella typhimurium*. *J. Bacteriol.* **171**:5436–5442.
1244. **Luckey, M., and J. B. Neilands.** 1976. Iron transport in *Salmonella typhimurium* LT-2: prevention, by ferrichrome, of adsorption of bacteriophages ES18 and ES18.h1 to a common cell envelope receptor. *J. Bacteriol.* **127**:1036–1037.
1245. **Luckey, M., J. R. Pollack, R. Wayne, B. N. Ames, and J. B. Neilands.** 1972. Iron uptake in *Salmonella typhimurium*: utilization of exogenous siderochromes as iron carriers. *J. Bacteriol.* **111**:731–738.
1246. **Luderitz, O., A. M. Staub, and O. Westphal.** 1966. Immunochemistry of O and R antigens of *Salmonella* and related *Enterobacteriaceae*. *Bacteriol. Rev.* **30**:192–255.
1247. **Luderitz, O., O. Westphal, A. M. Staub, and H. Nikaido.** 1971. Isolation and chemical and immunological characterization of bacterial lipopolysaccharides, p. 145–233. In G. Weinbaum, S. Kadis, and S. J. Ajl (ed.), *Bacterial Endotoxins*, vol. 4 of *Microbial Toxins*. Academic Press, Inc., New York.
1248. **Luginbuhl, G. H., J. G. Hofler, C. J. Decedue, and R. O. Burns.** 1974. Biodegradative L-threonine deaminase of *Salmonella typhimurium*. *J. Bacteriol.* **120**:559–561.
1249. **Lukat, G. S., B. H. Lee, J. M. Mottonen, A. M. Stock, and J. B. Stock.** 1991. Roles of the highly conserved aspartate and lysine residues in the response regulator of bacterial chemotaxis. *J. Biol. Chem.* **266**:8348–8354.
1250. **Lukat, G. S., A. M. Stock, and J. B. Stock.** 1990. Divalent metal ion binding to the CheY protein and its significance to phosphotransfer in bacterial chemotaxis. *Biochemistry* **29**:5436–5442.
1251. **Lupas, A., and J. Stock.** 1989. Phosphorylation of an N-terminal regulatory domain activates the CheB methylesterase in bacterial chemotaxis. *J. Biol. Chem.* **264**:17337–17342.
1252. **Luttinger, A. L., A. L. Springer, and M. B. Schmid.** 1991. A cluster of genes that affects nucleoid segregation in *Salmonella typhimurium*. *New Biol.* **3**:687–697.
1253. **Lyman, M. B., B. A. D. Stocker, and R. J. Roantree.** 1979. Evaluation of the immune response directed against the *Salmonella* antigenic factors O4,5 and O9. *Infect. Immun.* **26**:956–965.
1254. **MacAlister, T. J., W. R. Cook, R. Weigand, and L. I. Rothfield.** 1987. Membrane-murein attachment at the leading edge of the division septum: a second membrane-murein structure associated with morphogenesis of the gram-negative bacterial division septum. *J. Bacteriol.* **169**:3945–3951.
1255. **Macias, E. A., F. Rana, J. Blazyk, and M. C. Modrzakowski.** 1990. Bactericidal activity of magainin 2: use of lipopolysaccharide mutants. *Can. J. Microbiol.* **36**:582–584.

1256. **Mack, D. P., J. P. Sluka, J. A. Shin, J. H. Griffin, M. I. Simon, and P. B. Dervan.** 1990. Orientation of the putative recognition helix in the DNA-binding domain of Hin recombinase complexed with the *hix* site. *Biochemistry* **29**:6561–6567.
1257. **MacKay, D. A., A. Eisenstark, R. B. Webb, and M. S. Brown.** 1976. Action spectra for lethality in recombinationless strains of *Salmonella typhimurium* and *Escherichia coli*. *Photochem. Photobiol.* **24**:337–343.
1258. **MacLachlan, P. R., S. K. Kadam, and K. E. Sanderson.** 1991. Cloning, characterization, and DNA sequence of the *rfaLK* region for lipopolysaccharide synthesis in *Salmonella typhimurium* LT2. *J. Bacteriol.* **173**:7151–7163.
1259. **MacLachlan, P. R., and K. E. Sanderson.** 1985. Transformation of *Salmonella typhimurium* with plasmid DNA: differences between rough and smooth strains. *J. Bacteriol.* **161**:442–445.
1260. **Macnab, R., and D. E. Koshland, Jr.** 1972. Persistence as a concept in the motility of chemotactic bacteria. *J. Mechanochem. Cell Motil.* **2**:141–148.
1261. **Macnab, R., and D. E. Koshland, Jr.** 1974. Bacterial motility and chemotaxis: light-induced tumbling response and visualization of individual flagella. *J. Mol. Biol.* **84**:399–406.
1262. **Macnab, R., and D. E. Koshland, Jr.** 1974. The gradient mechanism in bacterial chemotaxis. *Proc. Natl. Acad. Sci. USA* **69**:2509–2512.
1263. **Macnab, R. M.** 1977. Bacterial flagella rotating in bundles: a study of helical geometry. *Proc. Natl. Acad. Sci. USA* **74**:221–225.
1264. **Macnab, R. M.** 1987. Flagella, p. 70–83. In F. C. Neidhardt, J. L. Ingraham, K. B. Low, B. Magasanik, M. Schaechter, and H. E. Umbarger (ed.), *Escherichia coli and Salmonella typhimurium: Cellular and Molecular Biology*. American Society for Microbiology, Washington, D.C.
1265. **Macnab, R. M., and M. K. Ornston.** 1977. Normal-to-curly flagellar transitions and their role in bacterial tumbling. *J. Mol. Biol.* **112**:1–30.
1266. **MacPhee, D. G.** 1973. Effect of *rec* mutations on the ultraviolet protecting and mutation-enhancing properties of the plasmid R-Utrecht in *Salmonella typhimurium*. *Mutat. Res.* **19**:357–359.
1267. **MacPhee, D. G., and M. R. Beazer.** 1973. Mutants of *Salmonella typhimurium* deficient in DNA polymerase I: detection by their failure to produce colicin E1. *Mol. Gen. Genet.* **127**:229–240.
1268. **MacPhee, D. G., and M. R. Beazer.** 1975. Mutants of *Salmonella typhimurium* deficient in DNA polymerase I: further characterization and genetic analysis. *Aust. J. Biol. Sci.* **28**:559–565.
1269. **Madonna, J. J., R. L. Fuchs, and J. E. Brenchley.** 1985. Fine structure analysis of *Salmonella typhimurium* glutamate synthase genes. *J. Bacteriol.* **161**:353–360.
1270. **Maeba, P., and B. D. Sanwal.** 1969. Phosphoenolpyruvate carboxylase of *Salmonella*. Some chemical and allosteric properties. *J. Biol. Chem.* **244**:2549–2557.
1271. **Magariyama, Y., S. Yamaguchi, and S. Aizawa.** 1990. Genetic and behavioral analysis of flagellar switch mutants of *Salmonella typhimurium*. *J. Bacteriol.* **172**:4359–4369.
1272. **Magasanik, B.** 1978. Regulation of the *hut* system. *Cold Spring Harbor Monogr. Ser.* **1978**:373–388.
1273. **Magnussen, K.-E., O. Stendahl, C. Tagesson, L. Edebo, and G. Johansson.** 1977. The tendency of smooth and rough *Salmonella typhimurium* bacteria and lipopolysaccharide to hydrophobic and ionic interaction as studied in aqueous polymer 2 phase systems. *Acta Pathol. Microbiol. Scand. Sect. B* **85**:212–218.
1274. **Mahan, M. J., J. Casadesus, and J. R. Roth.** 1992. The *Salmonella typhimurium* RecJ function permits growth of P22 abc phage on *recBCD*⁺ hosts. *Mol. Gen. Genet.* **232**:470–478.
1275. **Mahan, M. J., and L. N. Csonka.** 1983. Genetic analysis of the *proBA* genes of *Salmonella typhimurium*: physical and genetic analyses of the cloned *proB*^{A+} genes of *Escherichia coli* and of a mutant allele that confers proline overproduction and enhanced osmotolerance. *J. Bacteriol.* **156**:1249–1262.
1276. **Mahan, M. J., A. Garzon, and J. Casadesus.** 1993. Host RecJ is required for growth of P22 *erf* bacteriophage. *J. Bacteriol.* **175**:288–290.
1277. **Mahan, M. J., and J. R. Roth.** 1989. *recB* and *recC* genes of *Salmonella typhimurium*. *J. Bacteriol.* **171**:612–615.

1278. **Mäkelä, P. H.** 1964. Genetic homologies between flagellar antigens of *Escherichia coli* and *Salmonella abony*. *J. Gen. Microbiol.* **35**:503–510.
1279. **Mäkelä, P. H.** 1966. Genetic determination of the O antigens of *Salmonella* groups B (4, 5, 12) and C₁ (6, 7). *J. Bacteriol.* **91**:1115–1125.
1280. **Mäkelä, P. H.** 1973. Glucosylation of lipopolysaccharide in *Salmonella*: mutants negative for O antigen factor 12². *J. Bacteriol.* **116**:847–856.
1281. **Mäkelä, P. H., M. Jahkola, and O. Lüderitz.** 1970. A new gene cluster *rfe* concerned with the biosynthesis of *Salmonella* lipopolysaccharide. *J. Gen. Microbiol.* **60**:91–106.
1282. **Mäkelä, P. H., and O. Mäkelä.** 1966. *Salmonella* antigen 12₂: genetics of form variation. *Ann. Med. Exp. Biol. Fenn.* **44**:310–317.
1283. **Mäkelä, P. H., and H. Mayer.** 1974. Participation of lipopolysaccharide genes in the determination of the enterobacterial common antigen: analysis in *Salmonella* groups B and C₁. *J. Bacteriol.* **119**:765–770.
1284. **Mäkelä, P. H., and H. Mayer.** 1976. Enterobacterial common antigen. *Bacteriol. Rev.* **40**:591–632.
1285. **Mäkelä, P. H., H. Mayer, H. Y. Whang, and E. Neter.** 1974. Participation of lipopolysaccharide genes in the determination of the enterobacterial common antigen: analysis of R mutants of *Salmonella minnesota*. *J. Bacteriol.* **119**:760–764.
1286. **Mäkelä, P. H., G. Schmidt, H. Mayer, H. Nikaido, H. Y. Whang, and E. Neter.** 1976. Enterobacterial common antigen in *rfb* deletion mutants of *Salmonella typhimurium*. *J. Bacteriol.* **127**:1141–1149.
1287. **Mäkelä, P. H., and B. A. D. Stocker.** 1969. Genetics of polysaccharide biosynthesis. *Annu. Rev. Genet.* **3**:291–322.
1288. **Mäkelä, P. H., and B. A. D. Stocker.** 1981. Genetics of the bacterial cell surface. *Symp. Soc. Gen. Microbiol.* **31**:219–264.
1289. **Makover, S., and E. Telep.** 1978. The antibacterial potential of a phosphoenolpyruvate sugar phosphotransferase system blocking agent. *J. Antibiot.* **31**:237–238.
1290. **Maloy, S. R., and J. R. Roth.** 1983. Regulation of proline utilization in *Salmonella typhimurium*: characterization of *put::Mu d(Ap, lac)* operon fusions. *J. Bacteriol.* **154**:561–568.
1291. **Mankovich, J. A., C. A. McIntyre, and G. C. Walker.** 1989. Nucleotide sequence of the *Salmonella typhimurium mutL* gene required for mismatch repair: homology of MutL to HexB of *Streptococcus pneumoniae* and to PMS1 of the yeast *Saccharomyces cerevisiae*. *J. Bacteriol.* **171**:5325–5331.
1292. **Manuck, B. A., and C. Ho.** 1979. High-resolution proton nuclear magnetic resonance studies of histidine binding proteins J of *Salmonella typhimurium*. An investigation of substrate and membrane interaction sites. *Biochemistry* **18**:566–573.
1293. **Marcus, S. L., and E. Balbinder.** 1972. Purification of anthranilate-5-phosphoribosyl pyrophosphate phosphoribosyl transferase from *Salmonella typhimurium* using affinity chromatography: resolution of monomeric and dimeric forms. *Biochem. Biophys. Res. Commun.* **47**:438–444.
1294. **Mares, R., M. L. Urbanowski, and G. V. Stauffer.** 1992. Regulation of the *Salmonella typhimurium metA* gene by the *metR* protein and homocysteine. *J. Bacteriol.* **174**:390–397.
1295. **Margolies, M. N., and R. F. Goldberger.** 1967. Physical and chemical characterization of the isomerase of histidine biosynthesis in *Salmonella typhimurium*. *J. Biol. Chem.* **242**:256–264.
1296. **Margolies, M. N., and R. F. Goldberger.** 1968. Correlation between mutation type and the production of cross-reacting material in mutants of the A gene of the histidine operon in *Salmonella typhimurium*. *J. Bacteriol.* **95**:507–519.
1297. **Margolin, P.** 1963. Genetic fine structure of the leucine operon in *Salmonella*. *Genetics* **48**:441–457.
1298. **Marsh, M., and D. R. Hillyard.** 1988. Nucleotide sequence of the HU-1 gene of *Salmonella typhimurium*. *Nucleic Acids Res.* **16**:7196.
1299. **Marsh, M., and D. R. Hillyard.** 1990. Nucleotide sequence of *hns* encoding the DNA-binding

- protein H-NS of *Salmonella typhimurium*. *Nucleic Acids Res.* **18**:3397.
1300. **Martin, R. G.** 1968. Polarity in relaxed strains of *Salmonella typhimurium*. *J. Mol. Biol.* **31**:127–134.
1301. **Martin, R. G., M. A. Berberich, B. N. Ames, W. W. Davis, R. F. Goldberger, and J. Yourno.** 1971. Enzymes and intermediates of histidine biosynthesis in *Salmonella typhimurium*. *Methods Enzymol.* **17**:3–44.
1302. **Martin, R. G., and R. F. Goldberger.** 1967. Imidazolylacetolphosphate:L-glutamate aminotransferase. Purification and physical properties. *J. Biol. Chem.* **242**:1168–1174.
1303. **Martin, R. G., M. J. Voll, and E. Appella.** 1967. Imidazolylacetolphosphate:L-glutamate aminotransferase. Composition and substructure. *J. Biol. Chem.* **242**:1175–1181.
1304. **Marumo, K., L. Lindqvist, N. Verma, A. Weintraub, P. R. Reeves, and A. A. Lindberg.** 1992. Enzymatic synthesis and isolation of thymidine diphosphate-6-deoxy-D-xylo-4-hexulose and thymidine diphosphate-L-rhamnose. *Eur. J. Biochem.* **204**:539–545.
1305. **Masten, B. J., and T. M. Joys.** 1993. Molecular analyses of the *Salmonella g...* flagellar antigen complex. *J. Bacteriol.* **175**:5359–5365.
1306. **Matsubara, K., K. Ohnishi, and K. Kiritani.** 1987. Location of *livA* gene participating in the high-affinity transport of branched-chain amino acids in *Salmonella typhimurium* LT2. *Jpn. J. Genet.* **62**:189–196.
1307. **Matsubara, K., K. Ohnishi, and K. Kiritani.** 1988. The third general transport system for branched-chain amino acids in *Salmonella typhimurium*. *J. Gen. Appl. Microbiol.* **34**:183–189.
1308. **Matsubara, K., K. Ohnishi, and K. Kiritani.** 1992. Nucleotide sequences and characterization of *liv* genes encoding components of the high-affinity branched-chain amino acid transport system in *Salmonella typhimurium*. *J. Biochem. (Tokyo)* **112**:93–101.
1309. **Matsuyama, T., and H. Uetake.** 1972. Chromosomal locations of *Salmonella* conversion phages: mapping of prophages g_{341} , ϵ^{15} and ϵ^{24} in *Salmonella anatum*. *Virology* **49**:359–367.
1310. **Maurelli, A. T.** 1994. Virulence protein export systems in *Salmonella* and *Shigella*: a new family or lost relatives? *Trends Cell. Biol.* **4**:240–242.
1311. **Maurer, R., B. C. Osmond, and D. Botstein.** 1981. Genetic analysis of DNA replication in *Salmonella typhimurium*. *ICN-UCLA Symp. Mol. Cell. Biol.* **22**:375–386.
1312. **Maurer, R., B. C. Osmond, and D. Botstein.** 1984. Genetic analysis of DNA replication in bacteria: *dnaB* mutations that suppress *dnaC* mutations and the *dnaQ* mutations that suppress *dnaE* mutations in *Salmonella typhimurium*. *Genetics* **108**:25–38.
1313. **Maurer, R., B. C. Osmond, E. Shekhtman, A. Wong, and D. Botstein.** 1984. Functional interchangeability of DNA replication genes in *Salmonella typhimurium* and *Escherichia coli* demonstrated by a general complementation procedure. *Genetics* **108**:1–12.
1314. **Maurer, R., and A. Wong.** 1988. Dominant lethal mutations in the *dnaB* helicase gene of *Salmonella typhimurium*. *J. Bacteriol.* **170**:3682–3688.
1315. **May, S. G., and D. C. Old.** 1980. meso-Tartrate resistance and phylogenetic relationship of biotypes of *Salmonella typhimurium*. *Genet. Res.* **36**:327.
1316. **McCarter, L., K. Krajewska-Grynkiewicz, D. Trinh, G. Wei, and S. Kustu.** 1984. Characterization of mutations that lie in the promoter-regulatory region for *glnA*, the structural gene encoding glutamine synthetase. *Mol. Gen. Genet.* **197**:150–160.
1317. **McClatchy, J. K., and H. V. Rickenberg.** 1967. Heterogeneity of the stability of messenger ribonucleic acid in *Salmonella typhimurium*. *J. Bacteriol.* **93**:115–121.
1318. **McDonough, M. W.** 1965. Amino acid composition of antigenically distinct *Salmonella* flagellar proteins. *J. Mol. Biol.* **12**:342–355.
1319. **McFarland, N., L. McCarter, S. Artz, and S. Kustu.** 1971. Nitrogen regulatory locus “*glnR*” of enteric bacteria is composed of cistrons *ntrB* and *ntrC*: identification of their protein products. *Proc. Natl. Acad. Sci. USA* **78**:2135–2139.
1320. **McGinnis, E., and L. S. Williams.** 1972. Role of histidine transfer ribonucleic acid in regulation of synthesis of histidyl-transfer ribonucleic acid synthetase of *Salmonella typhimurium*. *J. Bacteriol.* **109**:505–511.

1321. **McHugh, G. L., and C. G. Miller.** 1974. Isolation and characterization of proline peptidase mutants of *Salmonella typhimurium*. *J. Bacteriol.* **120**:364–371.
1322. **Meadow, N. D., and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Isolation and characterization of a glucose-specific phosphocarrier protein (III^{Glc}) from *Salmonella typhimurium*. *J. Biol. Chem.* **257**:14526–14537.
1323. **Meadow, N. D., J. M. Rosenberg, H. M. Pinkert, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Evidence that *crr* is the structural gene for the *Salmonella typhimurium* glucose-specific phosphocarrier protein III^{Glc}. *J. Biol. Chem.* **257**:14538–14542.
1324. **Meadow, N. D., D. W. Saffen, R. P. Dottin, and S. Roseman.** 1982. Molecular cloning of the *crr* gene and evidence that it is the structural gene for III^{Glc}, a phosphocarrier protein of the bacterial phosphotransferase system. *Proc. Natl. Acad. Sci. USA* **79**:2528–2532.
1325. **Meier, U., and H. Mayer.** 1985. Genetic location of genes encoding enterobacterial common antigen. *J. Bacteriol.* **163**:756–762.
1326. **Meiss, H. K., W. J. Brill, and B. Magasanik.** 1969. Genetic control of histidine degradation in *Salmonella typhimurium*, strain LT-2. *J. Biol. Chem.* **244**:5382–5391.
1327. **Melton, T., P. E. Hartman, J. P. Stratis, T. L. Lee, and A. T. Davis.** 1978. Chemotaxis of *Salmonella* to amino acids and some sugars. *J. Bacteriol.* **133**:708–716.
1328. **Melton, T., W. Kundig, P. E. Hartman, and N. Meadow.** 1976. 3-Deoxy-3-fluoro-D-glucose-resistant *Salmonella typhimurium* mutants defective in the phosphoenolpyruvate:glycose phosphotransferase system. *J. Bacteriol.* **128**:794–800.
1329. **Menzel, R., and J. Roth.** 1980. Identification and mapping of a second proline permease in *Salmonella typhimurium*. *J. Bacteriol.* **141**:1064–1070.
1330. **Menzel, R., and J. Roth.** 1981. Regulation of the genes for proline regulation in *Salmonella typhimurium*: autogenous repression by the *putA* gene product. *J. Mol. Biol.* **148**:21–44.
1331. **Menzel, R., and J. Roth.** 1981. Purification of the *putA* gene product. A bifunctional membrane-bound protein from *Salmonella typhimurium* responsible for the two-step oxidation of proline to glutamate. *J. Biol. Chem.* **256**:9755–9761.
1332. **Mergeay, M., and J. Gerits.** 1983. Transduction of *Escherichia coli trp* genes in *Salmonella typhimurium* and effect of *N*-methyl-*N'*-nitro-*N*-nitrosoguanidine on transduction with heterogenetic DNA. *J. Gen. Microbiol.* **129**:321–335.
1333. **Meyers, M., F. Blasi, C. B. Bruni, R. G. Deeley, J. S. Kovach, M. Levinthal, K. P. Mullinix, T. Vogel, and R. G. Goldberger.** 1975. Specific binding of the first enzyme for histidine biosynthesis to the DNA of the histidine operon. *Nucleic Acids Res.* **2**:2021–2036.
1334. **Meyers, M., M. Levinthal, and R. F. Goldberger.** 1975. *trans*-Recessive mutation in the first structural gene of the histidine operon that results in constitutive expression of the operon. *J. Bacteriol.* **124**:1227–1235.
1335. **Michaels, G., and R. A. Kelln.** 1983. Construction and use of *pyr::lac* fusion strains to study regulation of pyrimidine biosynthesis in *Salmonella typhimurium*. *Mol. Gen. Genet.* **189**:463–470.
1336. **Michaels, G., R. A. Kelln, and F. E. Nargang.** 1987. Cloning, nucleotide sequence and expression of the *pyrBI* operon of *Salmonella typhimurium* LT2. *Eur. J. Biochem.* **166**:55–61.
1337. **Miesel, L., and J. R. Roth.** 1994. *Salmonella recD* mutations increase recombination in a short sequence transduction assay. *J. Bacteriol.* **176**:4092–4103.
1338. **Milburn, M. V., G. G. Prive, D. L. Milligan, W. G. Scott, J. Yeh, J. Jancarik, D. E. Koshland, Jr., and S. H. Kim.** 1991. Three-dimensional structures of the ligand-binding domain of the bacterial aspartate receptor with and without a ligand. *Science* **254**:1342–1347.
1339. **Miller, B. E., and N. M. Kredich.** 1987. Purification of the *cysB* protein from *Salmonella typhimurium*. *J. Biol. Chem.* **262**:6006–6009.
1340. **Miller, C. G.** 1975. Genetic mapping of *Salmonella typhimurium* peptidase mutations. *J. Bacteriol.* **122**:171–176.
1341. **Miller, C. G., and L. Green.** 1981. Degradation of abnormal proteins in peptidase-deficient mutants of *Salmonella typhimurium*. *J. Bacteriol.* **147**:925–930.
1342. **Miller, C. G., and L. Green.** 1983. Degradation of proline peptidases in peptidase-deficient

- strains of *Salmonella typhimurium*. *J. Bacteriol.* **153**:350–356.
1343. **Miller, C. G., L. Green, and R. Schultz.** 1982. *Salmonella typhimurium* mutations affecting utilization of L-leucine β -naphthylamide. *Mol. Gen. Genet.* **186**:228–234.
1344. **Miller, C. G., C. Helman, and C. Yen.** 1976. Mutants of *Salmonella typhimurium* deficient in an endoprotease. *J. Bacteriol.* **127**:490–497.
1345. **Miller, C. G., A. M. Kukral, J. L. Miller, and N. R. Movva.** 1989. *pepM* is an essential gene in *Salmonella typhimurium*. *J. Bacteriol.* **171**:5215–5217.
1346. **Miller, C. G., and K. Mackinnon.** 1974. Peptidase mutants of *Salmonella typhimurium*. *J. Bacteriol.* **120**:355–363.
1347. **Miller, C. G., J. L. Miller, and D. A. Bagga.** 1991. Cloning and nucleotide sequence of the anaerobically regulated *pepT* gene of *Salmonella typhimurium*. *J. Bacteriol.* **173**:3554–3558.
1348. **Miller, C. G., and J. R. Roth.** 1971. Recessive-lethal nonsense suppressors in *Salmonella typhimurium*. *J. Mol. Biol.* **59**:63–75.
1349. **Miller, C. G., K. L. Strauch, A. M. Kukral, J. L. Miller, P. T. Wingfield, G. J. Mazzei, R. C. Werlen, P. Graber, and N. R. Movva.** 1987. N-terminal methionine-specific peptidase in *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **84**:2718–2722.
1350. **Miller, C. G., and D. Zipser.** 1977. Degradation of *Escherichia coli* β -galactosidase fragments in protease-deficient mutants of *Salmonella typhimurium*. *J. Bacteriol.* **130**:347–353.
1351. **Miller, E. S., and J. E. Brenchley.** 1983. Cloning and characterization of *gdhA*, the structural gene for glutamate dehydrogenase of *Salmonella typhimurium*. *J. Bacteriol.* **157**:171–178.
1352. **Miller, J. B., and D. E. Koshland, Jr.** 1977. Membrane fluidity and chemotaxis: effects of temperature and membrane lipid composition on the swimming behavior of *Salmonella typhimurium* and *Escherichia coli*. *J. Mol. Biol.* **111**:183–201.
1353. **Miller, K., and S. Maloy.** 1990. DNA sequence of the *putP* gene from *Salmonella typhimurium* and predicted structure of proline permease. *Nucleic Acids Res.* **18**:3057.
1354. **Miller, S. I.** 1991. PhoP/PhoQ: macrophage-specific modulators of *Salmonella* virulence? *Mol. Microbiol.* **5**:2073–2078.
1355. **Miller, S. I., A. M. Kukral, and J. J. Mekalanos.** 1989. A two-component regulatory system (*phoP phoQ*) controls *Salmonella typhimurium* virulence. *Proc. Natl. Acad. Sci. USA* **86**:5054–5058.
1356. **Miller, S. I., and J. J. Mekalanos.** 1990. Constitutive expression of the *phoP* regulon attenuates *Salmonella* virulence and survival within macrophages. *J. Bacteriol.* **172**:2485–2490.
1357. **Miller, S. I., W. S. Pulkkinen, M. E. Selsted, and J. J. Mekalanos.** 1990. Characterization of defensin resistance phenotypes associated with mutations in the *phoP* virulence regulon of *Salmonella typhimurium*. *Infect. Immun.* **58**:3706–3710.
1358. **Miller, V. L., K. B. Beer, W. P. Loomis, J. A. Olson, and S. I. Miller.** 1992. An unusual *pagC::TnphoA* mutation leads to an invasion- and virulence-defective phenotype in salmonellae. *Infect. Immun.* **60**:3763–3770.
1359. **Mills, D. M., V. Bajaj, and C. A. Lee.** 1995. A 40 kilobase chromosomal fragment encoding *Salmonella typhimurium* invasion genes is absent from the corresponding region of the *Escherichia coli* K-12 chromosome. *Mol. Microbiol.* **15**:749–759.
1360. **Miloso, M., D. Limauro, P. Alifano, F. Rivellini, A. Lavitola, E. Gulletta, and C. B. Bruni.** 1993. Characterization of the *rho* genes of *Neisseria gonorrhoeae* and *Salmonella typhimurium*. *J. Bacteriol.* **175**:8030–8037.
1361. **Minamino, T., T. Iino, and K. Kutsukake.** 1994. Molecular characterization of the *Salmonella typhimurium flhB* operon and its protein products. *J. Bacteriol.* **176**:7630–7637.
1362. **Minson, A. C., and D. A. Smith.** 1972. Methionine regulatory defects in *Salmonella typhimurium* arising from amber-suppressible mutations. *J. Gen. Microbiol.* **70**:471–476.
1363. **Minton, N., J. Gunn, and I. R. Beacham.** 1979. Nucleoside diphosphate sugar hydrolase gene of *Salmonella typhimurium*: chromosomal location determined by intergeneric crosses. *J. Bacteriol.* **137**:1428–1429.
1364. **Miozarri, G. F., and C. Yanofsky.** 1979. Gene fusion during the evolution of the tryptophan operon in Enterobacteriaceae. *Nature (London)* **277**:486–489.

1365. **Misko, T. P., W. J. Mitchell, N. D. Meadow, and S. Roseman.** 1987. Sugar transport by the bacterial phosphotransferase system. *J. Biol. Chem.* **262**:16261–16266.
1366. **Mitchell, W. J., T. P. Misko, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Regulation of other transport systems (lactose and melibiose). *J. Biol. Chem.* **257**:14553–14564.
1367. **Miyake, T., and M. Demerec.** 1960. Proline mutants of *Salmonella typhimurium*. *Genetics* **45**:755–762.
1368. **Mizobuchi, K., M. Demerec, and D. H. Gillespie.** 1962. Cysteine mutants of *Salmonella typhimurium*. *Genetics* **47**:1617–1627.
1369. **Mizuno, T., N. Mutoh, S. M. Panasenko, and Y. Imae.** 1986. Acquisition of maltose chemotaxis in *Salmonella typhimurium* by the introduction of the *Escherichia coli* chemosensory transducer gene. *J. Bacteriol.* **165**:890–895.
1370. **Mizushima, K., S. Awakihara, M. Kuroda, T. Ishikawa, M. Tsuda, and T. Tsuchiya.** 1992. Cloning and sequencing of the *melB* gene encoding the melibiose permease of *Salmonella typhimurium* LT2. *Mol. Gen. Genet.* **234**:74–80.
1371. **Mojica-a, T.** 1975. Transduction by phage PICM *clr*-100 in *Salmonella typhimurium*. *Mol. Gen. Genet.* **138**:113–126.
1372. **Mojica-a, T., and E. Garcia.** 1976. Growth of coliphage BF23 on rough strains of *Salmonella typhimurium*. The *bfe* locus. *Mol. Gen. Genet.* **147**:195–202.
1373. **Mojica-a, T., E. Garcia, and C. Ascaso.** 1976. Mutants of coliphage BF-23 able to propagate on smooth strains of *Salmonella typhimurium*. *Arch. Int. Physiol. Biochim.* **84**:402–403.
1374. **Mojica-a, T., and R. B. Middleton.** 1972. *Salmonella typhimurium*-*Escherichia coli* hybrids for the tryptophan region. *Genetics* **71**:491–505.
1375. **Monroe, R. S., and N. M. Kredich.** 1988. Isolation of *Salmonella typhimurium cys* genes by transduction with a library of recombinant plasmids packaged in bacteriophage P22HT capsids. *J. Bacteriol.* **170**:42–47.
1376. **Monroe, R. S., J. Ostrowski, M. M. Hryniewicz, and N. M. Kredich.** 1990. In vitro interactions of CysB protein with the *cysK* and *cysJIH* promoter regions of *Salmonella typhimurium*. *J. Bacteriol.* **172**:6919–6929.
1377. **Morgan, D. G., R. M. Macnab, N. R. Francis, and D. J. DeRosier.** 1993. Domain organization of the subunit of the *Salmonella typhimurium* flagellar hook. *J. Mol. Biol.* **229**:79–84.
1378. **Morgan, R. W., M. F. Christman, F. S. Jacobson, G. Storz, and B. N. Ames.** 1986. Hydrogen peroxide-inducible proteins in *Salmonella typhimurium* overlap with heat shock and other stress proteins. *Proc. Natl. Acad. Sci. USA* **83**:8059–8063.
1379. **Mortlock, R. P., and D. C. Old.** 1979. Utilization of D-xylose by wild-type strains of *Salmonella typhimurium*. *J. Bacteriol.* **137**:173–178.
1380. **Morton, D. P., and S. M. Parsons.** 1977. Synergistic inhibition of ATP phosphoribosyltransferase by guanosine tetraphosphate and histidine. *Biochem. Biophys. Res. Commun.* **74**:172–177.
1381. **Morton, D. P., and S. M. Parsons.** 1977. Inhibition of ATP phosphoribosyltransferase by AMP and ADP in the absence and presence of histidine. *Arch. Biochem. Biophys.* **181**:643–648.
1382. **Movva, N. R., D. Semon, C. Meyer, E. Kawashima, P. Wingfield, J. L. Miller, and C. G. Miller.** 1990. Cloning and nucleotide sequence of the *Salmonella typhimurium pepM* gene. *Mol. Gen. Genet.* **223**:345–348.
1383. **Mowbray, S. L., and G. A. Petsko.** 1982. Preliminary X-ray data for the ribose binding protein from *Salmonella typhimurium*. *J. Mol. Biol.* **160**:545–547.
1384. **Muday, G. K., and K. M. Herrmann.** 1990. Regulation of the *Salmonella typhimurium aroF* gene in *Escherichia coli*. *J. Bacteriol.* **172**:2259–2266.
1385. **Muhradt, P.** 1969. Biosynthesis of *Salmonella* lipopolysaccharide. The in vitro transfer of phosphate to the heptose moiety of the core. *Eur. J. Biochem.* **11**:241–248.
1386. **Mukai, F. H., and P. Margolin.** 1963. Analysis of unlinked suppressors of an O^o mutation in *Salmonella*. *Proc. Natl. Acad. Sci. USA* **50**:140–148.

1387. **Mulford, C. A., and M. J. Osborn.** 1983. An intermediate step in translocation of lipopolysaccharide to the outer membrane of *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **80**:1159–1163.
1388. **Muller, E., A. Hinckley, and L. Rothfield.** 1972. Studies of phospholipid-requiring bacterial enzymes. III. Purification and properties of uridine diphosphate glucose: lipopolysaccharide glucosyltransferase I. *J. Biol. Chem.* **247**:2614–2622.
1389. **Muller, K.-H., T. J. Trust, and W. W. Kay.** 1988. Unmasking of bacteriophage Mu lipopolysaccharide receptors in *Salmonella enteritidis* confers sensitivity to Mu and permits Mu mutagenesis. *J. Bacteriol.* **170**:1076–1081.
1390. **Muller, N., H. G. Heine, and W. Boos.** 1982. Cloning of *mglB*, the structural gene for the galactose-binding protein of *Salmonella typhimurium* and *Escherichia coli*. *Mol. Gen. Genet.* **185**:473–480.
1391. **Muller, N., H. G. Heine, and W. Boos.** 1985. Characterization of the *Salmonella typhimurium* *mgl* operon and its gene products. *J. Bacteriol.* **163**:37–45.
1392. **Muller, V., C. J. Jones, I. Kawagishi, S. Aizawa, and R. M. Macnab.** 1992. Characterization of the *fliE* genes of *Escherichia coli* and *Salmonella typhimurium* and identification of the FliE protein as a component of the flagellar hook-basal body complex. *J. Bacteriol.* **174**:2298–2304.
1393. **Munford, R. S., C. L. Hall, and P. D. Rick.** 1980. Size heterogeneity of *Salmonella typhimurium* lipopolysaccharides in outer membranes and culture supernatant membrane fragments. *J. Bacteriol.* **144**:630–640.
1394. **Munson, R. S., Jr., N. S. Rasmussen, and M. J. Osborn.** 1978. Biosynthesis of lipid A. Enzymatic incorporation of 3-deoxy-D-mannoctulosonate into a precursor of lipid A in *Salmonella typhimurium*. *J. Biol. Chem.* **253**:1503–1511.
1395. **Murata-Matsubara, K., K. Ohnishi, and K. Kiritani.** 1985. Genetic and biochemical studies of *livS* mutation affecting the regulation of branched-chain amino acid transport in *Salmonella typhimurium*. *Jpn. J. Genet.* **60**:11–25.
1396. **Murooka, Y., and T. Harada.** 1981. Regulation of derepressed synthesis of arylsulfatase by tyramine oxidase in *Salmonella typhimurium*. *J. Bacteriol.* **145**:796–802.
1397. **Murphy-Corb, M., H.-L. Kong, and M. L. Murray.** 1980. Interaction of mutagenic spermidine-nitrous acid reaction products with *uvr*- and *recA*-dependent repair systems in *Salmonella typhimurium*. *J. Bacteriol.* **142**:191–195.
1398. **Murray, M. L., and T. Klopotoski.** 1968. Genetic map position of the gluconate-6-phosphate dehydrogenase gene in *Salmonella typhimurium*. *J. Bacteriol.* **95**:1279–1282.
1399. **Mustard, J. A., A. T. Thliveris, and D. W. Mount.** 1992. Sequence of the *Salmonella typhimurium* LT2 *lexA* gene and its regulatory region. *Nucleic Acids Res.* **20**:1813.
1400. **Myers, D. E., B. A. D. Stocker, and R. J. Roantree.** 1980. Mapping of genes determining penicillin-resistance and serum-sensitivity in *Salmonella enteritidis*. *J. Gen. Microbiol.* **118**:367–376.
1401. **Myers, R. S., D. Townsend, and S. Maloy.** 1991. Dissecting the molecular mechanism of ion-solute cotransport: substrate specificity mutations in the *putP* gene affect the kinetics of proline transport. *J. Membr. Biol.* **121**:201–214.
1402. **Nagano, H., and H. Zalkin.** 1970. Some physicochemical properties of anthranilate synthase component I from *Salmonella typhimurium*. *J. Biol. Chem.* **245**:3097–3103.
1403. **Nagano, H., H. Zalkin, and E. J. Henderson.** 1970. The anthranilate synthetase-anthranilate-5-phosphoribosyl pyrophosphate phosphoribosyltransferase aggregate. *J. Biol. Chem.* **245**:3810–3820.
1404. **Naide, Y., H. Nikaido, P. H. Makela, R. G. Wilkinson, and B. A. D. Stocker.** 1965. Semirough strains of *Salmonella*. *Proc. Natl. Acad. Sci. USA* **53**:147–153.
1405. **Nakake, T.** 1971. Multiple molecular forms of uridine diphosphate glucose pyrophosphorylase from *Salmonella typhimurium*. III. Interconversion between various forms. *J. Biol. Chem.* **246**:4404–4411.
1406. **Nakake, T., and H. Nikaido.** 1971. Multiple molecular forms of uridine diphosphate glucose pyrophosphorylase from *Salmonella typhimurium*. II. Genetic determination of multiple forms. *J. Biol. Chem.* **246**:4397–4403.

1407. Nakamura, K., R. M. Pirtle, and M. Inouye. 1979. Homology of the gene coding for outer membrane lipoprotein within various gram-negative bacteria. *J. Bacteriol.* **137**:595–604.
1408. Nakamura, T., Y. Kon, H. Iwahashi, and Y. Eguchi. 1983. Evidence that thiosulfate assimilation by *Salmonella typhimurium* is catalyzed by cysteine synthase B. *J. Bacteriol.* **156**:656–662.
1409. Nakayama, N., N. Arai, M. W. Bond, Y. Kaziro, and K. Arai. 1984. Nucleotide sequence of *dnaB* and the primary structure of the DnaB protein from *Escherichia coli*. *J. Biol. Chem.* **259**:97–101.
1410. Naumann, D., C. Schultz, J. Born, H. Labischinski, K. Brandenburg, G. von Busse, H. Brade, and U. Seydel. 1987. Investigations into the polymorphism of lipid A from lipopolysaccharides of *Escherichia coli* and *Salmonella minnesota* by Fourier-transform infrared spectroscopy. *Eur. J. Biochem.* **164**:159–169.
1411. Neal, B. L., P. K. Brown, and P. R. Reeves. 1993. Use of *Salmonella* phage P22 for transduction in *Escherichia coli*. *J. Bacteriol.* **175**:7115–7118.
1412. Negre, D., J. C. Cortay, P. Donini, and A. J. Cozzone. 1988. Inaccurate protein synthesis in a mutant of *Salmonella typhimurium* defective in transfer RNA pseudouridylation. *FEBS Lett.* **234**:165–168.
1413. Negre, D., J. C. Cortay, P. Donini, and A. J. Cozzone. 1989. Relationship between guanosine tetraphosphate and accuracy of translation in *Salmonella typhimurium*. *Biochemistry* **28**:1814–1819.
1414. Negre, D., J. C. Cortay, I. G. Old, A. Galinier, C. Richaud, I. Saint Girons, and A. J. Cozzone. 1991. Overproduction and characterization of the *iclR* gene product of *Escherichia coli* K-12 and comparison with that of *Salmonella typhimurium* LT2. *Gene* **97**:29–37.
1415. Nelson, S. O., B. J. Scholte, and P. W. Postma. 1982. Phosphoenolpyruvate:sugar phosphotransferase system-mediated regulation of carbohydrate metabolism in *Salmonella typhimurium*. *J. Bacteriol.* **150**:604–615.
1416. Nelson, S. O., A. R. J. Schuitema, R. Benne, L. H. T. van der Ploeg, J. S. Plijter, F. Aan, and P. W. Postma. 1984. Molecular cloning, sequencing, and expression of the *crr* gene: the structural gene for III^{Glc} of the bacterial PEP:glucose phosphotransferase system. *EMBO J.* **3**:1587–1593.
1417. Neufeld, B. R., L. R. Bullas, and M. M. Ball. 1978. Nonparental recombinants in intra-serotype phage P-1 transductions of the *hsd*-SB region of *Salmonella typhimurium*. *Genetics* **88**:S71–S72.
1418. Neuhard, J., and J. L. Ingraham. 1968. Mutants of *Salmonella typhimurium* requiring cytidine for growth. *J. Bacteriol.* **95**:2431–2433.
1419. Neuhard, J., K. F. Jensen, and E. Stauning. 1982. *Salmonella typhimurium* mutants with altered expression of the *pyrA* gene due to changes in RNA polymerase. *EMBO J.* **1**:1141–1145.
1420. Neuhard, J., and R. A. Kelln. 1988. A chromosomal mutation mediating increased expression of *pyrE* in *Salmonella typhimurium* is located within the proposed attenuator. *Can. J. Microbiol.* **34**:686–687.
1421. Neuhard, J., R. A. Kelln, and E. Stauning. 1986. Cloning and structural characterization of the *Salmonella typhimurium pyrC* gene encoding dihydroorotase. *Eur. J. Biochem.* **157**:335–342.
1422. Neuhard, J., E. Stauning, and R. A. Kelln. 1985. Cloning and characterization of the *pyrE* gene and of *PyrE::Mud1* (Ap^R *lac*) fusions from *Salmonella typhimurium*. *Eur. J. Biochem.* **146**:597–603.
1423. Newbury, S. F., N. H. Smith, E. C. Robinson, I. D. Hiles, and C. F. Higgins. 1987. Stabilization of translationally active mRNA by prokaryotic REP sequences. *Cell* **48**:297–310.
1424. Ni Bhriain, N., C. J. Dorman, and C. F. Higgins. 1989. An overlap between osmotic and anaerobic stress responses: a potential role for DNA supercoiling in the coordinate regulation of gene expression. *Mol. Microbiol.* **3**:933–942.
1425. Nichols, B. P., M. Blumenberg, and C. Yanofsky. 1981. Comparison of the nucleotide sequence of *trpA* and sequences immediately beyond the *trp* operon of *Klebsiella aerogenes*, *Salmonella typhimurium*, and *Escherichia coli*. *Nucleic Acids Res.* **9**:1743–1755.
1426. Nichols, B. P., G. F. Miozzari, M. Van Cleemput, G. N. Bennett, and C. Yanofsky. 1980. Nucleotide sequences of the *trpG* regions of *Escherichia coli*, *Shigella dysenteriae*, *Salmonella typhimurium* and *Serratia marcescens*. *J. Mol. Biol.* **142**:503–518.

1427. **Nichols, B. P., M. Van Cleemput, and C. Yanofsky.** 1981. Nucleotide sequence of *Escherichia coli trpE*: anthranilate synthetase component I contains no tryptophan residues. *J. Mol. Biol.* **146**:45–54.
1428. **Nichols, B. P., and C. Yanofsky.** 1979. Nucleotide sequences of *trpA* of *Salmonella typhimurium* and *Escherichia coli*: an evolutionary comparison. *Proc. Natl. Acad. Sci. USA* **76**:5244–5248.
1429. **Nicolaidis, A. A., and W. T. Drabble.** 1979. Plasmid replication in *Salmonella typhimurium* LT-2 and *Escherichia coli* K-12: a differential effect of nalidixic acid. *FEMS Microbiol. Lett.* **6**:261–264.
1430. **Nijkamp, H. J. J., and P. G. DeHaan.** 1967. Genetic and biochemical studies of the guanosine 5'-monophosphate pathway in *Escherichia coli*. *Biochim. Biophys. Acta* **145**:31–40.
1431. **Nikaido, H., S. Ah Song, L. Shaltiel, and M. Nurminen.** 1977. Outer membrane of *Salmonella typhimurium*. Part 14. Reduced transmembrane diffusion rates in porin deficient mutants. *Biochem. Biophys. Res. Commun.* **76**:324–330.
1432. **Nikaido, H., and T. Fukasawa.** 1961. The effect of mutation in a structural gene on the inducibility of the enzymes controlled by other genes of the same operon. *Biochem. Biophys. Res. Commun.* **4**:338–342.
1433. **Nikaido, H., M. Levinthal, K. Nikaido, and K. Nakane.** 1967. Extended deletions in the histidine-rough-B region of the *Salmonella* chromosome. *Proc. Natl. Acad. Sci. USA* **57**:1825–1832.
1434. **Nikaido, H., K. Nikaido, and P. H. Makela.** 1966. Genetic determination of enzymes synthesizing O-specific sugars of *Salmonella* lipopolysaccharides. *J. Bacteriol.* **91**:1126–1135.
1435. **Nikaido, H., Y. Takeuchi, S.-I. Ohnishi, and T. Nakae.** 1977. Outer membrane of *Salmonella typhimurium*. ESR studies. *Biochim. Biophys. Acta* **465**:152–164.
1436. **Nikkola, M., F. K. Gleason, J. A. Fuchs, and H. Eklund.** 1993. Crystal structure analysis of a mutant *Escherichia coli* thioredoxin in which lysine 36 is replaced by glutamic acid. *Biochemistry* **32**:5093–5098.
1437. **Nishioka, Y., M. Demerec, and A. Eisenstark.** 1967. Genetic analysis of aromatic mutants of *Salmonella typhimurium*. *Genetics* **56**:341–351.
1438. **Nishioka, Y., and A. Eisenstark.** 1970. Sequence of genes replicated in *Salmonella typhimurium* as examined by transduction techniques. *J. Bacteriol.* **102**:320–333.
1439. **Nishitani, J., and G. Wilcox.** 1991. Cloning and characterization of the L-rhamnose regulon in *Salmonella typhimurium* LT2. *Gene* **105**:37–42.
1440. **Nixon, B. T., C. W. Ronson, and F. M. Ausubel.** 1986. Two-component regulatory systems responsive to environmental stimuli share strongly conserved domains with the nitrogen assimilation regulatory genes *ntxB* and *ntxC*. *Proc. Natl. Acad. Sci. USA* **83**:7850–7854.
1441. **Nnalue, N. A., and B. A. D. Stocker.** 1986. Some *galE* mutants of *Salmonella choleraesuis* retain virulence. *Infect. Immun.* **54**:635–640.
1442. **Nnalue, N. A., and B. A. D. Stocker.** 1987. Test of the virulence and live-vaccine efficacy of auxotrophic and *galE* derivatives of *Salmonella choleraesuis*. *Infect. Immun.* **55**:955–962.
1443. **Nohmi, T., A. Hakura, Y. Nakai, M. Watanabe, S. Y. Murayama, and T. Sofuni.** 1991. *Salmonella typhimurium* has two homologous but different *umuDC* operons: cloning of a new *umuDC*-like operon (*samAB*) present in a 60-megadalton cryptic plasmid of *S. typhimurium*. *J. Bacteriol.* **173**:1051–1063.
1444. **Nohmi, T., M. Yamada, M. Watanabe, S. Y. Murayama, and T. Sofuni.** 1992. Roles of *Salmonella typhimurium umuDC* and *samAB* in UV mutagenesis and UV sensitivity. *J. Bacteriol.* **174**:6948–6955.
1445. **Norel, F., C. Coynault, I. Miras, D. Hermant, and M. Y. Popoff.** 1989. Cloning and expression of plasmid DNA sequences involved in *Salmonella* serotype *typhimurium* virulence. *Mol. Microbiol.* **3**:733–743.
1446. **Norel, F., M. R. Pisano, J. Nicoli, and M. Y. Popoff.** 1989. Nucleotide sequence of the plasmid-borne virulence gene *mkfA* encoding a 28 kDa polypeptide from *Salmonella typhimurium*. *Res. Microbiol.* **140**:263–265.
1447. **Norel, F., M. R. Pisano, J. Nicoli, and M. Y. Popoff.** 1989. Nucleotide sequence of the plasmid-

- borne virulence gene *mkfB* from *Salmonella typhimurium*. *Res. Microbiol.* **140**:455–457.
1448. **Norel, F., V. Robbe-Saule, M. Y. Popoff, and C. Coynault.** 1992. The putative sigma factor KatF (RpoS) is required for the transcription of the *Salmonella typhimurium* virulence gene *spvB* in *Escherichia coli*. *FEMS Microbiol. Lett.* **78**:271–276.
1449. **Novotny, M. J., W. L. Frederickson, E. B. Waygood, and M. H. Saier, Jr.** 1985. Allosteric regulation of glycerol kinase by enzyme III^{Glc} of the phosphotransferase system in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **162**:810–816.
1450. **Nurminen, M.** 1978. A mild procedure to isolate the 34K, 35K and 36K porins of the outer membrane of *Salmonella typhimurium*. *FEMS Microbiol. Lett.* **3**:331–334.
1451. **Nurminen, M., K. Lounatmaa, M. Sarvas, P. H. Makela, and T. Nakae.** 1976. Bacteriophage-resistant mutants of *Salmonella typhimurium* deficient in two major outer membrane proteins. *J. Bacteriol.* **127**:941–955.
1452. **Nurminen, M., and R. Oertli.** 1975. Bacteriophage P221-receptor in *Salmonella typhimurium*: purification and characterization. *Abstr. 10th Congr. Fed. Eur. Biochem. Soc.* 1975.
1453. **Nyman, K., M. Plosila, L. Howden, and P. H. Makela.** 1979. Genetic determination of lipopolysaccharide: locus of O specific unit polymerase in Group E of *Salmonella*. *Zentralbl. Bakteriol. Parasitenkd. Infektionskr. Hyg. Abt. 1 Orig. Reihe A* **243**:355–362.
1454. **O'Brien, E. J., and P. M. Bennett.** 1972. Structure of straight flagella from a mutant *Salmonella*. *J. Mol. Biol.* **70**:133–152.
1455. **O'Brien, K., G. Deno, P. Ostrovsky de Spicer, J. F. Gardner, and S. R. Maloy.** 1992. Integration host factor facilitates repression of the *put* operon in *Salmonella typhimurium*. *Gene* **118**:13–19.
1456. **O'Byrne, C. P., and C. J. Dorman.** 1994. The *spv* virulence operon of *Salmonella typhimurium* LT2 is regulated negatively by the cyclic AMP (cAMP)-cAMP receptor protein system. *J. Bacteriol.* **176**:905–912.
1457. **O'Byrne, C. P., N. Ni Bhriain, and C. J. Dorman.** 1992. The DNA supercoiling-sensitive expression of the *Salmonella typhimurium* *his* operon requires the *his* attenuator and is modulated by anaerobiosis and by osmolarity. *Mol. Microbiol.* **6**:2467–2476.
1458. **O'Connor, M., N. M. Willis, L. Bossi, R. F. Gesteland, and J. F. Atkins.** 1993. Functional tRNAs with altered 3' ends. *EMBO J.* **12**:2559–2566.
1459. **O'Donovan, G. A., and J. Neuhard.** 1970. Pyrimidine metabolism in microorganisms. *Bacteriol. Rev.* **34**:278–343.
1460. **Ohnishi, K., A. Hasegawa, K. Matsubara, T. Date, T. Okada, and K. Kiritani.** 1988. Cloning and nucleotide sequence of the *brnQ* gene, the structural gene for a membrane-associated component of the LIV-II transport system for branched-chain amino acids in *Salmonella typhimurium*. *Jpn. J. Genet.* **63**:343–357.
1461. **Ohnishi, K., M. Homma, K. Kutsukake, and T. Iino.** 1987. Formation of flagella lacking outer rings by *flaM*, *flaU*, and *flaY* mutants of *Escherichia coli*. *J. Bacteriol.* **169**:1485–1488.
1462. **Ohnishi, K., and K. Kiritani.** 1978. Glycyl-L-leucine resistance mutation affecting transport of branched chain amino acids in *Salmonella typhimurium*. *Jpn. J. Genet.* **53**:275–283.
1463. **Ohnishi, K., and K. Kiritani.** 1980. Close linkage relationship between *gleR*- and *brnQ* loci in *Salmonella typhimurium*. *Jpn. J. Genet.* **55**:67–70.
1464. **Ohnishi, K., K. Kutsukake, H. Suzuki, and T. Iino.** 1990. Gene *fliA* encodes an alternative sigma factor specific for flagellar operons in *Salmonella typhimurium*. *Mol. Gen. Genet.* **221**:139–147.
1465. **Ohnishi, K., K. Kutsukake, H. Suzuki, and T. Lino.** 1992. A novel transcriptional regulation mechanism in the flagellar regulon of *Salmonella typhimurium*: an antisigma factor inhibits the activity of the flagellum-specific sigma factor, sigma F. *Mol. Microbiol.* **6**:3149–3157.
1466. **Ohnishi, K., K. Murata, and K. Kiritani.** 1980. A regulatory transport mutant for branched-chain amino acids in *Salmonella typhimurium*. *Jpn. J. Genet.* **55**:349–360.
1467. **Ohnishi, K., A. Nakazima, K. Matsubara, and K. Kiritani.** 1990. Cloning and nucleotide sequences of *livB* and *livC*, the structural genes encoding binding proteins of the high-affinity

- branched-chain amino acid transport in *Salmonella typhimurium*. *J. Biochem.* (Tokyo) **107**:202–208.
1468. **Ohnishi, K., Y. Ohto, S. Aizawa, R. M. Macnab, and T. Iino.** 1994. FlgD is a scaffolding protein needed for flagellar hook assembly in *Salmonella typhimurium*. *J. Bacteriol.* **176**:2272–2281.
1469. **Ohta, N., P. R. Galsworthy, and A. B. Pardee.** 1971. Genetics of sulfate transport by *Salmonella typhimurium*. *J. Bacteriol.* **105**:1053–1062.
1470. **Okada, M., T. Watanabe, and T. Miyake.** 1968. On the nature of the recipient ability of *Salmonella typhimurium* for foreign deoxyribonucleic acids. *J. Gen. Microbiol.* **50**:241–252.
1471. **Okazaki, N., S. Matsuo, K. Saito, A. Tominaga, and M. Enomoto.** 1993. Conversion of the *Salmonella* phase 1 flagellin gene *fliC* to the phase 2 gene *fljB* on the *Escherichia coli* K-12 chromosome. *J. Bacteriol.* **175**:758–766.
1472. **Okino, H., M. Isomura, S. Yamaguchi, Y. Magariyama, S. Kudo, and S.-I. Aizawa.** 1989. Release of flagellar filament-hook-rod complex by a *Salmonella typhimurium* mutant defective in the M ring of the basal body. *J. Bacteriol.* **171**:2075–2082.
1473. **Old, D. C., P. F. H. Dawes, and R. M. Barker.** 1980. Transduction of inositol-fermenting ability demonstrating phylogenetic relationships among strains of *Salmonella typhimurium*. *Genet. Res.* **35**:215–224.
1474. **Old, I. G., D. Margarita, R. E. Glass, and I. Saint Girons.** 1990. Nucleotide sequence of the *metH* gene of *Escherichia coli* K-12 and comparison with that of *Salmonella typhimurium* LT2. *Gene* **87**:15–21.
1475. **Oliver, D. R., J. J. Manis, and H. J. Whitfield.** 1974. Evidence for a composite state of an F' *his gnd* element and a cryptic plasmid in a derivative of *Salmonella typhimurium* LT2. *J. Bacteriol.* **119**:192–201.
1476. **O'Mahony, D. J., D. Hughes, S. Thompson, and J. F. Atkins.** 1989. Suppression of a –1 frameshift mutation by a recessive tRNA suppressor which causes doublet decoding. *J. Bacteriol.* **171**:3824–3830.
1477. **O'Neal, C. R., W. M. Gabriel, A. K. Turk, S. J. Libby, F. C. Fang, and M. P. Spector.** 1994. RpoS is necessary for both the positive and negative regulation of starvation survival genes during phosphate, carbon, and nitrogen starvation in *Salmonella typhimurium*. *J. Bacteriol.* **176**:4610–4616.
1478. **O'Neill, J. P., and M. Freundlich.** 1972. Effect of cyclopentaneglycine on metabolism in *Salmonella typhimurium*. *J. Bacteriol.* **111**:510–515.
1479. **O'Neill, J. P., and M. Freundlich.** 1972. Two forms of biosynthetic acetohydroxy acid synthetase in *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.* **48**:437–443.
1480. **O'Neill, J. P., and M. Freundlich.** 1973. Temperature-sensitive growth inhibition by valine in *Salmonella typhimurium*: alteration of one form of acetohydroxy acid synthetase. *J. Bacteriol.* **116**:98–106.
1481. **Oosawa, K., T. Ueno, and S. Aizawa.** 1994. Overproduction of the bacterial flagellar switch proteins and their interactions with the MS ring complex in vitro. *J. Bacteriol.* **176**:3683–3691.
1482. **Oppezzo, O. J., B. Avanzati, and D. N. Anton.** 1991. Increased susceptibility to β -lactam antibiotics and decreased porin content caused by *envB* mutations of *Salmonella typhimurium*. *Antimicrob. Agents Chemother.* **35**:1203–1207.
1483. **O'Reilly, C., G. W. Black, R. Laffey, and D. J. McConnell.** 1990. Molecular analysis of an IS200 insertion in the *gpt* gene of *Salmonella typhimurium* LT2. *J. Bacteriol.* **172**:6599–6601.
1484. **O'Reilly, C., P. D. Turner, P. F. Smith-Keary, and D. J. McConnell.** 1984. Molecular cloning of genes involved in purine biosynthetic and salvage pathways of *Salmonella typhimurium*. *Mol. Gen. Genet.* **196**:152–157.
1485. **Ornellas, E. P., and B. A. D. Stocker.** 1974. Relation of lipopolysaccharide character to P1 sensitivity in *Salmonella typhimurium*. *Virology* **60**:491–502.
1486. **Orr, J. C., D. W. Bryant, D. R. McCalla, and M. A. Quilliam.** 1985. Dinitropyrene-resistant *Salmonella typhimurium* are deficient in an acetyl-CoA acetyltransferase. *Chem. Biol. Interact.* **54**:281–288.
1487. **Orrego, C., and E. Eisenstadt.** 1987. An inducible pathway is required for mutagenesis in *Salmonella typhimurium* LT2. *J. Bacteriol.* **169**:2885–2888.

1488. **Ortega, M. V., A. Cardenas, and D. Ubiera.** 1975. *panD*, a new chromosomal locus of *Salmonella typhimurium* for the biosynthesis of β -alanine. *Mol. Gen. Genet.* **140**:159–164.
1489. **Osborn, M. J.** 1968. Biochemical characterization of mutants of *Salmonella typhimurium* lacking glucosyl or galactosyl lipopolysaccharide transferases. *Nature* (London) **217**:957–960.
1490. **Osborn, M. J.** 1969. Structure and biosynthesis of the bacterial cell wall. *Annu. Rev. Biochem.* **29**:501–538.
1491. **Osborn, M. J., J. E. Gander, E. Parisi, and J. Carson.** 1972. Mechanism and assembly of the outer membrane of *Salmonella typhimurium*. Isolation and characterization of cytoplasmic and outer membrane. *J. Biol. Chem.* **247**:3962–3972.
1492. **Osborn, M. J., P. D. Rick, and N. S. Rasmussen.** 1980. Mechanism of assembly of the outer membrane of *Salmonella typhimurium*. Translocation and integration of an incomplete mutant lipid A into the outer membrane. *J. Biol. Chem.* **255**:4246–4251.
1493. **Osborn, M. J., S. M. Rosen, L. Rothfield, L. D. Zeleznick, and B. L. Horecker.** 1964. Lipopolysaccharide of the gram-negative cell wall. *Science* **145**:783–789.
1494. **Osborn, M. J., and L. I. Rothfield.** 1971. Biosynthesis of the core region of lipopolysaccharides, p. 331–350. In G. Weinbaum, S. Kadis, and S. J. Ajl (ed.), *Bacterial Endotoxins*, vol. 4 in *Microbial Toxins*. Academic Press, Inc., New York.
1495. **Ostapchuk, P., A. Anilionis, and M. Riley.** 1980. Conserved genes in enteric bacteria are not identical. *Mol. Gen. Genet.* **180**:475–478.
1496. **Ostrovsky de Spicer, P., and S. Maloy.** 1993. PutA protein, a membrane-associated flavin dehydrogenase, acts as a redox-dependent transcriptional regulator. *Proc. Natl. Acad. Sci. USA* **90**:4295–4298.
1497. **Ostrovsky de Spicer, P., K. O'Brien, and S. Maloy.** 1991. Regulation of proline utilization in *Salmonella typhimurium*: a membrane-associated dehydrogenase binds DNA in vitro. *J. Bacteriol.* **173**:211–219.
1498. **Ostrowski, J., M. J. Barber, D. C. Rueger, B. E. Miller, L. M. Siegel, and N. M. Kredich.** 1989. Characterization of the flavoprotein moieties of NADPH-sulfite reductase from *Salmonella typhimurium* and *Escherichia coli*. Physicochemical and catalytic properties, amino acid sequence deduced from DNA sequence of *cysJ*, and comparison with NADPH-cytochrome P-450 reductase. *J. Biol. Chem.* **264**:15796–15808.
1499. **Ostrowski, J., and D. Hulanicka.** 1979. Constitutive mutation of *cysJIH* operon in a *cysB* deletion strain of *Salmonella typhimurium*. *Mol. Gen. Genet.* **175**:145–150.
1500. **Ostrowski, J., and D. Hulanicka.** 1981. Effect of DNA gyrase inhibitors on gene expression of the cysteine regulon. *Mol. Gen. Genet.* **181**:363–366.
1501. **Ostrowski, J., G. Jagura-Burdzy, and N. M. Kredich.** 1987. DNA sequences of the *cysB* regions of *Salmonella typhimurium* and *Escherichia coli*. *J. Biol. Chem.* **262**:5999–6005.
1502. **Ostrowski, J., and N. M. Kredich.** 1989. Molecular characterization of the *cysJIH* promoters of *Salmonella typhimurium* and *Escherichia coli*: regulation by *cysB* protein and *N*-acetyl-L-serine. *J. Bacteriol.* **171**:130–140.
1503. **Ostrowski, J., and N. M. Kredich.** 1990. In vitro interactions of CysB protein with the *cysJIH* promoter of *Salmonella typhimurium*: inhibitory effects of sulfide. *J. Bacteriol.* **172**:779–785.
1504. **Ostrowski, J., and N. M. Kredich.** 1991. Negative autoregulation of *cysB* in *Salmonella typhimurium*: in vitro interactions of CysB protein with the *cysB* promoter. *J. Bacteriol.* **173**:2212–2218.
1505. **Ostrowski, J., J. Y. Wu, D. C. Rueger, B. E. Miller, L. M. Siegel, and N. M. Kredich.** 1989. Characterization of the *cysJIH* regions of *Salmonella typhimurium* and *Escherichia coli*. B. DNA sequences of *cysI* and *cysH* and a model for the siroheme-Fe₄S₄ active center of sulfite reductase hemoprotein based on amino acid homology with spinach nitrite reductase. *J. Biol. Chem.* **264**:15726–15737.
1506. **O'Toole, G. A., and J. C. Escalante-Semerena.** 1991. Identification and initial characterization of the *eutF* locus of *Salmonella typhimurium*. *J. Bacteriol.* **173**:5168–5172.
1507. **O'Toole, G. A., and J. C. Escalante-Semerena.** 1993. *cobU*-dependent assimilation of

- nonadenosylated cobinamide in *cobA* mutants of *Salmonella typhimurium*. *J. Bacteriol.* **175**:6328–6336.
1508. **O’Toole, G. A., M. R. Rondon, and J. C. Escalante-Semerena.** 1993. Analysis of mutants of *Salmonella typhimurium* defective in the synthesis of the nucleotide loop of cobalamin. *J. Bacteriol.* **175**:3317–3326.
1509. **O’Toole, G. A., J. R. Trzebiatowski, and J. C. Escalante-Semerena.** 1994. The *cobC* gene of *Salmonella typhimurium* codes for a novel phosphatase involved in the assembly of the nucleotide loop of cobalamin. *J. Biol. Chem.* **269**:26503–26511.
1510. **Overbeeke, N., G. Van Scharrenburg, and B. Lugtenburg.** 1980. Antigenic relationships between pore proteins of *Escherichia coli* K12. *Eur. J. Biochem.* **110**:247–254.
1511. **Overbye, K. M., S. K. Basu, and P. Margolin.** 1983. Loss of DNA topoisomerase I activity alters many cellular functions in *Salmonella typhimurium*. *Cold Spring Harbor Symp. Quant. Biol.* **47**:785–791.
1512. **Overbye, K. M., and P. Margolin.** 1981. Role of the *supX* gene in ultraviolet light-induced mutagenesis in *Salmonella typhimurium*. *J. Bacteriol.* **146**:170–178.
1513. **Overdier, D. G., and L. N. Csonka.** 1992. A transcriptional silencer downstream of the promoter in the osmotically controlled *proU* operon of *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **89**:3140–3144.
1514. **Overdier, D. G., E. R. Olson, B. D. Erickson, M. M. Ederer, and L. N. Csonka.** 1989. Nucleotide sequence of the transcriptional control region of the osmotically regulated *proU* operon of *Salmonella typhimurium* and identification of the 5' endpoint of the *proU* mRNA. *J. Bacteriol.* **171**:4694–4706.
1515. **Ow, D. W., V. Sundaresan, D. M. Rothstein, S. E. Brown, and F. M. Ausubel.** 1983. Promoters regulated by the *glnG* (*ntrC*) and *nifA* gene products share a heptameric consensus sequence in the –15 region. *Proc. Natl. Acad. Sci. USA* **80**:2524–2528.
1516. **Owen-Hughes, T. A., G. D. Pavitt, D. S. Santos, J. M. Sidebotham, C. S. Hulton, J. C. Hinton, and C. F. Higgins.** 1992. The chromatin-associated protein H-NS interacts with curved DNA to influence DNA topology and gene expression. *Cell* **71**:255–265.
1517. **Pace, J., M. J. Hayman, and J. E. Galan.** 1993. Signal transduction and invasion of epithelial cells by *S. typhimurium*. *Cell* **72**:505–514.
1518. **Pai, S. R., Y. Upshaw, and S. P. Singh.** 1992. Characterization of monoclonal antibodies to the outer membrane protein (OmpD) of *Salmonella typhimurium*. *Can. J. Microbiol.* **38**:1102–1107.
1519. **Palmer, D. T., P. H. Blum, and S. W. Artz.** 1983. Effects of the *hisT* mutation of *Salmonella typhimurium* on translation elongation rate. *J. Bacteriol.* **153**:357–363.
1520. **Palva, E. T.** 1978. Major outer membrane protein in *Salmonella typhimurium* induced by maltose. *J. Bacteriol.* **136**:286–294.
1521. **Palva, E. T.** 1979. Relationship between *ompB* genes of *Escherichia coli* and *Salmonella typhimurium*. *FEMS Microbiol. Lett.* **5**:205–210.
1522. **Palva, E. T., P. Liljestrom, and S. Harayama.** 1981. Cosmid cloning and transposon mutagenesis in *Salmonella typhimurium* using phage lambda vehicles. *Mol. Gen. Genet.* **181**:153–157.
1523. **Palva, E. T., and P. H. Makela.** 1980. Lipopolysaccharide heterogeneity in *Salmonella typhimurium* analyzed by sodium dodecyl sulfate/polyacrylamide gel electrophoresis. *Eur. J. Biochem.* **107**:137–143.
1524. **Pandey, N. K., and R. L. Switzer.** 1982. Mutant strains of *Salmonella typhimurium* with defective phosphoribosylpyrophosphate synthetase activity. *J. Gen. Microbiol.* **128**:1863–1871.
1525. **Pang, P. P., A. S. Lundberg, and G. C. Walker.** 1985. Identification and characterization of the *mutL* and *mutS* gene products of *Salmonella typhimurium* LT2. *J. Bacteriol.* **163**:1007–1015.
1526. **Pang, P. P., S. D. Tsen, A. S. Lundberg, and G. C. Walker.** 1984. The *mutH*, *mutL*, *mutS*, and *uvrD* genes of *Salmonella typhimurium* LT2. *Cold Spring Harbor Symp. Quant. Biol.* **49**:597–602.
1527. **Pang, P. P., and G. C. Walker.** 1983. The *Salmonella typhimurium* LT2 *uvrD* gene is regulated by the *lexA* gene product. *J. Bacteriol.* **154**:1502–1504.

1528. **Pang, P. P., and G. C. Walker.** 1983. Identification of the *uvrD* gene product of *Salmonella typhimurium* LT2. *J. Bacteriol.* **153**:1172–1179.
1529. **Papp-Szabo, E., M. Firtel, and P. D. Josephy.** 1994. Comparison of the sensitivities of *Salmonella typhimurium* *oxyR* and *katG* mutants to killing by human neutrophils. *Infect. Immun.* **62**:2662–2668.
1530. **Parada, J. L., and M. V. Ortega.** 1975. Lysis of a temperature conditional thiamineless mutant of *Salmonella typhimurium* by glucose and hexoses. *Rev. Assoc. Argent. Microbiol.* **7**:91–96.
1531. **Parada, J. L., M. V. Ortega, and G. Carrillo-Castaneda.** 1973. Biochemical and genetic characteristics of the C₄-dicarboxylic acids transport system of *Salmonella typhimurium*. *Arch. Mikrobiol.* **94**:65–76.
1532. **Pardee, A. B.** 1966. Purification and properties of a sulfate-binding protein from *Salmonella typhimurium*. *J. Biol. Chem.* **241**:5886–5892.
1533. **Pardee, A. B., L. S. Prestidge, M. B. Whipple, and J. Dreyfuss.** 1966. A binding site for sulfate and its relation to sulfate transport into *Salmonella typhimurium*. *J. Biol. Chem.* **241**:3962–3969.
1534. **Pardee, A. B., and K. Watanabe.** 1968. Location of sulfate-binding protein in *Salmonella typhimurium*. *J. Bacteriol.* **96**:1049–1054.
1535. **Park, U. E., B. M. Olivera, K. T. Hughes, J. R. Roth, and D. R. Hillyard.** 1989. DNA ligase and the pyridine nucleotide cycle in *Salmonella typhimurium*. *J. Bacteriol.* **171**:2173–2180.
1536. **Park, U. E., J. R. Roth, and B. M. Olivera.** 1988. *Salmonella typhimurium* mutants lacking NAD pyrophosphatase. *J. Bacteriol.* **170**:3725–3730.
1537. **Park, Y. M., and G. V. Stauffer.** 1989. *Salmonella typhimurium* *metC* operator-constitutive mutations. *FEMS Microbiol. Lett.* **51**:137–141.
1538. **Park, Y. M., and G. V. Stauffer.** 1989. DNA sequence of the *metC* gene and its flanking regions from *Salmonella typhimurium* LT2 and homology with the corresponding sequence of *Escherichia coli*. *Mol. Gen. Genet.* **216**:164–169.
1539. **Parker, J., M. Flashner, W. G. McKeever, and F. C. Neidhardt.** 1974. Metabolic regulation of the arginyl and valyl transfer ribonucleic acid synthetases in bacteria. *J. Biol. Chem.* **249**:1044–1053.
1540. **Parra-Lopez, C., M. T. Baer, and E. A. Groisman.** 1993. Molecular genetic analysis of a locus required for resistance to antimicrobial peptides in *Salmonella typhimurium*. *EMBO J.* **12**:4053–4062.
1541. **Parra-Lopez, C., R. Lin, A. Aspedon, and E. A. Groisman.** 1994. A *Salmonella* protein that is required for resistance to antimicrobial peptides and transport of potassium. *EMBO J.* **13**:3964–3972.
1542. **Parsons, S. M., and D. E. Koshland, Jr.** 1974. Multiple aggregation states of phosphoribosyladenosine triphosphate synthetase. *J. Biol. Chem.* **249**:4119–4126.
1543. **Parsons, S. M., and D. E. Koshland, Jr.** 1974. A rapid isolation of phosphoribosyladenosine triphosphate synthetase and comparison to native enzyme. *J. Biol. Chem.* **249**:4104–4109.
1544. **Parsons, S. M., and M. Lipsky.** 1975. Composition of the first enzyme of histidine biosynthesis isolated from wild-type and mutant operator strains of *Salmonella typhimurium*. *J. Bacteriol.* **121**:485–490.
1545. **Parsons, S. M., and M. Lipsky.** 1975. A unique reactive residue in adenosine triphosphate phosphoribosyltransferase sensitive to five conformation and dissociation sites. *J. Biol. Chem.* **250**:5660–5668.
1546. **Pascal, M.-C., F. Casse, and M. Chippaux.** 1977. Localization of *pfl* gene by transductional study of the *gal-aroA* segment of the *Salmonella typhimurium* LT2 chromosome. *Mol. Gen. Genet.* **150**:331–334.
1547. **Pascal, M.-C., F. Casse, M. Chippaux, and M. Lepelletier.** 1973. Genetic analysis of mutants of *Salmonella typhimurium* deficient in formate dehydrogenase activity. *Mol. Gen. Genet.* **120**:337–340.
1548. **Pascal, M.-C., F. Casse, M. Chippaux, and M. Lepelletier.** 1975. Genetic analysis of mutants of *Escherichia coli* K12 and *Salmonella typhimurium* LT2 deficient in hydrogenase activity. *Mol. Gen. Genet.* **141**:173–179.
1549. **Pasternak, C. A., R. J. Ellis, M. C. Jones-Mortimer, and C. E. Crichton.** 1965. The control of

- sulfate reduction in bacteria. *Biochem. J.* **96**:270–275.
1550. **Paton, E. B., M. I. Woodmaska, I. V. Kroupskaya, A. N. Zhyvoloup, and G. K. Matsuka.** 1990. Evidence for the ability of L10 ribosomal proteins of *Salmonella typhimurium* and *Klebsiella pneumoniae* to regulate *rplJL* gene expression in *Escherichia coli*. *FEBS Lett.* **265**:129–132.
1551. **Paton, E. B., S. B. Zolotukhin, M. I. Woodmaska, I. V. Kroupskaya, and A. N. Zhyvoloup.** 1990. The nucleotide sequence of gene *rplJ* encoding ribosomal protein L10 of *Salmonella typhimurium*. *Nucleic Acids Res.* **18**:2824.
1552. **Patterson-Delafield, J., R. J. Martinex, B. A. D. Stocker, and S. Yamaguchi.** 1973. A new *fla* gene in *Salmonella typhimurium*—*flaR*—and its mutant phenotype—superhooks. *Arch. Mikrobiol.* **90**:107–120.
1553. **Paveglio, M. T., J. S. Tang, R. E. Unger, and E. L. Barrett.** 1988. Formate-nitrate respiration in *Salmonella typhimurium*: studies of two *rha*-linked *fdn* genes. *J. Bacteriol.* **170**:213–217.
1554. **Payne, G. M., E. N. Spudich, and G. F.-L. Ames.** 1985. A mutational hot-spot in the *hisM* gene of the histidine transport operon in *Salmonella typhimurium* is due to deletion of repeated sequences and results in an altered specificity of transport. *Mol. Gen. Genet.* **200**:493–496.
1555. **Pearce, S. R., M. L. Mimmack, M. P. Gallagher, U. Gileadi, S. C. Hyde, and C. F. Higgins.** 1992. Membrane topology of the integral membrane components, OppB and OppC, of the oligopeptide permease of *Salmonella typhimurium*. *Mol. Microbiol.* **6**:47–57.
1556. **Pearce, U. B., and B. A. D. Stocker.** 1967. Phase variation of flagellar antigens in *Salmonella*: abortive transduction studies. *J. Gen. Microbiol.* **49**:335–349.
1557. **Pekkel, V. A., M. A. Abramova, and V. S. Levashev.** 1974. Role of polyamines in the process of bacterial cell division. *Zh. Mikrobiol. Epidemiol. Immunobiol.* **51**:8–13.
1558. **Persson, B. C., and G. R. Bjork.** 1993. Isolation of the gene (*miaE*) encoding the hydroxylase involved in the synthesis of 2-methylthio-*cis*-ribozeatin in tRNA of *Salmonella typhimurium* and characterization of mutants. *J. Bacteriol.* **175**:7776–7785.
1559. **Peterson, A. A., and E. J. McGroarty.** 1985. High-molecular-weight components in lipopolysaccharides of *Salmonella typhimurium*, *Salmonella minnesota*, and *Escherichia coli*. *J. Bacteriol.* **162**:738–745.
1560. **Pflugrath, J. W., and F. A. Quioco.** 1985. Sulphate sequestered in the sulphate-binding protein of *Salmonella typhimurium* is bound solely by hydrogen bonds. *Nature (London)* **314**:257–260.
1561. **Pflugrath, J. W., and F. A. Quioco.** 1988. The 2 Å resolution structure of the sulfate-binding protein involved in active transport in *Salmonella typhimurium*. *J. Mol. Biol.* **200**:163–180.
1562. **Piszkiwicz, D., B. E. Tilley, T. Rand-Meir, and S. M. Parsons.** 1979. Amino acid sequence of ATP phosphoribosyltransferase of *Salmonella typhimurium*. *Proc. Natl. Acad. Sci USA* **76**:1589–1592.
1563. **Pizarro, R. A., G. O. Boselli, and L. V. Orce.** 1985. Biochemical and phenotypical correction of an envelope mutant of *Salmonella typhimurium*. *Arch. Int. Physiol. Biochim.* **92**:333–337.
1564. **Plamann, L. S., and G. V. Stauffer.** 1987. Nucleotide sequence of the *Salmonella typhimurium metR* gene and the *metR-metE* control region. *J. Bacteriol.* **169**:3932–3937.
1565. **Plamann, L. S., M. L. Urbanowski, and G. V. Stauffer.** 1988. *Salmonella typhimurium metE* operator-constitutive mutations. *Gene* **73**:201–208.
1566. **Plosila, M., and P. H. Makela.** 1972. Mapping of a gene *oafA* determining antigen 1 in *Salmonella* of group E4. *Scand. J. Clin. Lab. Invest.* **29**(Suppl. 122):55.
1567. **Poland, J., and P. D. Ayling.** 1994. Methionine and glutamine transport systems in D-methionine utilising revertants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **194**:219–226.
1568. **Pollack, J. R., B. N. Ames, and J. B. Neilands.** 1970. Iron transport in *Salmonella typhimurium*: mutants blocked in the biosynthesis of enterobactin. *J. Bacteriol.* **104**:635–639.
1569. **Popham, D., J. Keener, and S. Kustu.** 1991. Purification of the alternative sigma factor, sigma 54, from *Salmonella typhimurium* and characterization of sigma 54 holoenzyme. *J. Biol. Chem.* **266**:19510–19518.
1570. **Popham, D. L., D. Szeto, J. Keener, and S. Kustu.** 1989. Function of a bacterial activator protein that binds to transcriptional enhancers. *Science* **243**:629–635.

1571. **Post, D. A., B. Hove-Jensen, and R. L. Switzer.** 1993. Characterization of the *hemA-prs* region of the *Escherichia coli* and *Salmonella typhimurium* chromosomes: identification of two open reading frames and implications for *prs* expression. *J. Gen. Microbiol.* **139**:259–266.
1572. **Post, D. A., and R. L. Switzer.** 1991. *prsB* is an allele of the *Salmonella typhimurium prsA* gene: characterization of a mutant phosphoribosylpyrophosphate synthetase. *J. Bacteriol.* **173**:1978–1986.
1573. **Postgate, J. R., and V. Krishnapillai.** 1977. Expression of *Klebsiella nif* and *his* genes in *Salmonella typhimurium*. *J. Gen. Microbiol.* **98**:379–385.
1574. **Postma, P. W.** 1976. Involvement of the phosphotransferase system in galactose transport in *Salmonella typhimurium*. *FEBS Lett.* **61**:49–53.
1575. **Postma, P. W.** 1977. Galactose transport in *Salmonella typhimurium*. *J. Bacteriol.* **129**:630–639.
1576. **Postma, P. W.** 1981. Defective enzyme II-B^{Glc} of the phosphoenolpyruvate:sugar phosphotransferase system leading to uncoupling of transport and phosphorylation in *Salmonella typhimurium*. *J. Bacteriol.* **147**:382–389.
1577. **Postma, P. W., J. C. Cordaro, and S. Roseman.** 1977. Sugar transport. A pleiotrophic membrane mutant of *Salmonella typhimurium*. *J. Biol. Chem.* **252**:3862–3876.
1578. **Postma, P. W., W. Epstein, A. R. J. Schuitema, and S. O. Nelson.** 1984. Interaction between III^{Glc} of the phosphoenolpyruvate:sugar phosphotransferase system and glycerol kinase of *Salmonella typhimurium*. *J. Bacteriol.* **158**:351–353.
1579. **Postma, P. W., H. G. Keizer, and P. Koolwijk.** 1986. Transport of trehalose in *Salmonella typhimurium*. *J. Bacteriol.* **168**:1107–1111.
1580. **Postma, P. W., and J. W. Lengeler.** 1985. Phosphoenolpyruvate:carbohydrate phosphotransferase system of bacteria. *Microbiol. Rev.* **49**:232–269.
1581. **Postma, P. W., A. Schuitema, and C. Kwa.** 1981. Regulation of methyl β -galactoside permease activity in *pts* and *crr* mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **181**:448–453.
1582. **Postma, P. W., and J. B. Stock.** 1980. Enzymes II of the phosphotransferase system do not catalyze sugar transport in the absence of phosphorylation. *J. Bacteriol.* **141**:476–484.
1583. **Powers, D. A., and S. Roseman.** 1984. The primary structure of *Salmonella typhimurium* HPr, a phosphocarrier protein of the phosphoenolpyruvate:glycose phosphotransferase system. A correction. *J. Biol. Chem.* **259**:15212–15214.
1584. **Prasad, R., A. K. Chopra, P. Chary, and J. W. Peterson.** 1992. Expression and characterization of the cloned *Salmonella typhimurium* enterotoxin. *Microb. Pathog.* **13**:109–121.
1585. **Prasad, R., A. K. Chopra, J. W. Peterson, R. Pericas, and C. W. Houston.** 1990. Biological and immunological characterization of a cloned cholera toxin-like enterotoxin from *Salmonella typhimurium*. *Microb. Pathog.* **9**:315–329.
1586. **Primakoff, P., and S. W. Artz.** 1979. Positive control of *lac* operon expression *in-vitro* by guanosine-5'-diphosphate-3'-diphosphate. *Proc. Natl. Acad. Sci. USA* **76**:1726–1730.
1587. **Primerano, D. A., and R. O. Burns.** 1982. Metabolic basis for the isoleucine, pantothenate, or methionine requirement of *ilvG* strains of *Salmonella typhimurium*. *J. Bacteriol.* **150**:1202–1211.
1588. **Primerano, D. A., and R. O. Burns.** 1983. Role of acetohydroxy acid isomeroreductase in biosynthesis of pantothenic acid in *Salmonella typhimurium*. *J. Bacteriol.* **153**:259–269.
1589. **Pritchard, D. G., S. C. Nivas, M. D. York, and B. S. Pomeroy.** 1979. Effects of *galE* mutant of *Salmonella typhimurium* on experimental salmonellosis in chickens. *Avian Dis.* **22**:562–575.
1590. **Prival, M. J., and T. A. Cebula.** 1992. Sequence analysis of mutations arising during prolonged starvation of *Salmonella typhimurium*. *Genetics* **132**:303–310.
1591. **Prossnitz, E.** 1991. Determination of a region of the HisJ binding protein involved in the recognition of the membrane complex of the histidine transport system of *Salmonella typhimurium*. *J. Biol. Chem.* **266**:9673–9677.
1592. **Pruss, G. J.** 1985. DNA topoisomerase I mutants. Increased heterogeneity in linking number and other replicon-dependent changes in DNA supercoiling. *J. Mol. Biol.* **185**:51–63.
1593. **Pruss, G. J., and K. Drlica.** 1985. DNA supercoiling and suppression of the *leu-500* promoter mutation. *J. Bacteriol.* **164**:947–949.
1594. **Pruss, G. J., and K. Drlica.** 1986. Topoisomerase I mutants: the gene on pBR322 that encodes

- resistance to tetracycline affects plasmid DNA supercoiling. *Proc. Natl. Acad. Sci. USA* **83**:8952–8956.
1595. **Pueyo, C.** 1978. Forward mutations to arabinose resistance in *Salmonella typhimurium* strains. A sensitive assay for mutagenicity testing. *Mutat. Res.* **54**:311–322.
1596. **Pueyo, C., and J. Lopez-Barea.** 1979. The L-arabinose resistance test with *Salmonella typhimurium* strain SV-3 selects forward mutations at several *ara* genes. *Mutat. Res.* **64**:249–258.
1597. **Pugsley, A. P., D. J. Conrad, C. A. Schnaitman, and T. I. Gregg.** 1980. *In vivo* effects of local anesthetics on the production of major outer membrane proteins by *Escherichia coli*. *Biochim. Biophys. Acta* **599**:1–12.
1598. **Pulkkinen, W. S., and S. I. Miller.** 1991. A *Salmonella typhimurium* virulence protein is similar to a *Yersinia enterocolitica* invasion protein and a bacteriophage lambda outer membrane protein. *J. Bacteriol.* **173**:86–93.
1599. **Purcell, B. K., J. Pruckler, and S. Clegg.** 1987. Nucleotide sequences of the genes encoding type 1 fimbrial subunits of *Klebsiella pneumoniae* and *Salmonella typhimurium*. *J. Bacteriol.* **169**:5831–5834.
1600. **Quay, S., and H. N. Christensen.** 1974. Basis of transport discrimination of arginine from other basic amino acids in *Salmonella typhimurium*. *J. Biol. Chem.* **249**:7011–7017.
1601. **Quay, S. C., and D. L. Oxender.** 1980. Role of tRNA^{leu} in branched-chain amino acid transport. *Cold Spring Harbor Monogr. Ser.* **9B**:481–491.
1602. **Quay, S. C., D. L. Oxender, S. Tsuyumu, and H. E. Umbarger.** 1975. Separate regulation of transport and biosynthesis of leucine, isoleucine, and valine in bacteria. *J. Bacteriol.* **122**:994–1000.
1603. **Qureshi, M. A., D. A. Smith, and A. J. Kingsman.** 1975. Mutants of *Salmonella typhimurium* responding to cysteine or methionine: their nature and possible role in the regulation of cysteine biosynthesis. *J. Gen. Microbiol.* **89**:353–370.
1604. **Qureshi, N., K. Takayama, D. Heller, and C. Fenselau.** 1983. Position of ester groups in the lipid A backbone of lipopolysaccharides obtained from *Salmonella typhimurium*. *J. Biol. Chem.* **258**:12947–12951.
1605. **Raetz, C. R. H., S. Purcell, M. V. Meyer, N. Qureshi, and K. Takayama.** 1985. Isolation and characterization of eight lipid A precursors from a 3-deoxy-D-manno-oculosonic acid-deficient mutant of *Salmonella typhimurium*. *J. Biol. Chem.* **260**:16080–16088.
1606. **Raha, M., I. Kawagishi, V. Muller, M. Kihara, and R. M. Macnab.** 1992. *Escherichia coli* produces a cytoplasmic alpha-amylase, AmyA. *J. Bacteriol.* **174**:6644–6652.
1607. **Raha, M., M. Kihara, I. Kawagishi, and R. M. Macnab.** 1993. Organization of the *Escherichia coli* and *Salmonella typhimurium* chromosomes between flagellar regions IIIa and IIIb, including a large non-coding region. *J. Gen. Microbiol.* **139**:1401–1407.
1608. **Raha, M., H. Sockett, and R. M. Macnab.** 1994. Characterization of the *fliL* gene in the flagellar regulon of *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **176**:2308–2311.
1609. **Raju, K. K., D. M. Bedwell, and J. E. Brenchley.** 1980. Characterization of a HinD-III generated NDA fragment carrying the glutamine synthetase gene in *Salmonella typhimurium*. *Gene* **11**:227–238.
1610. **Rao, R., and M. G. Pereira.** 1975. Isolation of a hybrid F' factor-carrying *Escherichia coli* lactose region and *Salmonella typhimurium* histidine region, F42–400 (F'_{ts114} lac⁺, his⁺): its partial characterization and behavior in *Salmonella typhimurium*. *J. Bacteriol.* **123**:779–791.
1611. **Rao, R. N., and C. V. S. Rao.** 1973. *Salmonella typhimurium* mutants affecting establishment of lysogeny. *Mol. Gen. Genet.* **125**:119–123.
1612. **Rao, R. N., and H. O. Smith.** 1968. Phage P22 lysogens of a *Salmonella typhimurium* mutant deleted at the normal prophage attachment site. *Virology* **36**:328–330.
1613. **Ratzkin, B., M. Grabnar, and J. R. Roth.** 1978. Regulation of the major proline permease gene of *Salmonella typhimurium*. *J. Bacteriol.* **133**:737–743.
1614. **Ratzkin, B., and J. R. Roth.** 1978. Cluster of genes controlling proline degradation in *Salmonella typhimurium*. *J. Bacteriol.* **133**:744–754.
1615. **Ravdonikas, L. E.** 1976. Production and characteristics of *Salmonella typhimurium* glycerin

- mutants. *Zh. Mikrobiol. Epidemiol. Immunobiol.* **12**:29–32.
1616. **Ravid, S., and M. Eisenbach.** 1984. Direction of flagellar rotation in bacterial cell envelopes. *J. Bacteriol.* **158**:222–230.
1617. **Rayssiguier, C., C. Dohet, and M. Radman.** 1991. Interspecific recombination between *Escherichia coli* and *Salmonella typhimurium* occurs by the RecABCD pathway. *Biochimie* **73**:371–374.
1618. **Rayssiguier, C., D. S. Thaler, and M. Radman.** 1989. The barrier to recombination between *Escherichia coli* and *Salmonella typhimurium* is disrupted in mismatch-repair mutants. *Nature* (London) **342**:396–401.
1619. **Rechler, M. M., and C. B. Bruni.** 1971. Properties of a fused protein formed by genetic manipulation. *J. Biol. Chem.* **246**:1806–1813.
1620. **Reeve, C. A., A. T. Bockman, and A. Matin.** 1984. Role of protein degradation in the survival of carbon-starved *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **157**:758–763.
1621. **Reeves, P., and G. Stevenson.** 1989. Cloning and nucleotide sequence of the *Salmonella typhimurium* LT2 *gnd* gene and its homology with the corresponding sequence of *Escherichia coli* K12. *Mol. Gen. Genet.* **217**:182–184.
1622. **Reeves, R. H., and J. R. Roth.** 1971. A recessive UGA suppressor. *J. Mol. Biol.* **56**:523–533.
1623. **Reeves, R. H., and J. R. Roth.** 1975. Transfer ribonucleic acid methylase deficiency found in UGA suppressor strains. *J. Bacteriol.* **124**:332–340.
1624. **Reiners, J. J., Jr., and H. Zalkin.** 1975. Immunological study of anthranilate synthetase. *J. Bacteriol.* **123**:620–630.
1625. **Rephaeli, A. W., and M. H. Saier, Jr.** 1976. Effects of *crp* mutations on adenosine 3',5'-monophosphate metabolism in *Salmonella typhimurium*. *J. Bacteriol.* **127**:120–127.
1626. **Rephaeli, A. W., and M. H. Saier, Jr.** 1980. Regulation of genes coding for enzyme constituents of the bacterial phosphotransferase system. *J. Bacteriol.* **141**:658–663.
1627. **Reyes, G. R., and V. Rocha.** 1977. Immuno-chemical comparison of phosphoribosylanthranilate isomerase-indoleglycerol phosphate synthetase among the *Enterobacteriaceae*. *J. Bacteriol.* **129**:1448–1456.
1628. **Rhen, M., and S. Sukupolvi.** 1988. The role of the *traT* gene of the *Salmonella typhimurium* virulence plasmid for serum resistance and growth within liver macrophages. *Microb. Pathog.* **5**:275–285.
1629. **Ricca, E., and J. M. Calvo.** 1990. The nucleotide sequence of *leuA* from *Salmonella typhimurium*. *Nucleic Acids Res.* **18**:1290.
1630. **Ricca, E., C. T. Lago, M. Sacco, and M. De Felice.** 1991. Absence of acetohydroxy acid synthase III in *Salmonella typhimurium* is due to early termination of translation within the *ilvI* gene. *Mol. Microbiol.* **5**:1741–1743.
1631. **Richardson, S. M., C. F. Higgins, and D. M. Lilley.** 1988. DNA supercoiling and the *leu-500* promoter mutation of *Salmonella typhimurium*. *EMBO J.* **7**:1863–1869.
1632. **Richardson, S. M. H., C. F. Higgins, and D. M. J. Lilley.** 1984. The genetic control of DNA supercoiling in *Salmonella typhimurium*. *EMBO J.* **3**:1745–1752.
1633. **Richarme, G., A. el Yaagoubi, and M. Kohiyama.** 1993. The MglA component of the binding protein-dependent galactose transport system of *Salmonella typhimurium* is a galactose-stimulated ATPase. *J. Biol. Chem.* **268**:9473–9477.
1634. **Richter-Dahlfors, A. A., and D. I. Andersson.** 1992. Cobalamin (vitamin B12) repression of the Cob operon in *Salmonella typhimurium* requires sequences within the leader and the first translated open reading frame. *Mol. Microbiol.* **6**:743–749.
1635. **Rick, P. D., W.-M. Fung, C. Ho, and M. J. Osborn.** 1977. Lipid A mutants of *Salmonella typhimurium*. *J. Biol. Chem.* **252**:4902–4912.
1636. **Rick, P. D., B. A. Neumeyer, and D. A. Young.** 1983. Effect of altered lipid A synthesis on the synthesis of the OmpA protein in *Salmonella typhimurium*. *J. Biol. Chem.* **258**:629–635.
1637. **Rick, P. D., and M. J. Osborn.** 1972. Isolation of a mutant of *Salmonella typhimurium* dependent on D-arabinose-5-phosphate for growth and synthesis of 3-deoxy-D-mannoctulosonate

- (ketodeoxyoctonate). *Proc. Natl. Acad. Sci. USA* **69**:3756–3760.
1638. **Rick, P. D., and M. J. Osborn.** 1977. Lipid A mutants of *Salmonella typhimurium*. Characterization of a conditional lethal mutant in 3-deoxy-D-mannoctulosonate-8-phosphate synthetase. *J. Biol. Chem.* **252**:4895–4903.
1639. **Rick, P. D., S. Wolski, K. Barr, S. Ward, and L. Ramsey-Sharer.** 1988. Accumulation of a lipid-linked intermediate involved in enterobacterial common antigen synthesis in *Salmonella typhimurium* mutants lacking dTDP-glucose pyrophosphorylase. *J. Bacteriol.* **170**:4008–4014.
1640. **Rick, P. D., and D. A. Young.** 1982. Relationship between cell death and altered lipid A synthesis in a temperature-sensitive lethal mutant of *Salmonella typhimurium* that is conditionally defective in 3-deoxy-D-manno-octulosonate-8-phosphate synthesis. *J. Bacteriol.* **150**:456–464.
1641. **Rick, P. D., and D. A. Young.** 1982. Isolation and characterization of a temperature-sensitive lethal mutant of *Salmonella typhimurium* that is conditionally defective in 3-deoxy-D-manno-octulosonate-8-phosphate synthesis. *J. Bacteriol.* **150**:447–455.
1642. **Riddle, D. L., and J. Carbon.** 1972. Frameshift suppression: a nucleotide addition in the anticodon of a glycine transfer RNA. *Nature (London) New Biol.* **242**:230–234.
1643. **Riddle, D. L., and J. R. Roth.** 1972. Frameshift suppressors. III. Effects of suppressor mutations on transfer RNA. *J. Mol. Biol.* **66**:495–506.
1644. **Riddle, D. L., and J. R. Roth.** 1972. Frameshift suppressors. II. Genetic mapping and dominance studies. *J. Mol. Biol.* **66**:483–493.
1645. **Riggs, D., and S. Artz.** 1984. The *hisD-hisC* gene border of the *Salmonella typhimurium* histidine operon. *Mol. Gen. Genet.* **196**:526–529.
1646. **Riggs, D. L., and E. Barrett.** 1983. Role for thiosulfate reductase in the chlorate sensitivity of *Salmonella typhimurium*, abstr. K246, p. 218. *Abstr. Annu. Meet. Am. Soc. Microbiol., 1983.*
1647. **Riggs, D. L., R. D. Mueller, H.-S. Kwan, and S. W. Artz.** 1986. Promoter domain mediates guanosine tetraphosphate activation of the histidine operon. *Proc. Natl. Acad. Sci. USA* **83**:9333–9337.
1648. **Riley, M., C. O'Reilly, and D. McConnell.** 1983. Physical map of *Salmonella typhimurium* LT2 DNA in the vicinity of the *proA* gene. *J. Bacteriol.* **157**:655–657.
1649. **Rioux, C. R., M. J. Friedrich, and R. J. Kadner.** 1990. Genes on the 90-kilobase plasmid of *Salmonella typhimurium* confer low-affinity cobalamin transport: relationship to fimbria biosynthesis genes. *J. Bacteriol.* **172**:6217–6222.
1650. **Rioux, C. R., and R. J. Kadner.** 1989. Two outer membrane transport systems for vitamin B₁₂ in *Salmonella typhimurium*. *J. Bacteriol.* **171**:2986–2993.
1651. **Ritchie, L. J., R. M. Hall, and D. M. Podger.** 1986. Mutant of *Salmonella typhimurium* LT2 deficient in DNA adenine methylation. *J. Bacteriol.* **167**:420–422.
1652. **Rivera, M., A. Bertasso, C. McCaffrey, and N. H. Georgopapadakou.** 1993. Porins and lipopolysaccharide of *Escherichia coli* ATCC 25922 and isogenic rough mutants. *FEMS Microbiol. Lett.* **108**:183–187.
1653. **Rizzino, A., M. Mastanduno, and M. Freundlich.** 1977. Partial derepression of the isoleucine-valine enzymes during methionine starvation in *Salmonella typhimurium*. *Biochim. Biophys. Acta* **475**:267–275.
1654. **Rizzino, A. A., R. S. Bresalier, and M. Freundlich.** 1974. Derepressed levels of the isoleucine-valine and leucine enzymes in *hisT1504*. *J. Bacteriol.* **117**:449–455.
1655. **Roberts, J. H., and A. P. Levin.** 1972. Normal synthesis of aminotransferase protein in a pyridoxineless strain of *S. typhimurium*. *Biochem. Biophys. Res. Commun.* **48**:802–807.
1656. **Roberts, J. H., and A. P. Levin.** 1973. Imidazolylacetol phosphate aminotransferase. Properties of the apoprotein produced in a pyridoxine auxotroph of *Salmonella typhimurium*. *J. Biol. Chem.* **248**:7748–7753.
1657. **Roberts, J. H., D. R. McCarroll, and A. P. Levin.** 1975. Properties of the imidazolylacetol phosphate aminotransferase produced in a mutant demonstrating no apparent genetic involvement of the structural gene. *J. Bacteriol.* **123**:233–241.
1658. **Robertson, B. C., and P. A. Hoffee.** 1973. Purification and properties of purine nucleoside

- phosphorylase from *Salmonella typhimurium*. *J. Biol. Chem.* **148**:2040–2043.
1659. **Robertson, B. C., P. Jargiello, J. Blank, and P. A. Hoffee.** 1970. Genetic regulation of ribonucleoside and deoxyribonucleoside catabolism in *Salmonella typhimurium*. *J. Bacteriol.* **102**:628–635.
1660. **Robinson, P. B., and H. R. Levy.** 1976. Metal ion requirement and tryptophan inhibition of normal and variant anthranilate synthase-anthranilate 5-phosphoribosylpyrophosphate. *Biochim. Biophys. Acta* **445**:475–485.
1661. **Robison, K., W. Gilbert, and G. M. Church.** 1994. Large scale bacterial gene discovery by similarity search. *Nat. Genet.* **7**:205–214.
1662. **Rodriguez, S. B., and J. L. Ingraham.** 1983. Location on the *Salmonella typhimurium* chromosome of the gene encoding nucleoside diphosphokinase (*ndk*). *J. Bacteriol.* **153**:1101–1103.
1663. **Rodriguez Lemoine, V., and R. J. Rowbury.** 1975. Instability of the *Flac*⁺ factor in a *dnaC* mutant of *Salmonella typhimurium*. *J. Gen. Microbiol.* **90**:360–364.
1664. **Roland, K. L., C. R. Esther, and J. K. Spitznagel.** 1994. Isolation and characterization of a gene, *pmrD*, from *Salmonella typhimurium* that confers resistance to polymyxin when expressed in multiple copies. *J. Bacteriol.* **176**:3589–3597.
1665. **Roland, K. L., L. E. Martin, C. R. Esther, and J. K. Spitznagel.** 1993. Spontaneous *pmrA* mutants of *Salmonella typhimurium* LT2 define a new two-component regulatory system with a possible role in virulence. *J. Bacteriol.* **175**:4154–4164.
1666. **Romana, L. K., F. S. Santiago, and P. R. Reeves.** 1991. High level expression and purification of thymidine diphospho-D-glucose 4,6-dehydratase (*rfbB*) from *Salmonella* serovar *typhimurium* LT2. *Biochem. Biophys. Res. Commun.* **174**:846–852.
1667. **Romeo, T., and J. Moore.** 1991. Comparison of the 5' flanking regions of the *Salmonella typhimurium* and *Escherichia coli glgC* genes, encoding ADP glucose pyrophosphorylases. *Nucleic Acids Res.* **19**:3452.
1668. **Ron, E. A.** 1975. Growth rate of *Enterobacteriaceae* at elevated temperatures: limitation by methionine. *J. Bacteriol.* **124**:243–246.
1669. **Rondon, M. R., and J. C. Escalante-Semerena.** 1992. The *poc* locus is required for 1,2-propanediol-dependent transcription of the cobalamin biosynthetic (*cob*) and propanediol utilization (*pdu*) genes of *Salmonella typhimurium*. *J. Bacteriol.* **174**:2267–2272.
1670. **Roof, D. M., and J. R. Roth.** 1988. Ethanolamine utilization in *Salmonella typhimurium*. *J. Bacteriol.* **170**:3855–3863.
1671. **Roof, D. M., and J. R. Roth.** 1989. Functions required for vitamin B₁₂-dependent ethanolamine utilization in *Salmonella typhimurium*. *J. Bacteriol.* **171**:3316–3323.
1672. **Roof, D. M., and J. R. Roth.** 1992. Autogenous regulation of ethanolamine utilization by a transcriptional activator of the *eut* operon in *Salmonella typhimurium*. *J. Bacteriol.* **174**:6634–6643.
1673. **Roseman, S., and N. D. Meadow.** 1990. Signal transduction by the bacterial phosphotransferase system. Diauxie and the *crr* gene (J. Monod revisited). *J. Biol. Chem.* **265**:2993–2996.
1674. **Rosenfeld, S. A., and J. E. Brenchley.** 1980. Regulation of nitrogen utilization in *hisT* mutants of *Salmonella typhimurium*. *J. Bacteriol.* **143**:801–808.
1675. **Rosenfeld, S. A., S. M. Dendinger, C. H. Murphy, and J. E. Brenchley.** 1982. Genetic characterization of the glutamate dehydrogenase gene (*gdhA*) of *Salmonella typhimurium*. *J. Bacteriol.* **150**:795–803.
1676. **Rosenthal, E. R., and J. M. Calvo.** 1987. Transcription termination sites at the distal end of the *leu* operon of *Salmonella typhimurium*. *J. Mol. Biol.* **194**:443–452.
1677. **Rosenthal, E. R., and J. M. Calvo.** 1990. The nucleotide sequence of *leuC* from *Salmonella typhimurium*. *Nucleic Acids Res.* **18**:3072.
1678. **Roth, J. R., and B. N. Ames.** 1966. Histidine regulatory mutants in *Salmonella typhimurium*. II. Histidine regulatory mutants having altered histidyl-tRNA synthetase. *J. Mol. Biol.* **22**:325–334.
1679. **Roth, J. R., D. N. Anton, and P. E. Hartman.** 1966. Histidine regulatory mutants in *Salmonella typhimurium*. I. Isolation and general properties. *J. Mol. Biol.* **22**:305–323.
1680. **Roth, J. R., and P. E. Hartman.** 1965. Heterogeneity in P22 transducing particles. *Virology*

- 27:297–307.
1681. **Roth, J. R., J. G. Lawrence, M. Rubenfield, S. Kieffer-Higgins, and G. M. Church.** 1993. Characterization of the cobalamin (vitamin B₁₂) biosynthetic genes of *Salmonella typhimurium*. *J. Bacteriol.* **175**:3303–3316.
1682. **Rothman-Denes, L., and R. G. Martin.** 1971. Two mutations in the first gene of the histidine operon of *Salmonella typhimurium* affecting control. *J. Bacteriol.* **106**:227–237.
1683. **Rowbury, R. J.** 1964. Synthesis of cystathionine and its control in *Salmonella typhimurium*. *Nature (London)* **203**:977–978.
1684. **Rowbury, R. J.** 1964. The accumulation of O-succinylhomoserine by *Escherichia coli* and *Salmonella typhimurium*. *J. Gen. Microbiol.* **37**:171–180.
1685. **Rowbury, R. J., D. A. Lawrence, and D. A. Smith.** 1968. Regulation of the methionine-specific aspartokinase and homoserine dehydrogenase of *Salmonella typhimurium*. *J. Gen. Microbiol.* **54**:337–342.
1686. **Rowen, L., J. A. Kabori, and S. Scherer.** 1982. Cloning of bacterial DNA replication genes. *Mol. Gen. Genet.* **187**:501–509.
1687. **Roy, A. M., and J. Coleman.** 1994. Mutations in *firA*, encoding the second acyltransferase in lipopolysaccharide biosynthesis, affect multiple steps in lipopolysaccharide biosynthesis. *J. Bacteriol.* **176**:1639–1646.
1688. **Roy, S., and M. Chakravorty.** 1986. Spontaneous deletions of drug-resistance determinants from *Salmonella typhimurium* in *Escherichia coli*. *J. Med. Microbiol.* **22**:119–123.
1689. **Rudd, K., and J. R. Roth.** 1983. Further studies on the role of ppGpp in the control of the *his* operon of *Salmonella*, abstr. H163, p. 112. *Abstr. Annu. Meet. Am. Soc. Microbiol., 1983.*
1690. **Rudd, K. E.** 1993. Maps, genes, sequences, and computers: an *Escherichia coli* case study. *ASM News* **59**:335–341.
1691. **Rudd, K. E., B. R. Bochner, M. Cashel, and J. R. Roth.** 1985. Mutations in the *spoT* gene of *Salmonella typhimurium*: effects of *his* operon expression. *J. Bacteriol.* **163**:534–542.
1692. **Rudd, K. E., and R. Menzel.** 1987. *his* operons of *Escherichia coli* and *Salmonella typhimurium* are regulated by DNA supercoiling. *Proc. Natl. Acad. Sci. USA* **84**:517–521.
1693. **Ruijter, G. J., P. W. Postma, and K. van Dam.** 1990. Adaptation of *Salmonella typhimurium* mutants containing uncoupled enzyme IIGlc to glucose-limited conditions. *J. Bacteriol.* **172**:4783–4789.
1694. **Ruijter, G. J., P. W. Postma, and K. van Dam.** 1991. Energetics of glucose uptake in a *Salmonella typhimurium* mutant containing uncoupled enzyme IIGlc. *Arch. Microbiol.* **155**:234–237.
1695. **Ruiz-Vazquez, R., C. Pueyo, and E. Cerda-Olmedo.** 1978. A mutagen assay detecting forward mutations in an arabinose-sensitive strain of *Salmonella typhimurium*. *Mutat. Res.* **54**:121–130.
1696. **Rundell, K., and C. W. Shuster.** 1973. Membrane-associated nucleotide sugar reactions. I. Properties of the first enzyme of O antigen synthesis. *J. Biol. Chem.* **248**:5436–5442.
1697. **Rundell, K., and C. W. Shuster.** 1975. Membrane-associated nucleotide sugar reactions: influence of mutations affecting lipopolysaccharide of the first enzyme of O-antigen synthesis. *J. Bacteriol.* **123**:928–936.
1698. **Russo, A. F., and D. E. Koshland, Jr.** 1983. Separation of signal transduction and adaptation functions of the aspartate receptor in bacterial sensing. *Science* **220**:1016–1020.
1699. **Russo, A. F., and D. E. Koshland, Jr.** 1986. Identification of the tip-encoded receptor in bacterial sensing. *J. Bacteriol.* **165**:276–282.
1700. **Sabe, H., T. Miwa, T. Kodaki, K. Izui, S. Hiraga, and H. Katsuki.** 1984. Molecular cloning of the phosphoenolpyruvate carboxylase gene, *ppc*, of *Escherichia coli*. *Gene* **31**:279–283.
1701. **Saier, M. H., Jr.** 1977. Bacterial phosphoenolpyruvate:sugar phosphotransferase systems: structural, functional, and evolutionary interrelationships. *Bacteriol. Rev.* **41**:856–871.
1702. **Saier, M. H., Jr., F. R. Bromberg, and S. Roseman.** 1973. Characterization of constitutive galactose permease mutants in *Salmonella typhimurium*. *J. Bacteriol.* **113**:512–514.
1703. **Saier, M. H., Jr., and B. U. Feucht.** 1976. Coordinate regulation of adenylate cyclase and carbohydrate permeases by the phosphoenolpyruvate:sugar phosphotransferase system in *Salmonella typhimurium*. *J. Biol. Chem.* **250**:7078–7080.

1704. **Saier, M. H., Jr., B. U. Feucht, and M. T. McCaman.** 1975. Regulation of intracellular adenosine cyclic 3'5'-monophosphate levels in *Escherichia coli* and *Salmonella typhimurium*. *J. Biol. Chem.* **250**:7593–7601.
1705. **Saier, M. H., Jr., B. U. Feucht, and W. K. Mora.** 1977. Sugar phosphate:sugar transphosphorylation and exchange group translocation catalyzed by the enzyme II complexes of the bacterial phosphoenolpyruvate:sugar phosphotransferase system. *J. Biol. Chem.* **252**:8899–8907.
1706. **Saier, M. H., Jr., F. C. Grenier, C. A. Lee, and E. B. Waygood.** 1985. Evidence for the evolutionary relatedness of the proteins of the bacterial phosphoenolpyruvate:sugar phosphotransferase system. *J. Cell. Biochem.* **27**:43–56.
1707. **Saier, M. H., Jr., M. J. Novotny, D. Comeau-Fuhrman, T. Osumi, and J. D. Desai.** 1983. Cooperative binding of the sugar substrates and allosteric regulatory protein (enzyme III^{Glc} of the phosphotransferase system) to the lactose and melibiose permeases in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **155**:1351–1357.
1708. **Saier, M. H., Jr., and S. Roseman.** 1972. Inducer exclusion and repression of enzyme synthesis in mutants of *Salmonella typhimurium* defective in enzyme I of the phosphoenolpyruvate:sugar phosphotransferase system. *J. Biol. Chem.* **247**:972–975.
1709. **Saier, M. H., Jr., and S. Roseman.** 1976. Sugar transport. Inducer exclusion and regulation of the melibiose, maltose, glycerol, and lactose transport systems by the phosphoenolpyruvate:sugar phosphotransferase system. *J. Biol. Chem.* **251**:6606–6615.
1710. **Saier, M. H., Jr., M. R. Schmidt, and M. Leibowitz.** 1978. Cyclic AMP-dependent synthesis of fimbriae in *Salmonella typhimurium*: effects of *cya pts* mutations. *J. Bacteriol.* **134**:356–358.
1711. **Saier, M. H., Jr., B. D. Simoni, and S. Roseman.** 1976. Sugar transport. Properties of mutant bacteria defective in proteins of the phosphoenolpyruvate:sugar phosphotransferase system. *J. Biol. Chem.* **251**:6584–6597.
1712. **Saier, M. H., Jr., H. Straud, L. S. Massman, J. J. Judice, M. H. Newman, and B. U. Feucht.** 1978. Permease-specific mutations in *Salmonella typhimurium* and *Escherichia coli* that release the glycerol, maltose, melibiose, and lactose transport systems from regulation by the phosphoenolpyruvate:sugar phosphotransferase system. *J. Bacteriol.* **133**:1358–1367.
1713. **Saier, M. H., Jr., D. L. Wentzel, B. U. Feucht, and J. J. Judice.** 1975. A transport system for phosphoenolpyruvate, 2-phosphoglycerate, and 3-phosphoglycerate in *Salmonella typhimurium*. *J. Biol. Chem.* **250**:5089–5096.
1714. **Sales, M., and J. E. Brenchley.** 1982. The regulation of the ammonia assimilatory enzymes in Rel⁺ and Rel⁻ strains of *Salmonella typhimurium*. *Mol. Gen. Genet.* **186**:263–268.
1715. **Sanderson, K. E., and M. Demerec.** 1965. The linkage map of *Salmonella typhimurium*. *Genetics* **51**:897–913.
1716. **Sanderson, K. E., and C. A. Hall.** 1970. F-prime factors of *Salmonella typhimurium* and an inversion between *Salmonella typhimurium* and *Escherichia coli*. *Genetics* **64**:215–228.
1717. **Sanderson, K. E., A. Hessel, and K. E. Rudd.** 1995. Genetic map of *Salmonella typhimurium*, edition VIII. *Microbiol. Rev.* **59**:241–303.
1718. **Sanderson, K. E., and J. A. Hurley.** 1987. Linkage map of *Salmonella typhimurium*, p. 877–918. In F. C. Neidhardt, J. L. Ingraham, K. B. Low, B. Magasanik, M. Schaechter, and H. E. Umbarger (ed.), *Escherichia coli and Salmonella typhimurium: Cellular and Molecular Biology*. American Society for Microbiology, Washington, D.C.
1719. **Sanderson, K. E., J. Janzer, and J. Head.** 1981. Influence of lipopolysaccharide and protein in the cell envelope on recipient capacity in conjunction of *Salmonella typhimurium*. *J. Bacteriol.* **148**:283–293.
1720. **Sanderson, K. E., S. K. Kadam, and P. R. MacLachlan.** 1983. Derepression of F factor function in *Salmonella typhimurium*. *Can. J. Microbiol.* **29**:1205–1212.
1721. **Sanderson, K. E., and J. R. Roth.** 1988. Linkage map of *Salmonella typhimurium*, edition VII. *Microbiol. Rev.* **52**:485–532.
1722. **Sanderson, K. E., and Y. A. Saeed.** 1972. Insertion of the F-factor into a cluster of *rfa* (rough A) genes of *Salmonella typhimurium*. *J. Bacteriol.* **112**:64–73.

1723. **Sanderson, K. E., and Y. A. Saeed.** 1972. P22-mediated transduction analysis of the rough A (*rfa*) region of the chromosome of *Salmonella typhimurium*. *J. Bacteriol.* **112**:58–63.
1724. **Sanderson, K. E., P. Sciore, S.-L. Liu, and A. Hessel.** 1993. Location of IS200 on the genomic cleavage map of *Salmonella typhimurium* LT2. *J. Bacteriol.* **175**:7624–7628.
1725. **Sanderson, K. E., and B. A. D. Stocker.** 1981. Gene *rfaH*, which affects lipopolysaccharide core structure in *Salmonella typhimurium*, is also required for expression of F-factor functions. *J. Bacteriol.* **146**:535–541.
1726. **Sandler, S. J., B. Chackerian, J. T. Li, and A. J. Clark.** 1992. Sequence and complementation analysis of *recF* genes from *Escherichia coli*, *Salmonella typhimurium*, *Pseudomonas putida* and *Bacillus subtilis*: evidence for an essential phosphate binding loop. *Nucleic Acids Res.* **20**:839–845.
1727. **Sankaran, K., and H. C. Wu.** 1994. Lipid modification of bacterial prolipoprotein. Transfer of diacylglyceryl moiety from phosphatidylglycerol. *J. Biol. Chem.* **269**:19701–19706.
1728. **Sarno, M. V., L. G. Tenn, A. Desai, A. M. Chin, F. C. Grenier, and M. H. Saier, Jr.** 1984. Genetic evidence for glucitol-specific enzyme III, an essential phosphocarrier protein of the *Salmonella typhimurium* glucitol phosphotransferase system. *J. Bacteriol.* **157**:953–955.
1729. **Sarvas, M.** 1967. Inheritance of *Salmonella* T1 antigen. *Ann. Med. Exp. Biol. Fenn.* **45**:447–471.
1730. **Sarvas, M., M. Malinen, M. Nurminen, and P. H. Makela.** 1976. T-2 lipopolysaccharide antigen of *Salmonella*. Comparison of the properties of T-2 and mucoid forms. *Infect. Immun.* **14**:839–842.
1731. **Sasarman, A., and M. Desrochers.** 1976. Uroporphyrinogen III cosynthase-deficient mutant of *Salmonella typhimurium* LT2. *J. Bacteriol.* **128**:717–721.
1732. **Sasarman, A., M. Desrochers, S. Sonea, K. E. Sanderson, and M. Surdenu.** 1976. Porphobilinogen-accumulating mutants of *Salmonella typhimurium*. *J. Gen. Microbiol.* **94**:359–366.
1733. **Sasarman, A., K. E. Sanderson, M. Surdenu, and S. Sonea.** 1970. Hemin-deficient mutants of *Salmonella typhimurium*. *J. Bacteriol.* **102**:531–536.
1734. **Sato, T., and T. Yura.** 1979. Chromosomal location and expression of the structural gene for major outer membrane protein Ia of *Escherichia coli* K-12 and of the homologous gene of *Salmonella typhimurium*. *J. Bacteriol.* **139**:468–477.
1735. **Savin, M. A., M. Flavin, and C. Slaughter.** 1972. Regulations of homocysteine biosynthesis in *Salmonella typhimurium*. *J. Bacteriol.* **111**:547–556.
1736. **Sawicka, T., and M. Bagdasarian.** 1976. Temperature sensitive carbon-14 galactose uptake by a division of *Salmonella typhimurium*. *Bull. Acad. Pol. Sci. Ser. Sci. Biol.* **24**:441–444.
1737. **Sawyer, M. E., and F. B. Armstrong.** 1970. Order of the *ilv* genes of *Salmonella montevideo*. *Mol. Gen. Genet.* **109**:370–372.
1738. **Scaife, J. G., J. S. Heilig, L. Rowen, and R. Calendar.** 1979. Gene for the RNA polymerase σ subunit mapped in *Salmonella typhimurium* and *Escherichia coli* by cloning and deletion. *Proc. Natl. Acad. Sci. USA* **76**:6510–6514.
1739. **Scapin, G., J. C. Sacchettini, A. Dessen, M. Bhatia, and C. Grubmeyer.** 1993. Primary structure and crystallization of orotate phosphoribosyltransferase from *Salmonella typhimurium*. *J. Mol. Biol.* **230**:1304–1308.
1740. **Schafer, M. P., W. H. Hannon, and A. P. Levin.** 1974. In vivo and in vitro complementation between *guaB* and in vivo complementation between *guaA* auxotrophs of *Salmonella typhimurium*. *J. Bacteriol.* **117**:1270–1279.
1741. **Schafer, R., and T. K. Eisenstein.** 1992. Natural killer cells mediate protection induced by a *Salmonella aroA* mutant. *Infect. Immun.* **60**:791–797.
1742. **Schlecht, S., E. Ferber, and I. Fromme.** 1979. The fatty acid composition of lipids from *Salmonella typhimurium* S and R forms. *Zentralbl. Bakteriол. Parasitenkd. Infektionskr. Hyg. Abt. 1 Orig. Reihe A* **245**:476–484.
1743. **Schlecht, S., and I. Fromme.** 1980. Growth of *Salmonella typhimurium* R-mutants in submerged cultures. 2. Influence of growth phases on the lipopolysaccharide content of the bacteria and on the chemical composition and serological behavior of the lipopolysaccharides. *Zentralbl. Bakteriол. Parasitenkd. Infektionskr. Hyg. Abt. 1 Orig. Reihe A* **248**:352–367.

1744. **Slecht, S., I. Fromme, E. Ferber, W. Meuller, and J. Gmeiner.** 1980. Chemische und biologische Eigenschaften von Revertanten aus einer *Salmonella typhimurium* Rd₁-Mutante. *Zentralbl. Bakteriol. Parasitenkd. Infektionskr. Hyg. Abt. 1 Orig. Reihe A* **247**:50–63.
1745. **Schleibinger, H., C. Leberl, and H. Ruden.** 1989. Nitrated polycyclic aromatic hydrocarbons (nitro-PAH) in the suspended substances of the atmosphere. 2. Comparison of the mutagenicity of nitro-PAH and dust extracts of the air in the Ames, SOS repair induction and SCE test. *Zentralbl. Hyg. Umweltmed.* **188**:421–438. (In German.)
1746. **Schlesinger, M. J., and R. Olsen.** 1968. Expression and localization of *Escherichia coli* alkaline phosphatase synthesized in *Salmonella typhimurium* cytoplasm. *J. Bacteriol.* **96**:1601–1605.
1747. **Schloss, J. V., D. E. Van Dyk, J. F. Vasta, and R. M. Kutny.** 1985. Purification and properties of *Salmonella typhimurium* acetolactate synthase isozyme II from *Escherichia coli* HB101/pDU9. *Biochemistry* **24**:4952–4959.
1748. **Schmid, M., and J. R. Roth.** 1980. Circularization of transduced fragments: a mechanism for adding segments to the bacterial chromosome. *Genetics* **94**:15–30.
1749. **Schmid, M. B.** 1990. A locus affecting nucleoid segregation in *Salmonella typhimurium*. *J. Bacteriol.* **172**:5416–5424.
1750. **Schmid, M. B., N. Kapur, D. R. Isaacson, P. Lindroos, and C. Sharpe.** 1989. Genetic analysis of temperature-sensitive lethal mutants of *Salmonella typhimurium*. *Genetics* **123**:625–633.
1751. **Schmid, M. B., and J. R. Roth.** 1987. Gene location affects expression level in *Salmonella typhimurium*. *J. Bacteriol.* **169**:2872–2875.
1752. **Schmid, M. B., and J. A. Sawitzke.** 1993. Multiple bacterial topoisomerases: specialization or redundancy? *Bioessays* **15**:445–449.
1753. **Schmidt, C., and H. Schmieger.** 1984. Selective transduction of recombinant plasmids with cloned *pac* sites by *Salmonella* phage P22. *Mol. Gen. Genet.* **196**:123–128.
1754. **Schmitt, C. K., S. C. Darnell, V. L. Tesh, B. A. Stocker, and A. D. O'Brien.** 1994. Mutation of *flgM* attenuates virulence of *Salmonella typhimurium*, and mutation of *fliA* represses the attenuated phenotype. *J. Bacteriol.* **176**:368–377.
1755. **Schmitz, G., P. Durre, G. Mullenbach, and G. F.-L. Ames.** 1987. Nitrogen regulation of transport operons: analysis of promoters *argTr* and *dhuA*. *Mol. Gen. Genet.* **209**:403–407.
1756. **Schmitz, G., K. Nikaido, and G. F. Ames.** 1988. Regulation of a transport operon promoter in *Salmonella typhimurium*: identification of sites essential for nitrogen regulation. *Mol. Gen. Genet.* **215**:107–117.
1757. **Schnaitman, C. A., and J. D. Klena.** 1993. Genetics of lipopolysaccharide biosynthesis in enteric bacteria. *Microbiol. Rev.* **57**:655–682.
1758. **Schnaitman, C. A., C. T. Parker, J. D. Klena, E. L. Pradel, N. B. Pearson, K. E. Sanderson, and P. R. MacLachlan.** 1991. Physical maps of the *rfa* loci of *Escherichia coli* K-12 and *Salmonella typhimurium*. *J. Bacteriol.* **173**:7410–7411.
1759. **Schneider, E., E. Francoz, and E. Dassa.** 1992. Completion of the nucleotide sequence of the “maltose B” region in *Salmonella typhimurium*: the high conservation of the *malM* gene suggests a selected physiological role for its product. *Biochim. Biophys. Acta* **1129**:223–227.
1760. **Schneider, E., and C. Walter.** 1991. A chimeric nucleotide-binding protein, encoded by a *hisP-malK* hybrid gene, is functional in maltose transport in *Salmonella typhimurium*. *Mol. Microbiol.* **5**:1375–1383.
1761. **Schneider, W. P., B. P. Nichols, and C. Yanofsky.** 1981. Procedure for production of hybrid genes and proteins and its use in assessing significance of amino acid differences in homologous tryptophan synthetase α polypeptides. *Proc. Natl. Acad. Sci. USA* **78**:2169–2173.
1762. **Schnierow, B. J., M. Yamada, and M. H. Saier, Jr.** 1989. Partial nucleotide sequence of the *pts* operon in *Salmonella typhimurium*: comparative analyses in five bacterial genera. *Mol. Microbiol.* **3**:113–118.
1763. **Scholte, B. J., and P. W. Postma.** 1980. Mutation in the *crp* gene of *Salmonella typhimurium* which interferes with inducer exclusion. *J. Bacteriol.* **141**:751–757.
1764. **Scholte, B. J., and P. W. Postma.** 1981. Competition between two pathways for sugar uptake by

- the phosphoenolpyruvate-dependent sugar phosphotransferase system in *Salmonella typhimurium*. *Eur. J. Biochem.* **114**:51–58.
1765. **Scholte, B. J., A. R. Schuitema, and P. W. Postma.** 1981. Isolation of III^{Glc} of the phosphoenolpyruvate-dependent glucose phosphotransferase system of *Salmonella typhimurium*. *J. Bacteriol.* **148**:257–264.
1766. **Scholte, B. J., A. R. J. Schuitema, and P. W. Postma.** 1982. Characterization of factor III^{Glc} in catabolite repression-resistant *crr* mutants of *Salmonella typhimurium*. *J. Bacteriol.* **149**:576–586.
1767. **Schroeder, C. J., and W. J. Dobrogosz.** 1986. Cloning and DNA sequence analysis of the wild-type and mutant cyclic AMP receptor protein genes from *Salmonella typhimurium*. *J. Bacteriol.* **167**:616–622.
1768. **Schulte, L. L., L. T. Stauffer, and G. V. Stauffer.** 1984. Cloning and characterization of the *Salmonella typhimurium metE* gene. *J. Bacteriol.* **158**:928–933.
1769. **Schumann, W., and E. G. Bade.** 1977. A *Salmonella typhimurium* endonuclease that converts native DNA to fragments of about 800,000 daltons. *J. Gen. Microbiol.* **101**:319–326.
1770. **Schwartz, M., and J. Neuhard.** 1975. Control of expression of the *pyr* genes in *Salmonella typhimurium*: effects of variations in uridine and cytidine nucleotide pools. *J. Bacteriol.* **121**:814–822.
1771. **Scott, J. F., J. R. Roth, and S. W. Artz.** 1975. Regulation of histidine operon does not require *hisG* enzyme. *Proc. Natl. Acad. Sci. USA* **72**:5021–5025.
1772. **Scott, T. N., and M. I. Simon.** 1982. Genetic analysis of the mechanism of the *Salmonella* phase variation site specific recombination system. *Mol. Gen. Genet.* **188**:313–321.
1773. **Searles, L. L., S. R. Wessler, and J. M. Calvo.** 1983. Transcription attenuation is the major mechanism by which the *leu* operon of *Salmonella typhimurium* is controlled. *J. Mol. Biol.* **163**:377–394.
1774. **Sedgwick, S. G., C. Ho, and R. Woodgate.** 1991. Mutagenic DNA repair in enterobacteria. *J. Bacteriol.* **173**:5604–5611.
1775. **Selker, E., and C. Yanofsky.** 1979. Nucleotide sequence of the *trpC-trpB* intercistronic region from *Salmonella typhimurium*. *J. Mol. Biol.* **130**:135–143.
1776. **Servos, S., S. Chatfield, D. Hone, M. Levine, G. Dimitriadis, D. Pickard, G. Dougan, N. Fairweather, and I. Charles.** 1991. Molecular cloning and characterization of the *aroD* gene encoding 3-dehydroquinase from *Salmonella typhi*. *J. Gen. Microbiol.* **137**:147–152.
1777. **Shaltiel, S., G. B. Henderson, and E. E. Snell.** 1974. Specific ion effects in affinity chromatography. The case of L-histidinolphosphate aminotransferase. *Biochemistry* **13**:4330–4335.
1778. **Shamanna, D. K., and K. E. Sanderson.** 1979. Genetics and regulation of D-xylose utilization in *Salmonella typhimurium* LT2. *J. Bacteriol.* **139**:71–79.
1779. **Shamanna, D. K., and K. E. Sanderson.** 1979. Uptake and catabolism of D-xylose in *Salmonella typhimurium* LT2. *J. Bacteriol.* **139**:64–70.
1780. **Shanabruch, W. G., I. Behlau, and G. C. Walker.** 1981. Spontaneous mutators of *Salmonella typhimurium* LT2 generated by insertion of transposable elements. *J. Bacteriol.* **147**:827–835.
1781. **Shanabruch, W. G., R. P. Rein, I. Beglau, and G. C. Walker.** 1983. Mutagenesis, by methylating and ethylating agents, in *mutH*, *mutS*, and *uvrD* mutants of *Salmonella typhimurium*. *J. Bacteriol.* **153**:33–44.
1782. **Shand, R. F., P. H. Blum, D. L. Holzschu, M. S. Urdea, and S. W. Artz.** 1989. Mutational analysis of the histidine operon promoter of *Salmonella typhimurium*. *J. Bacteriol.* **171**:6330–6337.
1783. **Shand, R. F., P. H. Blum, R. D. Mueller, D. L. Riggs, and S. W. Artz.** 1989. Correlation between histidine operon expression and guanosine 5'-diphosphate-3'-diphosphate levels during amino acid downshift in stringent and relaxed strains of *Salmonella typhimurium*. *J. Bacteriol.* **171**:737–742.
1784. **Shanmugam, K. T., V. Stewart, R. P. Gunsalus, D. H. Boxer, J. A. Cole, M. Chippaux, J. A. DeMoss, G. Giordano, E. C. Lin, and K. V. Rajagopalan.** 1992. Proposed nomenclature for the genes involved in molybdenum metabolism in *Escherichia coli* and *Salmonella typhimurium*. *Mol. Microbiol.* **6**:3452–3454. (Letter.)
1785. **Shannon, K. P., and R. J. Rowbury.** 1972. Alternation in the rate of cell division independent

- of the rate of DNA synthesis in a mutant of *Salmonella typhimurium*. *Mol. Gen. Genet.* **115**:122–125.
1786. **Shannon, K. P., B. G. Spratt, and R. J. Rowbury.** 1972. Cell division and the production of cells lacking nuclear bodies in a mutant of *Salmonella typhimurium*. *Mol. Gen. Genet.* **118**:185–197.
1787. **Sharp, P. M., J. E. Kelleher, A. S. Daniel, G. M. Cowan, and N. E. Murray.** 1992. Roles of selection and recombination in the evolution of type I restriction-modification systems in enterobacteria. *Proc. Natl. Acad. Sci. USA* **89**:9836–9840.
1788. **Sharp, P. M., D. C. Shields, K. H. Wolfe, and W. H. Li.** 1989. Chromosomal location and evolutionary rate variation in enterobacterial genes. *Science* **246**:808–810.
1789. **Shaw, K. J., and C. M. Berg.** 1980. Substrate channeling: α -ketobutyrate inhibition of acetohydroxy acid synthase in *Salmonella typhimurium*. *J. Bacteriol.* **143**:1509–1512.
1790. **Shaw, K. J., C. M. Berg, and T. J. Sobol.** 1980. *Salmonella typhimurium* mutants defective in acetohydroxy acid synthases I and II. *J. Bacteriol.* **141**:1258–1263.
1791. **Shaw, N. A., and P. D. Ayling.** 1991. Cloning of high-affinity methionine transport genes from *Salmonella typhimurium*. *FEMS Microbiol. Lett.* **62**:127–131.
1792. **Shematek, E. M., S. M. Arfin, and W. F. Diven.** 1973. A kinetic study of α -acetohydroxy acid isomerase from *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **158**:132–138.
1793. **Shematek, E. M., W. F. Diven, and S. N. Arfin.** 1973. Subunit structure of α -acetohydroxy acid isomerase from *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **158**:126–131.
1794. **Sheppard, D. E., and J. R. Roth.** 1994. A rationale for autoinduction of a transcriptional activator: ethanolamine ammonia-lyase (EutBC) and the operon activator (EutR) compete for adenosyl-cobalamin in *Salmonella typhimurium*. *J. Bacteriol.* **176**:1287–1296.
1795. **Shimamoto, T., H. Izawa, H. Daimon, N. Ishiguro, M. Shinagawa, Y. Sakano, M. Tsuda, and T. Tsuchiya.** 1991. Cloning and nucleotide sequence of the gene (*citA*) encoding a citrate carrier from *Salmonella typhimurium*. *J. Biochem. (Tokyo)* **110**:22–28.
1796. **Shirakihara, Y., and T. Wakabayashi.** 1979. Three-dimensional reconstruction of straight flagella from a mutant of *Salmonella typhimurium*. *J. Mol. Biol.* **131**:485–507.
1797. **Shiuan, D., and A. Campbell.** 1988. Transcriptional regulation and gene arrangement of *Escherichia coli*, *Citrobacter freundii* and *Salmonella typhimurium* biotin operons. *Gene* **67**:203–211.
1798. **Shuster, C. W., and K. Rundell.** 1969. Resistance of *Salmonella typhimurium* mutants to galactose death. *J. Bacteriol.* **100**:103–109.
1799. **Siitonen, A., V. Johansson, M. Nurminen, and P. H. Makela.** 1977. *Salmonella* bacteriophages that use outer membrane protein receptors. *FEMS Microbiol. Lett.* **1**:141–144.
1800. **Silbert, D. F., G. R. Fink, and B. N. Ames.** 1966. Histidine regulatory mutants in *Salmonella typhimurium*. III. A class of regulatory mutants deficient in tRNA for histidine. *J. Mol. Biol.* **22**:335–347.
1801. **Silva, D. O., and W. J. Dobrogosz.** 1978. Proton efflux associated with melibiose permease activity in *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.* **81**:750–755.
1802. **Silverman, M., and M. Simon.** 1980. Phase variation genetic analysis of switching mutants. *Cell* **19**:845–854.
1803. **Silverman, M., and M. I. Simon.** 1977. Bacterial flagella. *Annu. Rev. Microbiol.* **31**:397–419.
1804. **Silverman, M., J. Zieg, M. Hilmen, and M. Simon.** 1979. Phase variation in *Salmonella*: genetic analysis of a recombinational switch. *Proc. Natl. Acad. Sci. USA* **76**:391–395.
1805. **Silverman, M., J. Zieg, G. Mandel, and M. Simon.** 1981. Analysis of the functional components of the phase variation system. *Cold Spring Harbor Symp. Quant. Biol.* **45**:17–26.
1806. **Silverman, M., J. Zieg, and M. Simon.** 1979. Flagellar-phase variation: isolation of the *rhl* gene. *J. Bacteriol.* **137**:517–523.
1807. **Simms, S. A., E. W. Cornman, J. Mottonen, and J. Stock.** 1987. Active site of the enzyme which demethylates receptors during bacterial chemotaxis. *J. Biol. Chem.* **262**:29–31.
1808. **Simms, S. A., M. G. Keane, and J. Stock.** 1985. Multiple forms of the CheB methyltransferase in bacterial chemosensing. *J. Biol. Chem.* **260**:10161–10168.
1809. **Simms, S. A., A. M. Stock, and J. B. Stock.** 1987. Purification and characterization of the S-adenosylmethionine:glutamyl methyltransferase that modifies membrane chemoreceptor proteins in

- bacteria. *J. Biol. Chem.* **262**:8537–8543.
1810. **Singer, C. E., and G. R. Smith.** 1972. Histidine regulation in *Salmonella typhimurium*. XIII. Nucleotide sequence of histidine transfer ribonucleic acid. *J. Biol. Chem.* **247**:2989–3000.
1811. **Singer, C. E., G. R. Smith, R. Cortese, and B. N. Ames.** 1972. Mutant tRNA^{his} ineffective in repression and lacking two pseudouridine modifications. *Nature (London) New Biol.* **238**:72–74.
1812. **Singh, A. P., and P. D. Bragg.** 1977. Energetics of galactose transport in a cytochrome deficient mutant of *Salmonella typhimurium*. *J. Supramol. Struct.* **1**(Suppl.):136.
1813. **Sirisena, D. M., K. A. Brozek, P. R. MacLachlan, K. E. Sanderson, and C. R. Raetz.** 1992. The *rfaC* gene of *Salmonella typhimurium*. Cloning, sequencing, and enzymatic function in heptose transfer to lipopolysaccharide. *J. Biol. Chem.* **267**:18874–18884.
1814. **Sirisena, D. M., P. R. MacLachlan, S.-L. Liu, A. Hessel, and K. E. Sanderson.** 1994. Molecular analysis of the *rfaD* gene, for heptose synthesis, and the *rfaF* gene, for heptose transfer, in lipopolysaccharide synthesis in *Salmonella typhimurium*. *J. Bacteriol.* **176**:2379–2385.
1815. **Skavronskaya, A. G., I. V. Andreeva, and A. A. Kiryushkina.** 1973. Specifically UV-sensitive photoreactivable mutant of *Salmonella abony*. *Mutat. Res.* **18**:259–266.
1816. **Skavronskaya, A. G., I. V. Andreeva, and A. A. Kiryushkina.** 1974. The *uvrC* gene in *Salmonella*: phenotypic properties and a preliminary mapping. *Mutat. Res.* **23**:275–277.
1817. **Skavronskaya, A. G., N. F. Stepanova, and I. V. Andreeva.** 1982. UV-mutable hybrids of *Salmonella* incorporating *Escherichia coli* region adjacent to tryptophan operon. *Mol. Gen. Genet.* **185**:315–318.
1818. **Skovgaard, O., and F. G. Hansen.** 1987. Comparison of *dnaA* nucleotide sequences of *Escherichia coli*, *Salmonella typhimurium*, and *Serratia marcescens*. *J. Bacteriol.* **169**:3976–3981.
1819. **Skurnik, M., and P. Toivanen.** 1991. Intervening sequences (IVSs) in the 23S ribosomal RNA genes of pathogenic *Yersinia enterocolitica* strains. The IVSs in *Y. enterocolitica* and *Salmonella typhimurium* have a common origin. *Mol. Microbiol.* **5**:585–593.
1820. **Slater, S. C., and R. Maurer.** 1991. Requirements for bypass of UV-induced lesions in single-stranded DNA of bacteriophage phi X174 in *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **88**:1251–1255.
1821. **Sledziewska, E., and D. Hulanicka.** 1978. Method of isolation of cysteine constitutive mutants of the cysteine regulon in *Salmonella typhimurium*. *Mol. Gen. Genet.* **165**:289–294.
1822. **Slocum, H., and H. W. Boyer.** 1973. Host specificity of *Salmonella typhimurium* deoxyribonucleic acid restriction and modification. *J. Bacteriol.* **113**:724–726.
1823. **Sluka, J. P., S. J. Horvath, A. C. Glasgow, M. I. Simon, and P. B. Dervan.** 1990. Importance of minor-groove contacts for recognition of DNA by the binding domain of Hin recombinase. *Biochemistry* **29**:6551–6561.
1824. **Smando, R., E. B. Waygood, and B. D. Sanwal.** 1974. Cooperative interactions in the binding of allosteric effectors to phosphoenolpyruvate carboxylase. *J. Biol. Chem.* **249**:182–190.
1825. **Smit, J., Y. Kamio, and H. Nikaido.** 1975. Outer membrane of *Salmonella typhimurium*: chemical analysis and freeze fracture studies with lipopolysaccharide mutants. *J. Bacteriol.* **124**:942–958.
1826. **Smith, B. P., M. Reina-Guerra, S. K. Hoiseth, B. A. D. Stocker, F. Habasha, E. Johnson, and F. Merritt.** 1984. Aromatic-dependent *Salmonella typhimurium* as modified live vaccines for calves. *Am. J. Vet. Res.* **45**:59–66.
1827. **Smith, C. M., W. H. Koch, S. B. Franklin, P. L. Foster, T. A. Cebula, and E. Eisenstadt.** 1990. Sequence analysis and mapping of the *Salmonella typhimurium* LT2 *umuDC* operon. *J. Bacteriol.* **172**:4964–4978.
1828. **Smith, D., and R. H. Bauerle.** 1969. The anthranilate synthetase-5-phosphoribosyl transferase complex of the tryptophan pathway in *Salmonella typhimurium*. Purification by the in vitro assembly of its subunits. *Biochemistry* **8**:1451–1459.
1829. **Smith, D. A.** 1971. S-Amino acid metabolism and its regulation in *Escherichia coli* and *Salmonella typhimurium*. *Adv. Genet.* **16**:141–165.
1830. **Smith, D. A., and J. D. Childs.** 1966. Methionine genes and enzymes of *Salmonella*

- typhimurium*. *Heredity* **21**:265–268.
1831. **Smith, G. R.** 1971. Specialized transduction of the *Salmonella hut* operons by coliphage lambda: deletion analysis of the *hut* operons employing lambda *phut*. *Virology* **45**:208–223.
1832. **Smith, G. R., Y. S. Halpern, and B. Magasanik.** 1971. Genetic and metabolic control of enzymes responsible for histidine degradation in *Salmonella typhimurium*. *J. Biol. Chem.* **156**:3320–3329.
1833. **Smith, G. R., and B. Magasanik.** 1971. Nature and self-regulated synthesis of the repressor of the *hut* operons in *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **68**:1493–1497.
1834. **Smith, G. R., and B. Magasanik.** 1971. The two operons of the histidine utilization system in *Salmonella typhimurium*. *J. Biol. Chem.* **246**:3330–3341.
1835. **Smith, G. R., C. M. Roberts, and D. W. Schultz.** 1986. Activity of Chi recombinational hotspots in *Salmonella typhimurium*. *Genetics* **112**:429–439.
1836. **Smith, H. O., and M. Levine.** 1966. Gene order in prophage P22. *Virology* **27**:229–231.
1837. **Smith, H. R., G. O. Humphreys, N. D. F. Grindley, J. N. Grindley, and E. S. Anderson.** 1973. Molecular studies of an *fi*⁺ plasmid from strains of *Salmonella typhimurium*. *Mol. Gen. Genet.* **126**:143–151.
1838. **Smith, J. M., R. A. Kelin, and G. A. O'Donovan.** 1980. Repression and derepression of the enzymes of the pyrimidine biosynthetic pathway in *Salmonella typhimurium*. *J. Gen. Microbiol.* **121**:27–38.
1839. **Smith, J. M., E. H. Rowsell, J. Shioi, and B. L. Taylor.** 1988. Identification of a site of ATP requirement for signal processing in bacterial chemotaxis. *J. Bacteriol.* **170**:2698–2704.
1840. **Smith, N. H., P. Beltran, and R. K. Selander.** 1990. Recombination of *Salmonella* phase 1 flagellin genes generates new serovars. *J. Bacteriol.* **172**:2209–2216.
1841. **Smith, N. H., and R. K. Selander.** 1990. Sequence invariance of the antigen-coding central region of the phase 1 flagellar filament gene (*fliC*) among strains of *Salmonella typhimurium*. *J. Bacteriol.* **172**:603–609.
1842. **Smith, O., M. M. Meyers, T. Vogel, R. D. Deeley, and R. Goldberger.** 1974. Defective in vitro binding of histidyl-transfer ribonucleic acid to feedback resistant phosphoribosyl transferase of *Salmonella typhimurium*. *Nucleic Acids Res.* **1**:881–888.
1843. **Smith, R. L., J. L. Banks, M. D. Snavely, and M. E. Maguire.** 1993. Sequence and topology of the CorA magnesium transport systems of *Salmonella typhimurium* and *Escherichia coli*. Identification of a new class of transport protein. *J. Biol. Chem.* **268**:14071–14080.
1844. **Smith, R. L., J. W. Pelley, and R. M. Jeter.** 1991. Characterization of *lip* expression in *Salmonella typhimurium*: analysis of *lip::lac* operon fusions. *J. Gen. Microbiol.* **137**:2307–2312.
1845. **Smith-Keary, P. F.** 1966. Restricted transduction by bacteriophage P22 in *Salmonella typhimurium*. *Genet. Res.* **8**:73–82.
1846. **Smyer, J. R., and R. M. Jeter.** 1989. Characterization of phosphoenolpyruvate synthase mutants in *Salmonella typhimurium*. *Arch. Microbiol.* **153**:26–32.
1847. **Snavely, M. D., J. B. Florer, C. G. Miller, and M. E. Maguire.** 1989. Magnesium transport in *Salmonella typhimurium*: expression of cloned genes for three distinct Mg²⁺ transport systems. *J. Bacteriol.* **171**:4752–4760.
1848. **Snavely, M. D., J. B. Florer, C. G. Miller, and M. E. Maguire.** 1989. Magnesium transport in *Salmonella typhimurium*: ²⁸Mg²⁺ transport by the CorA, MgtA, and MgtB systems. *J. Bacteriol.* **171**:4761–4766.
1849. **Snavely, M. D., S. A. Gravina, T. T. Cheung, C. G. Miller, and M. E. Maguire.** 1991. Magnesium transport in *Salmonella typhimurium*. Regulation of *mgtA* and *mgtB* expression. *J. Biol. Chem.* **266**:824–829.
1850. **Snavely, M. D., C. G. Miller, and M. E. Maguire.** 1991. The *mgtB* Mg²⁺ transport locus of *Salmonella typhimurium* encodes a P-type ATPase. *J. Biol. Chem.* **266**:815–823.
1851. **Snellings, N. J., E. M. Johnson, and L. S. Baron.** 1977. Genetic basis of Vi antigen expression in *Salmonella paratyphi C*. *J. Bacteriol.* **131**:57–62.
1852. **Sockett, H., S. Yamaguchi, M. Kihara, V. M. Irikura, and R. M. Macnab.** 1992. Molecular

- analysis of the flagellar switch protein FlhM of *Salmonella typhimurium*. *J. Bacteriol.* **174**:793–806.
1853. **Sofia, H. J., V. Burland, D. L. Daniels, G. Plunkett, and F. R. Blattner.** 1994. Analysis of the *Escherichia coli* genome. V. DNA sequence of the region from 76.0 to 81.5 minutes. *Nucleic Acids Res.* **22**:2576–2586.
1854. **Sohel, I., J. L. Puente, W. J. Murray, J. Vuopio-Varkila, and G. K. Schoolnik.** 1993. Cloning and characterization of the bundle-forming pilin gene of enteropathogenic *Escherichia coli* and its distribution in *Salmonella* serotypes. *Mol. Microbiol.* **7**:563–575.
1855. **Somers, J. M., and W. W. Kay.** 1983. Genetic fine structure of the tricarboxylate transport (*tct*) locus of *Salmonella typhimurium*. *Mol. Gen. Genet.* **190**:20–26.
1856. **Somers, J. M., G. D. Sweet, and W. W. Kay.** 1981. Fluorocitrate resistant tricarboxylate transport mutants in *Salmonella typhimurium*. *Mol. Gen. Genet.* **181**:338–345.
1857. **Sonti, R. V., D. H. Keating, and J. R. Roth.** 1993. Lethal transposition of Mud phages in Restrains of *Salmonella typhimurium*. *Genetics* **133**:17–28.
1858. **Sorensen, K. I.** 1994. Conformational heterogeneity in the *Salmonella typhimurium pyrC* and *pyrD* leader mRNAs produced *in vivo*. *Nucleic Acids Res.* **22**:625–631.
1859. **Sorensen, K. I., K. E. Baker, R. A. Kelln, and J. Neuhard.** 1993. Nucleotide pool-sensitive selection of the transcriptional start site *in vivo* at the *Salmonella typhimurium pyrC* and *pyrD* promoters. *J. Bacteriol.* **175**:4137–4144.
1860. **Sorensen, K. I., and J. Neuhard.** 1991. Dual transcriptional initiation sites from the *pyrC* promoter control expression of the gene in *Salmonella typhimurium*. *Mol. Gen. Genet.* **225**:249–256.
1861. **Spears, K. R., R. E. Wooley, J. Brown, O. J. Fletcher, and J. B. Payeur.** 1990. Characteristics of *Salmonella* spp. and *Escherichia coli* isolated from broiler flocks classified as “good” or “poor” producers. *Avian Dis.* **34**:855–860.
1862. **Spector, M. P., Z. Aliabadi, T. Gonzalez, and J. W. Foster.** 1986. Global control in *Salmonella typhimurium*: two-dimensional electrophoretic analysis of starvation-, anaerobiosis-, and heat shock-inducible proteins. *J. Bacteriol.* **168**:420–424.
1863. **Spector, M. P., and C. L. Cubitt.** 1992. Starvation-inducible loci of *Salmonella typhimurium*: regulation and roles in starvation-survival. *Mol. Microbiol.* **6**:1467–1476.
1864. **Spector, M. P., and J. W. Foster.** 1983. Isolation and characterization of pyridine nucleotide uptake (*pnu*) mutants of *Salmonella typhimurium*, abstr. K51, p. 51. *Abstr. Annu. Meet. Am. Soc. Microbiol., 1983.*
1865. **Spector, M. P., J. M. Hill, E. A. Holley, and J. W. Foster.** 1985. Genetic characterization of pyridine nucleotide uptake mutants of *Salmonella typhimurium*. *J. Gen. Microbiol.* **131**:1313–1322.
1866. **Spector, M. P., Y. K. Park, S. Targari, T. Gonzalez, and J. W. Foster.** 1988. Identification and characterization of starvation-regulated genetic loci in *Salmonella typhimurium* by using Mu d-directed *lacZ* operon fusions. *J. Bacteriol.* **170**:345–351.
1867. **Spencer, J. B., N. J. Stolowich, C. A. Roessner, and I. Scott.** 1994. The *Escherichia coli cysG* gene encodes the multifunctional protein, siroheme synthase. *FEBS Lett.* **335**:57–60.
1868. **Spierings, G., R. Elders, B. van Lith, H. Hofstra, and J. Tommassen.** 1992. Characterization of the *Salmonella typhimurium phoE* gene and development of *Salmonella*-specific DNA probes. *Gene* **122**:45–52.
1869. **Spratt, B. G.** 1972. Replication of extrachromosomal elements in a DNA synthesis initiation mutant of *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.* **48**:496–501.
1870. **Spratt, B. G., and R. J. Rowbury.** 1971. Cell division in a mutant of *Salmonella typhimurium* which is temperature-sensitive for DNA synthesis. *J. Gen. Microbiol.* **65**:305–314.
1871. **Spratt, B. G., and R. J. Rowbury.** 1971. Physiological and genetical studies on a mutant of *Salmonella typhimurium* which is temperature-sensitive for DNA synthesis. *Mol. Gen. Genet.* **114**:35–49.
1872. **Springer, A. L., and M. B. Schmid.** 1993. Molecular characterization of the *Salmonella typhimurium parE* gene. *Nucleic Acids Res.* **21**:1805–1809.
1873. **Springer, W., H. Grimminger, and F. Lingens.** 1972. Isoleucine auxotrophy due to feedback hypersensitivity of biosynthetic threonine deaminase. *J. Bacteriol.* **112**:259–263.

1874. **Springer, W. R., and D. E. Koshland, Jr.** 1977. Identification of a protein methyltransferase as the *cheR* gene product in the bacterial sensing system. *Proc. Natl. Acad. Sci. USA* **74**:533–537.
1875. **Sprinson, D. B., E. G. Gollub, R. C. Hu, and K.-P. Liu.** 1976. Regulation of tyrosine and phenylalanine biosynthesis in *Salmonella typhimurium*. *Acta Microbiol. Acad. Sci. Hung.* **23**:167–170.
1876. **Spudich, J. L., and D. E. Koshland, Jr.** 1975. Quantitation of the sensory response in bacterial chemotaxis. *Proc. Natl. Acad. Sci. USA* **72**:710–713.
1877. **Spudich, J. L., and D. E. Koshland, Jr.** 1979. Specific inactivator of flagellar reversal in *Salmonella typhimurium*. *J. Bacteriol.* **139**:442–447.
1878. **Squires, C. H., M. DeFelice, C. T. Lago, and J. M. Calvo.** 1983. *ilvHI* locus of *Salmonella typhimurium*. *J. Bacteriol.* **154**:1054–1063.
1879. **Sroga, G. E., F. Nemoto, Y. Kuchino, and G. R. Bjork.** 1992. Insertion (*sufB*) in the anticodon loop or base substitution (*sufC*) in the anticodon stem of tRNA(Pro)₂ from *Salmonella typhimurium* induces suppression of frameshift mutations. *Nucleic Acids Res.* **20**:3463–3469.
1880. **St. Pierre, M. L., and M. Demerec.** 1968. Isolation and mapping of *Salmonella typhimurium* mutants defective in the utilization of trehalose. *J. Bacteriol.* **95**:1185–1186.
1881. **Stackhouse, T. M., J. J. Onuffer, C. R. Matthews, S. A. Ahmed, and E. W. Miles.** 1988. Folding of homologous proteins: conservation of the folding mechanism of the α subunit of tryptophan synthase from *Escherichia coli*, *Salmonella typhimurium*, and five interspecies hybrids. *Biochemistry* **27**:824–832.
1882. **Stalker, D. M., W. R. Hiatt, and L. Comai.** 1985. A single amino acid substitution in the enzyme 5-enolpyruvylshikimate-3-phosphate synthase confers resistance to the herbicide glyphosate. *J. Biol. Chem.* **260**:4724–4728.
1883. **Stan-Lotter, H., and P. D. Bragg.** 1985. Subunit distribution of the sulfhydryl groups of the F₁ adenosine triphosphatase of *Salmonella typhimurium*. *Arch. Biochem. Biophys.* **239**:280–285.
1884. **Stan-Lotter, H., M. Gupta, and K. E. Sanderson.** 1979. The influence of cations on the permeability of the outer membrane of *Salmonella typhimurium* and other gram negative bacteria. *Can. J. Microbiol.* **25**:475–485.
1885. **Staples, M. A., and L. L. Houston.** 1979. Proteolytic degradation of imidazoleglycerolphosphate dehydratase-histidinolphosphate from *Salmonella typhimurium* and the isolation of a resistant bi-functional core enzyme. *J. Biol. Chem.* **254**:1395–1401.
1886. **Staskawicz, K. N., and N. J. Panopoulos.** 1980. Phaseolotoxin transport in *Escherichia coli* and *Salmonella typhimurium* via the oligopeptide permease. *J. Bacteriol.* **142**:474–479.
1887. **Stauffer, G. V., C. A. Baker, and J. E. Brenchley.** 1974. Regulation of serine transhydroxymethylase activity in *Salmonella typhimurium*. *J. Bacteriol.* **120**:1017–1025.
1888. **Stauffer, G. V., and J. E. Brenchley.** 1974. Evidence for the involvement of serine transhydroxymethylase in serine and glycine interconversions in *Salmonella typhimurium*. *Genetics* **77**:185–198.
1889. **Stauffer, G. V., and J. E. Brenchley.** 1977. Influence of methionine biosynthesis on serine transhydroxymethylase regulation in *Salmonella typhimurium* LT2. *J. Bacteriol.* **129**:740–749.
1890. **Stauffer, G. V., and J. E. Brenchley.** 1978. Selection of *Salmonella typhimurium* mutants with altered serine transhydroxymethylase regulation. *Genetics* **88**:221–223.
1891. **Stauffer, G. V., and L. T. Stauffer.** 1988. *Salmonella typhimurium* LT2 *metF* operator mutations. *Mol. Gen. Genet.* **214**:32–36.
1892. **Stauffer, G. V., and L. T. Stauffer.** 1988. Cloning and nucleotide sequence of the *Salmonella typhimurium* LT2 *metF* gene and its homology with the corresponding sequence of *Escherichia coli*. *Mol. Gen. Genet.* **212**:246–251.
1893. **Stauffer, G. V., L. T. Stauffer, and M. D. Plamann.** 1989. The *Salmonella typhimurium* glycine cleavage enzyme system. *Mol. Gen. Genet.* **220**:154–156.
1894. **Steiert, J. G., M. L. Urbanowski, L. T. Stauffer, M. D. Plamann, and G. V. Stauffer.** 1990. Nucleotide sequence of the *Salmonella typhimurium* *glyA* gene. *DNA Seq.* **1**:107–113.
1895. **Steinberg, B., and M. Gough.** 1975. Altered DNA synthesis in a mutant of *Salmonella*

- typhimurium* that channels bacteriophage P22 toward lysogeny. *J. Virol.* **16**:1154–1160.
1896. **Steiner, K. E., and J. Preiss.** 1977. Biosynthesis of bacterial glycogen: genetic and allosteric regulation of glycogen biosynthesis in *Salmonella typhimurium* LT-2. *J. Bacteriol.* **129**:246–256.
1897. **Stepanova, N. F., I. V. Andreeva, A. A. Kiryushkina, Y. S. Kondrat'ev, L. Y. Likhoded, and A. G. Skavronskaya.** 1977. Intergeneric mating of *Escherichia coli* and *Salmonella typhimurium*. II. Transfer of *polA-1* mutation from *Escherichia coli* to *Salmonella typhimurium* and its phenotypic expression in the *Salmonella* genome. *Sov. Genet.* **13**:1474–1479.
1898. **Stepanova, N. F., I. V. Andreeva, and A. G. Skavronskaya.** 1977. Intergenous conjugation crossing of *Escherichia coli* and *Salmonella typhimurium*. Communication I. Production of a hybrid of *Salmonella* possessing increased activity of the recipient, in crosses with *Escherichia coli*. *Sov. Genet.* **13**:1358–1362.
1899. **Stephens, J. C., S. W. Artz, and B. N. Ames.** 1975. Guanosine 5'-diphosphate 3'-diphosphate (ppGpp): positive effector for histidine operon transcription and a general signal for amino acid deficiency. *Proc. Natl. Acad. Sci. USA* **72**:4389–4393.
1900. **Sterboul, C. C., J. E. Kleeman, and S. M. Parsons.** 1977. Purification and characterization of a mutant ATP phosphoribosyltransferase hypersensitive to histidine feedback inhibition. *Arch. Biochem. Biophys.* **181**:632–642.
1901. **Stern, M. J., C. F. Higgins, and G. F.-L. Ames.** 1984. Isolation and characterization of *lac* fusions to two nitrogen-regulated promoters. *Mol. Gen. Genet.* **195**:219–227.
1902. **Stetter, D. W., and R. B. Middleton.** 1979. Tryptophan requiring parental strains yield *Salmonella typhimurium* x *Escherichia coli* hybrid recombinants with functional tryptophan operons. *Can. J. Genet. Cytol.* **21**:255–260.
1903. **Stevenson, G., S. J. Lee, L. K. Romana, and P. R. Reeves.** 1991. The *cps* gene cluster of *Salmonella* strain LT2 includes a second mannose pathway: sequence of two genes and relationship to genes in the *rfb* gene cluster. *Mol. Gen. Genet.* **227**:173–180.
1904. **Stewart, V.** 1988. Nitrate respiration in relation to facultative metabolism in enterobacteria. *Microbiol. Rev.* **52**:190–232.
1905. **Stewart, V., J. T. Lin, and B. L. Berg.** 1991. Genetic evidence that genes *fdhD* and *fdhE* do not control synthesis of formate dehydrogenase-N in *Escherichia coli* K-12. *J. Bacteriol.* **173**:4417–4423.
1906. **Stieglitz, B. I., and J. M. Calvo.** 1971. Effect of 4-azaleucine upon leucine metabolism in *Salmonella typhimurium*. *J. Bacteriol.* **108**:95–104.
1907. **Stinavage, P. S., L. E. Martin, and J. K. Spitznagel.** 1990. A 59 kiloDalton outer membrane protein of *Salmonella typhimurium* protects against oxidative intraleukocytic killing due to human neutrophils. *Mol. Microbiol.* **4**:283–293.
1908. **Stirling, D. A., C. S. Hulton, L. Waddell, S. F. Park, G. S. Stewart, I. R. Booth, and C. F. Higgins.** 1989. Molecular characterization of the *proU* loci of *Salmonella typhimurium* and *Escherichia coli* encoding osmoregulated glycine betaine transport systems. *Mol. Microbiol.* **3**:1025–1038.
1909. **Stock, A., T. Chen, D. Welsh, and J. Stock.** 1988. CheA protein, a central regulator of bacterial chemotaxis, belongs to a family of proteins that control gene expression in response to changing environmental conditions. *Proc. Natl. Acad. Sci. USA* **85**:1403–1407.
1910. **Stock, A., D. E. Koshland, Jr., and J. Stock.** 1985. Homologies between the *Salmonella typhimurium* CheY protein and proteins involved in the regulation of chemotaxis, membrane protein synthesis, and sporulation. *Proc. Natl. Acad. Sci. USA* **82**:7989–7993.
1911. **Stock, A., J. Mottonen, T. Chen, and J. Stock.** 1987. Identification of a possible nucleotide binding site in the CheW, a protein required for sensory transduction in bacterial chemotaxis. *J. Biol. Chem.* **262**:535–537.
1912. **Stock, A., E. Schaeffer, D. E. Koshland, Jr., and J. Stock.** 1987. A second type of protein methylation reaction in bacterial chemotaxis. *J. Biol. Chem.* **262**:8011–8014.
1913. **Stock, A. M., E. Martinez-Hackert, B. F. Rasmussen, A. H. West, J. B. Stock, D. Ringe, and G. A. Petsko.** 1993. Structure of the Mg(2+)-bound form of CheY and mechanism of phosphoryl transfer in bacterial chemotaxis. *Biochemistry* **32**:13375–13380.

1914. **Stock, A. M., J. M. Mottonen, J. B. Stock, and C. E. Schutt.** 1989. Three-dimensional structure of CheY, the response regulator of bacterial chemotaxis. *Nature* (London) **337**:745–749.
1915. **Stock, A. M., and J. Stock.** 1987. Purification and characterization of the CheZ protein of bacterial chemotaxis. *J. Bacteriol.* **169**:3301–3311.
1916. **Stock, A. M., D. C. Wylie, J. M. Mottonen, A. N. Lupas, E. G. Ninfa, A. J. Ninfa, C. E. Schutt, and J. B. Stock.** 1988. Phosphoproteins involved in bacterial signal transduction. *Cold Spring Harbor Symp. Quant. Biol.* **53**:49–57.
1917. **Stock, J., G. Kersulis, and D. E. Koshland, Jr.** 1985. Neither methylation nor demethylating enzymes are required for bacterial chemotaxis. *Cell* **42**:683–690.
1918. **Stock, J. B., and D. E. Koshland, Jr.** 1979. A protein methyl esterase involved in bacterial sensing. *Proc. Natl. Acad. Sci. USA* **75**:3659–3663.
1919. **Stock, J. B., G. S. Lukat, and A. M. Stock.** 1991. Bacterial chemotaxis and the molecular logic of intracellular signal transduction networks. *Annu. Rev. Biophys. Biophys. Chem.* **20**:109–136.
1920. **Stock, J. B., E. B. Waygood, N. D. Meadow, P. W. Postma, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. The glucose receptors of the *Salmonella typhimurium* phosphotransferase system. *J. Biol. Chem.* **257**:14543–14552.
1921. **Stocker, B. A. D., and P. H. Mäkelä.** 1971. Genetic aspects of biosynthesis and structure of *Salmonella typhimurium* lipopolysaccharide, p. 369–438. In G. Weinbaum, S. Kadis, and S. J. Ajl (ed.), *Bacterial Endotoxins*, vol. 4 in *Microbial Toxins*. Academic Press, Inc., New York.
1922. **Stocker, B. A. D., and P. H. Makela.** 1978. Genetics of the (gram-negative) bacterial surface. *Proc. R. Soc. London Ser. B Biol. Sci.* **202**:5–30.
1923. **Stocker, B. A. D., B. M. Males, and W. Takano.** 1980. *Salmonella typhimurium* mutants of *rfaH* negative phenotype: genetics and antibiotic sensitivities. *J. Gen. Microbiol.* **116**:17–24.
1924. **Stocker, B. A. D., M. W. McDonough, and R. P. Ambler.** 1961. A gene determining presence or absence of ϵ -N-methyl-lysine in *Salmonella* flagellar protein. *Nature* (London) **189**:556–558.
1925. **Stocker, B. A. D., M. Nurminen, and P. H. Makela.** 1979. Mutants defective in the 33K outer membrane protein of *Salmonella typhimurium*. *J. Bacteriol.* **139**:376–383.
1926. **Stocker, B. A. D., S. M. Smith, and T. V. Subbaiah.** 1963. Mapping in *Salmonella typhimurium* with colicine factors to obtain fertility. *Microb. Genet. Bull.* **19**:22–24.
1927. **Stocker, B. A. D., R. G. Wilkinson, and P. H. Makela.** 1966. Genetic aspects of biosynthesis and structure of *Salmonella* somatic polysaccharide. *Ann. N.Y. Acad. Sci.* **133**:334–348.
1928. **Stocker, B. A. D., N. D. Zinder, and J. Lederberg.** 1953. Transduction of flagellar characters in *Salmonella*. *J. Gen. Microbiol.* **9**:410–433.
1929. **Storz, G., M. F. Christman, H. Sies, and B. N. Ames.** 1987. Spontaneous mutagenesis and oxidative damage to DNA in *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **84**:8917–8921.
1930. **Storz, G., F. S. Jacobson, L. A. Tartaglia, R. W. Morgan, L. A. Silveira, and B. N. Ames.** 1989. An alkyl hydroperoxide reductase induced by oxidative stress in *Salmonella typhimurium* and *Escherichia coli*: genetic characterization and cloning of *ahp*. *J. Bacteriol.* **171**:2049–2055.
1931. **Storz, G., L. A. Tartaglia, and B. N. Ames.** 1990. Transcriptional regulator of oxidative stress-inducible genes: direct activation by oxidation. *Science* **248**:189–194.
1932. **Storz, G., and M. B. Toledano.** 1994. Regulation of bacterial gene expression in response to oxidative stress. *Methods Enzymol.* **236**:196–207.
1933. **Stouthamer, A. H.** 1969. A genetical and biochemical study of chlorate-resistant mutants of *Salmonella typhimurium*. *Antonie Van Leeuwenhoek J. Microbiol. Serol.* **35**:505–521.
1934. **Stouthamer, A. H.** 1970. Genetics and biochemistry of reductase formation in Enterobacteriaceae. *Antonie Van Leeuwenhoek J. Microbiol. Serol.* **36**:181.
1935. **Stouthamer, A. H., and C. W. Bettenhausen.** 1970. Mapping of a gene causing resistance to chlorate in *Salmonella typhimurium*. *Antonie Van Leeuwenhoek J. Microbiol. Serol.* **36**:555–565.
1936. **Stover, C. K., J. Kemper, and R. C. Marsh.** 1988. Molecular cloning and characterization of *supQ/newD*, a gene substitution system for the *leuD* gene of *Salmonella typhimurium*. *J. Bacteriol.* **170**:3115–3124.
1937. **Strain, S. M., I. M. Armitage, L. Anderson, K. Takayama, N. Qureshi, and C. R. H. Raetz.**

1985. Location of polar substituents and fatty acid acyl chains on lipid A precursors from a 3-deoxy-D-manno-octulosonic acid-deficient mutant of *Salmonella typhimurium*. Studies by ^1H , ^{13}C , and ^{31}P nuclear magnetic resonance. *J. Biol. Chem.* **260**:16089–16098.
1938. **Strange, P. G., and D. E. Koshland, Jr.** 1976. Receptor interactions in a signalling system: competition between ribose receptor and galactose receptor in the chemotaxis response. *Proc. Natl. Acad. Sci. USA* **73**:762–766.
1939. **Strauch, K. L., T. H. Carter, and C. G. Miller.** 1983. Overproduction of *Salmonella typhimurium* peptidase T. *J. Bacteriol.* **156**:743–751.
1940. **Strauch, K. L., J. B. Lenk, B. L. Gamble, and C. G. Miller.** 1985. Oxygen regulation in *Salmonella typhimurium*. *J. Bacteriol.* **161**:673–680.
1941. **Strauch, K. L., and C. G. Miller.** 1983. Isolation and characterization of *Salmonella typhimurium* mutants lacking a tripeptidase (peptidase T). *J. Bacteriol.* **154**:763–771.
1942. **Straus, D. S., and B. N. Ames.** 1973. Histidyl transfer ribonucleic acid synthetase mutants requiring a high internal pool of histidine for growth. *J. Bacteriol.* **115**:188–197.
1943. **Straus, D. S., and G. R. Hoffman.** 1975. Selection for a large genetic duplication in *Salmonella typhimurium*. *Genetics* **80**:227–237.
1944. **Straus, D. S., and L. D. Straus.** 1976. Large overlapping tandem genetic duplications in *Salmonella typhimurium*. *J. Mol. Biol.* **103**:143–154.
1945. **Strugnell, R. A., D. Maskell, N. Fairweather, D. Pickard, A. Cockayne, C. Penn, and G. Dougan.** 1990. Stable expression of foreign antigens from the chromosome of *Salmonella typhimurium* vaccine strains. *Gene* **88**:57–63.
1946. **Stuttard, C.** 1972. Location of *trpR* mutations in the *serB-thr* region of *Salmonella typhimurium*. *J. Bacteriol.* **111**:368–374.
1947. **Stuttard, C.** 1973. Genetic analysis of *thr* mutations in *Salmonella typhimurium*. *J. Bacteriol.* **116**:1–11.
1948. **Stuttard, C.** 1975. Tryptophan biosynthesis in *Salmonella typhimurium*: location in *trpB* of a genetic difference between strains LT2 and LT7. *J. Bacteriol.* **123**:878–887.
1949. **Su, G. F., H. N. Brahmhatt, J. Wehland, M. Rohde, and K. N. Timmis.** 1992. Construction of stable Lamb-Shiga toxin B subunit hybrids: analysis of expression in *Salmonella typhimurium aroA* strains and stimulation of B subunit-specific mucosal and serum antibody responses. *Infect. Immun.* **60**:3345–3359.
1950. **Subbaiah, T. V., and B. A. D. Stocker.** 1964. Rough mutants of *Salmonella typhimurium*. I. *Genetics. Nature (London)* **201**:1298–1299.
1951. **Subbaramaiah, K., and S. A. Simms.** 1992. Photolabeling of CheR methyltransferase with S-adenosyl-L-methionine (AdoMet). Studies on the AdoMet binding site. *J. Biol. Chem.* **267**:8636–8642.
1952. **Sugiyama, T., N. Kido, T. Komatsu, M. Ohta, and N. Kato.** 1991. Expression of the cloned *Escherichia coli* O9 *rfb* gene in various mutant strains of *Salmonella typhimurium*. *J. Bacteriol.* **173**:55–58.
1953. **Suh, S. J., and J. C. Escalante-Semerena.** 1993. Cloning, sequencing and overexpression of *cobA* which encodes ATP:corrinoic adenosyltransferase in *Salmonella typhimurium*. *Gene* **129**:93–97.
1954. **Suh, S. J., and J. C. Escalante-Semerena.** 1995. Purification and initial characterization of the ATP:corrinoic adenosyltransferase encoded by the *cobA* gene of *Salmonella typhimurium*. *J. Bacteriol.* **177**:921–925.
1955. **Sukupolvi, S., I. M. Helander, R. Hukari, M. Vaara, and P. H. Makela.** 1985. Lipopolysaccharides of three classes of supersensitive mutants of *Salmonella typhimurium*. *FEMS Microbiol. Lett.* **30**:341–345.
1956. **Sukupolvi, S., and D. O'Connor.** 1987. Amino acid alterations in a hydrophobic region of the TraT protein of R6–5 increase the outer membrane permeability of enteric bacteria. *Mol. Gen. Genet.* **210**:178–180.
1957. **Sukupolvi, S., D. O'Connor, and M. F. Edwards.** 1986. The *traT* protein is able to normalize the phenotype of a plasmid-carried permeability mutation of *Salmonella typhimurium*. *J. Gen.*

- Microbiol.* **132**:2079–2085.
1958. **Sukupolvi, S., P. Riikonen, S. Taira, H. Saarilahti, and M. Rhen.** 1992. Plasmid-mediated serum resistance in *Salmonella enterica*. *Microb. Pathog.* **12**:219–225.
1959. **Sukupolvi, S., and M. Vaara.** 1989. *Salmonella typhimurium* and *Escherichia coli* mutants with increased outer membrane permeability to hydrophobic compounds. *Biochim. Biophys. Acta* **988**:377–387.
1960. **Sukupolvi, S., M. Vaara, I. M. Helander, P. Viljanen, and P. H. Makela.** 1984. New *Salmonella typhimurium* mutants with altered outer membrane permeability. *J. Bacteriol.* **159**:704–712.
1961. **Sukupolvi, S., R. Vuorio, S. Y. Qi, D. O'Connor, and M. Rhen.** 1990. Characterization of the *traT* gene and mutants that increase outer membrane permeability from the *Salmonella typhimurium* virulence plasmid. *Mol. Microbiol.* **4**:49–57.
1962. **Sundaram, T. K.** 1972. *myo*-Inositol catabolism in *Salmonella typhimurium*: enzyme repression dependent on growth history of organism. *J. Gen. Microbiol.* **73**:209–219.
1963. **Suryanarayana, T., and C. P. Burma.** 1975. Substrate specificity of *Salmonella typhimurium* RNase III and the nature of products formed. *Biochim. Biophys. Acta* **407**:459–468.
1964. **Sutherland, L., J. Cairney, M. J. Elmore, I. R. Booth, and C. F. Higgins.** 1986. Osmotic regulation of transcription: induction of the *proU* betaine transport gene is dependent on accumulation of intracellular potassium. *J. Bacteriol.* **168**:805–814.
1965. **Suzuki, H., and T. Iino.** 1966. An assay for newly synthesized intracellular flagellin. *Biochim. Biophys. Acta* **124**:212–215.
1966. **Suzuki, H., and T. Iino.** 1973. *In vitro* synthesis of phase-specific flagellin of *Salmonella*. *J. Mol. Biol.* **81**:57–70.
1967. **Suzuki, H., and T. Iino.** 1975. Absence of messenger ribonucleic acid specific for flagellin in non-flagellate mutants of *Salmonella*. *J. Mol. Biol.* **95**:549–556.
1968. **Suzuki, T., and T. Iino.** 1981. Role of the *flaR* gene in flagellar hook formation in *Salmonella* spp. *J. Bacteriol.* **148**:973–979.
1969. **Suzuki, T., T. Iino, T. Horiguchi, and S. Yamaguchi.** 1978. Incomplete flagella structures in nonflagellate mutants of *Salmonella typhimurium*. *J. Bacteriol.* **133**:904–915.
1970. **Sverdlov, E. D., N. A. Lisitsyn, S. O. Guryev, and G. S. Monastyrskaya.** 1986. Nucleotide sequence of the *Salmonella typhimurium rpoB* gene encoding the β -subunit of RNA polymerase. *Dokl. Akad. Nauk. SSSR* **287**:232–236. (In Russian.)
1971. **Sverdlov, E. D., N. A. Lisitsyn, S. O. Guryev, Y. V. Smirnov, V. M. Rostapshov, and G. S. Monastyrskaya.** 1986. Genes coding the β -subunit of bacterial RNA polymerases. I. Primary structure of the *rpoB* gene EcoRI-C fragment from *Salmonella typhimurium*. *Bioorg. Khim.* **12**:699–707. (In Russian with English abstract.)
1972. **Sweet, G. D., C. M. Kay, and W. W. Kay.** 1984. Tricarboxylate-binding proteins of *Salmonella typhimurium*. Purification, crystallization, and physical properties. *J. Biol. Chem.* **259**:1586–1592.
1973. **Sweet, G. D., J. M. Somers, and W. W. Kay.** 1979. Purification and properties of a citrate-binding transport component, the C protein of *Salmonella typhimurium*. *Can. J. Biochem.* **57**:710–716.
1974. **Swenson, D. L., and S. Clegg.** 1992. Identification of ancillary *fim* genes affecting *fimA* expression in *Salmonella typhimurium*. *J. Bacteriol.* **174**:7697–7704.
1975. **Swenson, D. L., K. J. Kim, E. W. Six, and S. Clegg.** 1994. The gene *fimU* affects expression of *Salmonella typhimurium* type 1 fimbriae and is related to the *Escherichia coli* tRNA gene *argU*. *Mol. Gen. Genet.* **244**:216–218.
1976. **Swenson, P. A., L. Riester, and T. V. Palmer.** 1983. Role of the *supX* gene in sensitizing *Salmonella typhimurium* cells to respiration shutoff induced by far ultraviolet irradiation. *Photochem. Photobiol.* **38**:305–310.
1977. **Switala, J., B. L. Triggs-Raine, and P. C. Loewen.** 1990. Homology among bacterial catalase genes. *Can. J. Microbiol.* **36**:728–731.
1978. **Syvanen, J. M., and J. R. Roth.** 1972. The structural genes for ornithine transcarbamylase in

- Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **110**:66–70.
1979. **Syvanen, J. M., and J. R. Roth.** 1973. Structural genes for catalytic and regulatory subunits of aspartate transcarbamylase. *J. Mol. Biol.* **76**:363–378.
1980. **Syvanen, J. M., Y. R. Yang, and M. W. Kirschner.** 1973. Preparation of ¹²⁵I-catalytic subunit of aspartate transcarbamylase and its use in studies of the regulatory subunit. *J. Biol. Chem.* **248**:3762–3768.
1981. **Szekely, E., and M. Simon.** 1981. Homology between the invertible deoxyribonucleic acid sequence that controls flagellar-phase variation in the *Salmonella* sp. and deoxyribonucleic acid sequences in other organisms. *J. Bacteriol.* **148**:829–836.
1982. **Szekely, E., and M. Simon.** 1983. DNA sequence adjacent to flagellar genes and evolution of flagellar-phase variation. *J. Bacteriol.* **155**:74–81.
1983. **Szwacka, M., Z. Ciesla, and T. Klopotoski.** 1979. Azide induced mutagenesis in gram negative bacteria is *recA* independent and *lexA* independent. *Mutat. Res.* **62**:221–226.
1984. **Tai, P. C., D. P. Kessler, and J. Ingraham.** 1966. Cold-sensitive mutations in *Salmonella typhimurium* which affect ribosome synthesis. *J. Bacteriol.* **97**:1298–1304.
1985. **Taillon, B. E., R. Little, and R. P. Lawther.** 1988. Analysis of the functional domains of biosynthetic threonine deaminase by comparison of the amino acid sequences of three wild-type alleles to the amino acid sequence of biodegradative threonine deaminase. *Gene* **63**:245–252.
1986. **Taillon, M. P., D. A. Gotto, and R. P. Lawther.** 1981. The DNA sequence of the promoter-attenuator of the *ilvGEDA* operon of *Salmonella typhimurium*. *Nucleic Acids Res.* **9**:3419–3432.
1987. **Taira, S., and M. Rhen.** 1989. Identification and genetic analysis of *mkaA*—a gene of the *Salmonella typhimurium* virulence plasmid necessary for intracellular growth. *Microb. Pathog.* **7**:165–173.
1988. **Taira, S., P. Riikonen, H. Saarilahti, S. Sukupolvi, and M. Rhen.** 1991. The *mkaC* virulence gene of the *Salmonella* serovar *typhimurium* 96 kb plasmid encodes a transcriptional activator. *Mol. Gen. Genet.* **228**:381–384.
1989. **Takayama, K., N. Qureshi, and P. Mascagni.** 1983. Complete structure of lipid A obtained from the lipopolysaccharides of the heptoseless mutant of *Salmonella typhimurium*. *J. Biol. Chem.* **258**:12801–12803.
1990. **Tame, J. R., G. N. Murshudov, E. J. Dodson, T. K. Neil, G. G. Dodson, C. F. Higgins, and A. J. Wilkinson.** 1994. The structural basis of sequence-independent peptide binding by OppA protein. *Science* **264**:1578–1581.
1991. **Tamir, H., and P. R. Srinivasan.** 1972. Studies of the mechanism of anthranilate synthase. Evidence for an acyl-enzyme. *J. Biol. Chem.* **247**:1153–1155.
1992. **Tanemura, S., and R. Bauerle.** 1977. Internal reinitiation of translation in polar mutants of the *trpB* gene of *Salmonella typhimurium*. *Mol. Gen. Genet.* **153**:135–143.
1993. **Tanemura, S., and R. Bauerle.** 1979. Suppression of a deletion mutation in the glutamine amidotransferase region of the *Salmonella typhimurium trpD* gene by mutations in *pheA* and *tyrA*. *J. Bacteriol.* **139**:573–582.
1994. **Tanemura, S., and R. Bauerle.** 1980. Conditionally expressed missense mutations: the basis for the unusual phenotype of an apparent *trpD* nonsense mutant of *Salmonella typhimurium*. *Genetics* **95**:545–560.
1995. **Tanemura, S., and J. Yourno.** 1969. Frameshift revertant of *Salmonella typhimurium* producing histidinol dehydrogenase with a sequence of four extra amino acid residues. *J. Mol. Biol.* **40**:459–466.
1996. **Tankersley, W. G., and J. M. Woodward.** 1974. Induction and isolation of a minicell-producing strain of *Salmonella typhimurium*. *Proc. Soc. Exp. Biol. Med.* **145**:802–805.
1997. **Tannock, G. W., R. V. H. Blumershine, and D. C. Savage.** 1975. Association of *Salmonella typhimurium* with, and its invasion of, the ileal mucosa in mice. *Infect. Immun.* **11**:365–370.
1998. **Tartaglia, L. A., G. Storz, and B. N. Ames.** 1989. Identification and molecular analysis of *oxyR*-regulated promoters important for the bacterial adaptation to oxidative stress. *J. Mol. Biol.* **210**:709–719.
1999. **Tartaglia, L. A., G. Storz, M. H. Brodsky, A. Lai, and B. N. Ames.** 1990. Alkyl hydroperoxide

- reductase from *Salmonella typhimurium*. Sequence and homology to thioredoxin reductase and other flavoprotein disulfide oxidoreductases. *J. Biol. Chem.* **265**:10535–10540.
2000. **Tate, C. G., J. A. Muiry, and P. J. Henderson.** 1992. Mapping, cloning, expression, and sequencing of the *rhaT* gene, which encodes a novel L-rhamnose-H⁺ transport protein in *Salmonella typhimurium* and *Escherichia coli*. *J. Biol. Chem.* **267**:6923–6932.
2001. **Taylor, B. L., and D. E. Koshland, Jr.** 1974. Reversal of flagellar rotation in monotrichous and peritrichous bacteria: generation of changes in direction. *J. Bacteriol.* **119**:640–642.
2002. **Taylor, B. L., and D. E. Koshland, Jr.** 1975. Intrinsic and extrinsic light responses of *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **123**:557–569.
2003. **Taylor, G., E. Vimr, E. Garman, and G. Laver.** 1992. Purification, crystallization and preliminary crystallographic study of neuraminidase from *Vibrio cholerae* and *Salmonella typhimurium* LT2. *J. Mol. Biol.* **226**:1287–1290.
2004. **Taylor, N. S., and I. R. Beacham.** 1976. Synthesis and localization of *Escherichia coli* UDP-glucose hydrolase (5'-nucleotidase), and demonstration of a cytoplasmic inhibitor of this enzyme in *Salmonella typhimurium*. *Biochim. Biophys. Acta* **411**:216–221.
2005. **Taylor, R. T., and H. Weissbach.** 1967. N⁵-methyltetrahydrofolate-homocysteine transmethylase. Partial purification and properties. *J. Biol. Chem.* **242**:1502–1508.
2006. **Theisen, M., R. A. Kelln, and J. Neuhard.** 1987. Cloning and characterization of the *pyrF* operon of *Salmonella typhimurium*. *Eur. J. Biochem.* **164**:613–619.
2007. **Theisen, M., and J. Neuhard.** 1990. Translational coupling in the *pyrF* operon of *Salmonella typhimurium*. *Mol. Gen. Genet.* **222**:345–352.
2008. **Theodore, T. S., and E. Engelsberg.** 1964. Mutant of *Salmonella typhimurium* deficient in the carbon dioxide-fixing enzyme phosphoenolpyruvic carboxylase. *J. Bacteriol.* **88**:946–955.
2009. **Thomas, S. M.** 1993. Extreme cold sensitivity of *Salmonella typhimurium umu* clones, effects of the *umu* region and flanking sequences. *Mutat. Res.* **285**:95–99.
2010. **Thomas, S. M., H. M. Crowne, S. C. Pidsley, and S. G. Sedgwick.** 1990. Structural characterization of the *Salmonella typhimurium* LT2 *umu* operon. *J. Bacteriol.* **172**:4979–4987.
2011. **Thomas, S. M., and S. G. Sedgwick.** 1989. Cloning of *Salmonella typhimurium* DNA encoding mutagenic DNA repair. *J. Bacteriol.* **171**:5776–5782.
2012. **Thomulka, K. W., and J. S. Gots.** 1982. Isolation and characterization of purine regulatory mutants of *Salmonella typhimurium* with an episomal *purE-lac* fusion. *J. Bacteriol.* **151**:153–161.
2013. **Thorne, G. M., and L. M. Corwin.** 1972. Genetic locus of a gene affecting leucine transport in *Salmonella typhimurium*. *J. Bacteriol.* **110**:784–785.
2014. **Thorne, G. M., and L. M. Corwin.** 1975. Mutations affecting aromatic amino acid transport in *Escherichia coli* and *Salmonella typhimurium*. *J. Gen. Microbiol.* **90**:203–216.
2015. **Thorner, L. K., J. P. Fandl, and S. W. Artz.** 1990. Analysis of sequence elements important for expression and regulation of the adenylate cyclase gene (*cya*) of *Salmonella typhimurium*. *Genetics* **125**:709–717.
2016. **Timme, T. L., C. B. Lawrence, and R. E. Moses.** 1989. Two new members of the OmpR superfamily detected by homology to a sensor-binding core domain. *J. Mol. Evol.* **28**:545–552.
2017. **Tirgari, S., M. P. Spector, and J. W. Foster.** 1986. Genetics of NAD metabolism in *Salmonella typhimurium* and cloning of the *nadA* and *pnuC* loci. *J. Bacteriol.* **167**:1086–1088.
2018. **Tittawella, I. P. B.** 1984. Evidence for clustering of RNA polymerase and ribosomal protein genes in six species of Enterobacteria. *Mol. Gen. Genet.* **195**:215–218.
2019. **Tittawella, I. P. B.** 1985. *Salmonella typhimurium rpoB* and *rpoC* genes cloned on the λ phages. *FEBS Lett.* **185**:33–36.
2020. **Tokunaga, H., M. Tokunaga, and T. Nakae.** 1979. Characterization of porins from the outer membrane of *Salmonella typhimurium*. 1. Chemical analysis. *Eur. J. Biochem.* **95**:433–440.
2021. **Tokunaga, M., H. Tokunaga, Y. Okajima, and T. Nakae.** 1979. Characterization of porins from the outer membrane of *Salmonella typhimurium*. 2. Physical properties of the functional oligomeric aggregates. *Eur. J. Biochem.* **95**:441–448.
2022. **Tokuno, S.-I., E. P. Goldschmidt, and M. Gough.** 1974. Mutant of *Salmonella typhimurium*

- that channels infecting bacteriophage P22 toward lysogenization. *J. Bacteriol.* **119**:508–513.
2023. **Tokuno, S.-I., and M. Gough.** 1975. Host influence on the activity of genes *c1* and *c3* in regulating the decision between lysis and lysogeny in bacteriophage P22. *J. Virol.* **16**:1184–1190.
2024. **Tokuno, S.-I., L. Roth, C. Weinberger, and M. Gough.** 1977. Effect of mutant host RNA polymerase on the bi-functional activities of phage P-22 gene C-1. *Mol. Gen. Genet.* **153**:205–210.
2025. **Trachtenberg, S., and D. J. DeRosier.** 1991. A molecular switch: subunit rotations involved in the right-handed to left-handed transitions of *Salmonella typhimurium* flagellar filaments. *J. Mol. Biol.* **220**:67–77.
2026. **Tran, P. V., T. A. Bannor, S. Z. Doktor, and B. P. Nichols.** 1990. Chromosomal organization and expression of *Escherichia coli pabA*. *J. Bacteriol.* **172**:397–410.
2027. **Tribhuwan, R. C., M. S. Johnson, and B. L. Taylor.** 1986. Evidence against direct involvement of cyclic GMP or cyclic AMP in bacterial chemotactic signaling. *J. Bacteriol.* **168**:624–630.
2028. **Tronick, S. R., J. E. Ciardi, and E. R. Stadtman.** 1973. Comparative biochemical and immunological studies of bacterial glutamine synthetases. *J. Bacteriol.* **115**:858–868.
2029. **Trucksis, M., E. I. Golub, D. J. Zabel, and R. F. Depew.** 1981. *Escherichia coli* and *Salmonella typhimurium supX* genes specify deoxyribonucleic acid topoisomerase I. *J. Bacteriol.* **147**:679–681.
2030. **Trzebiatowski, J. R., G. A. O'Toole, and J. C. Escalante-Semerena.** 1994. The *cobT* gene of *Salmonella typhimurium* encodes the NaMN:5,6-dimethylbenzimidazole phosphoribosyltransferase responsible for the synthesis of N¹-(5-phospho- α -D-ribose)-5,6-dimethylbenzimidazole, an intermediate in the synthesis of the nucleotide loop of cobalamin. *J. Bacteriol.* **176**:3568–3575.
2031. **Tsai, S. P., R. J. Hartin, and J. Ryu.** 1989. Transformation in restriction-deficient *Salmonella typhimurium* LT2. *J. Gen. Microbiol.* **135**:2561–2567.
2032. **Tubulekas, I., R. H. Buckingham, and D. Hughes.** 1991. Mutant ribosomes can generate dominant kirromycin resistance. *J. Bacteriol.* **173**:3635–3643.
2033. **Tubulekas, I., and D. Hughes.** 1993. Growth and translation elongation rate are sensitive to the concentration of EF-Tu. *Mol. Microbiol.* **8**:761–770.
2034. **Tubulekas, I., and D. Hughes.** 1993. A single amino acid substitution in elongation factor Tu disrupts interaction between the ternary complex and the ribosome. *J. Bacteriol.* **175**:240–250.
2035. **Tuohy, T. M., S. Thompson, R. F. Gesteland, D. Hughes, and J. F. Atkins.** 1990. The role of EF-Tu and other translation components in determining translocation step size. *Biochim. Biophys. Acta* **1050**:274–278.
2036. **Tupper, A. E., T. A. Owen-Hughes, D. W. Ussery, D. S. Santos, D. J. Ferguson, J. M. Sidebotham, J. C. Hinton, and C. F. Higgins.** 1994. The chromatin-associated protein H-NS alters DNA topology *in vitro*. *EMBO J.* **13**:258–268.
2037. **Turnbough, C. L., Jr., and B. R. Bochner.** 1985. Toxicity of the pyrimidine biosynthetic pathway intermediate carbamyl aspartate in *Salmonella typhimurium*. *J. Bacteriol.* **163**:500–505.
2038. **Turnowsky, F., K. Fuchs, C. Jeschek, and G. Hogenauer.** 1989. *envM* genes of *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **171**:6555–6565.
2039. **Tyler, B. M., A. B. DeLeo, and B. Magasanik.** 1974. Activation of transcription of *hut* DNA by glutamine synthetase. *Proc. Natl. Acad. Sci. USA* **71**:225–229.
2040. **Ueki, T., T. Mitsui, and H. Nikaido.** 1979. X-ray diffraction studies of outer membranes of *Salmonella typhimurium*. *J. Biochem.* **85**:173–182.
2041. **Ueno, T., K. Oosawa, and S. Aizawa.** 1992. M ring, S ring and proximal rod of the flagellar basal body of *Salmonella typhimurium* are composed of subunits of a single protein, FliF. *J. Mol. Biol.* **227**:672–677.
2042. **Ueno, T., K. Oosawa, and S. Aizawa.** 1994. Domain structures of the MS ring component protein (FliF) of the flagellar basal body of *Salmonella typhimurium*. *J. Mol. Biol.* **236**:546–555.
2043. **Uerkvitz, W., and C. F. Beck.** 1981. Periplasmic phosphatases in *Salmonella typhimurium* Lt-2. A biochemical, physiological, and partial genetic analysis of three nucleoside monophosphate dephosphorylating enzymes. *J. Biol. Chem.* **256**:382–389.

2044. **Umbarger, H. E.** 1980. Comments on the role of aminoacyl-tRNA in the regulation of amino acid biosynthesis. *Cold Spring Harbor Monogr. Ser.* **9B**:453–467.
2045. **Umbarger, H. E., M. A. Umbarger, and P. M. L. Sui.** 1963. Biosynthesis of serine in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **85**:1431–1439.
2046. **Uomini, J. R., and J. R. Roth.** 1974. Suppressor-dependent frameshift mutants of bacteriophage P22. *Mol. Gen. Genet.* **134**:237–247.
2047. **Urbanowski, M. L., L. S. Plamann, and G. V. Stauffer.** 1987. Mutations affecting the regulation of the *metB* gene of *Salmonella typhimurium* LT2. *J. Bacteriol.* **169**:126–130.
2048. **Urbanowski, M. L., M. D. Plamann, and G. V. Stauffer.** 1983. Comparison of the regulatory regions of the *glyA* genes of *Escherichia coli* and *Salmonella typhimurium*, abstr. H159, p. 112. *Abstr. Annu. Meet. Am. Soc. Microbiol.* 1983.
2049. **Urbanowski, M. L., M. D. Plamann, L. T. Stauffer, and G. V. Stauffer.** 1984. Cloning and characterization of the gene for *Salmonella typhimurium* serine hydroxymethyltransferase. *Gene* **27**:47–54.
2050. **Urbanowski, M. L., and G. V. Stauffer.** 1985. Cloning and initial characterization of the *metJ* and *metB* genes from *Salmonella typhimurium* LT2. *Gene* **35**:187–197.
2051. **Urbanowski, M. L., and G. V. Stauffer.** 1985. Nucleotide sequence and biochemical characterization of the *metJ* gene from *Salmonella typhimurium* LT2. *Nucleic Acids Res.* **13**:673–685.
2052. **Urbanowski, M. L., and G. V. Stauffer.** 1986. Autoregulation by tandem promoters of the *Salmonella typhimurium* LT2 *metJ* gene. *J. Bacteriol.* **165**:740–745.
2053. **Urbanowski, M. L., and G. V. Stauffer.** 1986. The *metH* gene from *Salmonella typhimurium* LT2: cloning and initial characterization. *Gene* **44**:211–217.
2054. **Urbanowski, M. L., and G. V. Stauffer.** 1987. Regulation of the *metR* gene of *Salmonella typhimurium*. *J. Bacteriol.* **169**:5841–5844.
2055. **Urbanowski, M. L., and G. V. Stauffer.** 1988. The control region of the *metH* gene of *Salmonella typhimurium* LT2: an atypical *met* promoter. *Gene* **73**:193–200.
2056. **Urbanowski, M. L., and G. V. Stauffer.** 1989. Role of homocysteine in *metR*-mediated activation of the *metE* and *metH* genes in *Salmonella typhimurium* and *Escherichia coli*. *J. Bacteriol.* **171**:3277–3281.
2057. **Urbanowski, M. L., and G. V. Stauffer.** 1989. Genetic and biochemical analysis of the MetR activator-binding site in the *metE metR* control region of *Salmonella typhimurium*. *J. Bacteriol.* **171**:5620–5629.
2058. **Urbanowski, M. L., L. T. Stauffer, L. S. Plamann, and G. V. Stauffer.** 1987. A new methionine locus, *metR*, that encodes a *trans*-acting protein required for activation of *metE* and *metH* in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **169**:1391–1397.
2059. **Vaara, M.** 1980. Increased outer membrane resistance to ethyleneaminetetraacetate and cations in novel lipid A mutants. *J. Bacteriol.* **148**:426–434.
2060. **Vaara, M.** 1981. Effect of ionic strength on polymyxin resistance of *pmrA* mutants of *Salmonella*. *FEMS Microbiol. Lett.* **11**:321–326.
2061. **Vaara, M., and T. Vaara.** 1981. Outer membrane permeability barrier disruption by polymyxin in polymyxin-susceptible and -resistant *Salmonella typhimurium*. *Antimicrob. Agents Chemother.* **19**:578–583.
2062. **Vaara, M., T. Vaara, M. Jensen, I. Helander, M. Nurminen, E. T. Rietschel, and P. H. Makela.** 1981. Characterization of the lipopolysaccharide from the polymyxin-resistant *pmrA* mutants of *Salmonella typhimurium*. *FEBS Lett.* **129**:145–149.
2063. **Vaara, M., T. Vaara, and M. Sarvas.** 1979. Decreased binding of polymyxin by polymyxin-resistant mutants of *Salmonella typhimurium*. *J. Bacteriol.* **139**:664–667.
2064. **Vaara, M., P. Viljanen, S. Sukupolvi, and T. Vaara.** 1985. Does polymyxin B nonapeptide increase outer membrane permeability in antibiotic supersensitive enterobacterial mutants? *FEMS Microbiol. Lett.* **26**:289–294.
2065. **Valtonen, M. V., U. M. Larinkari, M. Posila, V. V. Valtonen, and P. H. Makela.** 1976. Effect of enterobacterial common antigen on mouse virulence of *Salmonella typhimurium*. *Infect. Immun.*

- 13:1601–1605.
2066. **Van den Bosch, J. L., D. R. Kurlandsky, R. Urdangaray, and G. W. Jones.** 1989. Evidence of coordinate regulation of virulence in *Salmonella typhimurium* involving the *rsk* element of the 95-kilobase plasmid. *Infect. Immun.* **57**:2566–2568.
2067. **Van den Bosch, J. L., D. K. Rabert, D. R. Kurlandsky, and G. W. Jones.** 1989. Sequence analysis of *rsk*, a portion of the 95-kilobase plasmid of *Salmonella typhimurium* associated with resistance to the bactericidal activity of serum. *Infect. Immun.* **57**:850–857.
2068. **van der Vlag, J., K. van Dam, and P. W. Postma.** 1994. Quantification of the regulation of glycerol and maltose metabolism by IIA^{Glc} of the phosphoenolpyruvate-dependent glucose phosphotransferase system in *Salmonella typhimurium*. *J. Bacteriol.* **176**:3518–3526.
2069. **Van der Werf, R., and D. E. Koshland, Jr.** 1977. Identification of a γ -glutamyl methyl ester in bacterial membrane protein involved in chemotaxis. *J. Biol. Chem.* **252**:2793–2795.
2070. **van Dijl, J. M., A. de Jong, H. Smith, S. Bron, and G. Venema.** 1991. Lack of specific hybridization between the *lep* genes of *Salmonella typhimurium* and *Bacillus licheniformis*. *FEMS Microbiol. Lett.* **65**:345–351.
2071. **van Dijl, J. M., R. van den Bergh, T. Reversma, H. Smith, S. Bron, and G. Venema.** 1990. Molecular cloning of the *Salmonella typhimurium lep* gene in *Escherichia coli*. *Mol. Gen. Genet.* **223**:233–240.
2072. **Van Dyk, T. K., and R. A. LaRossa.** 1986. Sensitivity of a *Salmonella typhimurium aspC* mutant to sulfometuron methyl, a potent inhibitor of acetolactate synthase II. *J. Bacteriol.* **165**:386–392.
2073. **Van Dyk, T. K., and R. A. LaRossa.** 1987. Involvement of *ack-pta* operon products in alpha-ketobutyrate metabolism by *Salmonella typhimurium*. *Mol. Gen. Genet.* **207**:435–440.
2074. **Van Dyk, T. K., D. R. Smulski, and Y.-Y. Chang.** 1987. Pleiotropic effects of *poxA* regulatory mutations of *Escherichia coli* and *Salmonella typhimurium*, mutations conferring sulfometuron methyl and α -ketobutyrate hypersensitivity. *J. Bacteriol.* **169**:4540–4546.
2075. **Van Pel, A., and C. Colson.** 1974. DNA restriction and modification systems in *Salmonella*. II. Genetic complementation between the K and B systems of *Escherichia coli* and the *Salmonella typhimurium* system, SB. *Mol. Gen. Genet.* **135**:51–60.
2076. **Vartak, N. B., J. Reizer, A. Reizer, J. T. Gripp, E. A. Groisman, L. F. Wu, J. M. Tomich, and M. H. Saier, Jr.** 1991. Sequence and evolution of the FruR protein of *Salmonella typhimurium*: a pleiotropic transcriptional regulatory protein possessing both activator and repressor functions which is homologous to the periplasmic ribose-binding protein. *Res. Microbiol.* **142**:951–963.
2077. **Vary, P. S., and B. A. D. Stocker.** 1973. Nonsense motility mutants of *Salmonella typhimurium*. *Genetics* **73**:229–245.
2078. **Vaughan, P., and B. Sedgwick.** 1991. A weak adaptive response to alkylation damage in *Salmonella typhimurium*. *J. Bacteriol.* **173**:3656–3662.
2079. **Verma, N. K., N. B. Quigley, and P. R. Reeves.** 1988. O-antigen variation in *Salmonella* spp.: *rfb* gene clusters of three strains. *J. Bacteriol.* **170**:130–107.
2080. **Vimr, E. R., L. Green, and C. G. Miller.** 1983. Oligopeptidase-deficient mutants of *Salmonella typhimurium*. *J. Bacteriol.* **153**:1259–1265.
2081. **Vimr, E. R., and C. G. Miller.** 1983. Dipeptidyl carboxypeptidase-deficient mutants of *Salmonella typhimurium*. *J. Bacteriol.* **153**:1252–1258.
2082. **Vinitzky, A., H. Teng, and C. T. Grubmeyer.** 1991. Cloning and nucleic acid sequence of the *Salmonella typhimurium pncB* gene and structure of nicotinate phosphoribosyltransferase. *J. Bacteriol.* **173**:536–540.
2083. **Vogel, H. J., D. F. Baron, and A. Baich.** 1963. Induction of acetyl ornithine δ -transaminase during pathway-wide repression, p. 293–300. In H. J. Vogel, V. Bryson, and J. O. Lampen (ed.), *Informational Macromolecules*. Academic Press, Inc., New York.
2084. **Vogel, T., M. Meyers, J. S. Kovach, and R. F. Goldberger.** 1972. Specificity of interaction between the first enzyme for histidine biosynthesis and aminoacylated histidine transfer ribonucleic acid. *J. Bacteriol.* **112**:126–130.

2085. **Vogler, A. P., M. Homma, V. M. Irikura, and R. M. Macnab.** 1991. *Salmonella typhimurium* mutants defective in flagellar filament regrowth and sequence similarity of FlilI to F₀F₁, vacuolar, and archaeobacterial ATPase subunits. *J. Bacteriol.* **173**:3564–3572.
2086. **Voll, M. J., E. Appella, and R. G. Martin.** 1967. Purification and composition studies of phosphoribosyl-adenosine triphosphate:pyrophosphate phosphoribosyl transferase, the first enzyme of histidine biosynthesis. *J. Biol. Chem.* **242**:1760–1767.
2087. **Voll, M. J., L. A. Cohen, and J. J. Germida.** 1979. *his*-linked hydrogen sulfide locus of *Salmonella typhimurium* and its expression in *Escherichia coli*. *J. Bacteriol.* **139**:1082–1084.
2088. **Voll, M. J., L. M. Shiller, and J. Castrilli.** 1974. *his*-linked hydrogen sulfide locus in *Salmonella typhimurium*. *J. Bacteriol.* **120**:902–905.
2089. **Vuorio, R., T. Harkonen, M. Tolvanen, and M. Vaara.** 1994. The novel hexapeptide motif found in the acyltransferases LpxA and LpxD of lipid A biosynthesis is conserved in various bacteria. *FEBS Lett.* **337**:289–292.
2090. **Vuorio, R., L. Hirvas, and M. Vaara.** 1991. The Ssc protein of enteric bacteria has significant homology to the acyltransferase Lpxa of lipid A biosynthesis, and to three acetyltransferases. *FEBS Lett.* **292**:90–94.
2091. **Vuorio, R., and M. Vaara.** 1992. Mutants carrying conditionally lethal mutations in outer membrane genes *omsA* and *firA* (*ssc*) are phenotypically similar, and *omsA* is allelic to *firA*. *J. Bacteriol.* **174**:7090–7097.
2092. **Wainscott, V. J., and J. J. Ferretti.** 1978. Biochemical-genetic study of the first enzyme of histidine biosynthesis in *Salmonella typhimurium*: substrate and feedback binding regions. *J. Bacteriol.* **133**:114–121.
2093. **Walenga, R. W., and M. J. Osborn.** 1980. Biosynthesis of lipid A. *In-vivo* formation of an intermediate containing 3-deoxy-D-manno-octulosonate in a mutant of *Salmonella typhimurium*. *J. Biol. Chem.* **255**:4252–4256.
2094. **Walter, C., K. Honer zu Bentrup, and E. Schneider.** 1992. Large scale purification, nucleotide binding properties, and ATPase activity of the MalK subunit of *Salmonella typhimurium* maltose transport complex. *J. Biol. Chem.* **267**:8863–8869.
2095. **Walter, C., S. Wilken, and E. Schneider.** 1992. Characterization of side-directed mutations in conserved domains of MalK, a bacterial member of the ATP-binding cassette (ABC) family. *FEBS Lett.* **303**:41–44.
2096. **Wang, E., and D. E. Koshland, Jr.** 1980. Receptor structure in the bacterial sensing system. *Proc. Natl. Acad. Sci. USA* **77**:7157–7161.
2097. **Wang, J. Y. J., D. O. Clegg, and D. E. Koshland, Jr.** 1981. Molecular cloning and amplification of the adenylate cyclase gene. *Proc. Natl. Acad. Sci. USA* **78**:4684–4688.
2098. **Wang, L., and P. R. Reeves.** 1994. Involvement of the galactosyl-1-phosphate transferase encoded by the *Salmonella enterica rfbP* gene in O-antigen subunit processing. *J. Bacteriol.* **176**:4348–4356.
2099. **Wang, L., L. K. Romana, and P. R. Reeves.** 1992. Molecular analysis of a *Salmonella enterica* group E1 *rfb* gene cluster: O antigen and the genetic basis of the major polymorphism. *Genetics* **130**:429–443.
2100. **Wang, Q., M. Sacco, E. Ricca, C. T. Lago, M. DeFelice, and J. M. Calvo.** 1993. Organization of Lrp-binding sites upstream of *ilvIH* in *Salmonella typhimurium*. *Mol. Microbiol.* **7**:883–891.
2101. **Warner, T. G., R. Harris, R. McDowell, and E. R. Vimr.** 1992. Photolabelling of *Salmonella typhimurium* LT2 sialidase. Identification of a peptide with a predicted structural similarity to the active sites of influenza-virus sialidases. *Biochem. J.* **285**:957–964.
2102. **Warrick, H. M., B. L. Taylor, and D. E. Koshland, Jr.** 1977. Chemotactic mechanism of *Salmonella typhimurium*: preliminary mapping and characterization of mutants. *J. Bacteriol.* **130**:223–231.
2103. **Wasmuth, J. J., and H. E. Umbarger.** 1973. Effect of isoleucine, valine, or leucine starvation on the potential for formation of the branched-chain amino acid biosynthetic enzymes. *J. Bacteriol.* **116**:548–561.

2104. **Wasmuth, J. J., and H. E. Umbarger.** 1973. Participation of branched-chain amino acid analogues in multivalent repression. *J. Bacteriol.* **116**:562–570.
2105. **Wasserman, S. A., E. Daub, P. Grisafi, D. Botstein, and C. T. Walsh.** 1984. Catabolic alanine racemase from *Salmonella typhimurium*: DNA sequence, enzyme purification, and characterization. *Biochemistry* **23**:5182–5187.
2106. **Wasserman, S. A., C. T. Walsh, and D. Botstein.** 1983. Two alanine racemase genes in *Salmonella typhimurium* that differ in structure and function. *J. Bacteriol.* **153**:1439–1450.
2107. **Watanabe, H., H. Hashimoto, and S. Misuhashi.** 1980. *Salmonella typhimurium* LT-2 mutation affecting the deletion of resistance determinants on R plasmids. *J. Bacteriol.* **142**:145–152.
2108. **Watanabe, M., M. Ishidate, Jr., and T. Nohmi.** 1990. Nucleotide sequence of *Salmonella typhimurium* nitroreductase gene. *Nucleic Acids Res.* **18**:1059.
2109. **Watanabe, M., T. Sofuni, and T. Nohmi.** 1992. Involvement of Cys69 residue in the catalytic mechanism of N-hydroxyarylamine O-acetyltransferase of *Salmonella typhimurium*. Sequence similarity at the amino acid level suggests a common catalytic mechanism of acetyltransferase for *S. typhimurium* and higher organisms. *J. Biol. Chem.* **267**:8429–8436.
2110. **Watanabe, T., T. Arai, and T. Hattori.** 1970. Effects of cell wall polysaccharide on the mating ability of *Salmonella typhimurium*. *Nature (London)* **225**:70–71.
2111. **Waxman, L., and A. L. Goldberg.** 1985. Protease La, the *lon* gene product, cleaves specific fluorogenic peptides in an ATP-dependent reaction. *J. Biol. Chem.* **260**:12022–12028.
2112. **Way, J. C., M. A. Davis, D. Morisato, D. E. Roberts, and N. Kleckner.** 1984. New Tn10 derivatives for transposon mutagenesis and for construction of *lacZ* operon fusions by transposition. *Gene* **32**:369–379.
2113. **Wehr, C. T.** 1973. Isolation and properties of a ribonuclease-deficient mutant of *Salmonella typhimurium*. *J. Bacteriol.* **114**:96–102.
2114. **Wei, B. Y., C. Bradbeer, and R. J. Kadner.** 1992. Conserved structural and regulatory regions in the *Salmonella typhimurium* *btuB* gene for the outer membrane vitamin B12 transport protein. *Res. Microbiol.* **143**:459–466.
2115. **Wei, L.-N., and T. M. Joys.** 1985. Covalent structure of three phase-1 flagellar filament proteins of *Salmonella*. *J. Mol. Biol.* **186**:791–803.
2116. **Wei, L.-N., and T. M. Joys.** 1986. The nucleotide sequence of the H-1r gene of *Salmonella rubislaw*. *Nucleic Acids Res.* **14**:8227.
2117. **Wei, R. W., and S. Kustu.** 1981. Glutamine auxotrophs with mutations in a nitrogen regulatory gene, *ntnC*, that is near *glnA*. *Mol. Gen. Genet.* **183**:392–397.
2118. **Weigand, R. A., and L. I. Rothfield.** 1976. Genetic and physiological classification of periplasmic-leaky mutants of *Salmonella typhimurium*. *J. Bacteriol.* **125**:340–345.
2119. **Weigand, R. A., K. D. Vinci, and L. T. Rothfield.** 1976. Morphogenesis of the bacterial division septum: a new class of septation defective mutants. *Proc. Natl. Acad. Sci. USA* **73**:1882–1886.
2120. **Weigel, N., A. Kukuruzinska, A. Nakazawa, E. B. Waygood, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Phosphoryl transfer reactions catalyzed by enzyme I of *Salmonella typhimurium*. *J. Biol. Chem.* **257**:14477–14491.
2121. **Weigel, N., D. A. Powers, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Primary structure and active site of a general phosphocarrier protein (HPr) from *Salmonella typhimurium*. *J. Biol. Chem.* **257**:14499–14509.
2122. **Weigel, N., E. B. Waygood, M. A. Kukuruzinska, A. Nakazawa, and S. Roseman.** 1982. Sugar transport by the bacterial phosphotransferase system. Isolation and characterization of enzyme I from *Salmonella typhimurium*. *J. Biol. Chem.* **257**:14461–14469.
2123. **Weinberg, R. A., and R. O. Burns.** 1984. Regulation of expression of the *ilvB* operon in *Salmonella typhimurium*. *J. Bacteriol.* **160**:833–841.
2124. **Wek, R. C., and G. W. Hatfield.** 1986. Nucleotide sequence and in vivo expression of the *ilvY* and *ilvC* genes in *Escherichia coli* K12. Transcription from divergent overlapping promoters. *J. Biol. Chem.* **261**:2441–2450.

2125. **Weppelman, R., L. D. Kier, and B. N. Ames.** 1977. Properties of two phosphatases and a cyclic phosphodiesterase of *Salmonella typhimurium*. *J. Bacteriol.* **130**:411–419.
2126. **Wessler, S. R., and J. M. Calvo.** 1981. Control of *leu* operon expression in *Escherichia coli* by a transcription attenuation mechanism. *J. Mol. Biol.* **149**:579–597.
2127. **West, T. P., and G. A. O'Donovan.** 1982. Repression of cytosine deaminase by pyrimidines in *Salmonella typhimurium*. *J. Bacteriol.* **149**:1171–1174.
2128. **West, T. P., T. W. Traut, M. S. Shanley, and G. A. O'Donovan.** 1985. A *Salmonella typhimurium* strain defective in uracil catabolism and beta-alanine synthesis. *J. Gen. Microbiol.* **131**:1083–1090.
2129. **Westby, C. A., and J. S. Gots.** 1969. Genetic blocks and unique features in the biosynthesis of 5'-phosphoribosyl-*N*-formyl-glycinamide in *Salmonella typhimurium*. *J. Biol. Chem.* **244**:2095–2102.
2130. **Whalen, W. A., and C. M. Berg.** 1984. Gratuitous repression of *avtA* in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **158**:571–574.
2131. **Whitehouse, J. M., and D. A. Smith.** 1974. Methionine and vitamin B₁₂ repression and precursor induction in the regulation of homocysteine methylation in *Salmonella typhimurium*. *Mol. Gen. Genet.* **120**:341–353.
2132. **Whitehouse, J. M., and D. A. Smith.** 1974. The involvement of methionine regulatory mutants in the suppression of B₁₂-dependent homocysteine transmethylase (*metH*) mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **129**:259–267.
2133. **Whitfield, H. J., and G. Levine.** 1973. Isolation and characterization of a mutant of *Salmonella typhimurium* deficient in a major deoxyribonucleic acid polymerase activity. *J. Bacteriol.* **116**:54–58.
2134. **Whitfield, H. J., Jr.** 1971. Purification and properties of the wild type and a feedback resistant phosphoribosyladenosine triphosphate:pyrophosphate phosphoribosyltransferase. *J. Biol. Chem.* **246**:899–909.
2135. **Wiater, A., M. Filutowicz, and D. Hulanicka.** 1982. A new class of mutants of the *cysB* regulatory gene for cysteine biosynthesis in *Salmonella typhimurium*. *J. Gen. Microbiol.* **128**:1785–1790.
2136. **Wiater, A., and D. Hulanicka.** 1978. The regulatory *cysK* mutant of *Salmonella typhimurium*. *Acta Biochim. Pol.* **25**:281–288.
2137. **Wiater, A., and T. Kłopotowski.** 1972. Mutations rendering *Salmonella typhimurium* resistant to 3-amino triazole in the presence of histidine. *Acta Biochim. Pol.* **19**:191–199.
2138. **Widenhorn, K. A., W. Boos, J. M. Somers, and W. W. Kay.** 1988. Cloning and properties of the *Salmonella typhimurium* tricarboxylate transport operon in *Escherichia coli*. *J. Bacteriol.* **170**:883–888.
2139. **Widenhorn, K. A., J. M. Somers, and W. W. Kay.** 1988. Expression of the divergent tricarboxylate transport operon (*tctI*) of *Salmonella typhimurium*. *J. Bacteriol.* **170**:3223–3227.
2140. **Widenhorn, K. A., J. M. Somers, and W. W. Kay.** 1989. Genetic regulation of the tricarboxylate transport operon (*tctI*) of *Salmonella typhimurium*. *J. Bacteriol.* **171**:4436–4441.
2141. **Wild, J., M. Filutowicz, and T. Kłopotowski.** 1978. Utilization of D-amino acids by *dadR* mutants of *Salmonella typhimurium*. *Arch. Microbiol.* **118**:71–77.
2142. **Wild, J., and T. Kłopotowski.** 1975. Insensitivity of D-amino acid dehydrogenase synthesis to catabolite repression in *dadR* mutants of *Salmonella typhimurium*. *Mol. Gen. Genet.* **136**:63–73.
2143. **Wild, J., W. Walczak, K. Krajewska-Grynkiewicz, and T. Kłopotowski.** 1974. D-Amino acid dehydrogenase. The enzyme of the first step of D-histidine and D-methionine racemization in *Salmonella typhimurium*. *Mol. Gen. Genet.* **128**:131–146.
2144. **Wilkinson, R. G., P. Gemski, Jr., and B. A. D. Stocker.** 1972. Non-smooth mutants of *Salmonella typhimurium*: differentiation by phage sensitivity and genetic mapping. *J. Gen. Microbiol.* **70**:527–554.
2145. **Wilkinson, R. G., and B. A. D. Stocker.** 1968. Genetics and cultural properties of mutants of *Salmonella typhimurium* lacking glucosyl or galactosyl lipopolysaccharide transferases. *Nature (London)* **217**:955–957.
2146. **Williams, J. C., C. E. Lee, and J. R. Wild.** 1980. Genetics and biochemical characterization of

- distinct transport systems for uracil, uridine and cytidine in *Salmonella typhimurium*. *Mol. Gen. Genet.* **178**:121–130.
2147. **Williams, J. C., and G. A. O'Donovan.** 1973. Repression of enzyme synthesis of the pyrimidine pathway in *Salmonella typhimurium*. *J. Bacteriol.* **115**:1071–1076.
2148. **Williams, R. C., and C. H. Clarke.** 1974. The isolation and characterization of a mutant of *Salmonella typhimurium* defective in mutation frequency decline. *Mutat. Res.* **22**:243–253.
2149. **Willis, R. C., R. G. Morris, C. Cirakoglu, G. D. Schellenberg, N. H. Gerber, and C. E. Furlong.** 1974. Preparation of the periplasmic binding proteins from *Salmonella typhimurium* and *Escherichia coli*. *Arch. Biochem. Biophys.* **161**:64–75.
2150. **Winfield, S. L., and J. O. Falkinham, III.** 1981. Effect of *recA* and *polA* mutations on gene duplications in *Salmonella typhimurium*. *Mutat. Res.* **91**:15–20.
2151. **Wing, J. P.** 1968. Transduction by phage P22 in a recombination-deficient mutant of *Salmonella typhimurium*. *Virology* **36**:271–276.
2152. **Wing, J. P., M. Levine, and H. O. Smith.** 1968. Recombination-deficient mutant of *Salmonella typhimurium*. *J. Bacteriol.* **95**:1828–1834.
2153. **Wingfield, P., P. Graber, G. Turcatti, N. R. Movva, M. Pelletier, S. Craig, K. Rose, and C. G. Miller.** 1989. Purification and characterization of a methionine-specific aminopeptidase from *Salmonella typhimurium*. *Eur. J. Biochem.* **180**:23–32.
2154. **Winkler, M. E., D. J. Roth, and P. E. Hartman.** 1978. Promoter- and attenuator-related metabolic regulation of the *Salmonella typhimurium* histidine operon. *J. Bacteriol.* **133**:830–843.
2155. **Winkler, M. E., and C. Yanofsky.** 1981. Pausing of RNA polymerase during *in vitro* transcription of the tryptophan operon leader region. *Biochemistry* **20**:3738–3744.
2156. **Winston, F., and D. Botstein.** 1982. Control of lysogenization by phage P22. I. The P22 *cro* gene. *J. Mol. Biol.* **152**:209–232.
2157. **Winston, F., D. Botstein, and J. H. Miller.** 1979. Characterization of amber and ochre suppressors in *Salmonella typhimurium*. *J. Bacteriol.* **137**:433–439.
2158. **Woehlke, G., K. Wifling, and P. Dimroth.** 1992. Sequence of the sodium ion pump oxaloacetate decarboxylase from *Salmonella typhimurium*. *J. Biol. Chem.* **267**:22798–22803.
2159. **Wolf, R. E., Jr., and J. C. Loper.** 1970. The differential inactivation of histidinol dehydrogenase from *Salmonella typhimurium* by sulfhydryl reagents. *J. Biol. Chem.* **244**:6297–6303.
2160. **Wollin, R., E. S. Creeger, L. I. Rothfield, B. A. D. Stocker, and A. A. Lindberg.** 1983. *Salmonella typhimurium* mutants defective in UDP-D-galactose:lipopolysaccharide α 1,6-D-galactosyltransferase. *J. Biol. Chem.* **258**:3769–3774.
2161. **Wong, A., L. Kean, and R. Maurer.** 1988. Sequence of the *dnaB* gene of *Salmonella typhimurium*. *J. Bacteriol.* **170**:2668–2675.
2162. **Wong, K. K., and M. McClelland.** 1992. A *BlnI* restriction map of the *Salmonella typhimurium* LT2 genome. *J. Bacteriol.* **174**:1656–1661.
2163. **Wong, K. K., and M. McClelland.** 1992. Dissection of the *Salmonella typhimurium* genome by use of a Tn5 derivative carrying rare restriction sites. *J. Bacteriol.* **174**:3807–3811.
2164. **Wong, K. K., and M. McClelland.** 1994. Stress-inducible gene of *Salmonella typhimurium* identified by arbitrarily primed PCR of RNA. *Proc. Natl. Acad. Sci. USA* **91**:639–643.
2165. **Wong, K. K., K. L. Suen, and H. S. Kwan.** 1989. Transcription of *pfl* is regulated by anaerobiosis, catabolite repression, pyruvate, and *oxrA*: *pfl*::Mu *da* operon fusions of *Salmonella typhimurium*. *J. Bacteriol.* **171**:4900–4905.
2166. **Wong, K. K., R. M. Wong, K. E. Rudd, and M. McClelland.** 1994. High-resolution restriction map of a 240-kilobase region spanning 91 to 96 minutes on the *Salmonella typhimurium* LT2 chromosome. *J. Bacteriol.* **176**:5729–5734.
2167. **Woodgate, R., A. S. Levine, W. H. Koch, T. A. Cebula, and E. Eisenstadt.** 1991. Induction and cleavage of *Salmonella typhimurium* UmuD protein. *Mol. Gen. Genet.* **229**:81–85.
2168. **Wray, C., W. J. Sojka, J. A. Morris, and W. J. B. Morgan.** 1977. The immunization of mice and calves with *galE* mutants of *Salmonella typhimurium*. *J. Hyg.* **79**:17–24.
2169. **Wu, J. Y., L. M. Siegel, and N. M. Kredich.** 1991. High-level expression of *Escherichia coli*

- NADPH-sulfite reductase: requirement for a cloned *cysG* plasmid to overcome limiting siroheme cofactor. *J. Bacteriol.* **173**:325–333.
2170. **Wu, T. T.** 1966. A model for three-point analysis of random general transduction. *Genetics* **54**:405–410.
2171. **Wu, W. F., M. L. Urbanowski, and G. V. Stauffer.** 1992. Role of the MetR regulatory system in vitamin B₁₂-mediated repression of the *Salmonella typhimurium metE* gene. *J. Bacteriol.* **174**:4833–4837.
2172. **Wu, W. F., M. L. Urbanowski, and G. V. Stauffer.** 1993. MetJ-mediated regulation of the *Salmonella typhimurium metE* and *metR* genes occurs through a common operator region. *FEMS Microbiol. Lett.* **108**:145–150.
2173. **Wyche, J. H., B. Ely, T. A. Cebula, M. C. Snead, and P. E. Hartman.** 1974. Histidyl-transfer ribonucleic acid synthetase in positive control of the histidine operon in *Salmonella typhimurium*. *J. Bacteriol.* **117**:708–716.
2174. **Wyche, J. H., J. Kennedy, Z. Hartman, P. E. Hartman, and J. Diven.** 1974. Round-cell mutant of *Salmonella typhimurium*. *J. Bacteriol.* **120**:965–969.
2175. **Wyk, P., and P. Reeves.** 1989. Identification and sequence of the gene for abequoise synthase, which confers antigenic specificity on group B salmonellae: homology with galactose epimerase. *J. Bacteriol.* **171**:5687–5693.
2176. **Wylie, D., A. Stock, C.-Y. Wong, and J. Stock.** 1988. Sensory transduction in bacterial chemotaxis involves phosphotransfer between *che* proteins. *Biochem. Biophys. Res. Commun.* **151**:891–896.
2177. **Xu, K., J. Delling, and T. Elliott.** 1992. The genes required for heme synthesis in *Salmonella typhimurium* include those encoding alternative functions for aerobic and anaerobic coproporphyrinogen oxidation. *J. Bacteriol.* **174**:3953–3963.
2178. **Xu, K., and T. Elliott.** 1993. An oxygen-dependent coproporphyrinogen oxidase encoded by the *hemF* gene of *Salmonella typhimurium*. *J. Bacteriol.* **175**:4990–4999.
2179. **Xu, K., and T. Elliott.** 1994. Cloning, DNA sequence, and complementation analysis of the *Salmonella typhimurium hemN* gene encoding a putative oxygen-independent coproporphyrinogen III oxidase. *J. Bacteriol.* **176**:3196–3203.
2180. **Yagil, E., and E. Hermoni.** 1976. Repression of alkaline phosphatase in *Salmonella typhimurium* carrying a *phoA*⁺ *phoR*⁻ episome from *Escherichia coli*. *J. Bacteriol.* **128**:661–664.
2181. **Yamada, M., A. Hakura, T. Sofuni, and T. Nohmi.** 1993. New method for gene disruption in *Salmonella typhimurium*: construction and characterization of an *ada*-deletion derivative of *Salmonella typhimurium* TA1535. *J. Bacteriol.* **175**:5539–5547.
2182. **Yamada, T., and J. Davies.** 1971. A genetic and biochemical study of streptomycin and spectinomycin resistance in *Salmonella typhimurium*. *Mol. Gen. Genet.* **110**:197–210.
2183. **Yamada, T., Y. Murooka, and T. Harada.** 1978. Comparative immunological studies of arylsulfatase in bacteria of the family *Enterobacteriaceae*: occurrence of arylsulfatase protein regulated by sulfur compounds and tyramine. *J. Bacteriol.* **133**:536–541.
2184. **Yamagata, H., K. Nakamura, and M. Inouye.** 1980. Comparison of the lipoprotein gene among the *Enterobacteriaceae*. DNA sequence of *Erwinia amylovora* lipoprotein gene. *J. Biol. Chem.* **256**:2194–2198.
2185. **Yamaguchi, S., S.-I. Aizawa, M. Kihara, M. Isomura, C. J. Jones, and R. M. Macnab.** 1986. Genetic evidence for a switching and energy-transducing complex in the flagellar motor of *Salmonella typhimurium*. *J. Bacteriol.* **168**:1172–1179.
2186. **Yamaguchi, S., H. Fujita, A. Ishihara, S.-I. Aizawa, and R. M. Macnab.** 1986. Subdivision of flagellar genes of *Salmonella typhimurium* into regions responsible for assembly, rotation, and switching. *J. Bacteriol.* **166**:187–193.
2187. **Yamaguchi, S., H. Fujita, T. Kuroiwa, and T. Iino.** 1977. Sensitivity of non-flagellate *Salmonella* mutants to the flagellotropic bacteriophage chi. *J. Gen. Microbiol.* **99**:209–214.
2188. **Yamaguchi, S., H. Fujita, K. Sugata, T. Taira, and T. Iino.** 1984. Genetic analysis of H2, the structural gene for phase-2 flagellin in *Salmonella*. *J. Gen. Microbiol.* **130**:255–265.

2189. **Yamaguchi, S., H. Fujita, T. Taira, K. Kutsukake, M. Homma, and T. Iino.** 1984. Genetic analysis of three additional *fla* genes in *Salmonella typhimurium*. *J. Gen. Microbiol.* **130**:3339–3342.
2190. **Yamaguchi, S., and T. Iino.** 1969. Genetic determination of the antigenic specificity of flagellar protein in *Salmonella*. *J. Gen. Microbiol.* **55**:59–74.
2191. **Yamaguchi, S., and T. Iino.** 1970. Serological and fingerprinting analyses of mutant flagella antigens in *Salmonella*. *J. Gen. Microbiol.* **64**:311–318.
2192. **Yamaguchi, S., T. Iino, T. Horiguchi, and K. Ohta.** 1972. Genetic analysis of *fla* and *mot* cistrons closely linked to H1 in *Salmonella abortus-equi* and its derivatives. *J. Gen. Microbiol.* **70**:59–75.
2193. **Yamamoto, K., and Y. Imae.** 1993. Cloning and characterization of the *Salmonella typhimurium*-specific chemoreceptor Tcp for taxis to citrate and from phenol. *Proc. Natl. Acad. Sci. USA* **90**:217–221.
2194. **Yamamoto, N.** 1978. Somatic O1 antigen conversion of *Salmonella typhimurium* by a type B phage P221dis hybrid between P22 and FELS1 phages. *J. Gen. Virol.* **41**:367–376.
2195. **Yamamoto, N., and M. L. Droffner.** 1985. Mechanisms determining aerobic or anaerobic growth in the facultative anaerobe *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **82**:2077–2081.
2196. **Yamashita, M. M., R. J. Almassy, C. A. Janson, D. Cascio, and D. Eisenberg.** 1989. Refined atomic model of glutamine synthetase at 3.5 Å resolution. *J. Biol. Chem.* **264**:17681–17690.
2197. **Yan, Y., and M. Demerec.** 1965. Genetic analysis of pyrimidine mutants of *Salmonella typhimurium*. *Genetics* **52**:643–651.
2198. **Yancey, R. J., S. A. L. Breeding, and C. E. Lankford.** 1979. Enterochelin (enterobactin): virulence factor for *Salmonella typhimurium*. *Infect. Immun.* **24**:174–180.
2199. **Yang, H. J., B. Lee, and J. L. Haslam.** 1973. Studies on histidinol dehydrogenase. Preliminary crystallographic data. *J. Mol. Biol.* **81**:517–519.
2200. **Yang, S.-L., J. M. Becker, and F. Naider.** 1977. Transport of [¹⁴C]Gly-Pro in a proline peptidase mutant of *Salmonella typhimurium*. *Biochim. Biophys. Acta* **471**:135–144.
2201. **Yang, Y.-L., D. Goldrick, and J.-S. Hong.** 1988. Identification of the products and nucleotide sequences of two regulatory genes involved in the exogenous induction of phosphoglycerate transport in *Salmonella typhimurium*. *J. Bacteriol.* **170**:4299–4303.
2202. **Yanofsky, C., S. S.-L. Li, V. Horn, and J. Rowe.** 1977. Structure and properties of a hybrid tryptophan synthetase α chain produced by genetic exchange between *Escherichia coli* and *Salmonella typhimurium*. *Proc. Natl. Acad. Sci. USA* **74**:286–290.
2203. **Yanofsky, C., and M. Van Cleemput.** 1982. Nucleotide sequence of *trpE* of *Salmonella typhimurium* and its homology with the corresponding sequence of *Escherichia coli*. *J. Mol. Biol.* **154**:235–246.
2204. **Yen, C., L. Green, and C. G. Miller.** 1980. Degradation of intracellular protein in *Salmonella typhimurium* peptidase mutants. *J. Mol. Biol.* **143**:21–33.
2205. **Yen, C., L. Green, and C. G. Miller.** 1980. Peptide accumulation during growth of peptidase deficient mutants. *J. Mol. Biol.* **143**:35–48.
2206. **Yoakum, G., and A. Eisenstark.** 1972. Toxicity of L-tryptophan photoproduct on recombinationless (*rec*) mutants of *Salmonella typhimurium*. *J. Bacteriol.* **112**:653–655.
2207. **Yokoto, T., and J. S. Gots.** 1970. Requirement of adenosine-3',5'-cyclic phosphate for flagella formation in *Escherichia coli* and *Salmonella typhimurium*. *J. Bacteriol.* **103**:513–516.
2208. **Yoshioka, K., S.-I. Aizawa, and S. Yamaguchi.** 1995. Flagellar filament structure and cell motility of *Salmonella typhimurium* mutants lacking part of the outer domain of flagellin. *J. Bacteriol.* **177**:1090–1093.
2209. **Young, B. G., and P. E. Hartman.** 1966. Sites of P22 and P221 prophage integration in *Salmonella typhimurium*. *Virology* **28**:265–270.
2210. **Young, B. S., S. K. Guterman, and A. Wright.** 1976. Temperature-sensitive ribonucleic acid polymerase mutant of *Salmonella typhimurium* with a defect in the β' subunit. *J. Bacteriol.* **127**:1292–1297.

2211. **Young, B. S., and A. Wright.** 1977. Multiple effects of an RNA polymerase β -prime mutation on *in-vitro* transcription. *Mol. Gen. Genet.* **155**:191–196.
2212. **Yourno, J.** 1968. Composition and subunit structure of histidinol dehydrogenase from *Salmonella typhimurium*. *J. Biol. Chem.* **243**:3277–3288.
2213. **Yourno, J.** 1970. Nature of the compensating frameshift in the double frameshift mutant *hisD3018 R5* of *Salmonella typhimurium*. *J. Mol. Biol.* **48**:437–442.
2214. **Yourno, J.** 1972. Externally suppressible +1 “glycine” frameshift: possible quadruplet isomers for glycine and proline. *Nature (London) New Biol.* **239**:219–221.
2215. **Yourno, J., and I. Ino.** 1968. Purification and crystallization for histidinol dehydrogenase from *Salmonella typhimurium*. *J. Biol. Chem.* **243**:3273–3276.
2216. **Yourno, J., T. Kohno, and J. R. Roth.** 1970. Enzyme evolution: generation of a bifunctional enzyme by fusion of adjacent genes. *Nature (London)* **228**:820–824.
2217. **Yu, C.-Q., and J.-S. Hong.** 1986. Identification and nucleotide sequence of the activator gene of the externally induced phosphoglycerate transport system of *Salmonella typhimurium*. *Gene* **45**:51–57.
2218. **Yuasa, R., M. Levinthal, and H. Nikaido.** 1969. Biosynthesis of cell wall lipopolysaccharide in mutants of *Salmonella*. V. A mutant of *Salmonella typhimurium* defective in the synthesis of cytidine diphosphoabequose. *J. Bacteriol.* **100**:433–444.
2219. **Yutani, K., T. Sato, K. Ogasahara, and E. W. Miles.** 1984. Comparison of denaturation of tryptophan synthase alpha-subunits from *Escherichia coli*, *Salmonella typhimurium*, and an interspecies hybrid. *Arch. Biochem. Biophys.* **229**:448–454.
2220. **Zabel, D. J., M. Trucksis, and R. E. Depew.** 1980. *Salmonella typhimurium* mutants with reduced levels of transfer ribonucleic acid-inhibitable endodeoxyribonucleolytic activity. *J. Bacteriol.* **144**:173–178.
2221. **Zahrt, T. C., G. C. Mora, and S. Maloy.** 1994. Inactivation of mismatch repair overcomes the barrier to transduction between *Salmonella typhimurium* and *Salmonella typhi*. *J. Bacteriol.* **176**:1527–1529.
2222. **Zak, V. L., and R. A. Kelln.** 1978. 5-Fluoroorotate-resistant mutants of *Salmonella typhimurium*. *Can. J. Microbiol.* **24**:1339–1345.
2223. **Zak, V. L., and R. A. Kelln.** 1981. *Salmonella typhimurium* mutant dependent upon carbamyl aspartate for resistance to 5-fluorouracil is specifically affected in ubiquinone biosynthesis. *J. Bacteriol.* **145**:1095–1098.
2224. **Zarlengo, M. H., G. W. Robinson, and R. O. Burns.** 1968. Threonine deaminase from *Salmonella typhimurium*. II. The subunit structure. *J. Biol. Chem.* **243**:186–191.
2225. **Zaror, I., I. Gomez, G. Castillo, A. Yudelevich, and A. Venegas.** 1988. Molecular cloning and expression in *E. coli* of a *Salmonella typhi* porin gene. *FEBS Lett.* **229**:77–81.
2226. **Zhu, N., B. M. Olivera, and J. R. Roth.** 1988. Identification of a repressor gene involved in the regulation of NAD de novo biosynthesis in *Salmonella typhimurium*. *J. Bacteriol.* **170**:117–125.
2227. **Zhu, N., B. M. Olivera, and J. R. Roth.** 1989. Genetic characterization of the *pnuC* gene, which encodes a component of the nicotinamide mononucleotide transport system in *Salmonella typhimurium*. *J. Bacteriol.* **171**:4402–4409.
2228. **Zhu, N., B. M. Olivera, and J. R. Roth.** 1991. Activity of the nicotinamide mononucleotide transport system is regulated in *Salmonella typhimurium*. *J. Bacteriol.* **173**:1311–1320.
2229. **Zhu, N., and J. R. Roth.** 1991. The *nadI* region of *Salmonella typhimurium* encodes a bifunctional regulatory protein. *J. Bacteriol.* **173**:1302–1310.
2230. **Zhyvoloup, A. N., M. I. Woodmaska, I. V. Kroupskaya, and E. B. Paton.** 1990. Nucleotide sequence of the *rplJL* operon and the deduced primary structure of the encoded L10 and L7/L12 proteins of *Salmonella typhimurium* compared to that of *Escherichia coli*. *Nucleic Acids Res.* **18**:4620.
2231. **Ziebell, R., F. P. Imray, and D. G. MacPhee.** 1977. DNA degradation in wild-type and repair-deficient strains of *Salmonella typhimurium* exposed to ultraviolet light or photodynamic treatment. *J. Gen. Microbiol.* **101**:143–149.
2232. **Zieg, J., M. Hilmen, and M. Simon.** 1978. Regulation of gene expression by site specific

- inversion. *Cell* **15**:237–244.
2233. **Zieg, J., M. Silverman, M. Hilmen, and M. Simon.** 1977. Recombinational switch for gene expression. *Science* **196**:170–172.
2234. **Zieg, J., M. Silverman, M. Hilmen, and M. I. Simon.** 1978. The mechanisms of phase variation. *Cold Spring Harbor Monogr. Ser.* **1978**:411–424.
2235. **Zieg, J., and M. Simon.** 1980. Analysis of the nucleotide sequence of an invertible controlling element. *Proc. Natl. Acad. Sci. USA* **77**:4196–4200.
2236. **Zinder, N. D., and J. Lederberg.** 1952. Genetic exchange in *Salmonella*. *J. Bacteriol.* **64**:679–699.
2237. **Zukin, R. S., M. F. Klos, and R. E. Hirsch.** 1986. Conformational dynamics of two histidine-binding proteins of *Salmonella typhimurium*. *Biophys. J.* **49**:1229–1235.
2238. **Zukin, R. S., and D. E. Koshland, Jr.** 1976. Mg^{2+} , Ca^{2+} -dependent adenosine triphosphate as receptor for divalent cations in bacterial sensory receptor. *Proc. Natl. Acad. Sci. USA* **74**:1932–1936.
2239. **Zukin, R. S., P. G. Strange, L. R. Heavey, and D. E. Koshland, Jr.** 1977. Properties of galactose binding protein of *Salmonella typhimurium* and *Escherichia coli*. *Biochemistry* **16**:381–386.
2240. **Zyskind, J. W., L. T. Deen, and D. W. Smith.** 1979. Isolation and mapping of plasmids containing the *Salmonella typhimurium* origin of DNA replication. *Proc. Natl. Acad. Sci. USA* **76**:3097–3101.
2241. **Zyskind, J. W., and D. W. Smith.** 1980. Nucleotide sequence of the *Salmonella typhimurium* origin of replication. *Proc. Natl. Acad. Sci. USA* **77**:2460–2464.