Mutant Selections Linking Physiology, Inhibitors, and Genotypes

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OVERVIEW

Inhibitory conditions result in the selection of genetic variants. Such variants have been useful as selectable markers facilitating studies of rare genetic events such as recombination and mutagenesis (619). Many such selections have also defined the sites of agrichemical and drug action. These inhibitory agents, resultant selections, and mutants have been crucial probes allowing insights into the broad range of biological mechanisms occurring in bacteria. Studies of surface phenomena, transport, central and peripheral metabolic events, transcription, translation, specific and global regulatory mechanisms, protein folding, and replication have been advanced by such analyses. The aim of this chapter is to provide a catalog of such inhibitory agents and their targets. It is my belief that such a catalog provides an important connection between the genome and the physiology of an organism.

SELECTIONS AND SCREENS

Chemical, physical, and biological insults can be applied to *Escherichia coli* and *Salmonella typhimurium* (official designation, *Salmonella enterica* serovar Typhimurium). The response of a bacterial strain, i.e., its phenotype, is a complex function of the organism's genetic constitution, or genotype, its natural history, and its current environment. Conditions allowing all but a few cells to grow result in selections of genetic variants that overcome the environmental challenges. In other cases, rare mutants unable to grow under conditions in which the vast majority of organisms thrive can be obtained by screening. The analysis of both mutational classes can be most revealing; thorough study often rewards the dedicated researcher with fundamental new insights into biological phenomena.

SOME TOOLS OF THE TRADE

Environment

To devise a selection or a screen, the experimenter customizes the microbial environment. This customization may encompass manipulation of nutritional parameters and physical conditions such as temperature, pressure, and irradiation. Such manipulations by themselves can constitute positive selections or effective screens. These manipulations can also be utilized in conjunction with inhibitory agents to optimize selection or screening protocols.

Mutagenesis

Mutagenesis protocols can influence both the recovery of mutants and the spectrum of mutations obtained. It is thus useful to employ a variety of mutagens with a defined selection. For example, spontaneous hydrogen peroxide-resistant mutants have not been obtained from *S. typhimurium* despite repeated attempts with a tight and powerful selection; such mutants are recovered readily after chemical mutagenesis (131). Moreover, various protocols can lead to the preponderance of different mutational

classes. Many chemical treatments yield point mutations, while spontaneous mutations are often small deletions (460). Transposon mutagenesis most often results in loss of gene function (411). In addition, the high efficiency (=1) of recovering mutations by selection for drug resistance after exposure to transposons such as Tn*5*, Tn*10*, and Mud (Ap *lac*) facilitates selection of mutants resistant to a second agent and makes the screening for hypersensitive loss-of-function mutants manageable (411, 443, 796).

Inhibitory Agents

Energy, chemicals, and living things have the capacity to either inhibit bacterial growth or kill cells. Energy in many forms, including heat, visible light, UV rays, and gamma rays, can compromise cells. Chemical inhibitors may be elements, simple inorganic molecules, complex organic molecules, or natural products produced by an organism for a variety of reasons, including protection of its ecological niche or repelling of predators. A rich collection of antibacterial agents has arisen from the synthetic organic chemical practices of the modern pharmaceutical and agrichemical industries, the natural product isolation and screening of the pharmaceutical industry, and the development of novel compounds for a variety of uses by the chemical industry. Bacterial viruses, mammalian macrophages, and other microbes are also capable of efficient destruction of bacterial populations. These tools have been repeatedly exploited by bacterial geneticists to provide both fundamental and applied knowledge.

Modern Genetic Technologies

A wide variety of genetic methods are applicable to the characterization of selectable phenotypes. A few of general utility are mentioned here. Transposon-mediated insertion mutations that are linked to alleles conferring resistance or sensitivity or that are themselves responsible for the phenotype (411, 443, 796) can be physically isolated by using drug resistance as a selectable marker in in vivo or in vitro molecular cloning experiments (524). Such DNA fragments can be mapped accurately to the *E. coli* genome by powerful computer-assisted restriction digest matching and hybridization methodologies (414, 661). Multicopy plasmid libraries representative of the *E. coli* and *S. typhimurium* genomes are easy to construct. These libraries can be used to isolate resistant or hypersensitive variants that result from the amplification of small regions of the chromosome (see, e.g., reference 250 and 472). Again, such "meromultiploids" can be rapidly and accurately mapped by computer-assisted restriction enzyme digestion analyses or by hybridization to the ordered library of *E. coli* fragments present in phage lambda vectors (414, 661).

PATHWAY FOR INHIBITOR ACTION

To inhibit the growth of *E. coli* or *S. typhimurium*, a generic inhibitor must pass through the aqueous culture medium and one or both of the cellular membranes. Within the cytoplasm, periplasm, or cellular membranes, the inhibitory substance must compromise a vital cellular function. The response to the inhibitory substance may be modulated by altering (i) the efficiency with which it reaches its target, (ii) the target structure, (iii) the target quantity, (iv) the catabolism of the inhibitory substance, (v) the metabolic responses to target inhibition, or (vi) the functional alternatives to the inhibited target. Thus, inhibitor hypersensitivity (Fig. 1) can arise from (i) lessening of permeability barriers or efflux mechanisms (e.g., *tolC* [536, 653]), (ii) creation of targets with a greater affinity for the inhibitor (*hisG* [698]), (iii) decreased intracellular levels of targets (e.g., *his* promoter down-mutations [208]), (iv) increased conversion of a proinhibitor to an inhibitor, (v) destruction of inhibitor detoxification systems (e.g., inactivation of neomycin phosphotransferase) or inactivation of fueling pathways (e.g., *pta-ack*) that can degrade otherwise toxic products to more benign substances (see, e.g., reference 797), and (vi) destruction of

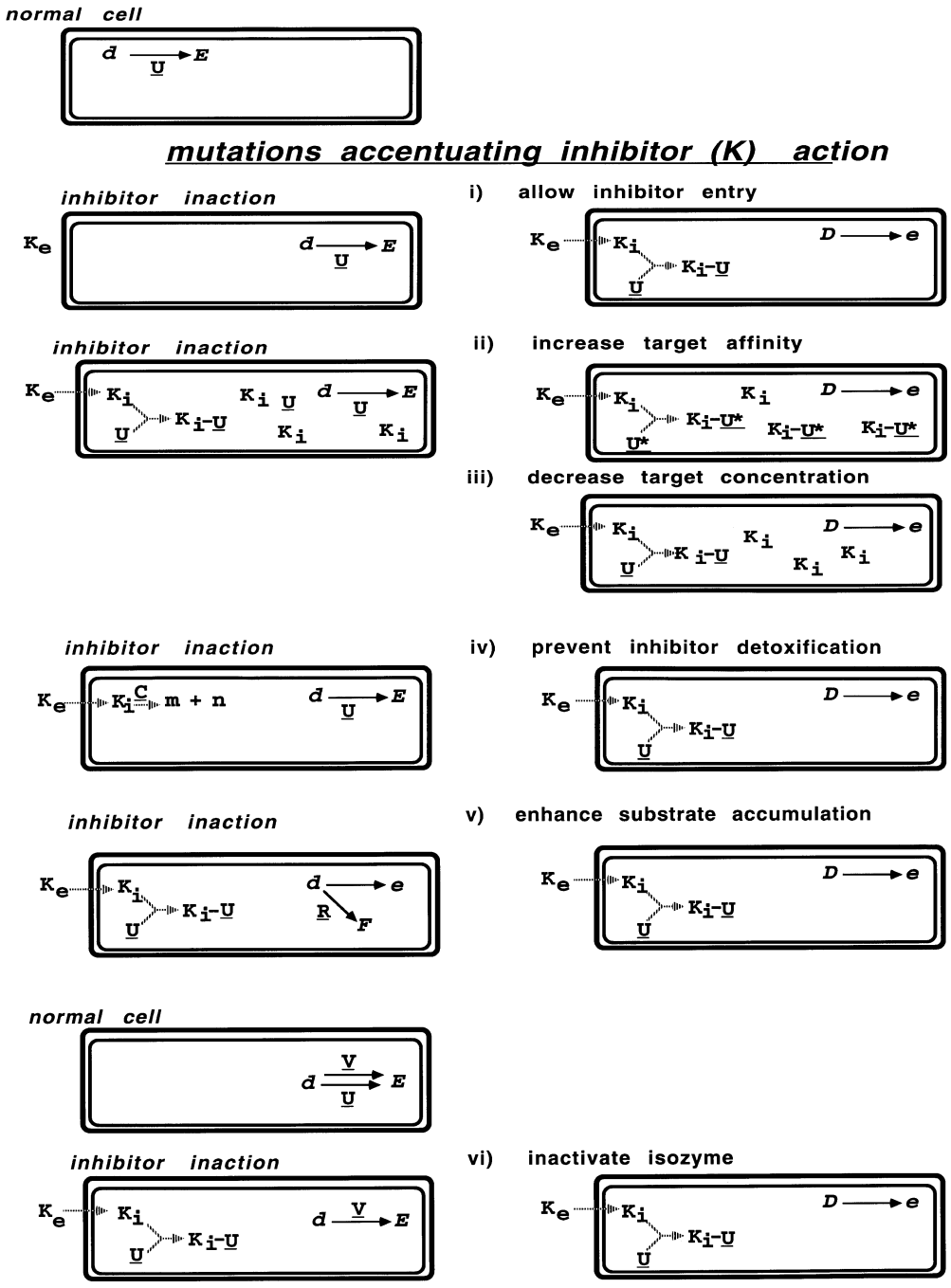

FIGURE 1 Some causes of inhibitor-hypersensitive mutants. Consider a cell in which enzyme U catalyzes the conversion of substrated to product e. The relative amounts of d and e are indicated by whether the symbol is an uppercase or lowercase letter (larger and smaller amounts, respectively). The inhibitor of enzyme U can be in the extracellular space (K_e) or internalized within the Cell (K_i). Within the cytoplasm, the inhibitor can bind to its target or be catabolized by a second protein, C, to metabolites m and n. Substrate d may be consumed by either enzyme U, an isozyme V, or another enzyme, R, yielding an alternative product, f. Inhibitor-hyper-sensitive mutants can arise by Ii) mutations that increase entry of the inhibitor into the cell, (ii) structural alterations of target enzyme U that result in increased affinity for the inhibitor, (iii) regulatory mutations that lower the concentration of enzyme U, (iv) alleles that prevent catabolism of inhibitor K by protein C, (v) mutations that cause the accumulation of metabolic intermediates to toxic levels, or (vi) loss-function mutations that inactivate inhibitor-resistant isozymes of enzyme U.

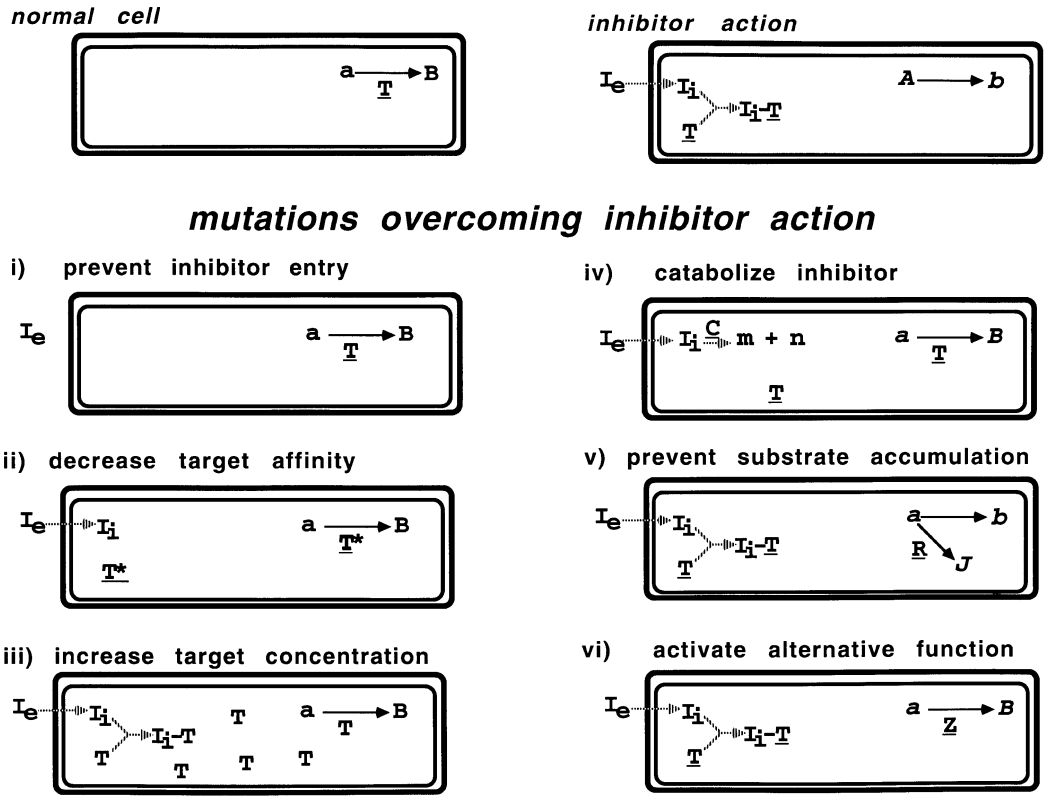

FIGURE 2 Some mechanisms underlying inhibitor-resistant mutants. A cell in which enzyme T catalyzes the conversion of substrate a to product b is depicted. The relative amounts of a and b are indicated by whether the symbol is an uppercase or lowercase letter (larger and smaller amounts, respectively). The inhibitor of enzyme T can be in the extracellular space (I_e) or internalized within the cell (I_1). Within the cytoplasm, the inhibitor can bind to its target or be catabolized by a second protein, C, to metabolites m and n. Substrate a may be consumed by enzyme T, an isozyme Z, or another enzyme, R, yielding an alternative product, j. Resistance can arise by (i) exclusion of inhibitor I from the cellular compartment containing enzyme T, (ii) structural alterations of enzyme T such that its affinity for inhibitor I is diminished. (iii) regulatory mutations increasing the intracellular concentration of enzyme T, (iv) mutations that cause the catabolism of inhibitor I, (v) alleles that prevent the accumulation of substrate a to toxic levels, and (vi) evolution of cryptic isozymes of enzyme T, the target of inhibitor I, that are unaffected by the inhibitor.

isozymes (see, e.g., reference 442). Conversely, resistance (Fig. 2) can arise by (i) preventing binding or permeation of molecules or organisms (e.g., phage λ [88, 134, 135, 253, 644, 766], colicin E1 [449, 536, 653], and histidine analogs [13–15]), (ii) creating target structures with lowered affinities for an inhibitor (781; e.g., *hisG* [540, 698, 699, 824]), (iii) elevating target levels (781; e.g., *hisO, hisR, hisS, hisT, hisU,* and *hisW* [23, 98, 126, 148, 657, 658, 660, 705, 706, 784]), (iv) transforming an inhibitor to an inactive form or preventing proinhibitor transformation to a toxic form (e.g., fluoroacetate to fluorocitrate [96, 281, 463, 797] and glycylvaline to valine [1, 178]), (v) obviating deleterious accumulations behind the block imposed by either a mutation or an inhibitor, and (vi) evolving cryptic enzyme activities (e.g., *ebg* [118] and *ilvF* [174, 610]).

ALTERING METABOLIC CAPACITY

E. coli and *S. typhimurium* utilize a large, though limited, number of organic compounds as sole sources of carbon, nitrogen, phosphorus, sulfur, and energy. Positive genetic selections that expand the metabolic repertoire of these organisms have been devised. These include the utilization of D-amino acids for protein synthesis, utilization of a single amino acid as a sole nitrogen or carbon source, utilization of organophosphates as a sole phosphorus source, utilization of djenkoic acid as a sole sulfur source, and utilization of many carbon compounds as energy sources. Although single mutations can expand metabolic capacity, mutation of several genes may be required to satisfy these selections.

An interesting twist on expanding metabolic capacity comes from gene amplification. In this regard, a discussion of the multiple transaminsases is illuminating. These enzymes have overlapping specificities in vitro. Amplification of *ilvE*, which encodes the branched-chain amino acid transaminase B, allows production of physiologically significant levels of tyrosine, which are not obtained with the haploid *ilvE* gene. Similarly, amplification of *tyrB* allows transaminase B to act in alanine synthesis, while overproduction of transaminase A or C is sufficient to meet the metabolic demand for leucine in an *ilvE* mutant. Thus, function may be modulated by changing enzyme concentrations in vivo via alteration of gene dosage or expression (61).

Loss of metabolic capacity can also be detected. Many positive selections for loss of function are known. Indirect screening methods (replica plating, indicator media) allow identification of interesting phenotypes. One such indirect method, hypersensitivity to a herbicide, has been useful in metabolic studies (443) and has led to the development of a new selection for *ilvA* alleles (231). Moreover, the indirect method has been extremely powerful in defining the responses of cells to DNA-damaging regimens (810).

LESSONS AND IMPACTS

Resistance-determining alleles have been exploited in several ways. They have served as selectable markers in genetic crosses. This utility is being supplanted by new techniques and use of drug resistance-specifying insertion alleles in strain construction. Nevertheless, a lasting legacy of these selections has been the definition of a very broad range of biological phenomena that have been intensively studied. A few examples illustrating this generality in conjunction with Fig. 2 may be illuminating.

Alleles preventing association of an inhibitory agent with the cell (Fig. 2, part i) have contributed much to our present understanding of surface architecture and membrane transport systems. Mutations that decrease inhibitor-target interactions (Fig. 2, part ii) have advanced our knowledge of antibiotic and agrichemical action, allostery, feedback inhibition, and repression. Mutations that increase the intracellular concentration of a target macromolecule (Fig. 2, part iii) have led directly to the genetic regulatory concepts of attenuation, repression, and activation.

Interference with inhibitor metabolism (Fig. 2, part iv) has led to findings both obvious and surprising. It is understood that fluoroacetate is a poison only if it enters the tricarboxylic acid cycle. Thus, mutations preventing the formation of fluoroacetyl coenzyme A are expected to confer resistance to fluoroacetate; such mutations have been obtained (96, 281, 463, 797). In contrast, if multiple phages are used as the inhibitory agents, bacterial Gro mutants both blocked in phage killing and defective in cellular metabolism are selected (256–260). It is worth emphasizing that this latter approach has had a profound effect on our understanding of protein folding, the cellular redox state, and transcription.

Preventing substrate accumulation (Fig. 2, part v) has been the basis of selections that have helped demonstrate that accumulations of sugar phosphates and 2-ketoacids are toxic (569, 752, 796, 797). These same selections are being used in the detailed dissection of protein structure-function and fine-structure genetic mapping (231). The recruitment of alternative functions (Fig. 2, part vi) has intriguing evolutionary implications. Selections have uncovered silent, cryptic genes that are activated by mutation (see, e.g., references 118, 174, 361, and 610). Further analyses have indicated that a gene encoding one isozyme may be cryptic in *E. coli* and expressed in *S. typhimurium*, while the gene encoding the second

isozyme is silent in *S. typhimurium* and functional in *E. coli* (782). Moreover, studies of evolved β-galactosidase and transaminases together indicate that a new in vivo function to meet a selection can be accomplished by changes in enzyme structure or changes in enzyme quantity or both (61, 118).

Analyses of hypersensitive and resistant alleles that use a single inhibitory agent can be most informative in the study of a single phenomenon. Analysis of mutations altered in both responses to an amino acid antagonist has defined the multiple components of the yeast general control system (841). Similarly, extensive genetic, physiological, and enzymatic studies of feedback-hypersensitive and feedback-resistant alleles of *hisG* have been most useful in understanding the role of the *hisG* gene product (698, 824). Several other such examples are well known.

An interesting contrast is provided by studies of sulfonylurea herbicide resistance and hypersensitivity in *S. typhimurium.* Resistance mutations precisely define acetolactate synthase as the site of action of these herbicides (441). Numerous transposon-induced, herbicide-hypersensitive mutations have also been collected (796). Studies of these mutations demonstrated that the accumulation of 2-ketobutyrate upon acetolactate synthase inhibition is toxic (443). This observation suggests that such toxic accumulation may be an important factor in herbicide target selection and that schemes can be conceived in which selections and screens may be used to mimic inborn errors of human metabolism (444).

These positive selections have also had direct economic and clinical impact. The sites of action of vital pharmaceutical and agrichemical agents have been and continue to be defined by mutant analyses of *E. coli* and *S. typhimurium.* Feedback-insensitive mutations of *E. coli, S. typhimurium,* and other bacteria play a critical role in pathway engineering designed to produce small biological molecules by schemes involving fermentation or agriculture.

LIMITATIONS OF INHIBITOR AND MUTANT ANALYSES

Mutations often cause an adverse situation in which cellular growth is not optimal. Even under permissive conditions, compensatory secondary mutations may accumulate. Conclusions attributing a phenotype to a mutation may be erroneous if that phenotype is actually a consequence of both the primary mutation and compensatory alterations. Hypotheses drawn from mutants can often be buttressed by analyzing growth disadvantages created by the addition of very specific chemical inhibitors of particular enzymes. In such cases, the time for selection and expression of compensatory mutations is minimized. Analysis of such transient phenocopies is, however, complicated; inhibitor specificity may not be absolute. For example, various oxayl hydroxamates inhibit both isopropyl malate dehydrogenase (the *leuB* product) and acetohydroxy acid isomeroreductase (the *ilvC* product [839]). Thus, mutually supportive physiological and genetic data derived from a single inhibitory condition are most desirable.

TABLES

Tables 1 through 3 build upon the splendid effort of Vinopal (803). Table 1 provides a list of selections by which mutations have been obtained. It is apparent that a single selection can often yield mutations in a wide variety of genes. Table 2 (p. 2551), cross-referencing Table 1, lists alphabetically those genes for which resistant alleles have been obtained by positive selections. From this table, one can see that alleles of single genes can often be obtained by a variety of selections. It is often useful to have access to a range of inhibitors interfering with a class of metabolic reactions. To address this need, the genes listed in Tables 1 and 2 are regrouped in Table 3 (p.2571) by metabolic function following the convention of Riley (643). As can be seen, selections for a broad spectrum of metabolic functions have been devised. For genes in the amino acid and cofactor biosynthesis domain, selections based on mechanisms other than false feedback inhibition are relatively few. By providing these three tables, I hope to provide maximal access to the contents of this chapter for geneticists, biochemists, and physiologists. An array of inhibitory agents with different specificities is therefore presented. As in the past, the utility of these tools for scientific investigation is limited only by the imagination of the experimenter.

A cautionary note is in order. I hope that the cross-referenced tables emphasize that, unlike the one-

to-one correspondence between gene and gene product, the relationship between phenotype and genotype is more complicated. Many different genotypes can give rise to a single phenotype. Similarly, many different selections can alter a single gene.

TABLE 1 Selections giving rise to mutants of *E.coli* and *S.typhimurium*[a]

Selection purpose and technique	Mutant gene
Expansion of metabolic capacity	
Acetate + gluconate as C source in *ppc*	*gntR*
Acetate + gluconate as C source in *ppc*	*gntS*
Acetyl(*N*)histidine + ornithine satisfaction of *his*	*argB*
Acetyl(*N*)histidine + ornithine satisfaction of *his*	*argC*
Acetyl(*N*)histidine + ornithine satisfaction of *his*	*argE*
Acetyl(*N*)histidine + ornithine satisfaction of *his*	*argH*
Acetylhistidine satisfaction of *his*	*argR*
Acetyl(*N*)lactonate as sole N source	*lacI*, operator
Acetylmethionine satisfaction of *met*	*argR*
Acetylornithine + uracil satisfaction of *car* (*pyrA*)	*argA*
Acetylornithine + uracil satisfaction of *car* (*pyrA*)	*argB*
Acetylornithine + uracil satisfaction of *car* (*pyrA*)	*argC*
Acetylornithine + uracil satisfaction of *car* (*pyrA*)	*argD*
Adenosine as C source in *upp deoD*	*xapR*
Aminobutyrate as N source	*gabC*
Arabinitol (D) resistance	*mtlA*
Arabinose (L) as C source in *cya* or *crp*	*rpoD*
Arabinose (L) as C source in presence of *lac* operon inducer	*lacY*
Arabinose (D) as C source	*fucA*
Arabitol as C source	*gatACD*
Arabitol (D) as C source in *fuc*	*dgd*
Arbutin as a C source	*bglBC*
Arbutin as C source)	*osmZ* (*bglY)*
Arginine as N source	*hisP*
Arginine-independent growth of *pyrH* in presence of uracil	*pyrB*
Arginine-independent growth of *pyrH* in presence of uracil	*pyrC*
Arginine-independent growth of *pyrH* in presence of uracil	*pyrD*
Arginine-resistant, proline-independent growth of Δ*pro*	*argR*
β-Glycerol-phosphate as C source in presence of high phosphate	*phoA*
β-Glycerol-phosphate as C source in presence of high phosphate	*phoR*
β-Glycerol-phosphate as C source in presence of high phosphate	*phoS*
β-Glycerol-phosphate as C source in presence of high phosphate	*phoT*
Biotin sulfoxide utilization in *chl bio*	*chlE*
Branched-chain amino acid satisfaction of Δ*ilvDC hisT*	*ilvA*
Butyrate as C source in *fadR*(Con)	*atoC*
Butyrate or valerate as better C source	*iclR*
Cellobiose as C source	*celABCDF*
Chemostat growth improved	*mut*
Citrate as C source	*cit*
Citrate as C source in presence of low cAMP	*cpd*
D-Amino acid satisfaction of amino acid auxotrophy	*dadA*
DAP-independent growth of Δ(*mal-asd*) in the presence of serine, methionine, and glycine	
D-Histidine + glycylglutamine satisfaction of *his* auxotrophs	*glnA*
Decanoate as C source	*fadR*
Deoxyadenosine (low) satisfaction of purine requirement	*add*

Selection purpose and technique	Mutant gene
Deoxyadenosine + hypoxanthine satisfaction of purine requirement	*add*
Diamino (2,6)purine satisfaction of purine auxotrophy	*deoR*
Erythromycin growth dependence	*mac*
Ethanol as C source	*adh*
Ethyleneglycol as C source in propanediol utilizer	*fucA*
Fructose as C source in *ptsF* or *ptsM*	*srlD*
Fructose 1-phosphate as C source	*uhpR*
Fucose (L) as C source in propanediol utilizer	*fucA*
Fucose + arabinose-supported growth in *galP*	*mglA*
Fucose + arabinose-supported growth in *galP*	*mglB*
Fucose + arabinose-supported growth in *galP*	*mglC*
Galactose as C source for *gal* (leader)::IS	*rho*
Galacturonide as C source	*uidA*
Galacturonide as C source	*uidR*
Glucanate as C source in *eda*	*edd*
Glucosamine as C source	*ptsG*
Glucosamine 6-phosphate as C source	*uhpR*
Glucosamine as anaerobic C source in *ptsG*	*dgsA*
Glucose 1-phosphate as C source	*uhpR*
Glucose as C source in Δ*ptsHI*	*galC*
Glucose as C source in *ppc*	*iclR*
Glucose as C source in Δ*ptsHI*	*galR*
Glucosides (β) as C source	*gyrA* (*hisU*)
Glucosides (β) as C source	*gyrB* (*hisW)*
Glutamate as C source	*gadS*
Glutamate as C source	*gltH*
Glutamate as C source	*gltS*
Glutamate as C source at 42°C	*gltR*
Glutamine as C source	*glnP*
Glycerol as C source in *ppc*	*iclR*
Glycerol + gluconate as C source in *eda*	*gntM*
Glycerol + methylglucuronide as C source in *eda*	*gurBCD*
Glycerol 3-phosphate as C source in *glpT ugpAB*	
Hemin satisfaction of *hemA* auxotroph	*hemB*
Hemin satisfaction of *hemA* auxotroph	*rfa*
Hexuronate as C source in noninducible strain	*exuR*
Histidinal satisfaction of *his* auxotroph requirement at 30°C	*his* structural genes
Histidinal satisfaction of *his* auxotroph requirement at 30°C	*hisG*
Histidine (D) satisfaction of *his* auxotroph requirement	*his* structural genes
Histidine (D) satisfaction of *his* auxotroph requirement	*hisG*
Histidine (D) satisfaction of *his* auxotroph requirement	*dhuA*
Histidine as C source	*hut*
Histidine as N source	*hut*
Improved growth in *icd*	*gltA*
Inosine as C source in *upp deoD*	*xapR*
Inosine as improved C source	*deoR*
Keto(2)-3-deoxygalactonate as C source	*kdgR*
Keto(2)-3-deoxygalactonate as C source	*dgoR*
Lactate + fumarate as anaerobic energy source	*chlABDE*
Lactate + nitrate as anaerobic energy source (*chl* to *chl*$^+$)	*chlE*
Lactitol as C source	*lacI*, operator

Selection purpose and technique	Mutant gene
Lactobionic acid as C source	*lacI*, operator
Lactobionic acid as C source	*lacZ*
Lactose utilization after conjugation of F′*lac* into *Salmonella* sp.	*hsd*
Lactose utilization in Δ*lacZ*	*ebgA*
Leucine (D) satisfaction of *leu* auxotrophs	*lrp* (*livR, lstR, lss, mbl, oppl)*
Lyxose (D) as C source	*manC*
Malate (L) as improved C source	*dct*
Malate (D) as C source	*dml*
Maltose as C source in *malT*	*malP*
Maltose as C source in *malT*	*malQ*
Maltose utilization in *malT*	*bymA*
Mannitol (limiting) as C source	*mtlC*
Mannose as C source	*ptdG*
Melibiose as C source	*lacI*, operator
Melibiose as C source and acetyl(*N*)lactonate as N source	*lacI*, operator
Methyl-β-galactoside-supported growth	*mglD*
Methylgalacturonide as C source	*uidA*
Methylgalacturonide as C source	*uidR*
Methylgalacturonide as C source	*uxuR*
Methyl(β)glucoside as C source	*bglT*
Methylglucuronide + glycerol-supported growth	*uidA*
Neolactose as C source	*lacI*, operator
Nicotinamide as sole N source	*pncA*
Phenylgalactoside as C source	*lacI*, operator
Proline as sole N source with glucose as C source	*putA*
Proline-independent growth of *proAB*	*argD*
Propanediol as C source	*fucA*
Propionate as C source	*prp*
Raffinose as C source in *lacI*	*mel* (generic)
Raffinose as C source	*lacI*, operator
Ribitol utilization	*gatACD*
Salicin as C source	*bglB,C*
Salicin as C source	*osmZ*
Serine (L) as C source	*cpxA*
Serine (L) as C source	*ecfB*
Sorbose (L) as C source in crosses with wild strains	*sorAT*
Streptomycin independence of *rpsL*	*rpsD*
Streptomycin independence of *rpsL*	*rpsE*
Succinate as improved C source	*cpd*
Succinate-independent growth in *lpd*	*sdh*
Sucrose as C source	*dsdA*
Sucrose as C source	*dsdC*
Threonine as N source	*ilvA*
Tyramine as N source	*tyn*
Uridine as C source, improved utilization	*cytR*
Valerate as C source in *fadR*(Con)	*atoC*
Xylitol as C source in propanediol utilizer	*fucA*
Resistance to inorganic chemicals	
Acid resistance	*atr*
Acid resistance	*phoE*
Arsenate resistance	*glpT*

Selection purpose and technique	Mutant gene
Arsenate resistance	*phoR*
Arsenate resistance	*phoS*
Arsenate resistance	*phoT*
Arsenate resistance	*pstABCS*
Arsenate resistance	*pit*
Azide resistance	*atpA–atpE*
Azide resistance	*cysB*
Azide resistance	*cysK*
Azide resistance	*secA*
Chlorate resistance	*chlABCDEG*
Chlorate resistance	*narCG*
Chlorate resistance	*narH*
Chromate + selenate resistance	*cysL*
Chromate resistance	*cysA*
Chromate resistance	*cysB*
Chromate resistance	*cysC*
Chromate resistance	*cysD*
Chromate resistance	*cysH*
Chromate resistance	*cysI*
Chromate resistance	*cysJ*
Copper resistance in *ompC*	*ompF*
Copper resistance	*ompR*
Diazoborine resistance	*envM*
Lithium resistance (multicopy)	*nhaA*
Lithium-resistant utilization of melibiose	*melB*
Manganese resistance	*corABCD*
Manganese resistance	*fur*
Manganese resistance	*mng*
Nickel resistance	*corABCD*
Osmotolerance	*crp*
Osmotolerance	*cyaA*
Osmotolerance	*osmB*
Osmotolerance	*proA*
Osmotolerance	*proB*
Peroxide resistance	*oxyR*
Selenate resistance	*cysA*
Selenate resistance	*cysB*
Selenate resistance in *cysM*	*cysB*
Selenate resistance	*cysK*
Selenate resistance	*cysL*
Selenite resistance	*cysK*
Selenite resistance	*gshA*
Selenite resistance	*gshB*
Tellurite resistance	*phoB*
Tributyl tin resistance	*atpA–atpE*
Resistance to biological and organic chemicals	
Acetylnorvaline resistance in *argR*(Con)	*argE*
Acetylnorvaline resistance in *argR*(Con)	*argR*
Acridine resistance	*dnaE*
Actinomycin D resistance in the presence of EDTA	*pldA*
Adenine resistance in *hpt gpt*	*apt*
Adenine resistance in *hpt gpt*	*purR*
Alafosfalin resistance	*pepA*
Alafosfalin resistance	*tpp*
Alanyl-2-aminopropionate resistance	*oppA*
Albicidin resistance	*tsx*

Selection purpose and technique	Mutant gene
Albomycin resistance	*exbB*
Albomycin resistance	*fhuA*
Albomycin resistance	*fhuB*
Albomycin resistance	*pepN*
Albomycin resistance	*sidCF*
Albomycin resistance	*sidK*
Albomycin resistance	*tonB*
Aldohexuronate resistance in *eda*	*exuT*
Aldohexuronate resistance in *eda*	*exuR*
Allyl alcohol resistance	*adhE*
Amidinopenicillin tolerance	*sloB*
Amikacin resistance	*cpxA*
Amino(2)purine resistance in *dam*	*mutH*
Amino(2)purine resistance in *dam*	*mutL*
Amino(2)purine resistance in *dam*	*mutS*
Amino(4)phenylalanine resistance	*aroF*
Amino(4)phenylalanine resistance	*tyrA*
Amino(4)phenylalanine resistance	*tyrR*
Amino(6)nicotinamide resistance	*nadA*
Amino(6)nicotinamide resistance	*nadD*
Amino(6)nicotinamide resistance	*pncA*
Amino(6)nicotinamide resistance	*pncB*
Amino(6)nicotinamide resistance	*pncX*
Amino(6)nicotinate resistance	*pncB*
Aminobutyrate resistance	*ilv* structural genes
Aminobutyrate resistance	*ilvB*
Aminobutyrate resistance	*ilvH*
Aminobutyrate resistance	*ilvI*
Aminoethylcysteine (thialysine) resistance	*lysC*
Aminoethylcysteine (thialysine) resistance	*lysP*
Aminoethylcysteine (thialysine) resistance	*lysS*
Aminoglycoside resistance	*nek*
Amino(2)hydroxy(3)pentoate resistance	*thr* structural genes
Aminopterin resistance	*thyA*
Aminotriazole resistance	*amtA*, *amtB*
Aminotriazole resistance	*his* structural genes
Aminotriazole resistance in *relA*	*gyrB*
Ampicillin resistance	*ampC*
Ampicillin resistance	*ampD*
Ampicillin resistance	*ampE*
Ampicillin resistance	*envZ*
Ampicillin resistance	*galU*
Ampicillin resistance	*hipA*
Ampicillin resistance	*hipQ*
Ampicillin resistance	*ompC*
Ampicillin resistance	*ompF*
Ampicillin resistance	*ompR*
Ampicillin resistance	*ptsI*
Ampicillin resistance	*rfa* (general)
Ampicillin resistance	*tolD*
Ampicillin resistance	*tolE*
Arabinitol (D) resistance	*mtlA*
Arbitol (D) resistance	*gatACD*
Arbutin resistance in *dgk*	*mdoB*
Arginine-resistant, proline-independent growth of Δ*pro*	*argR*
Auroventin resistance	*atpA–atpE*
Aza(5)cytidine resistance	*dcm*
Azadeoxycytidine resistance	*cdd*
Aza(6)uracil resistance	*gpt*

Selection purpose and technique	Mutant gene
Aza(8)guanine resistance	*ndk*
Aza(8)guanine resistance	*upp*
Azaleucine resistance	*aroP*
Azaleucine resistance	*azl*
Azaleucine resistance	*tolB*
Azaleucine resistance	*leuS*
Azaleucine resistance	*livG*
Azaleucine resistance	*livH*
Azaserine + tryptophan resistance	*dhuA*
Azaserine + tryptophan resistance in *dhuA*	*hisJ*
Azaserine resistance	*aroP*
Azaserine resistance	*azaAB*
Azaserine resistance	*cysA*
Azaserine resistance	*cysB*
Azaserine resistance	*cysC*
Azaserine resistance	*cysD*
Azaserine resistance	*cysE*
Azaserine resistance	*cysG*
Azaserine resistance	*cysH*
Azaserine resistance	*cysI*
Azaserine resistance	*cysJ*
Azaserine resistance	*cysK*
Azaserine resistance	*cysM*
Azaserine resistance	*mut* (generic)
Azetidine carboxylate resistance	*proB*
Azetidine carboxylate resistance	*putA*
Azetidine carboxylate resistance	*putP*
Azidothymidine resistance	*tdk*
Bacilysin resistance	*dppA*
Bacitracin resistance	*rfa*
Bacteriocin resistance	*tol*
Bacteriocin 4-59 resistance	*ompA*
Bacteriocin 4-59 resistance	*tonB*
Bacteriocin JF246 resistance	*ompA*
Baikiain resistance in constitutive background	*putA*
β-Glycerol-phosphate resistance in *glpD*	*phoA*
Beta-lactam conjugate resistance	*fhuA*
Beta-lactam resistance (see mecillinam resistance)	*crp*
Beta-lactam resistance	*cyaA*
Beta-lactam resistance	*lyt*
Beta-lactam resistance	*alaS*
Beta-lactam resistance	*argS*
Bialaphos resistance	*dppA*
Borrelidin resistance	*thrS*
Bromodeoxyuridine + UV light resistance	*ung*
Cadaverine resistance	*cadB*
Caffeine resistance	*glnV*
Calmodulin inhibitor resistance	*leuW*
cAMP + glucose 6-phosphate + D-xylose + L-arabinose resistance	*crp*
cAMP + glucose 6-phosphate resistance	*crp*
Camphor resistance	*mbrABCD*
Canavanine + azauracil resistance	*argR*
Canavanine + thiouracil resistance	*upp*
Canavanine + thiouracil resistance	*argP*
Canavanine resistance	*argS*
Canavanine resistance	*argP*
Canavanine resistance	*argR*
CCCP resistance	*atpA–atpE*
CCCP resistance due to gene dosage	*emrB*

Selection purpose and technique	Mutant gene
Cephalosporin E-0702 resistance	*tonB*
Cephalothin resistance	*rfa*
Chelator resistance	*ompA*
Chloramphenicol resistance	*cmlA*
Chloramphenicol resistance	*marA*
Chloramphenicol resistance	*rrn*
Chloramphenicol resistance	*ompF*
Chloramphenicol resistance	*ompR*
Chloro(β)-D-alanine resistance	*dadA*
Chloro(β)-D-alanine resistance	*metC* (*ecfA*)
Chloro-3-hydroxyacetone resistance in *uhp*(Con)	*uhpT*
Chloroacetaldehyde resistance	*adhCE*
Chloroacetate(β) resistance	*cbt*
Chlorobiocin resistance	*gyrB*
Chloroethanol resistance	*adhCE*
Chlorohydroxyacetone phosphate resistance	*glpT*
Chlorpromazine resistance	*lon*
Chuangxinmycin resistance	*trpR*
Cloacin DF13 resistance	*ompF*
Coenzyme A feedback resistance	*coaA*
Colicin "K-type" tolerance	*hemB*
Colicin (multiple) resistance	*envZ*
Colicin (other) resistance	*exbB*
Colicin (other) resistance	*exbC*
Colicin A tolerance	*cpxA*
Colicin A tolerance	*ompF*
Colicin A group tolerance	*cirA*
Colicin A group tolerance	*tolQ*
Colicin B resistance	*exbC*
Colicin B resistance	*fepABCDG*
Colicin B resistance	*tonB*
Colicin B tolerance	*cbt*
Colicin D resistance	*cbt*
Colicin D tolerance	*tolB*
Colicin E resistance	*tolC*
Colicin E1 tolerance	*cet*
Colicin E1 tolerance	*tolQAB*
Colicin E2 tolerance	*ompF*
Colicin E3 tolerance	*btuB*
Colicin E3 tolerance	*tolR*
Colicin E2 and E3 tolerance	*tolE*
Colicin E2 and E3 tolerance	*tolZ*
Colicin E2, E3, D, Ia, and Ib tolerance	*tolI*
Colicin I resistance	*exbB*
Colicin I resistance	*exbC*
Colicin I resistance	*ecfB*
Colicin Ia and Ib tolerance	*tolJ*
Colicin K resistance	*metC* (*ecfA*)
Colicin K resistance	*tsx*
Colicin K resistance	*ompA*
Colicin K tolerance	*ompA*
Colicin K tolerance	*ompF*
Colicin L tolerance	*envZ*
Colicin L tolerance	*ompF*
Colicin L tolerance	*fhuA*
Colicin L, A, and S4 tolerance	*fepABCDG*
Colicin M resistance	*tonB*
Colicin M resistance	*tolM*
Colicin M tolerance	*tolD*
Coumermycin resistance	*gyrB*
Coumermycin resistance	*hisW*
Cyclopentane glycine resistance	*ilv* structural genes
Cyclopentane glycine resistance	*ilvA*
Cycloserine resistance	*hipA*
Cycloserine (D) resistance	*cycA*
Dapsone resistance	*thdA*

Selection purpose and technique	Mutant gene
Dehydrobiotin resistance	*bio* operon
Dehydrobiotin resistance	*bioP*
Dehydrobiotin resistance	*birA*
Dehydroproline + azetidine carboxylate resistance at high osmolarity in *putA putP*	*proU*
Dehydroproline resistance	*proB*
Dehydroproline resistance in *putA putP*	*proP*
Deoxy(2)adenosine resistance in *deoC*	*deoD*
Deoxyadenosine + fluorouracil resistance in *upp*	*deoA*
Deoxyadenosine + fluorouracil resistance in *upp*	*deoD*
Deoxydihydroxyphosphonyl methyl fructose resistance	*uhpT*
Deoxy(3)-3-fluoroglucose-independent utilization of lactate	*ptsHIG*
Deoxy(3)-3-fluoroglucose-independent utilization of fructose	*ptsG*
Deoxy(3)-3-fluoroglucose resistance	*ptsI*
Deoxy(2)galactitol resistance in galicitol utilizer	*gatACD*
Deoxy(2)galactose resistance	*gal* operon
Deoxy(2)galactose resistance	*galE*
Deoxy(2)galactose resistance	*galK*
Deoxy(2)galactose resistance	*galP*
Deoxy(2)glucose-resistant utilization of melibiose	*melB*
Deoxyglucose resistance	*manXYZ*
Deoxy(2)glucose-6-phosphate resistance	*uhpT*
Deoxy(2)glucose-resistant fructose utilization	*fruA*
Deoxy(2)glucose-resistant fructose utilization	*ptsG*
Deoxy(2)-2-iodoacetamidoglucose resistance	*nagE*
Diamino(2,6)purine resistance	*apt*
Diamino(2,6)purine resistance in *pnp*	*apt*
Dicyclohexylcarbodiimide resistance in *rfa*	*rfb*
Dideoxy(2′,3′)thymidine resistance	*tmk*
Dihydroproline resistance	*putP*
Dihydroxybutylphosphonate resistance	*cls*
Dihydroxybutylphosphonate resistance	*glpT*
Dihydroxybutylphosphonate resistance in *glpT*	*ugpA,B*
Dihydroxybutylphosphonate resistance in *uhp*(Con)	*uhpT*
Dimethyl sulfoxide resistance	*pss*
Dinitropyrene resistance	*atoB*
Dipeptide (valine containing) resistance	*dppA*
Drug-resistant gene maintenance	*dor*
Erythromycin growth dependence	*rrn*
Erythromycin resistance	*eryC*
Erythromycin resistance	*eryD*
Erythromycin resistance	*mac*
Erythromycin resistance	*rplD*
Erythromycin resistance	*rplV*
Erythromycin resistance	*rplC*
Ethanol resistance	*pss*
Ethionine resistance	*metG*
Ethionine resistance	*metJ*
Fluoroacetate resistance	*ack*
Fluoroacetate resistance	*pta*
Fluorocitrate resistance	*tct*
Fluoro(5)cytosine resistance	*codA*
Fluoro(5)cytosine resistance	*cod*
Fluorodeoxycytidine resistance	*cdd*

Selection purpose and technique	Mutant gene
Fluorodeoxycytidine resistance	*nupC*
Fluorodeoxycytidine resistance	*nupG*
Fluoro(5)deoxyuridine resistance	*tdk*
Fluorodeoxyuridine resistance	*nupC*
Fluorodeoxyuridine resistance	*nupG*
Fluorodeoxyuridine + uracil resistance in *deoA*	*tdk*
Fluoro(2)-L-erythrocitrate resistance	*tct*
Fluoro-3-hydroxyacetone resistance in *uhp*(Con)	*uhpT*
Fluorohydroxyacetone phosphate resistance	*ugpAB*
Fluorohydroxyacetone phosphate resistance	*glpT*
Fluoro(3)malate resistance	*dct*
Fluoro(5)orotic acid resistance	*pyrF*
Fluoro(5)orotic acid resistance	*pyrH*
Fluoro(4)phenylalanine resistance	*tyrR*
Fluoro(4)phenylalanine resistance	*pheA*
Fluoro(4)phenylalanine resistance	*pheR*
Fluoro(4)phenylalanine resistance	*pheS*
Fluoro(4)phenylalanine resistance	*pheU*
Fluorophenylalanine resistance	*aroF*
Fluorophenylalanine resistance	*aroG*
Fluorophenylalanine resistance	*aroP*
Fluorophenylalanine resistance	*tyrA*
Fluoro(5)tryptophan resistance	*aroP*
Fluoro(6)tryptophan resistance	*trp* (generic)
Fluorotyrosine resistance	*tyrR*
Fluorotyrosine resistance	*tyrS*
Fluoro(5)uracil + fluoro(5)uridine resistance	*guaB*
Fluoro(5)uracil + 5′-AMP resistance in *upp*	*ushA*
Fluoro(5)uracil + 5-fluorouridine resistance in *udp*	*pyrH*
Fluoro(5)uracil + nucleotide resistance	*ompF*
Fluoro(5)uracil + nucleotide resistance	*ompR*
Fluoro(5)uracil + adenosine resistance	*udp*
Fluorouracil + adenosine resistance in *upp deoD xapR*(Con)	*xapA*
Fluoro(5)uracil + adenosine resistance in *upp*, *phoS*, or *phoT*	*phoA*
Fluoro(5)uracil + adenosine resistance in *upp*, *phoS*, or *phoT*	*phoB*
Fluoro(5)uracil and 3′-AMP resistance	*cpdB*
Fluoro(5)uracil + 5′-AMP + 3′-AMP resistance	*crp*
Fluoro(5)uracil + carbamylaspartate resistance	*ubiF*
Fluoro(5)uracil resistance	*upp*
Fluorouracil resistance	*nupC*
Fluorouracil resistance	*nupG*
Fluorouracil resistance	*pyrH*
Fluorouracil resistance	*rpoB*
Fluoro(5)uridine + uracil resistance	*udk*
Fluoro(5)uridine resistance	*udhA*
Fluoro(5)uridine resistance in *upp*	*udk*
Fluorouridine resistance	*pyrH*
Fluorouridine resistance	*nupC*
Fluorouridine resistance	*nupG*
Fosfomycin resistance due to increased gene dosage	*murZ*
Fosfomycin + fructose-6-phosphate resistance	*pgi*
Fosfomycin resistance	*crp*
Fosfomycin resistance	*cyaA*
Fosfomycin resistance	*glpT*
Fosfomycin resistance	*hipA*
Fosfomycin resistance	*mrb*
Fosfomycin resistance	*ptsI*
Fosfomycin resistance	*uhpT*
Fucitol resistance in galactitol-utilizing strains	*gatACD*

Selection purpose and technique	Mutant gene
Fucose + arabinose-supported growth in *galP*	*mglA*
Fucose + arabinose-supported growth in *galP*	*mglB*
Fucose + arabinose-supported growth in *galP*	*mglC*
Fucose resistance (arabinose as C source)	*araC*
Fusaric acid resistance of Tn*10* insertion mutants	*tet*
Fusidic acid resistance	*fusA*
Galactose resistance in *galE*	*galK*
Galactose resistance in *galT*	*galK*
Galactose resistance in *galU*	*gal* operon
Galactose resistance in *galU*	*galK*
Galactose resistance in $galT^{+K+E+}$/*galU* $galT^{+K+E+}$ merodiploid	*galR*
Galactose utilization in presence of thiomethylglucoside	*gal* operon
Gentamicin resistance	*rplF*
Gentamicin resistance	*ubiF*
Globomicin resistance	*dnaE*
Globomicin resistance	*lpp*
Glucarate (D) resistance in *ppc*	*garA*
Glucose + gluconate-independent motility	*pts* (general)
Glucose-resistant satisfaction of *trp* by indole + 5-methyltryptophan	*tna*
Glutamate (D) resistance in *gltS* (increased)	*gltS*
Glutamine (D) resistance	*glnP*
Glutamyl(γ)hydrazide resistance	*glnF*
Glutamyl(γ)hydrazide resistance	*glnH*
Glutamyl(γ)hydrazide resistance	*glnP*
Glutamyl(γ)methyl ester resistance	*gltX*
Glutamyl(γ)methyl ester resistance	*metJ*
Glutamyl(γ)methyl ester resistance	*metK*
Glyceraldehyde (DL) 3-phosphate resistance	*glpT*
Glyceraldehyde (L) 3-phosphate resistance in *uhp*(Con)	*uhpT*
Glyceraldehyde (L) resistance	*glpF*
Glyceraldehyde (L) resistance	*glpK*
Glycerol 3-phosphorothioate resistance	*glpT*
Glycine tolerance	*qmeACDE*
Glycylglycyl-*N*-phosphonoacetylornithine resistance	*argR*
Glycylleucine resistance	*ilvA*
Glycylleucine resistance	*ilvB*
Glycylleucine resistance	*ilvH*
Glycylleucine resistance	*ilvI*
Glycylleucine resistance	*oppA*
Glycylleucine resistance in *ilv*	*gleR*
Glycylglycyl histidinol phosphate ester resistance	*oppA*
Glycylglycyl-*N*-phosphonoacetylornithine resistance	*oppA*
Glyphosate resistance	*aroA*
Hexuronate resistance in *eda*	*uxaBC*
Hexuronate resistance in *eda*	*uxuAB*
Homocysteic acid resistance	*gltS*
Hydrazino (α) imidazole propionic acid resistance	*argT*
Hydrazino (α) imidazole propionic acid resistance	*hisG*
Hydrazino (α) imidazole propionic acid resistance	*hisJ*
Hydrazino (α) imidazole propionic acid resistance	*hisQ*
Hydrazino (α) imidazole propionic acid resistance in *dhuA*	*hisP*
Hydroxy (β) norvaline resistance	*metL*
Hydroxyaspartate resistance	*pan*
Hydroxybutylphosphonate resistance in *uhp*(Con)	*uhpT*
Hydroxyurea resistance	*nrdA*

Selection purpose and technique	Mutant gene
Hydroxyurea resistance	*nrdB*
Indole acrylic acid resistance	*aroT*
Indolmycin resistance	*trpS*
Indospicine resistance	*argR*
Iodoacetylglucosamine resistance	*nagA*
Iodoacetylglucosamine resistance	*nagB*
Iodoacetylglucosamine resistance	*nagE*
Isoniazid resistance	*pdx*
Kanamycin resistance	*atpA–atpE*
Kanamycin resistance	*cpxA*
Kanamycin resistance	*ecfB*
Kanamycin resistance	*hemA*
Kanamycin resistance	*hemB*
Kanamycin resistance	*hemL*
Kanamycin resistance	*topA*
Kasugamycin resistance	*ksgA*
Kasugamycin resistance	*ksgB*
Kasugamycin resistance	*ksgC*
Kasugamycin resistance	*ksgD*
Kasugamycin resistance	*rplK*
Kasugamycin resistance	*rplB*
Kasugamycin resistance	*rpsN*
Kasugamycin resistance	*rpsM*
Kasugamycin resistance	*rpsR*
Kasugamycin resistance and dependence	*rpsI*
Keto(2)butyrate resistance	*ilvA*
Kirromycin resistance	*tufAB*
Lambda *c*II phage + rifampin coresistance	*rpoB*
Lambda phage + nalidixic acid resistance	*crp*
Lambda phage + nalidixic acid resistance	*cyaA*
Levallorphan resistance	*lev*
Lincomycin resistance	*linB*
Lincomycin resistance	*rplN*
Lincomycin resistance	*rplO*
Lincomycin resistance	*rpsG*
Lithium-resistant use of proline as C source	*putP*
Lysine hydroxamate resistance	*lysC*
Mecillinam resistance (see beta-lactam resistance)	*alaS*
Mecillinam resistance	*argS*
Mecillinam resistance	*crp*
Mecillinam resistance	*cyaA*
Mecillinam resistance	*envB*
Mecillinam resistance	*mrdA*
Mecillinam resistance	*mrdB*
Mecillinam resistance	*mreB*
Mecillinam resistance	*mreC*
Mecillinam resistance	*mreD*
Menadionine resistance	*marA*
Mercaptopurine resistance in *gpt*	*hpt*
Methionine sulfoximine + methyl(α)methionine resistance	*metJ*
Methionine sulfoximine resistance	*asm*
Methionine sulfoximine resistance	*glnP*
Methionine sulfoximine resistance	*metP*
Methionine sulfoximine resistance in *glnG*	*glnA*
Methylammonium resistance	*glnA*
Methyl(3)anthranilate resistance	*trpE*
Methyl(3)anthranilate resistance	*aroG*

Selection purpose and technique	Mutant gene
Methyl(α)glutamate resistance in *gltS* (increased)	*gltS*
Methylglucoside(α)-resistant utilization of lactose	*lacIO*
Methylglucoside(α)-resistant utilization of maltose	*malE*
Methylglucoside(α)-resistant utilization of maltose	*malF*
Methylglucoside(α)-resistant utilization of maltose	*malG*
Methylglucoside(α)-resistant utilization of maltose	*malK*
Methylglucoside(α)-resistant utilization of mannitol + lactose	*ptsG*
Methylglucoside(α) resistance	*ptsG*
Methylglucoside(α)-resistant utilization of glycerol in Δ*ptsHI*	*crr*
Methylglucoside(α)-resistant utilization of lactose in *ptsH*	*lacI*, operator
Methylglucoside(α)-resistant utilization of melibiose	*mel*
Methylglyoxal resistance	*gsh*
Methyl(2)histidine resistance + aminotriazole resistance	*hisR*
Methyl methanesulfonate resistance in *lon*	*sulA*
Methyl methanesulfonate resistance in *lon*	*ftsZ*
Methyl(α)methionine resistance	*metA*
Methyl(α)methionine resistance	*metD* (*metP*)
Methyl(α)methionine resistance	*metK*
Methyl(6)purine resistance	*apt*
Methyl(6)purine + hypoxanthine resistance	*purA*
Methyl(*o*)threonine resistance	*brnQ*
Methyl(4)tryptophan resistance in *aroP*	*aroT*
Methyl(5)tryptophan resistance	*mtr*
Methyl(5)tryptophan resistance	*aroP*
Methyl(5)tryptophan resistance	*trp* (generic)
Methyl(5)tryptophan resistance	*trpE*
Methyl(5)tryptophan resistance	*trpR*
Methyl(5)tryptophan + thienylalanine resistance	*aroP*
Methyl viologen resistance	*mvrA*
Methyl viologen resistance (multicopy)	*mvrC*
Methyl viologen resistance	*gor*
Metronidazole resistance	*nar* (general)
Microcin B17 resistance	*sbmA*
Microcin E492 resistance	*semA*
Mitomycin C resistance of *lexA*(Con)	*lexA*
Mocimycin resistance	*tufA,B*
Nalidixic acid resistance	*hisU*
Nalidixic acid resistance	*icdE*
Nalidixic acid tolerance	*sloB*
Nalidixic acid resistance	*gyrA*
Nalidixic acid resistance	*gyrB*
Nalidixic acid resistance	*nalB*
Nalidixic acid resistance	*nalD*
Nalidixic acid resistance	*purB*
Nalidixic acid resistance due to gene dosage	*emrB*
Neamine resistance	*rpsL*
Neamine resistance	*rpsQ*
Neamine resistance	*neaB*
Negamycin resistance	*prfB*
Neomycin resistance	*atpA–atpE*
Neomycin resistance	*ecfB*
Neomycin resistance	*hemA*
Neomycin resistance	*hemC*
Neomycin resistance	*hemD*
Neomycin resistance	*hemE*
Neomycin resistance	*hemG*
Neomycin resistance	*metC* (*ecfA*)
Neomycin resistance	*topA*
Neomycin resistance	*ubi* (generic)

Selection purpose and technique	Mutant gene
Neutrophil granule protein resistance	*pmrA*
Nitro(4)pyridine *N*-oxide resistance	*proA*
Nitro(4)pyridine *N*-oxide resistance	*proB*
Nitro(*o*)-phenyl galactoside resistance	*lacZ*
Nitro(*o*)-phenylthiogalactoside resistance	*lacY*
Nitro(*o*)-phenylthiogalactoside resistance in *lacI*(Con) or *lacO*(Con)	*lacI*, operator
Nitrofurantoin resistance	*nfnA*
Nitrofurantoin resistance	*nfnB*
Nitrofurantoin resistance in *lon*	*sulA*
Nitrofurantoin resistance in *lon*	*ftsZ*
Nitrofuranzone resistance	*nfsA*
Nitrofuranzone resistance	*nfsB*
Nitrosoguanidine resistance	*ada*
Nitrosoguanidine resistance	*gsh* (generic)
Norfloxacin resistance	*hipQ*
Norleucine resistance	*metJ*
Norleucine resistance	*metK*
Norleucine resistance	*nol*
Norleucylglycyl glycine resistance	*oppA*
Novobiocin resistance	*cysB*
Novobiocin resistance	*cysE*
Novobiocin resistance	*gyrB*
Novobiocin resistance	*nov*
Novobiocin resistance	*ompA*
Oxolinic acid resistance	*gyrA*
Paromycin resistance or dependence	*rpsL*
Pentachlorophenol resistance	*atpA–atpE*
Penten(4)oate resistance in *atoC*(Con)	*atoC*
Pentylpantothenamide resistance	*pan*
Peptide (toxic, valine containing) resistance	*pepA*
Peptide (toxic, valine containing) resistance	*pepD*
Peptide (toxic, valine containing) resistance	*pepN*
Peptide (toxic, valine containing) resistance	*pepQ*
Peroxide (organic) resistance	*oxyR*
Phaseolotoxin resistance	*oppA*
Phenethyl alcohol resistance	*dnaB*
Phenethyl alcohol resistance	*dnaP*
Phenethyl alcohol resistance	*secA*
Phenethylyl galactoside resistance	*lacY*
Phenethylyl galactoside resistance	*lacZ*
Phenyl galactoside resistance of *lacP lacI*(nonsense) *supE*	*hisT*
Phenyl galactoside resistance of *lacP lacI*(nonsense) *supE*	*prfA*
Phenyl galactoside resistance of *lacP lacI*(nonsense) *supE*	*rpsL*
Phenyl galactoside resistance of $lacI^q$/*lacP lacI*(nonsense) *supL*	*lysS*
Phenyl galactoside resistance of $lacI^q$/*lacP lacI*(nonsense) *supL*	*strM*
Phenyl galactoside resistance of $lacI^q$/*lacP lacI*(nonsense) *supL*	*trmE*
Phenyl galactoside resistance	*lacY*
Phenyl galactoside resistance	*lacZ*
Phenylalanylleucine resistance	*ilvB*
Phenylalanylleucine resistance	*ilvH*
Phenylalanylleucine resistance	*ilvI*
Plasmid maintenance	*polA*
Polymyxin resistance	*pmrA*
Promethazine resistance	*lon*
Pseudomonic acid resistance	*ileS*
Psicofuranine resistance	*guaAB*

Selection purpose and technique	Mutant gene
Psoralen + UV irradiation resistance	*puvA*
Pyrithiamine resistance	*thi*
Quinaldic acid resistance of Tn*10* insertion mutants	*tet*
Quinolone resistance	*gyrA*
Ribitol resistance in *araC*(Con)	*araB*
Ribitol resistance in *araC*(Con)	*araC*
Rifampin + kasugamycin dependence	*ridA*
Rifampin dependence	*ridB*
Rifampin resistance	*crp*
Rifampin resistance	*cyaA*
Rifampin resistance	*rpoB*
Rifampin resistance in *rpoB*$^+$/*rpoB* (*rif*) diploids	*rpoB*
Salicylate resistance	*pan*
Serine (D) resistance	*cycA*
Serine + methionine + glycine resistance in *relA*	*glyA*
Serine hydroxamate resistance	*serA*
Serine hydroxamate resistance	*serS*
Serine resistance	*sbaA*
Serine resistance	*thrA*
Serine resistance in *relA*	*crp*
Serine resistance in *relA*	*cyaA*
Serine resistance in *relA*	*relA*
Serine resistance in *relA*	*rpoB*
Serine resistance in *relA*	*rpoC*
Showdomycin resistance	*nupC*
Showdomycin resistance	*pnp*
Siderophore–beta-lactam conjugate resistance	*cirA*
Sorbitol + xylitol resistance	*srlA*
Sorbose (L) resistance	*fruA*
Sorbose resistance	*ptsG*
Spectinomycin resistance	*rpsE*
Spectinomycin resistance	*rrn*
Spectinomycin resistance	*spcB*
Spectinomycin resistance and sucrose dependence	*rpsC*
Spectinomycin resistance and sucrose dependence	*rpsD*
Spectinomycin resistance and sucrose dependence	*rpsE*
Streptolydigin resistance	*rpoB*
Streptomycin + cAMP resistance	*crp*
Streptomycin resistance	*hem* (generic)
Streptomycin resistance	*rpsL*
Streptomycin resistance	*strB*
Streptomycin resistance	*strC*
Streptomycin resistance	*strM*
Streptomycin resistance	*ubiF*
Streptomycin resistance	*mut* (generic)
Streptomycin resistance	*topA*
Streptovaricin resistance	*rpoB*
Streptozotocin resistance	*fba*
Streptozotocin resistance	*galT*
Streptozotocin resistance	*manA*
Streptozotocin resistance	*nagA*
Streptozotocin resistance	*nagE*
Streptozotocin resistance	*pfkA*
Streptozotocin resistance	*ptsI*
Streptozotocin resistance	*glpD*
Sulfanilamide + hypoxanthine resistance	*hpt*
Sulfanilamide + hypoxanthine resistance	*pspABCDE*
Sulfanilamide resistance	*folP*

Selection purpose and technique	Mutant gene
Sulfanilamide resistance	*gpt*
Sulfometuron methyl + valine resistance	*ilv* structural genes
Sulfometuron methyl + valine resistance	*ilvG*
Sulfonamide resistance	*folA*
Sulfonamide resistance	*pab*
Tartrate resistance	*dct*
Tetracycline resistance	*cmlA*
Tetracycline resistance	*marA*
Tetracycline resistance	*ompF*
Thiaisoleucine resistance	*ileS*
Thiaisoleucine resistance	*ilvU*
Thialysine resistance	*thrA*
Thiazolealanine resistance	*hisG*
Thiazolealanine resistance	*hisR*
Thienylalanine resistance	*aroP*
Thienylalanine resistance	*aroG*
Thiodigalactoside resistance	*lacY*
Thio(5)glucose resistance	*crr*
Thiolactomycin resistance	*emrB*
Thiolactomycin resistance (due to gene dosage)	*fadB*
Thiolactomycin resistance (due to gene dosage)	*emrB*
Thiolutin resistance	*tlnA*
Thiomaltose resistance	*lamB*
Thiomaltose resistance	*malE*
Thiomaltose resistance	*malF*
Thiomaltose resistance	*malG*
Thiomaltose resistance	*malK*
Thiomaltose resistance	*malT*
Thiomethylgalactoside-independent utilization of galactose in *galR*(Con)	*galR*
Thiopeptin resistance	*rplE*
Thiosine resistance	*argP*
Thymidine resistance in *deoC*	*deoA*
Thymidine resistance in *deoC*	*deoB*
Thymineless death prevention by low thymine levels in *thyA*	*deoB*
Thymineless death prevention by low thymine levels in *thyA*	*deoC*
Thymineless death resistance in *thyA*	*recF*
Thymineless death resistance in *thyA*	*recJ*
Thymineless death resistance in *thyA*	*recO*
Thymineless death resistance in *thyA*	*recQ*
Thymineless death resistance in *thyA*	*alaS*
Thymineless death resistance in *thyA*	*pheS*
Thymineless death resistance in *thyA*	*valS*
Tiamulin resistance	*rplC*
Tiamulin resistance	*rplD*
Triazole resistance	*cysB*
Triazole resistance	*cysE*
Triazole resistance	*cysG*
Triazole resistance	*trzA*
Triazole resistance in *cysM*	*cysB*
Triazole resistance in *cysM*	*cysE*
Triazolealanine + aminotriazole resistance	*gyrA*
Triazolealanine + aminotriazole resistance	*gyrB*
Triazolealanine + aminotriazole resistance	*his* structural genes
Triazolealanine + aminotriazole resistance	*hisR*

Selection purpose and technique	Mutant gene
Triazolealanine + aminotriazole resistance	*hisS*
Triazolealanine + aminotriazole resistance	*hisT*
Triazolealanine + aminotriazole resistance	*hisU*
Triazolealanine + aminotriazole resistance	*hisW*
Trifluorocitrate resistance	*tct*
Trifluoroleucine resistance	*flrB*
Trifluoroleucine resistance	*ileR*
Trifluoroleucine resistance	*leuA*
Trifluoroleucine resistance	*leuJ*
Trifluoroleucine resistance	*leu* (generic)
Trifluoroleucine resistance	*leuS*
Trilysine resistance	*oppA*
Trimethoprim resistance	*folA*
Trimethoprim resistance	*thyA*
Triornithine resistance	*oppA*
Triornithine resistance in *opp*	*tpp*
Tripeptide (toxic amino acid containing) resistance	*oppAE*
Tripeptide (toxic amino acid containing) resistance	*tppA*
Tripeptide (toxic amino acid containing) resistance	*tppB*
Tryptophan analog resistance	*aroH*
Uncoupler resistances	*atpA–atpE*
Uridine resistance of *thyA deoB*	*deoR*
Valine resistance	*ilv* structural genes
Valine resistance	*ilvB*
Valine resistance	*ilvF*
Valine resistance	*ilvG*
Valine resistance	*ilvH*
Valine resistance	*ilvI*
Valine resistance	*ilvJ*
Valine resistance	*livG*
Valine resistance	*livH*
Valine resistance	*livJ*
Valine resistance	*livK*
Valine resistance	*brnQ*
Vinylglycolate resistance	*dld*
Vinylglycolate resistance	*lct*
Xylitol resistance	*fruA*
Xylose resistance in *fda*	*xylE*
Xylose (D) + cAMP resistance	*cxm*
Resistance to biological agents	
9NA phage resistance	*pmi*
9NA phage resistance in *galE*	*kdsA*
Bf23 phage resistance	*btuB*
C21 phage resistance	*rfaD*
Chi phage resistance	*fliC (hag)*
Chi phage resistance	*motA*
Chi phage resistance	*motB*
ES18 phage resistance	*fhuA*
ES18 phage resistance	*prbA,B*
ES18 phage resistance	*sidK*
ES18 phage resistance	*tonB*
Felix O phage resistance	*galE*
Felix O phage resistance	*galU*
Felix O phage resistance	*rfaC,D,E,F,H*
Filamentous phage tolerance	*tolR*
Filamentous phage tolerance	*tolQ*
HK009 phage resistance	*prh*
HK068 phage resistance	*prk*
Host range phage (from *Serratia marcescens*) resistance	*ompC*
K10 phage resistance	*lamB*

Selection purpose and technique	Mutant gene
K3 phage resistance	*ompA*
Lambda + 434 phage resistance	*mopA*
Lambda + 434 phage resistance	*mopB*
Lambda *c*II + rifampin coresistance	*rpoB*
Lambda mutant infection resistance	*gyrB* (*hisW*)
Lambda mutant phage infection, survival of	*himA*
Lambda mutant phage resistance	*hflC*
Lambda mutant phage resistance	*hflK*
Lambda mutant phage resistance	*hflX*
Lambda mutant prophage induction, survival of	*grpD*
Lambda mutant prophage induction, survival of	*grpE*
Lambda phage + nalidixic acid resistance	*crp*
Lambda phage + nalidixic acid resistance	*cyaA*
Lambda phage + 434 phage cross-resistance	*rpoB*
Lambda phage gamma mutant resistance	*polA*
Lambda phage induction, resistance to	*dnaJ*
Lambda phage induction, resistance to	*dnaK*
Lambda phage resistance	*envZ*
Lambda phage resistance	*gprAB*
Lambda phage resistance	*lamB*
Lambda phage resistance	*malK*
Lambda phage resistance	*malT*
Lambda phage resistance	*rap*
Lambda phage resistance with maltose and arabinose as C sources	*crp*
Lambda phage resistance with maltose and arabinose as C sources	*cyaA*
Lambda prophage induction deficiency during thymine deprivation	*recA*
Lambda prophage induction, resistance to	*rpsJ*
Lambda prophage induction, resistance to	*rpsM*
Lambda prophage induction, survival of	*nusA*
Lambda prophage induction, survival of	*nusB*
Lambda *sus N7 nin-5* resistance in P2 lysogen	*rho*
Lambda *vir* resistance after infection with heteromodified lambda *c*I857	*hsd*
Lambdoid phage resistance	*nusB*
Lambdoid phage mixture coinfection resistance	*dnaB*
Lambdoid phage mixture coinfection resistance	*dnaJ*
Lambdoid phage mixture coinfection resistance	*dnaK*
Lambda *c*I71 resistance	*rpoD*
Lambda *Nmar* mutant phage resistance	*rpoB*
Male-specific phage resistance	*arcA* (*fexA*)
Me1 phage resistance	*envZ*
Me1 phage resistance	*ompC*
Me1 phage resistance	*ompF*
Me1 phage resistance	*ompR*
Mu phage lytic growth resistance	*himA*
Mu phage lytic growth resistance	*himD*
Mu prophage induction, survival of	*himA*
Mu prophage induction, survival of	*himD*
N4 phage resistance	*manXYZ*
Ox2 phage resistance	*ompA*
P1 phage resistance	*galE*
P1 phage resistance	*galU*
P1 phage resistance	*lpcA*
P1 phage resistance	*rfaD*
P1 phage specialized transduction of drug resistance to *Salmonella* sp.	*sspA*
P2 *vir1* phage resistance	*rpoA*
P2 phage + lambda phage coinfection resistance	*dnaJ*
P2 phage + lambda phage coinfection resistance	*dnaK*
P2 phage resistance	*rep*
P22 phage resistance	*galE*
P22 phage resistance	*pmi*
P221 phage resistance	*praAB*
PH105 phage resistance	*ompB* (*ompR* of *E. coli*)
PH105 phage resistance	*ompC*

Selection purpose and technique	Mutant gene
PH105 phage resistance	*ompF*
PH105 phage resistance	*praAB*
PH51 phage resistance	*ompB* (*ompR* of *E. coli*)
PH51 phage resistance	*ompC*
PH51 phage resistance	*ompF*
PH51 phage resistance	*praAB*
PH51 phage resistance	*prdB*
ϕX174 phage resistance	*phxB*
ϕ80 phage resistance	*fhuA*
ϕ80 phage resistance	*tonB*
Q phage resistance	*cpxA* (*ecfB, ssd, eup*)
T-even phage resistance	*ompA*
T1 phage (UV irradiated) resistance	*phr*
T1 phage resistance	*fhuA*
T1 phage resistance	*tonB*
T2 phage resistance in *ompF*$^{+}$ or *ompF*	*fadL*
T3 phage resistance	*lpcA*
T4 mutant phage resistance	*lit*
T4 phage *lig* mutant nibbling of colonies yielding *lig*-overproducing strain	*lig*
T4 phage *lig* mutant resistance from *lig*-overproducing strain	*lig*
T4 phage resistance	*lpcA*
T4 phage resistance	*lpcB*
T4 phage resistance	*mopA*
T4 phage resistance	*mopB*
T4 phage resistance	*rho*
T4 phage resistance	*tabC*
T4 phage resistance	*lit*
T4 phage (uracil containing) resistance	*ung*
T5 phage resistance	*fhuA*
T6 phage resistance	*crp*
T6 phage resistance	*cyaA*
T6 phage resistance	*tsx*
T7 phage gene 1.2 mutant resistance	*optA*
T7 phage gene 2 resistance	*rpoC*
T7 phage resistance	*groM*
T7 phage resistance	*lpcA*
T7 phage resistance	*lpcB*
T7 phage resistance	*rpoB*
T7 phage resistance	*trxA*
TC45 phage resistance	*phoB*
TC45 phage resistance	*phoE*
TC45 phage resistance	*phoR*
TC45 phage resistance	*phoS*
TC45 phage resistance	*phoT*
TC45 phage resistance	*pstABCS*
TP1 phage resistance	*envZ*
TuIa phage resistance	*envZ*
TuIa phage resistance	*ompC*
TuIa phage resistance	*ompF*
TuIa phage resistance	*ompR*
TuIa phage resistance	*tolQAB*
TuIb phage resistance	*ompF*
TuII* phage resistance	*ompA*
U3 phage + K3 phage coresistance	*rfaP*
U3 phage resistance	*galE*
U3 phage resistance	*galU*
U3 phage resistance	*pgi*
U3 phage resistance	*pgm*

Selection purpose and technique	Mutant gene
U3 phage resistance	*rfa* (general)
UV-irradiated lytic phage resistance	*uvrA*
UV-irradiated lytic phage resistance	*uvrB*
UV-irradiated lytic phage resistance	*uvrC*
UV-irradiated lytic phage resistance	*uvrD*
Resistance to physical extremes	
Cold resistance in *rpsE* cold-sensitive mutants	*rpsB*
Cold-resistant growth	*crg*
Filter retention	*fts* (generic)
Freeze-thaw resistance	*envZ*
Gamma irradiation resistance	*garA*
Gamma irradiation resistance	*garB*
Growth at 42°C in *his*-overexpressing strain	*his* structural genes
Near-UV irradiation resistance	*nuvA*
Near-UV irradiation resistance	*nuvC*
Near-UV irradiation resistance	*relA*
Osmotolerance	*crp*
Osmotolerance	*cyaA*
Osmotolerance	*osmB*
Osmotolerance	*proA*
Osmotolerance	*proB*
Phage (UV-irradiated T1) resistance	*phr*
Psoralen + UV irradiation resistance	*puvA*
Temperature resistance in *rpoD* (Ts)	*rpoH*
Thermotolerance	*gyrA*
UV light resistance	*crp*
UV light resistance	*cyaA*
UV light resistance	*envB*
UV light resistance	*relA*
UV irradiation resistance in *lon*	*sulA*
UV irradiation resistance in *lon*	*ftsZ*
UV light + bromodeoxyuridine resistance	*tdk*
UV light + bromodeoxyuridine resistance	*ung*
UV light + psoralen resistance	*puvA*
UV-irradiated lytic phage resistance	*uvrA*
UV-irradiated lytic phage resistance	*uvrB*
UV-irradiated lytic phage resistance	*uvrC*
UV-irradiated lytic phage resistance	*uvrD*
Movement	
Migration in a chemical gradient	*che*
Static cultivation (prolonged)	*fliC*

[a]References to selections and species used in selections can be found in Table 2. Note that a single selection can give rise to mutations in several distinct genes. Abbreviations: cAMP, cyclic AMP; DAP, diaminopimelate; IS, insertion sequence; CCCP, carbonyl cyanide *m*-chlorophenylhydrazone, an uncoupling agent. Abbreviations following gene names: (Con), constitutive; (Ts), heat sensitive.

TABLE 2 Genes for which selections exist in *E.coli* and *S. typhimurium*

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
ackA	E, S	Fluoroacetate resistance	96, 281, 463, 797	L
ada	E	Nitrosoguanidine resistance	693	
add	E	Deoxyadenosine + hypoxanthine satisfaction of *purB* requirement	370	L
add	S	Deoxyadenosine (low) satisfaction of *purA* requirement	326	L
adhCE	E	Chloracetaldehyde resistance	157	

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
adhCE	E	Chlorethanol resistance	157	
adhE	E	Allyl alcohol resistance	476	L
adh	E	Ethanol as C source	132	C
alaS	E	Thymineless death resistance in *thyA*	394	S
alaS	E	Mecillinam resistance (beta-lactam resistance)	802	S
ampC	E	Ampicillin resistance	139, 570	D
ampC	E	Ampicillin resistance	210, 212, 362	C
amtAB	S	Aminotriazole resistance	828	
apeA	E, S	*N*-Acetyl-L-phenylalanine-β-naphthyl ester hydrolysis	421, 516	L
apt	E	6-Methylpurine resistance	60	L
apt	E	Adenine resistance in *hpt gpt*	462	
apt	E	2,6-Diaminopurine resistance in *pnp*	470	L
apt	E, S	2,6-Diaminopurine resistance	107, 390	L
araB	E	Ribitol resistance from *araC*(Con)	396	L
araC	E	Fucose resistance (arabinose as C source)	67	C
araC	E	Ribitol resistance from *araC*(Con)	396	L
arcA	E	Male-specific phage resistance; also called *fexA*	110, 651, 711	L
argA	E	Acetylornithine + uracil satisfaction of *car* (*pyrA*)	153	L
argB	E	*N*-Acetylhistidine + ornithine satisfaction of *his*	50	C
argB	E	Acetylornithine + uracil satisfaction of *car* (*pyrA*)	153	L
argC	E	*N*-Acetylhistidine + ornithine satisfaction of *his*	50	C
argC	E	Acetylornithine + uracil satisfaction of *car* (*pyrA*)	153	L
argD	E, S	Proline-independent growth of Δ*proAB*	62, 403	L
argD	E	Acetylornithine + uracil satisfaction of *car* (*pyrA*)	153	L
argE	E	*N*-Acetylhistidine + ornithine satisfaction of *his*	50	C
argE	E	Acetylnorvaline resistance in *argR*(Con)	402	L
argH	E	*N*-Acetylhistidine + ornithine satisfaction of *his*	50	C
argP	E	Canavanine resistance	483, 655	L
argP	E	Thiosine resistance	293, 716	L
argP	E	Canavanine + thiouracil resistance	605	L
argR	E, S	Arginine-resistant, proline-independent growth of Δ*pro*	62, 403	C
argR	E	Acetylhistidine satisfaction of *his*	49, 50, 403	C
argR	E	Acetylmethionine satisfaction of *met*	402	C
argR	E	Indospicine resistance	454	C
argR	E	Canavanine resistance	482, 523	C
argR	E	Glycylglycyl-*N*-phosphonoacetylornithine resistance	604	C
argR	E	Canavanine + azauracil resistance	605	C
argR	E	Canavanine + thiouracil resistance	605	C
argR	E	Acetylnorvaline resistance in *argR*(Con)	402	
argS	E	Canavanine resistance	322	S
argS	E	Mecillinam resistance (beta-lactam resistance)	802	S
argT	S	Hydrazino (α) imidazole propionic acid resistance	432, 433	
aroA	E, S	Glyphosate resistance	512, 731; Comai[d]	C, D
aroF	E	Amino(4)phenylalanine resistance	504	C
aroF	S	Fluoro(4)phenylalanine resistance	270, 729	C
aroG	E, S	Methyl(3)anthranilate resistance	307	FBI, S
aroG	E	Thienylalanine resistance	215	FBI, S
aroG	E	Fluorophenylalanine resistance	351	FBI, S
aroH	E	Tryptophan analog resistance	637	FBI, S
aroP	E, S	Methyl(5)tryptophan resistance	12, 94, 288, 303, 393, 437–439	L, C
aroP	E, S	Fluoro(5)tryptophan resistance	12, 94, 288, 303, 393, 437–439	L
aroP	E, S	Azaserine resistance	12, 94, 288, 303,	L

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
			393, 437–439, 836, 837	
aroP	E, S	Thienylalanine resistance	12, 94, 288, 303, 393, 437–439	L
aroP	E, S	Fluorophenylalanine resistance	12, 94, 288, 303, 393, 437–439	L
aroP	E, S	Azaleucine resistance	12, 94, 288, 303, 393, 437–439	L
aroP	E, S	Methyl(5)tryptophan + thienylalanaine resistance	12, 94, 288, 303, 393, 437–439	L
aroT	E, S	Indole acrylic acid resistance	769	L
aroT	E	Methyl(4)tryptophan resistance in *aroP*	594	L
asm	S	Methionine sulfoxamine resistance	188	
atoB	S	Dinitropyrene resistance	590	L
atoC	E	Butyrate as C source in *fadR*(Con)	602	C
atoC	E	Valerate as C source in *fadR*(Con)	602	C
atoC	E	Penten(4)oate resistance in *atoC*(Con)	669	L
atpA–atpE	E	Uncoupler resistances, including DCCD	225, 226, 229, 355, 537	L
atpA–atpE	E	Tributyl tin resistance	355	
atpA–atpE	E	CCCP resistance	355	
atpA–atpE	E	Pentachlorophenol resistance	355	
atpA–atpE	E	Auroventin resistance	451, 685, 818	L
atpA–atpE	E	Kanamycin resistance	768	L
atpA–atpE	E	Neomycin resistance	392	L
atpA–atpE	E	Azide resistance	355	
atr	S	Acid resistance	233	
azaAB	E	Azaserine resistance	836	
azl	E	Azaleucine resistance	610	
bglBC	E	Arbutin as C source	523, 616, 640	
bglBC	E	Salicin as C source	523, 616, 640	
bglT	E	Methyl(β)glucoside as C source	686	C
bio operon	E	Dehydrobiotin resistance	206	
bioP	E	Dehydrobiotin resistance	206	L
birA	E	Dehydrobiotin resistance	206, 597	
brnQ	E	Methyl(*o*)threonine resistance	278	L
brnQ	E	Valine resistance	277	L
btuB	E	Colicin E3 tolerance	46, 47, 109, 284, 388, 620	
btuB	E, S	Bf23 phage resistance	46, 47, 109, 284, 388, 528, 620	
bymA	E	Maltose utilization in *malT*	327	
cbt	E	Chloroacetate(β) resistance	68	L
cbt	E	Colicin B tolerance	623	L
cbt	E	Colicin D tolerance	623	L
cdd	E	Aza(5)-2′-deoxycytidine resistance	196	L
cdd	E, S	Fluoro(5)deoxycytidine resistance	53, 579	L
celABCDF	E	Cellobiose as C source	426	
cet	E	Colicin E2 tolerance	201	
che	S	Migration in a chemotaxis gradient	34	
chlABDEG	E, S	Chlorate resistance	2, 121, 122, 228, 266, 523, 743, 744	L
chlABDE	E	Lactate + fumarate as anaerobic energy source	436	L
chlC	S	Chlorate resistance	45	L
chlE	E	Lactate + nitrate as anaerobic energy source	799	
chlE	E	Biotin sulfoxide utilization in *chl bio*	180	
cirA	E	Colicin I resistance	77, 93, 620	L
cirA	E	Siderophore–beta-lactam conjugate resistance	93	L

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
cit	E	Citrate as C source	290	
cls	E	Dihydroxy(3,4)butyl-1-phosphonate resistance	345	L
cmlA	E	Chloramphenicol resistance	48	
cmlA	E	Tetracycline resistance	523, 638	
coaA	E	Coenzyme A feedback resistance	789, 790	FBI, S
codA(*cod*)	E, S	Fluoro(5)cytosine resistance	4, 54	L
corABCD	E, S	Cobalt resistance	262, 600, 817	
corABCD	E	Manganese resistance	600	
corABCD	E	Nickel resistance	817	
cpd	S	Succinate as improved C source	8, 530	L
cpd	S	Citrate as C source in presence of low cAMP	8	L
cpdB	E	Fluorouracil(5) and 3′-AMP resistance	51	L
cpxA	E	Amikacin resistance	629	
cpxA	E	Colicin A tolerance	629	
cpxA	E	Kanamycin resistance	768	
cpxA	E	Q phage resistance	508, 711	
cpxA	E	Serine (L) as C source	567	
crg	E	Cold-resistant growth	398	
crp	S	Fosfomycin resistance	10	L
crp	E	Serine (L) resistance in *relA*	167	L
crp	E	Lambda phage + nalidixic acid resistance	429	L
crp	E	Streptomycin + cAMP resistance	31	L
crp	E	Lambda phage resistance with maltose and arabinose as C sources	92, 766	L
crp	E	cAMP + glucose 6-phosphate resistance	1a	L
crp	E	cAMP + glucose 6-phosphate + D-xylose + L-arabinose resistance	1a	L
crp	E	Fluorouracil(5) + 5′-AMP + 3′-AMP resistance	52	L
crp	E	Osmotolerance	282	L
crp	E	Beta-lactam resistance	362	L
crp	E	Mecillinam resistance	25, 168, 857	L
crp	E	UV light resistance	627	L
crp	E	Rifampin resistance	413	L
crp	E	T6 phage resistance	6	L
crr	E	Thio(5)glucose resistance	419	L
crr	S	Methylglucoside(α)-resistant utilization of glycerol in *ptsHI*	563	L
cxm	E	Xylose (D) + cAMP resistance	1a	L
cyaA	E	Lambda phage resistance with maltose and arabinose as C sources	92	L
cyaA	E	Lambda phage + nalidixic acid resistance	429	L
cyaA	E	Serine (L) resistance in *relA*	167	L
cyaA	S	Fosfomycin resistance	10	L
cyaA	E	Osmotolerance	282	L
cyaA	E	Beta-lactam resistance	362	L
cyaA	E	Mecillinam resistance	25, 168, 857	L
cyaA	E	UV light resistance	627	L
cyaA	E	Rifampin resistance	413	L
cyaA	E	T6 phage resistance	6	L
cycA	E	Cycloserine (D) resistance	150, 646, 813	L
cycA	E	Serine (D) resistance	689	L
cysA	S	Chromate resistance	581	L
cysA	E	Selenate resistance	728	L
cysA	S	Azaserine resistance	340, 689	L
cysB	S	Chromate resistance	340	L
cysB	S	Azide resistance	227	C
cysB	S	Selenate resistance	339	L
cysB	E	Novobiocin resistance	631	L
cysB	S	Triazole resistance	227	C
cysB	S	Azaserine resistance	340	L

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
cysC	S	Azaserine resistance	340	L
cysC	S	Chromate resistance	581	L
cysD	S	Azaserine resistance	340	L
cysD	S	Chromate resistance	581	L
cysE	S	Triazole resistance in *cysM*	717, 825	C
cysE	S	Triazole resistance	341	C
cysE	E	Novobiocin resistance	631	L
cysG	S	Azaserine resistance	340	L
cysH	S	Azaserine resistance	340	L
cysH	S	Chromate resistance	581	L
cysI	S	Azaserine resistance	340	L
cysI	S	Chromate resistance	581	L
cysJ	S	Azaserine resistance	340	L
cysJ	S	Chromate resistance	581	L
cysK	S, E	Azaserine resistance	340, 827	L
cysK	S	Azide resistance	147, 227	L
cysK	E	Selenate resistance	230	L
cysK	E, S	Triazole resistance	147, 227, 826, 827	L, C
cysK	E	Selenite resistance	230	L
cysL	S	Selenate resistance	673, 674	
cysL	S	Chromate + selenate resistance	338	
cysM	S	Azaserine resistance	340	L
cytR	E	Uridine as C source, improved utilization	546	
dadA	E, S	Chloro(β)-D-alanine resistance	832	L
dadA	E, S	D-Amino acid satisfaction of amino acid auxotrophy	428, 831	C
dcm	E	Aza(5)cytidine resistance	247	L
dct	E	Fluoro(3)malate resistance	401	L
dct	E	Tartrate resistance	687	L
dct	S	Malate (L) as improved C source	745	D
deoA	E	Deoxyadenosine + fluorouracil resistance in *upp*	3	L
deoA	E	Thymidine resistance in *deoC*	3	
deoB	E	Thymidine resistance in *deoC*	3, 651	L
deoB	E, S	Thymineless death prevention by low thymine levels in *thyA*	71, 471	
deoC	E	Thymineless death prevention by low thymine levels in *thyA*	325, 471, 651	L
deoD	E	Deoxy(2)adenosine resistance in *deoC*	651	L
deoD	E	Deoxyadenosine + fluorouracil resistance in *upp*	3	L
deoR	E	Inosine as improved C source	546	C
deoR	S	Diamino(2,6)purine satisfaction of purine auxotrophy	251	
deoR	S	Uridine resistance in *thyA deoB*	71	
dgd	E	Arabitol (D) as C source in *fuc*	849	
dgoR	E	Keto(2)-3-deoxygalactonate as C source	144	C
dgsA	E	Glucosamine as anaerobic C source in *ptsG*	652	L
dhuA	E, S	Histidine (D) satisfaction of *his* auxotrophs	422, 428, 546	
dhuA	S	Azaserine + tryptophan resistance	432	
dld	E	Vinylglycolate resistance	696	L
dml	S	Malate (D) as C source	737	
dnaB	E	Lambdoid phage mixture coinfection resistance	259	
dnaB	E	Phenethyl alcohol resistance	494	
dnaE	E	Acriflavin (acridine) resistance	553–555	

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
dnaE	E	Globomycin resistance	668	S
dnaJ	E	Lambda phage induction, resistance to	667	S
dnaJ	E	Lambdoid phage mixture coinfection resistance	257, 259	S
dnaJ	E	P2 phage + lambda phage coinfection resistance	753	S
dnaK	E	Lambda phage induction, resistance to	667	S
dnaK	E	Lambdoid phage mixture coinfection resistance	257, 259	S
dnaK	E	P2 phage + lambda phage coninfection resistance	753	S
dnaP	E	Phenethyl alcohol resistance	809	
dor	S	Drug-resistant gene maintenance	814	
dppA	E, S	Bacilysin resistance	1	L
dppA	E, S	Bialaphos resistance	1	L
dppA	E, S	Valine-containing dipeptide resistance	1	L
dppA	E	Lysyl-2-aminoxypropionate resistance	603	L
dppA	E	Glycylleucine resistance	269	L
dppA	E	Phenylalanylleucine resistance	269	L
dppA	E	Glycylvaline resistance in *opp*	178	L
dsdA	E	Sucrose as C source	5	L
dsdC	E	Sucrose as C source	5	
ebgA	E	Lactose utilization in Δ*lacZ*	118	Q
ecfB	E	Serine (L) as C source	567, 768	
ecfB	E	Kanamycin resistance	567, 768	
ecfB	E	Neomycin resistance	608	
ecfB	E	Colicin K resistance	608	
edd	E	Gluconate as C source in *eda*	239, 240	L
emrB	E	CCCP resistance due to gene dosage	472	D
emrB	E	Nalidixic acid resistance due to gene dosage	472	D
emrB	E	Thiolactomycin resistance due to gene dosage	250	D
emrB	E	Thiolactomycin resistance	250	
envB	E, S	Mecillinam resistance	359, 587	
envB	E	UV light resistance	24	
envM	E, S	Diazoborine resistance	63	S
envZ	E	Ampicillin resistance	362, 363	
envZ	E	Colicin L tolerance	812	
envZ	E	Lambda phage resistance	812	
envZ	E	Me1 phage resistance	801	
envZ	E	TPI phage resistance	812	
envZ	E	TuIa phage resistance	801	
envZ	E	Freeze-thaw resistance	112	
envZ	E	Colicin (multiple) resistance	626	
eryC	E	Erythromycin resistance	599	
eryD	E	Erythromycin resistance	830	
exbB	E	Albomycin resistance	205	
exbB	E	Colicin I resistance	283, 624	
exbB	E	Colicin (other) resistance	283, 624	
exbC	E	Colicin B resistance	624	
exbC	E	Colicin I resistance	283, 624	
exbC	E	Colicin (other) resistance	283, 624	
exuR	E	Aldohexuronate resistance in *eda*	612	
exuR	E	Hexuronate as C course in noninducible *exuR eda*	612	C
exuT	E	Aldohexuronate resistance in *eda*	612	L
fadB	E	Thiolactomycin resistance (due to gene dosage)	778	D
fadL	E	T2 phage resistance in *ompF*$^+$ or *ompF*	70, 534	L
fadR	E	Decanoate as C source	713	L
fba	E	Streptozotocin resistance	456	L
fepABCDG	E	Colicin B resistance	623, 624	L
fepABDCG	E	Colicin D resistance	623	L

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
fhuA	E, S	Albomycin resistance	87, 387, 388, 478, 479	S
fhuA	S	ES18 phage resistance	87, 478, 479	S
fhuA	E	T1 phage resistance	93, 409; Lin et al.[e]	S, L
fhuA	E	T5 phage resistance	93, 151, 387; Lin et al.[e]	L
fhuA	E	Φ80 phage resistance	151, 387, 409; Lin et al.[e]	L, S
fhuA	E	Colicin M resistance	151, 387, 409	L, S
fhuA	E	Beta-lactam conjugate resistance	93	L
fhuB	E	Albomycin resistance	618	L
fliC	E, S	Chi phage resistance	347, 349, 416, 417, 513, 710	
fliC	S	Prolonged static cultivation	249	
flrB	S	Trifluoroleucine resistance	115, 117	
folA	E	Sulfonamide resistance	607, 697	S, D
folA	S	Trimethoprim resistance	405, 654, 718, 719	S, D
folP	E	Sulfonamide resistance	756	S
fruA	E	Deoxy(2)glucose-independent fructose utilization	11	
fruA	E	Xylitol resistance	614, 639	L
fruA	E	Sorbose (L) resistance	715	L
fts (generic)	E	Filter retention	55	
ftsZ	E	UV irradiation resistance in *lon*	373	
ftsZ	E	Methyl methanesulfonate resistance in *lon*	373	
ftsZ	E	Nitrofurantoin resistance in *lon*	252	
fucA	E	Propanediol as C source	287	
fucA	E	Ethyleneglycol as C source in propanediol utilizer	79	
fucA	E	Fucose (L) as C source in propanediol utilizer	287	
fucA	E	Xylitol as C source in propanediol utilizer	848	
fucA	E	Arabinose (D) as C source	450	
fur	E	Manganese resistance	300	C
fusA	E	Fusidic acid resistance	65, 434, 695, 761	S
gabC	E	Aminobutyrate as N source	197	
gadS	E	Glutamate as C source	292	L
gal operon	E	Galactose utilization in the presence of thiomethylglucoside	636	D
gal operon	S	Deoxy(2)galactose resistance	9, 552	L
gal operon	E	Galactose resistance in *galU*	664	L
galC	S	Glucose as C source in Δ*ptsHI*	613	
galE	E, S	P1 phage infection of *Salmonella* sp. monitored by drug resistance	527	L
galE	E	U3 phage resistance	816	L
galE	S	Deoxy(2)galactose resistance	408	L
galE	S	Felix O phage resistance	334, 527, 591, 833	L
galE	S	P22 phage resistance	334, 527, 591, 833	L
galK	S	Deoxy(2)galactose resistance	408	L
galK	E, S	Galactose resistance in *galE*	569, 752	L
galK	E	Galactose resistance in *galT*	859	L
galK	E	Galactose resistance in *galU*	664	L
galP	S	Deoxy(2)galactose resistance	552	L
galR	E	Thiomethylgalactoside-independent utilization of galactose in *galR*(Con)	108	
galR	S	Glucose utilization in Δ*ptsHI*	613	
galR	E	Galactose resistance in $galT^{+K+E+}$/$galT^{+K+E+}$ *galU*	664	
galT	E	Streptozotocin resistance	456	L

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
galU	E	Ampicillin resistance	212	L
galU	E	P1 phage resistance	242	L
galU	E	U3 phage resistance	816	L
galU	S	Felix O phage resistance	334	L
garA	S	Gamma irradiation resistance	346	
garA	E	Glucarate (D) resistance in *ppc*	647	L
garB	S	Gamma irradiation resistance	346	
gatACD	E	Fucitol resistance in galactitol-utilizing strains	184	L
gatACD	E	Deoxy(2)galactitol resistance in galactitol-utilizing strains	184	L
gatACD	E	Arabitol utilization	466, 845	
gatACD	E	Ribitol utilization	466, 845	
gatACD	E	Arbitol (D) resistance	639	L
gleR	S	Glycylleucine resistance in *ilv*	580	
glnA	S	Histidine(D) + glycylglutamine satisfaction of *his* auxotrophs	819	L
glnA	E	Methylammonium resistance	694	S
glnA	E	Methionine sulfoxamine resistance in *glnG*	592	C
glnA	S	Glutamyl(γ)hydrazide resistance	518; Miller[f]	S
glnF	S	Glutamyl(γ)hydrazide resistance	433	L
glnH	S	Glutamyl(γ)hydrazide resistance	433	L
glnP	E	Glutamine as C source	433, 501, 820	
glnP	E, S	Methionine sulfoxamine resistance	37, 501	L
glnP	E	Glutamyl(γ)hydrazide resistance	501, 821	L
glnP	E	Glutamine (D) resistance	501	L
glnV	E	Caffeine resistance	185	S
glpD	E	Streptozotocin resistance	456	L
glpF	E	Glyceraldehyde (L) resistance	762	L
glpK	E	Glyceraldehyde (L) resistance	762	L
glpK	E, S	Methyl(α)glucoside-resistant glycerol utilization in *ptsI*	64, 665	
glpT	E, S	Fosfomycin resistance	10, 29, 313, 707, 800	L
glpT	E	Glyceraldehyde (DL) 3-phosphate resistance	762	L
glpT	E	Arsenate resistance	838	L
glpT	E	Dihydroxybutyl phosphonate resistance	285, 453	L
glpT	E	Fluorohydroxyacetone phosphate resistance	515	L
glpT	E	Chlorohydroxyacetone phosphate resistance	515	L
glpT	E	Glycerol 3-phosphorothioate resistance	295	L
gltA	E	Improved growth in *icd*	435	L
gltH	E	Glutamate as C source	496, 497, 687	
gltR	E	Glutamate as C source at 42°C	497	
gltS	E	Glutamate as C source	496, 687	Q
gltS	E	Glutamate as C source	496, 497, 687	
gltS	E	Glutamate (D) resistance in *gltS* (increased)	525, 716	L
gltS	E	Methyl(α)glutamate resistance in *gltS* (increased)	391, 525, 716	L
gltS	E	Homocysteic acid resistance	213	L
gltX	E	Glutamyl-γ-methyl ester resistance	425	
glyA	E	Serine + methionine + glycine resistance in *relA*	783	
gntM	E	Glycerol + gluconate as C source in *eda*	217	L
gntR	E	Acetate + gluconate as C source in *ppc*	39	
gntS	E	Acetate + gluconate as C source in *ppc*	39	L
gor	E	Methyl viologen tolerance	430	L
gprAB	E	Lambda phage resistance	578, 670	
gpt	S	Aza(8)guanine resistance	272, 764	L
gpt	E	Sulfanilamide resistance in presence of guanine	97	L
groM	E	T7 phage resistance	427	

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
grpD	E	Lambda mutant prophage induction, survival of	667	
grpE	E	Lambda mutant prophage induction, survival of	667	
gsh (generic)	E	Nitrosoguanidine resistance	693	L
gsh (generic)	E	Methylglyoxal resistance	548	
gshAB	E, S	Selenite resistance	423	L
guaAB	E	Psicofuranine resistance	779	
guaB	S	Fluoro(5)uracil + fluoro(5)uridine resistance	367	L
gurBCD	E	Glycerol + methylglucuronide a C source in *eda*	572	L
gyrA	E, S	Triazolealanine + aminotriazole resistance	660	S
gyrA	E, S	Nalidixic acid resistance	200, 298	S
gyrA	E	Quinolone resistance	860	S
gyrA	E	Oxolinic acid resistance	734	S
gyrA	E	Glucosides (β) as C source	194	
gyrA	S	Thermotolerance	200	
gyrB	S	Triaolealanine + aminotriazole resistance	660	S
gyrB	E	Aminotriazole resistance in *relA*	772	S
gyrB	E	Novobiocin resistance	255	S
gyrB	E	Coumermycin resistance	181, 255, 593	D, S
gyrB	E	Chlorobiocin resistance	589	
gyrB	E	Glucosides (β) as C source	194	
gyrB	E	Lambda mutant infection resistance	521	
gyrB	E	Nalidixic acid resistance	333, 855	S
hem (generic)	E	Streptomycin resistance	57	L
hemA	E	Kanamycin resistance	585	L
hemA	E, S	Neomycin resistance	683	L
hemB	E	Kanamycin resistance	585	L
hemB	E	Kanamycin-resistant, hemin-supported growth of *hemA*	507	L
hemB	E	Colicin "K-type" tolerance	83	
hemC	S	Neomycin resistance	682	L
hemD	S	Neomycin resistance	681	L
hemE	S	Neomycin resistance	189, 680	L
hemBCF	E	Plate method	506	L
hemG	E	Neomycin resistance	679	L
hemL	E	Kanamycin resistance	350	L
hflC	E	Lambda mutant phage resistance	56	
hflK	E	Lambda mutant phage resistance	56	
hflX	E	Lambda mutant phage resistance	56	
himA	E	Mu prophage induction, survival of	520, 522	
himA	E	Mu phage lytic growth resistance	81	
himA	E	Lambda mutant phage infection, survival of	519, 521	
himA (himC)	E	Lambda mutant phage resistance	519, 521	
himD	E	Mu prophage induction, survival of	520, 522	
himD	E	Mu phage lytic growth resistance	81	
hipA	E	Cycloserine resistance	541	
hipA	E	Ampicillin resistance	541	
hipA	E	Fosfomycin resistance	541	
hipQ	E	Norfloxacin resistance	842	
hipQ	E	Ampicillin resistance	842	
his structural genes	E, S	Triazolealanine + aminotriazole resistance	98, 126, 658	C, Q
his structural genes	S	Aminotriazole resistance	20, 21	D
his structural genes	S	Growth at 42°C in *his*-overexpressing strain	804	Q
his structural genes	S	Histidinal satisfaction of *his* auxotroph requirement at 30°C	374, 375	Q
his structural genes	S	Histidine (D) satisfaction of *his* auxotroph requirement	374, 375	Q

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
hisG	E, S	Thiazolealanine resistance	540, 698, 824	S, FBI
hisG	S	Hydrazino (α) imidazole propionic acid resistance	699	S, FBI
hisG	S	Histidinal satisfaction of *his* auxotroph requirement at 30°C	374, 375	L
hisG	S	Histidine (D) satisfaction of *his* auxotroph requirement	374, 375	L
hisG	E	Histidine-resistant adenine → guanine nucleotide conversion in *deoD purF add*	33	S,FBI
hisJ	S	Hydrazino (α) imidazole propionic acid resistance	13, 15	L
hisJ	S	Azaserine + tryptophan resistance in *dhuA*	15, 432	
hisP	S	Hydrazino (α) imidazole propionic acid resistance in *dhuA*	14, 15	L
hisP	S	Arginine as N source	13, 15, 432	D
hisQ	S	Hydrazino (α) imidazole propionic acid resistance	13, 15	L
hisR	S	Triazolealanine + aminotriazole resistance	658	Q
hisR	S	Thiazolealanine resistance	706	Q
hisR	S	Methyl(2)histidine resistance + aminotriazole resistance	658	Q
hisS	S	Triazolealanine + aminotriazole resistance	658	S
hisS	S	Thiazolealanine resistance	657	S
hisT	E, S	Triazolealanine + aminotriazole resistance	98, 148, 658, 705, 784	L
hisT	E	Azaleucine resistance	98, 784	L
hisT	E	Serine resistance	98, 784	L
hisT	S	Amino(3)tyrosine resistance	148, 658, 705	L
hisT	S	Thialysine resistance	148, 658, 705	L
hisT	S	Trifluoroleucine resistance	148, 658, 705	L
hisT	S	Norleucine resistance	148, 658, 705	L
hisT	S	Hydroxy (β) leucine resistance	148, 658, 705	L
hisT	E	Phenyl galactoside resistance of *lacP lacI* (nonsense) *supE*	747	
hisU	S, E	Triazolealanine + aminotriazole resistance	23, 660	
hisU	S	Nalidixic acid resistance	593, 660	
hisW	S, E	Triazolealanine + aminotriazole resistance	23	
hisW	S	Coumermycin resistance	593, 660	
hpt	E	Mercapto(6)purine resistance in *gpt*	371	
hpt	E	Sulfanilamide + hypoxanthine resistance	97	L
hsd	E	Lambda *vir* resistance after infection with heteromodified lambda *c*I857	183	L
hsd	S	Lactose utilization after conjugation of *F′lac* into *Salmonella* sp.	103	L
hut	S	Histidine as sole N or C source	509	
icdE	E, S	Nalidixic acid resistance	91, 311	L
iclR	E	Butyrate or valerate as better C source	602	C
iclR	E	Glucose or glycerol as C source in *ppc*	488	
ileR	E	Trifluoroleucine resistance	412	
ileS	E	Pseudomonic acid resistance	858	S
ileS	E	Thiaisoleucine resistance	757	S
ilv structural genes	S	Sulfometuron methyl + valine resistance	Epelbaum et al.[g]	C
ilv structural genes	E	Aminobutyrate resistance	633, 780	C
ilv structural genes	E	Valine resistance	268	C
ilv structural genes	S	Cyclopentane glycine resistance	586	C
ilvA	S	Cyclopentane glycine resistance	586	S, FBI
ilvA	E	Glycylleucine resistance	806	S, FBI

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
ilvA	S	Threonine as sole N source	106	S, FBI
ilvA	E	Growth on minimal medium of *ilvA*$^+$ (multicopy) *ilvDC hisT* overcoming 2-ketobutyrate accumulation	231	L
ilvB	E	Aminobutyrate resistance	633, 780	S, FBI
ilvB	E	Valine resistance	633, 755	S, FBI
ilvB	E	Glyclleucine resistance	269	S
ilvB	E	Phenylalanylleucine resistance	269	S
ilvF	E	Valine resistance	174, 610	G
ilvG	E, S	Sulfometuron methyl + valine resistance	441, 851; Epelbaum et al.[g]	S, Q
ilvG	E	Valine resistance	221, 448, 720	G
ilvH	E	Aminobutyrate resistance	633, 780	S, FBI
ilvH	E	Valine resistance	633, 755	S, FBI
ilvH	E	Glyclleucine resistance	269	S
ilvH	E	Phenylalanylleucine resistance	269	S
ilvI	E	Aminobutyrate resistance	633, 780	S
ilvI	E	Valine resistance	633, 755	
ilvI	E	Glyclleucine resistance	269	
ilvI	E	Phenylalanylleucine resistance	269	
ilvJ	E	Valine resistance	174, 361, 649	G
ilvU	E	Thiaisoleucine resistance	222	
kdgR	E	Keto(2)-3-deoxygluconate as C source	377, 615	C
kdsA	S	9NA phage resistance in *galE*	452, 641	
ksgA	E	Kasugamycin resistance	312, 726, 793	L
ksgB	E	Kasugamycin resistance	238, 726	
ksgC	E	Kasugamycin resistance	861	
ksgD	E	Kasugamycin resistance	238	
lac	E	Growth in lactose-limited chemostats	330	D
lacI, operator	E	Methyl(α)glucoside-resistant utilization of lactose in *ptsH*	665	C
lacI, operator	E	Raffinose as C source	459	C
lacI, operator	E	Neolactose as C source	459	C
lacI, operator	E	Phenyl galactoside as C source	523	C
lacI, operator	E	Lactobionic acid as C source	440	C
lacI, operator	E	Lactitol as C source	457	C
lacI, operator	E	Melibiose as C source	475	C
lacI, operator	E	Melibiose as C source and acetyl(*N*)lactonate as N source	475	C
lacI, operator	E	Lactobionic acid as C source	474	
lacI, operator	E	Acetyl(*N*)lactonate as N source	474	Q
lacI, operator	E	Nitro(*o*)-phenylthiogalactoside resistance in *lacI*(Con) or *lacO*(Con)	543, 571	Q
lacI, operator	E	Methyl(α)glucoside-resistant lactose utilization	406	C
lacY	E	Nitro(*o*)-phenylthiogalactoside resistance	523, 543, 721	L
lacY	E	Phenyl galactoside resistance	376	L
lacY	E	Phenethylyl galactoside resistance	376	L
lacY	E	Arabinose (L) growth in the presence of *lac* operon inducer	812	L
lacY	E	Thiodigalactoside resistance	241	
lacZ	E	Lactobionic acid as C source	440	D
lacZ	E	Phenyl galactoside resistance	376, 500	L
lacZ	E	Phenethylyl galactoside resistance	376, 500	L
lacZ	E	Nitro(*o*)-phenyl galactoside resistance	376, 500	L

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
lamB	E	Lambda phage resistance	88, 134, 135, 253, 644, 766	L, S
lamB	E	K10 phage resistance	644	
lamB	E	Thio(5)maltose resistance	223	L
lct	E	Vinylglycolate resistance	696	
leuA	S	Trifluoroleucine resistance	115	FBI, S
leuJ	E	Trifluoroleucine resistance	575	
leu (structural genes)	S	Trifluoroleucine resistance	115, 116	C
leuS	S, E	Azaleucine resistance	477, 514	S
leuS	S	Trifluoroleucine resistance	7	S
leuW	E	Calmodulin inhibitor resistance	129	S
lev	E	Levallorphan resistance	164	
lexA	E	Mitomycin C resistance of *recA* (SOS-induced) *sfi lexA3*(Con)	538	L
lig	E	T4 phage *lig* mutant nibbling of colonies yielding *lig* overproducer	254	Q
lig	E	T4 phage *lig* mutant resistance from *lig* overproducer	254	L
linB	E	Lincomycin resistance	26, 343	
lit	E	T4 mutant phage resistance	143	
livG	E	Azaleucine resistance	303, 561	L
livH	E	Valine resistance in *leu*	17, 595	L
livH	E	Azaleucine resistance	561	L
livJ	E	Valine resistance in *leu*	17, 595	L
livK	E	Valine resistance in *leu*	17, 595	L
lon	E, S	Chlorpromazine resistance	198, 529	L
lon	E	Promethazine resistance	529	L
lpp	E	Globomycin resistance	140, 344, 854, 868	L
lpcA	E	T3 phage resistance	792	L
lpcA	E	T4 phage resistance	792	L
lpcA	E	T7 phage resistance	792	L
lpcA	E	P1 phage resistance	40, 41	
lpcB	E	T4 phage resistance	760	
lpcB	E	T7 phage resistance	760	
lrp	E	Leucine (D) satisfaction of *leu* auxotrophs	18, 428	
lysC	E	Aminoethylcysteine (thialysine) resistance	82, 765	S, FBI
lysC	E	Lysine hydroxamate resistance	82, 765	S, FBI
lysP	E	Aminoethylcysteine (thialysine) resistance	611, 736	L
lysS	E	Aminoethylcysteine (thialysine) resistance	323	S
lysS	E	Phenyl galactoside resistance of $lacI^{q\ lacI}$(nonsense) *lacP supL*	748	
lyt	E	Beta-lactam tolerance	700	
mac	E	Erythromycin growth dependence	725	
malE	E, S	Methylglucoside(α)-resistant utilization of maltose	665	
malE	E	Thio(5)maltose resistance	223	L
malF	E, S	Methylglucoside(α)-resistant utilization of maltose	665	
malF	E	Thio(5)maltose resistance	223	L
malG	E, S	Methylglucoside(α)-resistant utilization of maltose	665	
malG	E	Thio(5)maltose resistance	223	L
malK	E	Lambda phage resistance	766	L
malK	E, S	Methylglucoside(α)-resistant utilization of maltose	177, 665	
malK	E	Thio(5)maltose resistance	223	L
malP	E	Maltose as C source in *malT*	327	

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
malQ	E	Maltose as C source in *malT*	327	
malT	E	Lambda phage resistance	766	L
malT	E	Thiomaltose resistance	223	L
manA	E	Streptozotocin resistance	456	
manC	E	Lyxose (D) as C source	738	
manXYZ	E	Phage N4 resistance	410	
manXYZ	E	Deoxyglucose resistance	158, 379	L
marA	E	Menadionine resistance	274	
marA	E	Chloramphenicol resistance	286	
marA	E	Tetracycline resistance	286, 329	
mbrABCD	E	Camphor resistance	776, 777	
mdoB	E	Arbutin resistance in *dgk*	360	L
mel (generic)	E	Raffinose as C source in *lacI*	459	
mel (generic)	S	Methylglucoside(α)-resistant utilization of melibiose	665	
melB	E	Deoxy(2)glucose-resistant utilization of melibiose	431	S
melB	E	Lithium-resistant utilization of melibiose	397	S
metA	S	Methyl(α)methionine resistance	127, 447	FBI, S
metC (*ecfA*?)	E	Neomycin resistance	464	
metC (*ecfA*?)	E	Colicin K resistance	465	
metC (*ecfA*?)	E	Chloro(β)alanine resistance	832	
metG	E	Ethionine resistance	28	S
metJ	E, S	Ethionine resistance	447	
metJ	E	Glutamyl-γ-methyl ester resistance	425	S
metJ	E, S	Norleucine resistance	128	
metJ	E	Methionine sulfoximine + methyl(α)methionine resistance	386	S
metK	E, S	Ethionine resistance	275, 289, 447, 735	S
metK	E	Glutamyl-γ-methyl ester resistance	425	S
metK	E, S	Norleucine resistance	128, 447, 735	S
metK	S	Methyl(α)methionine resistance	447, 735	S
metL	E	Hydroxy (β) norvaline resistance	138	S, FBI
metPD	E, S	Methyl(α)methionine resistance	37, 38, 386	L
metPD	E, S	Methionine sulfoximine resistance	37, 38, 386	L
mglA	E	Fucose + arabinose-supported growth in *galP*	209, 613	
mglB	E	Fucose + arabinose-supported growth in *galP*	209, 613	
mglC	E	Fucose + arabinose-supported growth in *galP*	209, 613	
mglD	E	Methyl-β-galactoside-supported growth	645	C
mng	E	Manganese resistance	708	
mopA (*groEL*)	E	T4 phage resistance	258	S
mopA (*groEL*)	E	Lambda + 434 phage resistance	258	S
mopB (*groES*)	E	T4 phage resistance	258	S
mopB (*groES*)	E	Lambda + 434 phage resistance	258	S
motAB	E	Chi phage resistance	349, 709, 710	
mrb	E	Fosfomycin resistance	800	
mrdA	E	Mecillinam resistance	759	
mrdB	E	Mecillinam resistance	358, 502, 759	
mreBCD	E	Mecillinam resistance	582, 807	
mtlA	E	Arabinitol (D) resistance	614	L
mtlC	E	Mannitol (limiting) as C source	722	C
mtr	E	Methyl(5)tryptophan resistance	305, 320, 523	L
murZ	E	Fosfomycin resistance due to increased gene dosage	499	D

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
mut (generic)	E	Streptomycin resistance	309	
mut (generic)	E	Azaserine resistance	703	
mut (generic)	E	Chemostat growth	152	
mutH	E	Amino(2)purine resistance in *dam*	267	L
mutL	E	Amino(2)purine resistance in *dam*	267	L
mutS	E	Amino(2)purine resistance in *dam*	267	L
mvrC	E	Methyl viologen resistance	532	D
nadB	S	Amino(6)nicotinamide resistance	142, 336	S
nadD	S	Amino(6)nicotinamide resistance	336, 337	L
nagA	E	Streptozotocin resistance	456	L
nagA	E	Iodoacetylglucosamine resistance	823	L
nagB	E	Iodoacetylglucosamine resistance	823	L
nagE	E	Streptozotocin resistance	456	L
nagE	E	Iodoacetylglucosamine resistance	823	L
nagE	E	Deoxy(2)-2-iodoacetamideoglucose resistance	379	L
nalB	E	Nalidixic acid resistance	298	
nalD	E	Nalidixic acid resistance	333	
nar (general)	E	Metronidazole resistance	677	L
narC	E	Chlorate resistance	266, 280	L
narG	E	Chlorate resistance	739	L
narH	E	Chlorate resistance	739	L
ndk	S	Aza(8)guanine resistance	264, 650	
neaB	E, S	Neamine resistance	119, 182, 495	
nek	E	Aminoglycoside resistance	27, 342	
nfnA	E	Nitrofurantoin resistance	684	
nfnB	E	Nitrofurantoin resistance	684	
nfsA	E	Nitrofuranzone resistance	90, 505	
nfsB	E	Nitrofuranzone resistance	90, 505	
nhaA	E	Lithium resistance (multicopy)	628	D
nol	S	Norleucine resistance	324	
nov	E	Novobiocin resistance	630	
nrdA	E	Hydroxyurea resistance	609	D
nrdB	E	Hydroxyurea resistance	609	D
nupC	E	Showdomycin resistance	415, 545	L
nupC	E	Fluorouracil resistance	544	L
nupC	E	Fluorodeoxyuridine resistance	545	L
nupC	E	Fluoruridine resistance	544	L
nupC	E	Fluorodeoxycytidine resistance	544	L
nupG	E	Fluorouracil resistance	544	L
nupG	E	Fluorodeoxyuridine resistance	545	L
nupG	E	Fluorouridine resistance	544	L
nupG	E	Fluorodeoxycytidine resistance	544	L
nusA	E	Lambda prophage induction, survival of	244	
nusB	E	Lambda prophage induction, survival of	245, 260	
nusB	E	Lambdoid phage resistance	260	
nuvA	E, S	Near-UV irradiation resistance	424, 468, 767	L
nuvC	E	Near-UV irradiation resistance	663	
ompA	E	K3 phage resistance	306, 489, 491, 493	L
ompA	E	T-even-like phage resistance	199, 533, 535	S
ompA	E	TuII* phage resistance	171, 314, 493	L
ompA	E	Ox2 phage resistance	199, 493, 642	
ompA	E	Bacteriocin JF246 resistance	124, 491	
ompA	S	Bacteriocin 4-59 resistance	741	L
ompA	E	Colicin K tolerance	491	
ompA	E	Colicin L tolerance	491	
ompA	E	Chelator resistance	493	
ompA	E	Novobiocin resistance	493	

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
ompB	S	PH51 phage resistance	372	
ompB	S	PH105 phage resistance	372	
ompC	E	Me1 phage resistance	791, 801	L
ompC	E	TuIa phage resistance	801	L
ompC	S	PH51 phage resistance	372	L
ompC	S	PH105 phage resistance	372	L
ompC	E	Host range *Serratia marcescens* phage resistance	702	
ompD	S	PH51 phage resistance	741	L
ompD	S	Bacteriocin 4-59 resistance	741	L
ompF	E	Beta-lactam (ampicillin, cefoxitin) resistance	362, 363	L
ompF	E	Chloramphenicol resistance	235, 523	L
ompF	E	Tetracycline resistance	235, 523	L
ompF	E	Fluoro(5)uracil + nucleotide resistance	52	L
ompF	E	Colicin A tolerance	125, 235	
ompF	E	Cloacin DF13 resistance	846	L
ompF	E	Colicin L tolerance	235, 291	L
ompF	E	Colicin K tolerance	235	L
ompF	E	Colicin E2 tolerance	235	
ompF	E	Colicin E3 tolerance	235	
ompF	E	Me1 phage resistance	801	L
ompF	E	TuIa phage resistance	801	L
ompF	E	TuIb phage resistance	237	
ompF	S	PH51 phage resistance	372	L
ompF	S	PH105 phage resistance	372	L
ompF	E	Copper resistance in *ompC*	480	
ompR	E	Me1 phage resistance	801	
ompR	E	TuIa phage resistance	801	
ompR	E	Copper resistance	52, 625	
ompR	E	Beta-lactam (ampicillin, cefoxitin) resistance	362, 363	L
ompR	E	Chloramphenicol resistance	625	
ompR	E	Fluoro(5)uracil + nucleotide resistance	52	
oppA	E, S	Triornithine resistance	43, 317	L
oppA	E	Glycylleucine resistance	806	L
oppA	E	Alanyl-2-aminopropionate resistance	603	L
oppA	E, S	Trilysine resistance	317	L
oppA	E, S	Norleucylglycyl glycine resistance	317	L
oppA	S	Glycylglycyl histidinol phosphate ester resistance	317	L
oppA	E, S	Phaseolotoxin resistance	733	L
oppA	E	Tripeptide (toxic amino acid containing) resistance	604	L
oppA	E	Glycylglycyl-*N*-*S*-(phosphonoacetyl)-L-ornithine resistance	604	L
oppE	E	Tripeptide (toxic amino acid containing) resistance	22	L
optA	E	T7 phage gene 1.2 mutant resistance	666	
osmB	E	Osmotolerance	384	L
osmZ	E	Arbutin as C source	179	
osmZ	E	Salicin as C source	179	
oxyR	E, S	Peroxide resistance	131	C
pab	E	Sulfonamide resistance	97	C
pan	E	Salicylate resistance	481	C
pan	E	Hydroxyaspartate resistance	701	C
pan	E	Pentylpantothenamide resistance	136	C
pdx	E	Isoniazid resistance	186	C
pepA	S	Alafosfalin resistance	263	L
pepA	E, S	Peptide (toxic, valine containing) resistance in *pepN*	517	L
pepD	E, S	Peptide (toxic, valine containing) resistance in *pepN pepA*	517	L
pepN	E, S	Albomycin resistance	86	L
pepN	E, S	Peptide (toxic, valine containing) resistance	517	L
pepN	E, S	Indicator plate	445	

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
pepQ	E, S	Peptide (toxic, valine containing) resistance	517	L
pfkA	E	Streptozotocin resistance	456	L
pgi	E	U3 phage resistance	816	L
pgi	E	Fosfomycin + fructose-6-phosphate resistance	243	L
pgm	E	U3 phage resistance	816	L
pheA	E	Fluoro(4)phenylalanine resistance	351, 564	C, FBI
pheR	S	Fluoro(4)phenylalanine resistance	271	C
pheS	E	Fluoro(4)phenylalanine resistance	78, 218, 395	S
pheS	E	Thymineless death resistance in *thyA*	394	S
pheU	S	Fluoro(4)phenylalanine resistance	729	
pho	S	Glycerol(β)-phosphate as C source in the presence of high phosphate	407	C
phoA	E	Fluoro(5)uracil + adenosine resistance in *upp*, *phoS*, or *phoT*	315	
phoA	E	Glycerol(β)-phosphate as C source in the presence of high phosphate	773	C
phoA	E	Glycerol(β)-phosphate resistance in *glpD*	678	
phoB	E	Tellurite resistance	770	
phoB	E	TC45 phage resistance	771	L
phoB	E	Fluoro(5)uracil + adenosine resistance in *upp*, *phoS*, or *phoT*	316	
phoE	E	Acid resistance	659	D
phoE	E	TC45 phage resistance	420, 771	S, L
phoR	E	Arsenate resistance	852	
phoR	E	Glycerol(β)-phosphate as C source in the presence of high phosphate	204, 838	
phoR	E	TC45 phage resistance	621	S
phoS	E	Arsenate resistance	852	
phoS	E	Glycerol(β)-phosphate as C source in the presence of high phosphate	204, 838	
phoS	E	TC45 phage resistance	621	S
phoT	E	Arsenate resistance	852	
phoT	E	Glycerol(β)-phosphate as C source in the presence of high phosphate	204, 838	
phoT	E	TC45 phage resistance	621	S
phr	E	T1 phage (UV irradiated) resistance	332	L
phxB	E	ϕX174 phage resistance	547	L
pit	E	Arsenate resistance	59, 727	L
pldA	E	Actinomycin D resistance in the presence of EDTA	301, 805	L
pmi	S	P22 phage resistance	656, 833	L
pmi	S	9NA phage resistance	656, 833	L
pmrA	E, S	Polymyxin resistance	219, 297, 485, 785–788	
pmrA	S	Neutrophil granule protein resistance	219	
pncA	E, S	Amino(6)nicotinamide resistance	234, 455, 822	L
pncA	E	Nicotinamide as sole N source	598	Q
pncB	E, S	Amino(6)nicotinamide resistance	234, 455	L
pncB	E, S	Amino(6)nicotinate resistance	234, 455	L
pncX	S	Amino(6)nicotinamide resistance	336	
pnp	E	Showdomycin resistance	58	
polA	E	Lambda γ mutant phage resistance	867	L
praA,B	S	P221 phage resistance	576, 674	L
praA,B	S	PH51 phage resistance	576	L
praA,B	S	PH105 phage resistance	576	L
prbA,B	S	ES18 phage resistance	674	

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
prdB	S	PH51 phage resistance	674	
prfA	E	Phenylgalactoside resistance of *lacP lacI*(nonsense) *supE*	747	
prfB	E	Negamycin resistance	145	
prh	S	HK009 phage resistance	674	
prk	S	HK068 phage resistance	674	
proAB	S	Osmotolerance	155	
proA	E	Nitro(4)pyridine *N*-oxide resistance	62, 222, 321	L
proB	E, S	Dehydroproline resistance	62, 155, 635	FBI, S
proB	E	Nitro(4)pyridine *N*-oxide resistance	62, 222, 321	
proB	E, S	Azetidine carboxylate resistance	62, 155, 635	FBI, S
proP	E, S	Dehydroproline resistance in *putA putP*	156, 732	L
proU	S	Dehydroproline + azetidine carboxylate resistance at high osmolarity in *putA putP*	156	L
prp	E	Propionate as C source	400	Q
pspABCDE	E	Sulfanilamide + hypoxanthine resistance	97	
pss	E	Ethanol resistance	133	
pss	E	Dimethyl sulfoxide resistance	133	
pstABCS	E	Arsenate resistance	727, 838	L
pstABCS	E	TC45 phage resistance	621	S
pta	S	Fluoroacetate resistance	96, 281, 463, 797	
pts (general)	E	Glucose + gluconate-independent motility	30	
ptsG	E	Methyl(α)-glucoside resistance	102, 104	
ptsG	E	Sorbose resistance	715	L
ptsG	E, S	Deoxy(2)glucose-independent utilization of fructose	418, 510	L
ptsG	E, S	Deoxy(3)-3-fluoroglucose-independent utilization of fructose	418, 510	L
ptsG	E	Methyl(α)-glucoside-independent lactose + mannitol utilization	80	L
ptsG	E	Glucosamine as C source	379	
ptsG	E	Mannose as C source	379	
ptsHI	E, S	Deoxy(3)-3-fluoroglucose-independent utilization of lactate	510	L
ptsHI	E, S	Fosfomycin resistance	146, 800	L
ptsHI	E	Streptozotocin resistance	16; Freitag[h]	L
ptsI	E	Ampicillin resistance	212	
ptsI	S	Deoxy(3)-3-fluoroglucose resistance	510	L
purA	E	Methyl(6)purine + hypoxanthine resistance	60	
purB	E	Nalidixic acid resistance	310	L
purR	E	Adenine resistance in *hpt gpt*	461, 462	
putA	E, S	Azetidine carboxylic acid resistance	511, 635, 775	L
putAP	S	Baikiain resistance in constitutive background	187	L
putA	S	Proline as N source with glucose as C source	566	
putP	E, S	Dehydroproline resistance	193, 511, 635, 732, 775, 843	L
putP	E, S	Azetidine carboxylic acid resistance	193, 511, 635, 775, 843	L
putP	S	Lithium-resistant proline utilization as C source	551	S
puvA	E	Psoralen + UV irradiation resistance	328	C
pyrB	S	Arginine-independent growth of *pyrH* in the presence of uracil	366	L
pyrC	S	Arginine-independent growth of *pyrH* in the presence of uracil	366	L
pyrD	S	Arginine-independent growth of *pyrH* in the presence of uracil	366	L
pyrF	E	Fluoro(5)orotic acid resistance	74	L
pyrH	S	Fluoro(5)orotic acid resistance	865	C
pyrH	S	Fluorouracil resistance	385	C
pyrH	S	Fluorouridine resistance	385	C

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
pyrH	E	Fluoro(5)uracil + 5-fluorouridine resistance in *udp*	606	
qmeACDE	E	Glycine tolerance	829	
rap	E	Lambda phage resistance	279	
recA	E	Lambda prophage induction deficiency during thymine deprivation	190	
recF	E	Thymineless death resistance in *thyA*	558	
recJ	E	Thymineless death resistance in *thyA*	558	
recO	E	Thymineless death resistance in *thyA*	558	
recQ	E	Thymineless death resistance in *thyA*	557	
relA	E	UV (near) irradiation resistance	632	L
relA	E	Serine resistance in *relA*	167	
rep	E	P2 phage resistance	113	
rfa (general)	E, S	U3 and FO phage resistance	35, 484, 486, 588, 833	
rfa (general)	E, S	Ampicillin resistance	212, 550, 562	
rfa (general)	S	Hemin satisfaction of *hemA* auxotrophy	364	
rfa (general)	S	Cephalothin resistance	562	
rfa (general)	S	Bacitracin resistance	562	
rfaCDEF	S	FO phage resistance	676	
rfaD	E	C21 phage resistance	141	
rfaD	E	P1 phage resistance	141	
rfaH	S	FO phage resistance	458, 675	
rfaP	E	U3 phage + K3 phage coresistance	601	
rfb	S	DCCD resistance in *rfa*	833	
rho	E	T4 phage resistance	740	
rho	E	Lambda *sus N7 nin-5* resistance in P2 lysogen	352, 353	
rho	E, S	Polarity suppression of *gal* leader insertion	169, 331	
ridA	E	Rifampin + kasugamycin dependence	162	
ridB	E	Rifampin dependence	160	
rplC	E	Tiamulin resistance	73	
rplD	E	Erythromycin resistance	725, 840	S
rplE	E	Thiopeptin resistance	467	
rplF	E	Gentamicin resistance	101	S
rplK	E	Kasugamycin resistance	159	
rplK	E	DAP starvation of Δ(*mal-asd*) in the presence of serine, methionine, and glycine	165	
rplN	E	Kasugamycin resistance	159	
rplN	E	Lincomycin resistance	343	
rplO	E	Lincomycin resistance	343	
rplV	E	Erythromycin resistance	840	
rpoA	E	P2 *vir1* phage resistance	754	S
rpoB	E	Lambda *c*II + rifampin coresistance	296	S
rpoB	E	Streptovaricin resistance	863	S
rpoB	E	Rifampin resistance	216, 359, 369	S
rpoB	E	Streptolydigin resistance	357, 469, 688	S
rpoB	S	Fluorouracil resistance	368	S
rpoB	E	Lambda phage + 434 phage cross-resistance	256	S
rpoB	E	Lambda *Nmar* mutant phage resistance	261	S
rpoB	E	Serine resistance in *relA*	784	S
rpoB	E	Rifampin resistance in $rpoB^{+}$/*rpoB* (*rif*) merodiploids	36	L
rpoB	E	T7 phage resistance	690	S
rpoC	E	T7 phage gene 2 resistance	100	
rpoD	E	Lambda *c*I71 resistance	556	
rpoD	E	Arabinose (L) as C source in *cya* or *crp*	712	S
rpoH	E	Temperature resistance in *rpoD*(Ts)	577	S
rpsB	E	Kasugamycin resistance	583, 861	S

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
rpsB	E	Cold resistance in *rpsE* cold-sensitive mutants	559	
rpsC	E	Spectinomycin resistance and sucrose dependence	195	S
rpsD	E	Spectinomycin resistance and sucrose dependence	195	S
rpsD	E	Streptomycin independence of streptomycin-dependent *rpsL*	304	
rpsE	E	Spectinomycin resistance and sucrose dependence	195, 526	S
rpsE	E, S	Spectinomycin resistance	172, 495, 634, 672, 853	S
rpsE	E	Streptomycin independence of streptomycin-dependent *rpsL*	304	
rpsG	E	Lincomycin resistance	343	S
rpsI	E	Kasugamycin resistance and dependence	161, 163	S
rpsJ	E	Lambda prophage induction, resistance to	170, 246	S
rpsL	E, S	Streptomycin resistance	89, 495, 853	S
rpsL	E	Neamine dependence	798	
rpsL	E	Paromomycin resistance or dependence	853	S
rpsL	E	Phenyl galactoside resistance of *lacP lacI* (nonsense) *supE*	747	
rpsM	E	Kasugamycin resistance	159	
rpsQ	E	Neamine resistance	76, 119	S
rpsR	E	Kasugamycin resistance	159	
rrn	E	Erythromycin resistance	704	S
rrn	E	Chloramphenicol resistance	704	S
rrn	E	Spectinomycin resistance	704	S
sbaA	E	Serine resistance	166	
sbmA	E	Microcin B17 resistance	446	
sdh	E	Succinate-independent growth in *lpd*	154	
secA	E, S	Azide resistance	227, 232, 584, 808, 864	
secA	E	Phenethyl alcohol resistance	808, 864	
semA	E	Microcin E492 resistance	622	
serA	E	Serine hydroxamate resistance	774	FBI, S
serS	E	Serine hydroxamate resistance	774	S
sidCF	S	Albomycin resistance	87, 478, 479, 674	
sidK	S	Albomycin resistance	87, 478, 479, 674	
sidK	S	ES18 phage resistance	87, 478, 479, 674	
sloB	E	Nalidixic acid tolerance	473	
sloB	E	Amidinopenicillin tolerance	473	
sorAT	E	Sorbose (L) as C source in crosses with wild strains	844	
spcB	S	Spectinomycin resistance	853	
srlA	E	Sorbitol + xylitol resistance	639	L
srlD	E	Fructose as C source in *ptsF* or *ptsM*	378	
sspA	E	P1 phage resistance	835	L
strB	S	Streptomycin resistance	273, 853	
strC	S	Streptomycin resistance	648	
strM	E	Streptomycin resistance	671	
strM	E	Phenyl galactoside resistance of $lacI^q$ *lacI*(nonsense) *lacP supL*	748	
sulA	E	UV irradiation resistance in *lon*	373	L
sulA	E	Methyl methanesulfonate resistance in *lon*	373	L
sulA	E	Nitrofurantoin resistance in *lon*	252	L
tabC	E	T4 phage resistance	258	
tct	S	Fluorocitrate resistance	724	L
tct	S	Trifluorocitrate resistance	723	L
tct	S	2-Fluoro-L-erythrocitrate resistance	32	L
tdk	E, S	Azidothymidine resistance	207	L

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
tdk	S	Fluorodeoxyuridine + uracil resistance in *deoA*	54	
tdk	E	Fluoro(5)deoxyuridine resistance	749	L
tdk	E	Bromo(5)deoxyuridine + UV irradiation resistance	319, 348	L
"*tet*"	E, S	Fusaric acid resistance	72, 487	L
"*tet*"	S	Quinaldic acid resistance	72	L
thdA	E	Dapsone resistance	383	
thi	E	Pyrithiamine resistance	399	C
thrA	E, S	Thialysine resistance	365	S, FBI
thrA	E	Serine resistance	294	S, FBI
thrABC	E	Amino(2)-hydroxy(3)-pentoate resistance	847	D
thrS	E	Borrelidin resistance	248, 276, 560, 596	S, Q
thyA	E, S	Aminopterin resistance	66, 123, 325, 730	L
thyA	E	Trimethoprim resistance	66, 730	L
tinA (*tlr*)	E, S	Thiolutin resistance	381, 382, 714	
tmk	E	Dideoxy(2′,3′)thymidine resistance	176	S
tnaA	E	Tryptophan-supported growth at 13°C	568	C
tna	E	Indole + methyl(5)tryptophan-supported, glucose-resistant growth in Δ*trp*	862	
tol	E	Bacteriocin tolerance	85, 120, 173, 236	
tolQAB	E	Colicin E1 resistance	449	
tolQAB	E	TuIa phage resistance	449	
tolB	E	Colicin E resistance	19	L
tolB	E	Azaleucine resistance	19	L
tolC	E	Colicin E1 tolerance	536, 653	L
tolD	E	Colicin E2 and E3 tolerance	210	
tolD	E	Ampicillin resistance	105, 210	
tolE	E	Colicin E2 and E3 tolerance	210, 211	
tolE	E	Ampicillin resistance	210, 211	
tolI	E	Colicin Ia and Ib tolerance	120	
tolJ	E	Colicin L, A, and S4 tolerance	173	
tolM	E	Colicin M tolerance	302	
tolQ	E	Colicin group A tolerance	84a, 750	
tolQ	E	Filamentous phage tolerance	84a, 750	
tolR	E	Colicin group A tolerance	84a, 750	
tolR	E	Filamentous phage tolerance	84a, 750, 751	
tolZ	E	Colicin E2, E3, D, 1a, and 1b tolerance	503	
tonB	S	ES18 phage resistance	149, 741	
tonB	E	T1 phage resistance	46	
tonB	E	ϕ80 phage resistance	46	
tonB	E	Colicin B resistance	46, 623	
tonB	E, S	Albomycin resistance	85, 505, 741	
tonB	E	Colicin M resistance	85, 523	
tonB	S	Bacteriocin 4-59 resistance	741	
tonB	E	Cephalosporin E-0702 resistance	815	
topA	S	Kanamycin resistance	202	
topA	S	Neomycin resistance	202	
topA	S	Streptomycin resistance	202	
tpp	E	Alafosfalin resistance	603	L
tpp	E	Triornithine resistance in *opp*	44	L
tppA	S	Tripeptide (toxic) resistance	263	
tppB	S	Tripeptide (toxic) resistance	263	
trmE?	E	Phenyl galactoside resistance of *lacI*^{q} *lacI*(nonsense) *lacP supL*	748	
trp (generic)	E, S	Fluoro(6)tryptophan resistance	42, 318	C

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
trp (generic)	E, S	Methyl(5)tryptophan resistance	42, 318	C
trpE	E, S	Methyl(5)tryptophan resistance	114, 539	S, FBI
trpE	E	Methyl(3)anthranilate resistance	308	S, FBI
trpR	E, S	Methyl(5)tryptophan resistance	42, 137, 523, 746	
trpR	E	Chuangxinmycin resistance	850	
trpS	E	Indolmycin resistance	75	D
trxA	E	T7 phage resistance	498	L
trzA	S	Triazole resistance	339	
tsx	E	T6 phage resistance	99, 299, 490, 492, 620	L, S
tsx	E	Colicin K resistance	99, 299, 490, 492, 620	L, S
tsx	E	Albicidin resistance	69	
tufAB	E	Kirromycin resistance	220, 356, 763, 795	
tufAB	E, S	Mocimycin resistance	335, 794	
tyn	S	Tyramine as N source	549	
tyrA	E, S	Fluorophenylalanine resistance	270, 729	C
tyrA	E	Amino(4)phenylalanine resistance	504	C
tyrR	E, S	Amino(4)phenylalanine resistance	95, 504, 811	
tyrR	E	Fluorotyrosine resistance	130	
tyrR	S	Fluoro(4)phenylalanine resistance	729	
tyrS	E	Fluorotyrosine resistance	662	S
ubi (generic)	E	Neomycin resistance	265	L
ubiF	S	Fluoro(5)uracil + carbamylaspartate resistance	404, 866	L
ubiF	E	Gentamicin resistance	542	
ubiF	E	Streptomycin resistance	542	
udhA	S	Fluoro(5)uridine resistance	834	L
udk	E	Fluoro(5)uridine + uracil resistance	380	L
udk	E	Fluoro(5)uridine resistance in *upp*	565	L
udp	E	Fluoro(5)uracil + adenosine resistance	606, 617	L
ugpAB	E	Fluorohydroxyacetone phosphate resistance	515	L
ugpAB	E	Dihydroxybutylphosphonate resistance in *glpT*	691, 692	L
ugpAB	E	Glycerol-3-phosphate as C source in *glpT*	691	C
uhpR	E	Glucosamine 6-phosphate as C source	191	C
uhpR	S	Glucose 1-phosphate as C source	192	C
uhpR	E	Fructose 1-phosphate as C source	224	C
uhpT	E	Chloro-3-hydroxyacetone resistance in *uhp*(Con)	515	L
uhpT	E	Fluoro-3-hydroxyacetone resistance in *uhp*(Con)	515	L
uhpT	E	Dihydroxybutylphosphonate resistance in *uhp*(Con)	285	L
uhpT	E	Hydroxybutylphosphonate resistance in *ubp*(Con)	285	L
uhpT	E	Deoxydihydroxyphosphonyl methyl fructose resistance	285	L
uhpT	E	L-Glyceraldehyde-3-phosphate resistance in *uhp*(Con)	285	L
uhpT	E	Fosfomycin resistance	230, 389, 800	L
uhpT	E	Deoxy(2)glucose-6-phosphate resistance	214	L
uidA	E	Galacturonide as C source	742	C
uidA	E	Methylgalacturonide as C source	573	C
uidA	E	Methylglucuronide + glycerol-supported growth in *eda*	572	L
uidR	E	Galacturonide as C source	742	C
uidR	E	Methylgalacturonide as C source	573	C
ung	E	Bromodeoxyuridine + UV light resistance	856	L
ung	E	T4 phage (uracil containing) resistance	203	L
upp	E, S	Fluoro(5)uracil resistance	53, 605, 617	L
upp	E	Aza(6)uracil resistance	605, 617	L

Gene	Organism[a]	Selection[b]	Reference(s)	Alteration[c]
upp	E	Canavanine + aza(6)uracil resistance	605, 617	L
ushA	E	Fluoro(5)uracil + 5′-AMP resistance in *upp*	52	L
uvrA	E	UV-irradiated lytic phage resistance	332	
uvrB	E	UV-irradiated lytic phage resistance	332	
uvrC	E	UV-irradiated lytic phage resistance	332	
uvrD	E	UV-irradiated lytic phage resistance	332	
uxaBC	E	Hexuronate resistance in *eda*	742	L
uxuAB	E	Hexuronate resistance in *eda*	742	L
uxuR	E	Methylgalacturonide as C source	574	C
valS	E	Thymineless death resistance in *thyA*	394	S
xapA	E	Fluoro(5)uracil + adenosine resistance in *upp deoD xapR*(Con)	111	L
xapR	E	Adenosine as C source in *upp deoD*	111	C
xapR	E	Inosine as C source in *upp deoD*	111	C
xylE	E	Xylose resistance in *fda*	175	L

[a] E, *E. coli;* S, *S. typhimurium.*

[b] Abbreviations: DCCD, *N,N* ¢-dicyclohexylcarbodiimide; CCCP, carbonyl cyanide *m*-chlorophenylhydrazone; cAMP, cyclic AMP; DAP, diaminopimelic acid; (Con), constitutive; (Ts), heat sensitive.

[c] S, structure; FBI, site of feedback inhibition; D, increased gene dosage; C, constitutive gene expression; Q, altered amount of gene product; G, gain of function; L, loss of function.

[d] L. Comai, U.S. Patent 4,535,060, 1988; L. Comai, European patent application 389066, 1984.

[e] N. S. C. Lin, D. T. Palmer, and H. I. Miller, European patent application EP 85-308408 and U.S. patent application 84-673955, 1986.

[f] E. S. Miller, thesis, Purdue University, West Lafayette, Ind., 1984.

[g] S. Epelbaum, Z. Barak, R. LaRossa, and D. Chipman, unpublished data.

[h] C. S. Freitag, Ph.D. thesis, North Carolina State University, Raleigh, 1982.

TABLE 3 Selectable genes grouped by metabolic function[a]

I. Intermediary metabolism

A. Degradation

aceE, aceF, ackA, araA, araB, araC, atoB, atoC, dadA, dgd, dgoR, dsdA, dsdC, edd, exuR, fadB, fadL, fadR, fba, fucA, galK, galR, garA, garB, gatC, gatD, hut, kdgR, lacA, lacI, lacZ, malP, malQ, malT, manC, melA, mtlC, pfkA, pgi, pgm, phoA, prp, pta, putA, sorA, sorT, srlD, thdA, tnaA, udp, uidA, uidR, uxaB, uxaC, uxuA, uxuB, uxuR, xapA, xapR

B. Central intermediary metabolism

gabC, gadA, gltA, gnd, icdE, iclR, lpdA, metK, zwf

C. Respiration (aerobic and anaerobic)

chl, chlA, chlB, chlC, chlD, chlE, cydA, cydB, glpD, glpR, narC, narG, narH, sdHABCD

D. Fermentation

adhE, dld, frdABCD, hyb, hyc, hyd, hyp, lctD

E. ATP-proton motive force interconversion

atpA–I

F. Broad regulatory functions

arcA, cpxA, crp, cyaA, cytR, envZ, fur, lexA, lon, ompR, oxyR, phoB, phoR, relA, rpoD, sspA

II. Biosynthesis of small molecules

A. Amino acids

1. Glutamate family, nitrogen assimilation
   argA, argB, argC, argD, argR, glnA, gltH, proA, proB, proC
2. Aspartate family, pyruvate family
   asd, azl, ileR, ilvA, ilvB, ilvH, ilvI, leuA, leuJ, leuO, lrp, lysA, lysC, metA, metC, metJ, metL, thrA, thrB, thrC
3. Glycine-serine family, sulfur metabolism
   cysB, cysE, cysG, cysK, cysL, cysM, glyA, sbaA, serA
4. Aromatic amino acid family
   aroA, aroF, aroG, aroH, pheA, pheR, trp, trpE, trpR, tyrA
5. Histidine
   his, hisG

B. Nucleotides

1. Purine ribonucleotides
   guaA, guaB, purA, purB, purR
2. Pyrimidine ribonucleotides
   carA, pyrB, pyrC, pyrD, pyrF, pyrH
3. 2′-Deoxyribonucleotides
   dcd, dut, ndk, nrdA, nrdB, thyA, tmk
4. Salvage and interconversions
   apt, cdd, codA, cpdB, deoA, deoB, deoC, deoD, deoR, gpt, hpt, optA, spoT, tdk, upp

C. Sugars and sugar nucleotides

galE, galT, manA, nagA, nagB, nagR, rfbA, rfbB, rfbD, ushA

D. Cofactors, prosthetic groups, electron carriers

1. Biotin
   bioA, bioB, bioC, bioD, bioF, bioH, birA
2. Folic acid
   folA, pabA, pabB
3. Pantothenate
   coaA
4. Pyridoxine
   pdxA, pdxB
5. Pyridine nucleotides
   nadA, nadB, nadC, nadD, pncA, pncB, pncH, pncX
6. Thiamine
   thiA
7. Thioredoxin, glutaredoxin, and glutathione
   gor, gshA, gshB, trxA
8. Menaquinone and ubiquinones
   ubiF
9. Heme and porphyrins
   hemA, hemB, hemE, hemF, hemG, hemH, hemL

E. Fatty acids and lipids

clsA, glpK, pldA, pssA

III. Macromolecular metabolism

A. Synthesis and modification

1. Ribosomal proteins and their modification
   ksgC, rplC, rplD, rplE, rplF, rplK, rplN, rplO, rplT, rplV, rpsB, rpsD, rpsE, rpsG, rpsI, rpsJ, rpsL, rpsM, rpsQ
2. tRNAs and their modification, aminoacyl-tRNA synthetases
   alaS, argS, glnV, hemM, hisR, hisS, hisT, ileS, ilvU, leuS, leuW, lysS, metG, miaA, nuvA, nuvC, pheS, pheU, serS, thrS, trmE, trpS, tyrS, valS
3. RNA synthesis and modification and DNA transcription
   nusA, nusB, nusG, pnp, rho, ridA, rpoA, rpoB, rpoC
4. DNA (replication, restriction-modification, recombination, and repair)
   dcm, dnaB, dnaE, dnaG, dnaJ, dnaK, gyrA, gyrB, himA, himD, lig, mcrC, msp, mutA, mutC, mutH, mutL, mutS, mutY, phr, polA, recA, recF, recJ, recO, recQ, rep, sbcB, topA, ung, uvrA, uvrB, uvrC, uvrD
5. Proteins (translation and modification)
   fusA, prfA, prfB, tufA, tufB
6. Polysaccharides (cytoplasmic)
   glgA, glgB, glgC

B. Degradation of macromolecules
1. DNA
   hsdR, mcrA, mcrB
2. Proteins
   pepA, pepD, pepN, pepQ, sulA

IV. Cell structure
A. Membrane components
mvrC, ompA, phoE, qmeA, qmeC, qmeD, qmeE

B. Murein sacculus
hipA, hipQ, lpp, mrbA, mrdA, mreB, mreC, mreD, murZ

C. Surface polysaccharides and antigens
kdsA, lpcA, rfaB, rfaC, rfaH, rfaP

D. Surface structures
fliC

V. Cellular processes
A. Transport-binding proteins
araF, argP, argT, aroP, aroT, bioP, brnQ, btuB, bymA, cadB, cbt, codB, corA, corB, crr, cycA, cysA, dctA, dctB, dgsA, dppA, exbB, exbC, fepA, fepB, fepD, fepG, fhuA, fhuB, fruA, galP, gatA, glnP, glpF, glpT, gltR, gltS, gntS, hisJ, hisM, hisP, hisQ, lacY, livG, livH, livJ, livK, lysP, malE, malF, malG, malK, manX, manY, manZ, mdoB, melB, metD, mglD, mtlA, mtr, nagE, nhaA, nupC, nupG, oppA, oppE, panF, pit, proP, proU, pstA, pstB, pstC, pstS, ptsG, ptsH, ptsI, putP, srlA, tct, tonB, tpp, tsx, tyrR, udhA, ugpA, ugpB, uhpA, uhpB, uhpC, uhpT, xyIE
B. Cell division
envB, ftsY, ftsZ, mbrA, mbrB, mbrC

C. Chemotaxis and mobility
che, mglA, mglB, mglC, motA, motB

D. Protein secretion
lspA, secA

E. Osmotic adaptation
envM, ompC, ompF, osmB

VI. Other functions
A. Cryptic genes
bglB, bglT, celA, celB, celC, celD, celF, citA, ebgA, ebgC, ebgR, ilvF, ilvG, ilvM, ilvJ

B. Phage-related functions and prophages
gprA, gprB, grpD, grpE, groM, hflC, hflK, hflX, lamB, lit, mopA, mopB, phxB, pmi, pmrA, praAB, prbAB, prdB, prh, rap, tabC

C. Colicin-related functions
cet, cirA, tolA, tolB, tolC, tolD, tolE, tolI, tolJ, tolM, tolQ, tolR, tolZ

D. Drug or analog sensitivity
ampC, ampD, ampE, azaA, azaB, can, cmlA, eryC, eryD, ksgA, ksgB, ksgD, lev, linB, lytA, marA, mbrD, mng, mvrA, nalB, nalD, neaB, nek, nfnA, nfnB, nfsA, nfsB, nol, nov, pmrA, puvA, ridB, sbmA, semA, sloB, spcB , strB, strC, strM, tet, tlnA, trzA

E. Radiation sensitivity
garA, garB

F. Adaptations to atypical conditions
crg

[a]References to selections and species used in selections are given in Table 2.

FUTURE DIRECTIONS

Inhibitory conditions will continue to be important genetic tools with which to probe *E. coli* and *S. typhimurium* physiology. The study of mutants hypersensitive to environmental insults, alluded to earlier, is a most fertile area for exploitation. In addition, bacteriophage-resistant mutations have recently been of prime importance in defining pathway-assisted protein folding in the cell (531). Vigorous investigation of several such ill-defined mutants may reveal other new challenges to our orthodoxies. Relatively few natural product inhibitors of essential amino acid and cofactor biosynthetic pathways are identified (Table 1). Searches for such products and molecular biological definition of their modes of action may contribute both to our understanding of the establishment of microbial niches and to the development of a bioagrichemical industry akin to the antibiotic industry. These possibilities, and several others, portend an integrative understanding of biology emanating from the continued detailed study of the selectable phenotypes in *E. coli* and *S. typhimurium.*

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