Two-Component Signal Transduction
Two-Component Signal Transduction

edited by
James A. Hoch
DIVISION OF CELLULAR BIOLOGY
DEPARTMENT OF MOLECULAR AND EXPERIMENTAL MEDICINE
THE SCRIPPS RESEARCH INSTITUTE, LA JOLLA, CALIFORNIA

and

Thomas J. Silhavy
DEPARTMENT OF MOLECULAR BIOLOGY
PRINCETON UNIVERSITY, PRINCETON, NEW JERSEY

ASM Press • Washington, D.C.
Contents

Contributors ix
Preface xv

1. Historical Perspective
Boris Magasanik
1

I GENERAL PRINCIPLES 7

2. Genetic Approaches for Signaling Pathways and Proteins
John S. Parkinson
9

3. Two-Component Signal Transduction Systems: Structure-Function Relationships and
Mechanisms of Catalysis
Jeffry B. Stock, Michael G. Surette, Mikhail Levit, and Peter Park
25

4. Structural and Functional Conservation in Response Regulators
Karl Volz
53

II PARADIGMS 65

5. Control of Nitrogen Assimilation by the NRs-NRt Two-Component System of Enteric Bacteria
67

6. Chemotactic Signal Transduction in Escherichia coli and Salmonella typhimurium
Charles D. Amsler and Philip Matsumura
89
7. Porin Regulon of *Escherichia coli*
   Leslie A. Pratt and Thomas J. Silhavy
   105

8. Control of Cellular Development in Sporulating Bacteria
   by the Phosphorelay Two-Component Signal Transduction System
   James A. Hoch
   129

III  RESPONSE REGULATOR FUNCTIONS  145

9. Mechanism of Transcriptional Activation by NtrC
   Susan C. Porter, Anne K. North, and Sydney Kustu
   147

10. Transcription Regulation by the *Bacillus subtilis*
    Response Regulator Spo0A
    George B. Spiegelman, Terry H. Bird, and Valerie Voon
    159

11. Flagellar Switch
    Robert M. Macnab
    181

IV  CELLULAR PHYSIOLOGY  201

12. Signal Transduction and Cross Regulation in the
    *Escherichia coli* Phosphate Regulon by PhoR, CreC, and
    Acetyl Phosphate
    Barry L. Wanner
    203

13. Signal Transduction in the Arc System for Control of
    Operons Encoding Aerobic Respiratory Enzymes
    Shiro Iuchi and E. C. C. Lin
    223

14. Dual Sensors and Dual Response Regulators Interact to
    Control Nitrate- and Nitrite-Responsive Gene Expression in
    *Escherichia coli*
    Valley Stewart and Ross S. Rabin
    233

15. Regulation of Capsule Synthesis: Modification of the
    Two-Component Paradigm by an Accessory Unstable Regulator
    Susan Gottesman
    253

16. Expression of the Uhp Sugar-Phosphate Transport
    System of *Escherichia coli*
    Robert J. Kadner
    263
17. Symbiotic Expression of *Rhizobium meliloti* Nitrogen Fixation Genes Is Regulated by Oxygen
   Peter G. Agron and Donald R. Helinski
   275

18. Complex Phosphate Regulation by Sequential Switches in *Bacillus subtilis*
   F. Marion Hulett
   289

V PATHOGENESIS 303

19. Two-Component Signal Transduction and Its Role in the Expression of Bacterial Virulence Factors
   Michelle Dziejman and John J. Mekalanos
   305

20. Regulation of *Salmonella* Virulence by Two-Component Regulatory Systems
   Eduardo A. Groisman and Fred Heffron
   319

21. *Bordetella pertussis* BvgAS Virulence Control System
   M. Andrew Uhl and Jeff F. Miller
   333

22. Three-Component Regulatory System Controlling Virulence in *Vibrio cholerae*
   Victor J. DiRita
   351

23. Ti Plasmid and Chromosomally Encoded Two-Component Systems Important in Plant Cell Transformation by *Agrobacterium* Species
   Joe Don Heath, Trevor C. Charles, and Eugene W. Nester
   367

24. Regulation of Glycopeptide Resistance Genes of Enterococcal Transposon Tn1546 by the VanR-VanS Two-Component Regulatory System
   Michel Arthur, Florence Depardieu, Theodore Holman, Zhen Wu, Gerard Wright, Christopher T. Walsh, and Patrice Courvalin
   387

25. Tetracycline Regulation of Conjugal Transfer Genes
   Abigail A. Salyers, Nadja B. Shoemaker, and Ann M. Stevens
   393

VI CELLULAR COMMUNICATION AND DEVELOPMENT 401

26. Switches and Signal Transduction Networks in the *Caulobacter crescentus* Cell Cycle
   Todd Lane, Andrew Benson, Gregory B. Hecht, George J. Burton, and Austin Newton
   403
27. The frz Signal Transduction System Controls Multicellular Behavior in Myxococcus xanthus
   Wenyuan Shi and David R. Zusman 419

28. Intercellular Communication in Marine Vibrio Species: Density-Dependent Regulation of the Expression of Bioluminescence
   Bonnie L. Bassler and Michael R. Silverman 431

   Tarek Msadek, Frank Kunst, and Georges Rapoport 447

Index 473
Contributors

Peter G. Agron
Department of Biology and Center for Molecular Genetics, University of California,
San Diego, La Jolla, California 92093-0634
Present address: Division of Infectious Disease, University of California, San Francisco,
San Francisco, California 94143-0654

Charles D. Amsler
Department of Biology, University of Alabama at Birmingham,
Birmingham, Alabama 35294-1170

Michel Arthur
Unité des Agents Antibactériens, Centre National de la Recherche Scientifique,
Institut Pasteur, Paris, France

Mariette R. Atkinson
Department of Biological Chemistry, University of Michigan Medical School,
Ann Arbor, Michigan 48109-0606

Bonnie L. Bassler
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

Andrew Benson
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

Terry H. Bird
Department of Microbiology and Immunology, University of British Columbia,
Vancouver, Canada V6T 1Z3

George J. Burton
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

Trevor C. Charles
Department of Natural Resource Sciences, McGill University, Macdonald Campus,
Ste. Anne de Bellevue, Quebec, Canada H9X 3V9
CONTRIBUTORS

Patrice Courvalin
Unité des Agents Antibactériens, Centre National de la Recherche Scientifique,
Institut Pasteur, Paris, France

Florence Depardieu
Unité des Agents Antibactériens, Centre National de la Recherche Scientifique,
Institut Pasteur, Paris, France

Victor J. DiRita
Unit for Laboratory Animal Medicine and Department of Microbiology and Immunology,
University of Michigan Medical School, Ann Arbor, Michigan 48109

Michelle Dziejman
Department of Microbiology and Molecular Genetics, Harvard Medical School,
Boston, Massachusetts 02115-5701

Junli Feng
Department of Biological Chemistry, University of Michigan Medical School,
Ann Arbor, Michigan 48109-0606

Susan Gottesman
Laboratory of Molecular Biology, National Cancer Institute,
Bethesda, Maryland 20892-4255

Eduardo A. Groisman
Department of Molecular Microbiology, Washington University School of Medicine,
St. Louis, Missouri 63110

Joe Don Heath
Department of Microbiology, University of Washington, Seattle, Washington 98195

Gregory B. Hecht
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

Fred Heffron
Department of Microbiology and Immunology, Oregon Health Sciences University,
Portland, Oregon 97201

Donald R. Helinski
Department of Biology and Center for Molecular Genetics, University of California,
San Diego, La Jolla, California 92093-0634

James A. Hoch
Division of Cellular Biology, Department of Molecular and Experimental Medicine,
The Scripps Research Institute, La Jolla, California 92037

Theodore Holman
Department of Biological Chemistry and Molecular Pharmacology,
Harvard Medical School, Boston, Massachusetts 02115

F. Marion Hulett
Laboratory for Molecular Biology, Department of Biological Sciences,
University of Illinois at Chicago, Chicago, Illinois 60607

Shiro Iuchi
Department of Microbiology and Molecular Genetics, Harvard Medical School,
Boston, Massachusetts 02115
CONTRIBUTORS

Robert J. Kadner
Department of Microbiology, School of Medicine, University of Virginia,
Charlottesville, Virginia 22908

Emmanuel S. Kamberov
Department of Biological Chemistry, University of Michigan Medical School,
Ann Arbor, Michigan 48109-0606

Frank Kunst
Unité de Biochimie Microbiennne, Centre National de la Recherche Scientifique,
Département des Biotechnologies, Institut Pasteur, Paris, France

Sydney Kustu
Departments of Plant Biology and Molecular and Cell Biology, University of California,
Berkeley, Berkeley, California 94270

Todd Lane
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

Mikhail Levit
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

E. C. C. Lin
Department of Microbiology and Molecular Genetics, Harvard Medical School,
Boston, Massachusetts 02115

Robert M. Macnab
Department of Molecular Biophysics and Biochemistry, Yale University,
New Haven, Connecticut 06520-8114

Boris Magasanik
Department of Biology, Massachusetts Institute of Technology,
Cambridge, Massachusetts 02139

Philip Matsumura
Department of Microbiology and Immunology (M/C 790),
University of Illinois at Chicago, Chicago, Illinois 60612-7344

John J. Mekalanos
Department of Microbiology and Molecular Genetics, Harvard Medical School,
Boston, Massachusetts 02115-5701

Jeff F. Miller
Molecular Biology Institute, University of California, Los Angeles,
Los Angeles, California 90024

Tarek Msadek
Unité de Biochimie Microbiennne, Centre National de la Recherche Scientifique,
Département des Biotechnologies, Institut Pasteur, Paris, France
Present address: Division of Cellular Biology, The Scripps Research Institute,
La Jolla, California 92037

Eugene W. Nester
Department of Microbiology, University of Washington, Seattle, Washington 98195

Austin Newton
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544
Alexander J. Ninfa  
Department of Biological Chemistry, University of Michigan Medical School,  
Ann Arbor, Michigan 48109-0606

Elizabeth G. Ninfa  
Department of Biological Chemistry, University of Michigan Medical School,  
Ann Arbor, Michigan 48109-0606

Anne K. North  
Departments of Plant Biology and Molecular and Cell Biology, University of California,  
Berkeley, California 94270

Peter Park  
Departments of Molecular Biology and Chemistry, Princeton University,  
Princeton, New Jersey 08544

John S. Parkinson  
Biology Department, University of Utah, Salt Lake City, Utah 84112

Susan C. Porter  
Departments of Plant Biology and Molecular and Cell Biology, University of California,  
Berkeley, California 94270

Leslie A. Pratt  
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

Ross S. Rabin  
NeXagen, Inc., Boulder, Colorado 80301

Georges Rapoport  
Unité de Biochimie Microbienne, Centre National de la Recherche Scientifique,  
Département des Biotechnologies, Institut Pasteur, Paris, France

Abigail A. Salyers  
Department of Microbiology, University of Illinois, Urbana, Illinois 61801

Wenyuan Shi  
Department of Molecular and Cell Biology, University of California, Berkeley,  
Berkeley, California 94720

Nadja B. Shoemaker  
Department of Microbiology, University of Illinois, Urbana, Illinois 61801

Thomas J. Silhavy  
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

Michael R. Silverman  
The Agouron Institute, La Jolla, California 92037

George B. Spiegelman  
Department of Microbiology and Immunology, University of British Columbia,  
Vancouver, Canada V6T 1Z3

Ann M. Stevens  
Department of Microbiology, University of Iowa, Iowa City, Iowa 52242

Valley Stewart  
Sections of Microbiology and Genetics and Development, Cornell University,  
Ithaca, New York 14853-8101
Jeffry B. Stock  
Departments of Molecular Biology and Chemistry, Princeton University,  
Princeton, New Jersey 08544

Michael G. Surette  
Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544

M. Andrew Uhl  
Department of Microbiology and Immunology, School of Medicine,  
University of California, Los Angeles, Los Angeles, California 90024

Karl Volz  
Department of Microbiology and Immunology, University of Illinois at Chicago,  
Chicago, Illinois 60612

Valerie Voon  
Department of Microbiology and Immunology, University of British Columbia,  
Vancouver, Canada V6T 1Z3

Christopher T. Walsh  
Department of Biological Chemistry and Molecular Pharmacology,  
Harvard Medical School, Boston, Massachusetts 02115

Barry L. Wanner  
Department of Biological Sciences, Purdue University, West Lafayette, Indiana 47907

Gerard Wright  
Department of Biological Chemistry and Molecular Pharmacology,  
Harvard Medical School, Boston, Massachusetts 02115

Zhen Wu  
Department of Biological Chemistry and Molecular Pharmacology,  
Harvard Medical School, Boston, Massachusetts 02115

David R. Zusman  
Department of Molecular and Cell Biology, University of California, Berkeley,  
Berkeley, California 94720
Cells must sense and respond to their environment, a process that requires signal transduction across biological membranes. A major mechanism of signal transduction, widespread in bacteria, is the so-called two-component system that has adopted phosphorylation as a means of information transfer. Two-component systems are central to much of the cellular physiology that results from alterations in the environment. Starvation for phosphate or nitrogen, responses to oxygen limitation, and adaptation to new carbon and nitrogen sources are but a few of the environmental insults that cells overcome with modified cellular physiology mediated by two-component systems. Pathogenesis requires two-component modification of cellular physiology as well. There is no doubt that cells sense when they need to express virulence factors, but in most cases what is sensed remains obscure. It is unlikely that any pathogen can survive the varied and changing environments of the human body without involving at least one two-component pathway.

We are only now beginning to understand the bacterial cell cycle and the role of cell-cell communication in population dynamics and development. Yet we can cite examples in which two-component switches process signals required to trigger these events. Because two-component systems form networks that involve more than one system and show dependencies and hierarchies, they are easily adapted for very complex processes. In fact, two-component systems are so widespread, and so important, that without them bacteria would be rendered the equivalent of deaf, dumb, and blind.

In this book we have tried to highlight the global nature of two-component systems and summarize the enormous progress that has been made in less than a decade in our understanding of how these systems work. The book is divided into several sections, each of which deals with a particular aspect of two-component regulation. A few two-component systems have been studied in depth by several investigative groups, and these systems form a reservoir of information about how these systems function. Although some of the systems are complex, the two-component paradigm forms the basis for a common information flow.
Scientists studying microbial physiology, pathogenesis, motility and chemotaxis development, or a variety of other behavioral characteristics of bacteria need to be aware of and understand two-component signal transduction. The functions of two-component systems in eukaryotes such as yeasts and plants are now being appreciated, and astute investigators of these systems will take advantage of the vast knowledge base in bacteria. This book was therefore designed to appeal to the wide variety of disciplines in which signal transduction is a vital component and knowledge of its mechanism is essential.

For those of us who have witnessed the virtual explosion of information on two-component systems in the ten years since we became aware of their existence, the amount of knowledge accumulated seems enormous. Despite this progress, many fundamental issues regarding two-component systems still remain unresolved. We hope that this book will help focus attention on these critical problems and stimulate research to solve them.

The editors would like to thank Susan DiRenzo for service above and beyond the call in keeping the chapters, as well as the authors and editors, organized. We are also grateful to the ASM Press editorial staff—especially Ellie Tupper, Pamela Wilks, and Patrick Fitzgerald—for their continuing help and encouragement.

JAMES A. HOCH
THOMAS J. SILHAVY
The page numbers for entries occurring in figures are followed by an f; those for entries occurring in tables, by a t.

OA boxes, 164, 165f, 167–168, 169
reverse, 164, 166

ABC protein, 206
Ablations, 15, 16
abrB gene, 160
promotion repression in, 166–167
Spo0A–P repression in, 293
transcriptional activation in, 168
transcriptional repression in, 167, 168
AbrB protein, 139, 160, 293, 455, 458, 461
abrBp gene, 160, 162, 167
abrBlp gene, 168f
abbr2p gene, 168f
Accessory colonization factor (ACF), 353–354
Acetate, 226
Acetosyringone (AS), 369, 371, 372, 374, 376, 378, 379, 380
Acetyl coenzyme A (CoA), 73, 75
Acetyl phosphate, 3, 42–43, 73, 210, 212–213
Acetyl adenylate, 191
Acetylation, 191
af gene, 360
afA gene, 353
afB gene, 353
afC gene, 353
afD gene, 353
Acidity, 373–374, 375
ackA gene, 73, 75, 213
Acyl phosphates, 133–134
addAB gene, 461
Adenosine diphosphate (ADP)
bacterial virulence factors and, 352
histidine protein kinase and, 30, 31, 32
magnesium, 32
nitrogen fixation genes and, 280
nitrogen regulator I and, 80
nitrogen regulator II and, 75
protein II and, 83
thermodynamics and, 42
Adenosine triphosphate (ATP), see also Magnesium
adenosine triphosphate
ArcA and, 226
ArcB and, 225, 226
BvgS and, 338
DegU and, 451
EnvZ and, 109
FrzE and, 426
histidine protein kinases and, 25, 30, 31, 32
nitrogen fixation genes and, 275, 280, 282–283
nitrogen regulator I and, 70, 74, 74, 75, 82, 147, 150,
153–154, 156, 173
nitrogen regulator II and, 75–76, 80
phosphatase regulation and, 44
phosphate incorporation into, 203, 215
protein II and, 83–84
thermodynamics and, 42
Uhp system and, 264
uridylyltransferase/uridylyl and, 81
VanR/VanS and, 389
Adenylyltransferase (ATase), 3, 68–69, 81
adkE gene, 237
ADP, see Adenosine diphosphate
aeg-46.5 locus, 235, 236–237, 238, 242
Aerobic respiratory enzymes, 223–229
AgrA protein, 309, 310, 312
AgrB protein, 309

473
### Agrobacterium
- **Ti plasmid of**: 367–381
- **virulence factors of**: 307

#### Agrobacterium radiobacter
- 367, 373

#### Agrobacterium rhizogenes
- 367

#### Agrobacterium tumefaciens
- **Ti plasmid of**: 308, 367, 434
- **virulence factors of**: 306t, 307t, 308, 438

#### Agrobacterium vitis
- 367

#### AlgR protein
- 312

#### AlgRl protein
- 307

#### AlgR2 protein
- 307

#### AlgRN protein
- 312

#### AlgRN protein
- 307

#### AlgR protein
- 312

#### AlgRN protein
- 307

#### AlgRN protein
- 307

#### AlgRN protein
- 307

#### AlgRN protein
- 307

#### Ail protein
- 325, 326

#### Alcaligenes eutrophus
- 237

#### Alkaline phosphatase genes
- 290

#### Amino acid sequence analysis
- of dipI, 405–106
- of divK, 405–406
- of pleC, 405–406
- of Spo0A, 161f

#### of transmitters and receivers, 19–21

#### of VanR/VanS, 389

#### amyE gene
- 450

#### Anabaena
- 403

#### Antimicrobials
- 62

#### APase
- 289, 290, 293

#### APase A
- 289, 290, 293

#### APase B
- 289, 290, 293

#### Apo-CheY
- 56–57

#### aprA gene
- 434

#### aprE gene
- 139, 450–451, 461, 462

#### Arabidopsis
- 409, 447

#### Arabidopsis thaliana
- 409, 447

#### AraC protein
- 307

#### Arc system
- 223–229

#### arcA gene
- 213, 223, 227–228

#### arcA protein
- 35, 228

#### bacterial virulence factors and, 320, 321

#### Lux compared with, 439, 441

#### phosphorylation by ArcB-P, 226

#### phosphotransfer to, 346

#### primary structures of, 225

#### ArcA-P protein
- 227, 228

#### arcB gene
- 223, 227–228

#### ArcB protein
- 34–35, 227, 229f

#### autophosphorylation of, 225–226

#### bacterial virulence factors and, 320, 321, 338, 339, 342

#### Bvg compared with, 338–342

#### compounds controlling activity of, 226

#### Lux compared with, 438, 439, 441

#### phosphorylation of ArcA and, 226

#### phosphotransfer from, 346

#### primary structures of, 225

#### ArcB-P protein
- 226, 227

#### Association–dissociation mechanism
- 209–210

#### ATase, see Adenylyltransferase

#### ATP, see Adenosine triphosphate

#### att gene
- 369

#### atx gene
- 313

#### aut gene
- 71

#### Autophosphatase, 40–41

#### Autophosphorylation, see also Phosphorylation
- of ArcB, 225–226
- of BvgS, 338–342
- of CheA, 31–33, 110
- of EnvZ, 33–34, 109, 110–111
- of FixL, 279–280
- of FrzE, 426

#### of histidine protein kinases, 31–34

#### of nitrogen regulator II, 32, 33, 75–76, 80

#### Azorhizobium caulinodans
- 284, 285

#### Bacillus
- 135, 403

#### Bacillus anthracis
- 307t, 313

#### Bacillus brevis
- 449

#### Bacillus subtilis

#### competence gene expression in, 454–457
degradative enzyme synthesis in, 449–454

#### Pho regulon of, 289–300

#### phosphatase regulation and, 44

#### phosphorelay and, 137

#### phosphorylation and, 30

#### transcriptional regulation in, 159–176

#### Bacterial alkaline phosphatase (Bap), 203, 211, 212–213

#### Bacterial virulence factors
- 305–314, 434, 438

#### Bordetella pertussis

#### Clostridium perfringens
- 306t, 311

#### group A streptococci
- 312–313

#### Klebsiella pneumoniae
- 306t, 311, 312

#### Neisseria gonorrhoeae
- 306t, 310–311, 356

#### Salmonella
- 307, 308, 311, 319–330

#### Shigella flexneri
- 306, 307f, 308–309, 328

#### Staphylococcus aureus
- 309–310, 312

#### Vibrio cholerae

#### Bacteroides fragilis
- 306t

#### Bacteroides transposons
- 393–399

#### Bap, see Bacterial alkaline phosphatase

#### BarA protein
- 342

#### Bioluminescence
- 431–443

#### autoinduction of, 432

#### quorum sensing in, 432–434, 442

#### Bordetella
- 307, 363

#### Bordetella avium
- 334

#### Bordetella bronchiseptica
- 334, 344–345

#### Bordetella parapertussis
- 334

#### Bordetella pertussis

#### bpr gene
- 450

#### Bradyrhizobium japonicum
- 279, 285

#### G-Bromoacetosyringone, 372

#### BrpA protein
- 449

#### Brute-force screens
- 9, 13

#### Bryophyllum diagremontiana
- 380

#### bug gene
- 334

#### repression by, 344–345
transcriptional regulation by operon, 335

BvgA protein, 307, 333–346
  activation of virulence factors by, 343–344
  domain organization of, 334–335
  mutational analysis of, 337–338
  phosphorylation of, 342
  phosphotransfer to, 342, 346

BvgS protein, 307, 333–346, 358
  autophosphorylation of, 338–342
  domain organization of, 334–335
  intramolecular complementation of mutations, 337
  requirements for domains in vivo, 336–337
  signal-insensitive mutations in, 336

Bypass suppression, 22

C ring, 185, 186
cadA gene, 354
CadC protein, 354, 362, 363
Calcium
  bacterial virulence factors and, 306, 308
  flagellar switch and, 191–192

cAMP see Cyclic adenosine-3′,5′-cyclic monophosphate
Capsule synthesis, see Colanic acid capsule synthesis
Carbamyl phosphate, 73
Carbon sufficiency, 83–84
cat gene, 389–390
Catabolite control
  by acetyl phosphate, 212–213
  by CreC, 210–212
Catabolite gene activator protein (CAP), 175

Caulobacter crescentus
  cell cycle of, 403–415
  response regulator of, 39

ΦChk receptors, 403, 407
Cecropins, 324

Cell division cycle checkpoints, 404–409
Cell separation (CS), 404

cheA gene, 2, 94, 95
CheA protein, 3, 270, 448
  autophosphorylation of, 31–33, 110
  Bvg compared with, 334, 339
  catabolite control by CreC and, 212
  chemotaxis and, 93, 94–95, 96–97, 98
  CheY and, 39, 389
  crosstalk and, 214
  dimerization and, 29–30, 31–32
  failure to function as phosphatase, 44
  flagellar switch and, 189, 190
  Frz compared with, 421, 424–426
  phosphorylation of, 29–30, 38
  phosphotransfer and, 43–44

CheA2 protein, 94–95, 96, 97
CheA3 protein, 30, 94–95, 96, 97
CheB protein, 34, 39, 41, 448
  chemotaxis and, 93, 94, 96–97, 98
  Frz compared with, 421
  phosphorylation of, 38, 42, 283

phosphotransfer and, 43

CheB–P protein, 96, 97
CHEMOTAXIS, 13, 89–98, 454
  flagellar regulon motility and expression in, 89–91
  frz in, 421–424
  membrane receptors in, 93–94
CheR protein, 93, 96–97, 421, 427
CheW protein, 270
  chemotaxis and, 93, 94–95, 96–97, 98
  CheY autophosphorylation and, 33
  flagellar switch and, 190
  Frz compared with, 421, 426
  phosphotransfer and, 44
cheY gene, 2, 95, 98, 184, 187

CheY protein, 4, 20, 34, 41, 115, 448
  active site structure of, 56–57
  amino acid sequence analysis of, 406
  chemotaxis and, 93, 94, 95–96, 97, 98
  core and tertiary structure conservation in, 57
  flagellar switch and, 183, 184, 187, 188, 189–191, 192, 193, 196
  FlbD compared with, 413
  Frz compared with, 421, 424–426
  historical perspective on, 53–54
  Lux compared with, 439
  magnesium puzzle and, 60–61
  molecular structure of, 54–57
  phosphatase regulation and, 44
  phosphorelay and, 133, 134
  phosphotransfer and, 43–44, 110
  possible activation mechanism for, 61–62
  secondary structure conservation in, 57–58
  Spo0A compared with, 129, 163
  structural roles of conserved residues in, 59t
  structure-function relationships in, 35–38
  as tertiary template, 61
  VanR and, 389

CheY–P (CheY-P) protein, 133
  chemotaxis and, 95–96, 97, 98
  flagellar switch and, 181, 182, 188, 190, 192, 193

cheZ gene, 40, 96, 184, 187

CheZ protein
  chemotaxis and, 93, 96, 97, 98
  CheY and, 38, 40, 44
  flagellar switch and, 187, 188, 189–191
  Frz compared with, 421
  as phosphatase, 44
  phosphorelay and, 136

chvA gene, 369

chvB gene, 369

chvE gene, 369, 372–373

ChvE protein, 373
  Lux compared with, 439
  vir regulation by, 376–379

chvG gene, 369, 380–381

ChvG protein, 379–381
chvl gene, 369, 380–381
Chvl protein, 379–381
Citrobacter freundii, 255, 306t
Clostridium, 135
Clostridium perfringens, 306t, 311–312
cipB gene, 462
ClpC protein, 458–459
ClpP protein, 462
CoA, see Acetyl coenzyme A
coi gene, 163
Colanic acid capsule synthesis, 253–260
comA gene, 133, 455, 458, 459
ComA protein, 271, 300, 448, 449, 461, 462
Comensation genes and, 455—456
Mec and, 459, 460
phosphorelay and, 136, 137
phosphorylation of, 457
comC gene, 456–457
comE gene, 456–457
comF gene, 456–457
comG gene, 456
comK gene, 450, 457–458, 460, 461, 462
ComK protein, 455, 456–457, 459–460, 461
Communication modules, 19—22
comP gene, 455, 458, 459
ComP protein, 300, 448, 449, 461, 462
Comensation genes and, 455–456
Mec and, 459, 460
phosphorelay and, 136, 137
Comensation genes, 454–457
Complementation analysis, 14
ComQ protein, 455, 457, 462
comS gene, 456, 458
ComS protein, 455, 456, 458, 460, 462
comX gene, 141
ComX protein, 455, 457, 458, 462
Conformational change mechanism, 209–210
Conformational suppression, 22
Coniferin, 371
Conjugal transfer genes, 393–399
Conservation, 53–62
CopR protein, 307
CopS protein, 307
Core structure conservation, 57
Corynebacterium diphtheriae, 306, 307
cotB gene, 449
cotC gene, 449
eps gene, 255, 258
CrC protein, 204, 290
creA gene, 211, 213
CreA protein, 211
creABCD gene, 210–212
creB gene, 211, 213
CreB protein, 210, 211, 214, 215, 217, 218
creC gene, 211, 212–213
CreC protein, 30, 203, 211, 213, 214, 215, 408
catabolite control of Pho regulon by, 210–212
cross regulation and, 216, 217, 218
creD gene, 211, 213
Cross regulation, 203, 213–218
Crostalk, 21, 213–214, 442
crp gene, 1, 213
Crp protein, 233, 277, 319, 322
Cryptococcus neqformans, 313
tiaA gene, 295
CtaA protein, 295
tx gene, 359, 360–361
Ctx protein, 360, 361
cy gene, 1, 213, 338, 343–344
cyc gene, 235
Cyclic adenosine-3',5'-cyclic monophosphate (cAMP), 1, 212, 352
Cycloheximide, 371
cydAB gene, 228
cysA gene, 458
Defensins, 324–325
DegM protein, 448
degQ gene, 448, 449, 450, 455–456, 460
DegQ protein, 450
degR gene, 449, 450, 461
DegR protein, 450
Degradative enzyme synthesis, 449–454
degS gene, 449, 451, 452, 453, 460
DegS protein, 300, 448, 449, 462
Comensation genes and, 455
Degradative enzyme synthesis and, 450–451
DegU phosphorylation and, 451–454
functions and properties of, 460–461
degS(Hy) mutants, 461–462
degU gene, 458, 459
Degradative enzyme synthesis and, 449
DegU protein, 271, 295, 300, 448, 449, 458, 462
DegU phosphorylation and, 451–454
functions and properties of, 460–461
DegU (Hy) mutants, 300, 461–462
Dehydroconiferyl acid, 371
2-Deoxy-glucose-6-phosphate, 265–266
Dephosphorylation, see also Phosphorylation
of CheY-P, 190
of FixJ, 280–281
of nitrogen regulator II, 32, 80
Deuridylylation, 81
Dimerization
of histidine protein kinases, 29–32
of nitrogen regulator I, 147, 150–151
of ToxR, 358–359
dinR gene, 461
divJ gene, 405–406, 407–408
DivJ protein, 409, 414
INDEX

amino acid sequence analysis of, 405–406
catalytic activities of, 406
cell division and, 407–408
divK gene, 405–406, 407
DivK protein, 409, 414–415
amino acid sequence analysis of, 405–406
catalytic activities of, 406
cell cycle checkpoints and, 406–408
flagellar switch and, 410
PleD compared with, 409
divL gene, 405, 408–409
DivL protein, 409
dmsA gene, 237, 248
DNA binding
by Arc, 225
by FixJ, 284
by FlbD, 413
by Lux O, 441
by nitrogen regulator I, 149, 150, 151, 154, 156–157
by OmpR, 112–114, 115–117, 119, 120
receivers and, 11
by response regulators, 34
by RtcE, 398
by Spo0A, 135, 160–162, 164, 167–168, 175
by ToxR, 354, 355, 358, 359–360, 363
by UhpA, 449
by VirG, 375–376
dnaf gene, 259
dnaJ protein, 98, 259
dnaK gene, 259
DnaK protein, 98, 259
Domain liberation, 17–19
dsbA gene, 257
dsbB gene, 257
dsrA gene, 260
DsrA protein, 260

dmm6 gene, 313
Enteric bacteria, 67–85; see also Nitrogen assimilation; specific types
Enterobacter cloacae, 326
Enterococcus faecium, 306t, 394
eNZ gene, 2
bacterial virulence factors and, 308–309, 330
porin regulation and, 105, 109–110, 114
EnvZ protein, 164
autophosphorylation of, 33–34, 109, 110–111
bacterial virulence factors and, 308, 310, 320, 321, 354, 356
CreC compared with, 212
crosstalk and, 214
domain structure of, 108f
kinase:phosphatase ratio regulated by, 243
phosphatase regulation by, 44, 45
phosphorylation of, 29
porin regulation and, 105–112, 114, 115, 307
quenching and, 17–18

transplantations and, 17
Epistasis, 14–15
Envenia amylovora, 255, 306t, 312, 449
Envenia tarotovora, 434
Envenia stewartii, 255, 449
aerobic respiratory enzymes in, 223, 226
bioluminescence in, 432, 434, 435
catabolite repression protein in, 175
chemotaxis and, 13, 89–98, 421, 454
CheY in, 55
colic acid capsule synthesis in, 253, 255, 259
flagellar switch and, 181–196
glutamine synthetase in, 3
jamming and, 18
mutations in genes of, 1
nifA regulation by, 281–282
nitrate/nitrite gene expression in, 233–249, 408
nitrogen assimilation in, 2, 67, 69, 71, 72f
nitrogen fixation genes in, 277, 279, 281–282, 284
Pho regulon of, 203–218, 290–292
porin regulon of, 105–124, 174, 307
response regulator of, 54
RNA polymerase of, 69, 169, 173, 282–283, 284, 389, 411
succinyl-CoA synthetase of, 29
Uhp system of, 263–273
Ethyl ferulate, 371
ETR1, 409
expl gene, 434
Factor Z, 294, 295
FapR protein, 307
fhaG gene, 233, 234, 236, 238, 239, 240, 242, 243, 249
narX null mutants and, 244
operon control region of, 245, 247
Ferulic acid, 371
fha gene, 335, 338, 343, 344
fhaB gene, 338, 344
fim gene, 335, 343
FIS protein, 54
fixGHIS gene, 277
fixJ gene, 277–278, 281–282, 283
FixL* and, 278, 279
phosphorylation of, 283, 453
principal domains of, 283–284
RcsB compared with, 255, 258
transcriptional activation and, 282–283
fixK gene, 281, 284
fixL/fixJ and, 277–278
promoters of, 284
transcriptional activation and, 282
FixK protein, 277
fixL gene, 277–278, 281–282
FixL protein, 242, 282
amino acid sequence analysis of, 405
principal domains of, 279
properties of, 277–278
transcriptional activation and, 282
fixL* gene, 282
FixL* protein, 278
autophosphorylation of, 279–280
FixJ dephosphorylation and, 280–281
transcriptional activation and, 282–283
fixLJ gene, 277
fixNOQP gene, 277

fla gene, 404, 415
ai-acting sequences in transcription of, 412
flagellar switch and, 410–411
FlbD in transcription of, 414
specialized nature of promoters, 411–412
flaA gene, 344
Flagellar protein transport apparatus, 410
Flagellar regulon, 89–91
Flagellar switch, 96, 181–196
in Caulobacter crescentus, 409–414
components of, 183–184
functional analysis of, 187–188
interaction among, 194–195
location of, 184–185
model for, 192–193, 194f
proteins in, 95, 184
rotor versus stator of, 186–187
stoichiometric composition of, 186
flaN gene, see flgK gene
Flavobacterium, 399
flbD gene, 412
FlbD protein, 39, 404, 415
in fla transcription, 414
as flagellar switch protein, 409–414
at ftr sequence elements, 412–413
regulation of activity, 413–414
flbG gene, 412–413
flgK gene, 412
flgL gene, 412
flhC gene, 90
FlhC protein, 90
flhCD gene, 344
flhD gene, 90, 97–98
FlhD protein, 90
flkA gene, 90
flkC gene, 90
flkF gene, 185, 412–413
FlkF protein, 185, 186
flkG gene, 95, 183, 184–185
FlkG protein, 95, 97, 183–184, 190, 192, 193
biochemical properties of, 184
CheY and, 426
description of, 189
functional analysis of, 187, 188
location of, 184–185
stoichiometric composition of, 186
flkM gene, 95, 183
FlkM protein, 34, 95, 97, 183–184, 190, 192, 193
biochemical properties of, 184
CheY and, 39, 196, 426
description of, 189
functional analysis of, 187, 188
location of, 185
stoichiometric composition of, 186
flkN gene, 183
FlkN protein, 95, 183–184, 190, 192, 193
biochemical properties of, 184
CheY and, 426
description of, 189
functional analysis of, 187, 188
location of, 185
stoichiometric composition of, 186
FN516 protein, 227
FN517 protein, 227
fur gene, 227
Fnr protein, 233, 245, 247, 248, 277
Fosfomycin, 265
frdA gene, 233, 234, 236, 238, 239, 240, 242, 243, 249
operon control region of, 248
ftrAB gene, 344–345
FruR protein, 319, 322
frz gene, 419–429
biochemical analysis of, 424–427
chemotaxis and, 421–424
social behaviors and, 427–429
frzA gene, 421, 422, 428
FrzA protein, 421
frzB gene, 421, 422, 428
frzC gene, 421, 422
frzCD gene, 421, 422, 428
FrzCD protein, 421, 427–428, 429
frzE gene, 421, 422, 428
FrzE protein, 424–426, 429
autophosphorylation of, 426
Bvg compared with, 334, 338, 339
chemotaxis and, 421
FrzZ phosphorylation and, 427
Lux compared with, 438
frzF gene, 421, 422, 428
FrzF protein, 421
frzG protein, 39, 421
frzZ gene, 421, 427
FrzZ protein, 421, 426–427, 429
frx gene, 412–413
FtsY protein, 310
frzZ gene, 257
Fumarate, 191
Functional analysis, 187–188
Gain-of-function mutants, 14, 15
<table>
<thead>
<tr>
<th>Term</th>
<th>Page Numbers</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>β-Galactosidase</td>
<td>3, 13</td>
<td></td>
</tr>
<tr>
<td>gbpR gene</td>
<td>373</td>
<td></td>
</tr>
<tr>
<td>GbpR protein</td>
<td>373</td>
<td></td>
</tr>
<tr>
<td>GetE protein</td>
<td>449</td>
<td></td>
</tr>
<tr>
<td>glnA gene</td>
<td>2, 67, 153, 154, 156</td>
<td>in absence of nitrogen regulator II, 72</td>
</tr>
<tr>
<td></td>
<td></td>
<td>derivatives of, 150</td>
</tr>
<tr>
<td>glnA mutations and, 78, 79</td>
<td></td>
<td>mutations in histidine kinase C-terminal, 76, 78</td>
</tr>
<tr>
<td>glnA mutations in histidine kinase C-terminal domain</td>
<td></td>
<td>nitrogen regulator I dimer binding to, 150–151</td>
</tr>
<tr>
<td>glnB gene</td>
<td>2, 69, 79, 85</td>
<td></td>
</tr>
<tr>
<td>glnD gene</td>
<td>68, 81</td>
<td></td>
</tr>
<tr>
<td>glnD::Tn10</td>
<td>78–79</td>
<td></td>
</tr>
<tr>
<td>glnE gene</td>
<td>68</td>
<td></td>
</tr>
<tr>
<td>glnG (ntrC) gene</td>
<td>2, 67, 71, 276</td>
<td></td>
</tr>
<tr>
<td>glnH gene</td>
<td>153</td>
<td></td>
</tr>
<tr>
<td>glnH::Tn10</td>
<td>78–79</td>
<td></td>
</tr>
<tr>
<td>glnI gene</td>
<td>71</td>
<td></td>
</tr>
<tr>
<td>glnI mutations in histidine kinase C-terminal domain</td>
<td>76–78</td>
<td></td>
</tr>
<tr>
<td>glnL (ntrB) gene</td>
<td>2, 67, 71, 276</td>
<td></td>
</tr>
<tr>
<td>glnL gene</td>
<td>68</td>
<td></td>
</tr>
<tr>
<td>GlcA gene</td>
<td>387–390</td>
<td></td>
</tr>
<tr>
<td>Glu-6-phosphate (Glu6P)</td>
<td>263, 265–266, 268, 272, 273</td>
<td>Glutamate synthase, 75</td>
</tr>
<tr>
<td>Glutamate synthase</td>
<td>75</td>
<td></td>
</tr>
<tr>
<td>Glutamine</td>
<td>68, 69</td>
<td></td>
</tr>
<tr>
<td>Glutamine synthase</td>
<td>3, 85</td>
<td></td>
</tr>
<tr>
<td>Glutamine synthetase</td>
<td>85</td>
<td></td>
</tr>
<tr>
<td>Glutamine synthetase</td>
<td>85</td>
<td>in absence of nitrogen regulator II, 71, 72–73, 73</td>
</tr>
<tr>
<td>Glutamine synthetase</td>
<td>85</td>
<td>mechanisms of regulation of, 67–69</td>
</tr>
<tr>
<td>Glutamine synthetase</td>
<td>85</td>
<td>regulation of expression, 70–71</td>
</tr>
<tr>
<td>Glutamine synthetase-adenosine monophosphate (AMP)</td>
<td>69</td>
<td>Glutamine synthetase-adenosine monophosphate (AMP), 69</td>
</tr>
<tr>
<td>Glycerol</td>
<td>73</td>
<td></td>
</tr>
<tr>
<td>Glycopeptide resistance genes</td>
<td>387–390</td>
<td></td>
</tr>
<tr>
<td>Group A streptococci</td>
<td>312–313</td>
<td></td>
</tr>
<tr>
<td>GrpE protein</td>
<td>98</td>
<td></td>
</tr>
<tr>
<td>gsiA gene</td>
<td>136, 137, 455–456, 460–461, 462</td>
<td>HAI, 432</td>
</tr>
<tr>
<td>HAI-1</td>
<td>435–439, 441</td>
<td></td>
</tr>
<tr>
<td>HAI-2</td>
<td>435–439, 442</td>
<td></td>
</tr>
<tr>
<td>Heparin</td>
<td>171</td>
<td></td>
</tr>
<tr>
<td>hfl gene</td>
<td>326</td>
<td></td>
</tr>
<tr>
<td>hsp gene</td>
<td>253</td>
<td></td>
</tr>
<tr>
<td>HisP protein</td>
<td>207</td>
<td></td>
</tr>
<tr>
<td>Histidine protein kinases</td>
<td>25–34</td>
<td>dimerization of, 29–32</td>
</tr>
<tr>
<td></td>
<td></td>
<td>mutations in C-terminal domain of, 76–78</td>
</tr>
<tr>
<td></td>
<td></td>
<td>phosphatase regulation and, 44–45</td>
</tr>
<tr>
<td></td>
<td></td>
<td>phosphotransfer regulation and, 43–44</td>
</tr>
<tr>
<td></td>
<td></td>
<td>as response regulators, 34–43</td>
</tr>
<tr>
<td></td>
<td></td>
<td>structure-function relationships between domains, 26–29</td>
</tr>
<tr>
<td>HOG1 protein</td>
<td>409</td>
<td></td>
</tr>
<tr>
<td>hpr gene</td>
<td>462</td>
<td></td>
</tr>
<tr>
<td>Hpr protein</td>
<td>139–140</td>
<td></td>
</tr>
<tr>
<td>hrp gene</td>
<td>312</td>
<td></td>
</tr>
<tr>
<td>HrpR protein</td>
<td>307</td>
<td></td>
</tr>
<tr>
<td>HrpS protein</td>
<td>307, 312</td>
<td></td>
</tr>
<tr>
<td>hut gene</td>
<td>71</td>
<td></td>
</tr>
<tr>
<td>hutC gene</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>hutU gene</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Hydroxy-acetosyringone, 371</td>
<td></td>
<td>Hydroxy-acetosyringone, 371</td>
</tr>
<tr>
<td>N-(3-hydroxybutanoyl)-L-homoserine lactone, see HAI</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>HAI</td>
<td></td>
<td></td>
</tr>
<tr>
<td>idc gene</td>
<td>213</td>
<td></td>
</tr>
<tr>
<td>In vitro transcription regulation</td>
<td>167–173</td>
<td></td>
</tr>
<tr>
<td>Initiation of division (DIVi)</td>
<td>404, 407</td>
<td></td>
</tr>
<tr>
<td>Input-output communication</td>
<td>15–17</td>
<td></td>
</tr>
<tr>
<td>Integration host factor (IHF)</td>
<td>121, 245–247</td>
<td></td>
</tr>
<tr>
<td>iup gene</td>
<td>450</td>
<td></td>
</tr>
<tr>
<td>iuv gene</td>
<td>369</td>
<td></td>
</tr>
<tr>
<td>Jamming</td>
<td>18</td>
<td></td>
</tr>
<tr>
<td>2-Ketogluutarate</td>
<td>68, 69, 75, 80</td>
<td>nitrogen regulator I phosphorylation and, 82–83</td>
</tr>
<tr>
<td></td>
<td></td>
<td>protein II as carbon sufficiency sensor and, 83–84</td>
</tr>
<tr>
<td></td>
<td></td>
<td>uridylyltransferase/uridylyl and, 81</td>
</tr>
<tr>
<td>3-Ketogluutarate</td>
<td>83</td>
<td></td>
</tr>
<tr>
<td>kinA gene</td>
<td>133</td>
<td></td>
</tr>
<tr>
<td>KinA protein</td>
<td>129, 132–133, 135, 136, 448</td>
<td>Kinase-phosphatase antagonist, 137–139</td>
</tr>
<tr>
<td>KinA–P protein</td>
<td>135</td>
<td></td>
</tr>
<tr>
<td>Kinase–phosphatase antagonism</td>
<td>137–139</td>
<td></td>
</tr>
<tr>
<td>Kinase–phosphatase ratio</td>
<td>243</td>
<td>EnvZ regulation of, 243</td>
</tr>
<tr>
<td></td>
<td></td>
<td>in porin regulation, 110–111</td>
</tr>
<tr>
<td>KinB gene</td>
<td>132</td>
<td></td>
</tr>
<tr>
<td>KinB protein</td>
<td>129, 132–133, 448</td>
<td>Klebsiella, 255, 307, 312, 456</td>
</tr>
<tr>
<td>Klebsiella</td>
<td>255, 307, 312, 456</td>
<td>Klebsiella aerogenes, 1, 71, 72f</td>
</tr>
<tr>
<td>Klebsiella pneumoniae</td>
<td>2, 4, 449</td>
<td>colanic acid capsule synthesis in, 259, 260</td>
</tr>
<tr>
<td></td>
<td></td>
<td>nitrogen assimilation in, 71, 72f</td>
</tr>
<tr>
<td></td>
<td></td>
<td>nitrogen fixation genes in, 276, 277</td>
</tr>
<tr>
<td></td>
<td></td>
<td>virulence factors of, 306t, 311, 312</td>
</tr>
<tr>
<td>D-Lactate</td>
<td>226</td>
<td></td>
</tr>
<tr>
<td>LacZ protein</td>
<td>266</td>
<td></td>
</tr>
<tr>
<td>lasA gene</td>
<td>434</td>
<td></td>
</tr>
<tr>
<td>lasB gene</td>
<td>434</td>
<td></td>
</tr>
</tbody>
</table>
lasI gene, 434
lasR gene, 434
LasR protein, 449
licS gene, 450
Listeria monocytogenes, 307t, 308
Lorn protein, 325-326
lon gene, 255, 257, 259
Lon protease, 253
Loss-of-function mutants, 15
lux gene, 431, 432-434
luxA gene, 432
luxB gene, 432
luxC gene, 432
luxCDABEG gene, 432
luxCDABEGH gene, 434, 435-436, 438, 439, 441, 442
luxD gene, 432
luxE gene, 432
luxG gene, 432
luxH gene, 432
luxI gene, 434
LuxI protein, 308, 434, 442
luxICDABEG gene, 432
LuxL protein, 435
luxL gene, 435, 436, 438, 443
LuxM protein, 435, 438
luxM gene, 435, 438, 443
LuxN protein, 437, 438, 442, 443
LuxO protein, 439-443
luxP gene, 437, 438, 443
LuxP protein, 437, 438, 439
luxPQ gene, 437
LuxPQ protein, 438
luxQ gene, 437, 438, 443
LuxQ protein, 437, 438-442, 443
luxR gene, 432, 433, 434, 435-436
LuxR protein, 271, 434, 442, 449
bacterial virulence factors and, 308, 362, 363
quorum sensing and, 433-434
RcsB compared with, 255, 258
luxR-luxI signal response system, see Quorum sensing system
LysR protein, 311, 371-372
M protein, 313
M ring, 186
Magainins, 324-325, 328-329
Magnesium
CheY and, 36-37, 40, 41, 53, 60-61
histidine protein kinases and, 26, 28, 45
phosphatase regulation and, 44
thermodynamics and, 41
MalT protein, 255, 270, 449
Manganese
FixL* and, 279-280
methylation of, 96-97
nar compared with, 235
Methyl-accepting chemotaxis proteins (MCPs), 93-95, 98
Frz compared with, 421, 426, 427
Methyl syringate, 371
Methylation, 96-97
micF gene, 122-123
modA (chlD) gene, 237
Monosaccharides, 372-373
MotA protein, 184, 185, 186, 187
MotB protein, 184, 185, 186
MotX protein, 271
mpr gene, 450
Mry protein, 313
MS ring, 181-182, 183, 184-185, 186, 193, 410
Mutations, see also Null mutants
BvgA, 337-338
BvgS, 336, 337
in communication modules, 21-22
complementation analysis of, 14
frz, 421
in C-terminal histidine kinase domain, 76-78
enha, 15
in response regulators, 58-60
sporulation, 297-299
ToxR DNA binding analysis and, 359–360

*Mycobacterium*, 13, 438

chemotaxis in, 421–424
response regulator of, 39
social behaviors of, 427–429

*nac* gene, 71
NAC protein, 311
NapAB protein, 237
*Kap-cyc* fusion gene, 235, 236–237, 238, 242, 248
Nar protein, 233, 460
*narG* gene, 233, 236, 238, 240, 242, 243, 249
*narX* null mutants and, 244
operon control region of, 245–247

Narigenin, 371–372
*narK* gene, 236, 238, 247
*narQ* gene, 233, 238, 240, 242, 243, 249
identification and characterization of, 234–235
null mutations of, 238, 239–240
*narQ narL* double null strain, 242, 244
NarQ protein, 233, 238, 240, 242, 408
equilibrium model for functions of, 242–244
negative regulation by, 244–245
phosphatase regulation and, 44
structure of, 235

*narX* gene, 236, 237
identification and characterization of, 234–235
null mutations of, 238, 239–240

*narX* null mutants and, 244
operon control region of, 245–247

*NtB* gene, 247–248

*Nitrate-nitrite responsive gene expression, 233–249, 408
equilibrium model for, 242–244
negative regulation of, 244–245
target operon control regions for, 245–248

Nitrate-responsive gene expression, see Nitrate-nitrite responsive gene expression

Nitrogen assimilation, 2, 67–85
in absence of nitrogen regulator II, 71–75
redundancy of uridylyltransferase/uridylyl and protein II in, 84–85

Nitrogen fixation genes, 275–276
Nitrogen regulator I (NR-I/NtrC), 2, 3–4, 34, 54, 67, 69–70, 71, 73–74, 207
autophosphorylation of, 33
background information on, 147–150
bacterial virulence factors and, 310, 311
central activation domain of, 154–156
dimerization of, 147, 150–151
FlbD compared with, 412
mode of action of, 284
nitrogen regulator II/protein II regulated phosphatase and, 79–80
oligomerization of, 147, 148, 151–156, 173
phosphorylation of, 35, 39, 41, 74, 80, 82–83, 150–151, 180
Spo0A compared with, 173, 174
transcriptional activation by, 147–157
UhpA distinguished from, 270
Nitrogen regulator II (NR-II/NtrB), 2, 3, 67, 70–71, 270
autophosphorylation of, 32, 33, 75–76, 80
bacterial virulence factors and, 311
crosstalk and, 214
dehphosphorylation of, 32, 80
dimerization of, 31
glnL alteration of protein II interaction, 78–79
nitrogen regulation in absence of, 71–75
nitrogen regulator I phosphorylation and, 82, 83, 151
phosphatase regulation and, 44, 45
protein II as carbon sufficiency sensor and, 84
reconstitution of phosphatase regulated by, 79–80
structure-function analysis of, 75–79

NDPK, see Nucleotide diphosphate kinase

*negA* gene, 428–429

*Neisseria gonorrhoeae*, 306c, 310–311, 356

*nif* gene, 4, 71
*nifA* gene, 276, 277, 284, 449
fixL/fxL and, 277–278
negative and positive regulation of, 281–282
promoters of, 284
transcriptional activation and, 282

*NifA* protein, 4, 312
*nifHDK* gene, 276, 277
*NifL* protein, 311
*nifLA* gene, 71, 153

*nirB* gene, 247–248, 249

Nitrate-nitrite responsive gene expression, 233–249, 408
equilibrium model for, 242–244
negative regulation of, 244–245
target operon control regions for, 245–248

Nitrate-responsive gene expression, see Nitrate-nitrite responsive gene expression

Nitrogen regulator I phosphorylation and, 82, 83, 151
phosphatase regulation and, 44, 45
nod gene, 371–372
NodD protein, 371–372
Nonreplicating Bacteroides units (NBUs), 394–395, 398, 399
nprE gene, 139, 450, 461
nrgA gene, 237, 242–243, 244, 248, 249
NtrB, see Nitrogen regulator II
ntrB (glnL) gene, see glnL (ntrB) gene
NtrC, see Nitrogen regulator I
ntrC (glnG) gene, see glnG (ntrC) gene
Nucleotide diphosphate kinase (NDPK), 28
Null mutants, 15
  functional defects of, 14
  narL, 235–238
  narP, 235–238
  narQ, 238, 239–240
  narX, 238, 239–240, 243, 244
obg gene, 141
Obg protein, 141
Oligomerization, 147, 149, 151–156, 173
ompB gene, 105, 107, 309
  bacterial virulence factors and, 309, 321
  DNA binding and, 115, 117
  promoter of, 121–122
  transcriptional activation of, 117, 118
  transcriptional repression of, 167
OmpC protein, 105, 106, 107, 123–124, 174
  bacterial virulence factors and, 308, 309, 321
  bacterial virulence factors and, 321
  DNA binding and, 115, 117
  promoter of, 120–121
  transcriptional activation of, 117
  transcriptional repression of, 118–119, 167
OmpF protein, 105, 106, 107, 122–124, 174
  bacterial virulence factors and, 308, 321
ompR gene, 2, 105, 109–110, 114
  bacterial virulence factors and, 308, 39, 321, 330
  Pho regulon and, 213
  bacterial virulence factors and, 308, 309, 310, 319, 320, 321, 322, 323, 354, 356, 359
  domain structure of, 108f
EnvZ and, 243
  mode of action of, 284
  phosphatase regulation and, 44
  phosphorylation of, 453
  porin promoters and, 120–122
  quenching and, 17–18
Spo0A compared with, 162, 164, 167, 174
  transcriptional activation in, 117–118
  transcriptional repression in, 118–119
  transplantations and, 17
UhpA distinguished from, 270
  VanR compared with, 389
OmpR–P protein, 109, 110, 112, 117
OmpT protein, 363
ompU gene, 361
OmpU protein, 360
OmpX protein, 326
opp gene, see spotk (opp) gene
ops gene, 213
ORF1 protein, 387
ORF2 protein, 387
ORFX–17 protein, 448
ORFX–18 protein, 448
orgA gene, 321
otT gene, 394, 395, 398
Oxaloacetate, 83
OxyR protein, 266
P4, see Protein II
pagA gene, 323
pagB gene, 323
pagC gene, 325–326, 327, 329
PagC protein, 323, 325–326
pai gene, 462
Paracoccus denitrificans, 271
Penicillin G, 404
Petunia extracts, 371
PfhCDE protein, 215
PheR protein, 307
PheS protein, 307
PfxK protein, 284–285
pgf gene, 228, 237
pgfR gene, 312
pgf gene, 372
PgtP protein, 265
Pho regulon, 213
Pho box, 290–291
Pho regulon, 73, 203–218, 289–300
  alkaline phosphatase genes as reporters of, 290
  catabolite control by acetyl phosphate, 212–213
  catabolite control by CreC, 210–212
  cross regulation of, 203, 213–218
  regulatory network of, 292–295
  regulatory site mechanism for, 207, 208f, 210
  stoichiometric mechanism for, 207, 208f, 209–210
phoA gene, 203, 289, 290, 291
  bacterial virulence factors and, 327
  cross regulation and, 218
  induction of, 292
ToxR and, 354
PhoA protein, 266
phoB gene, 2, 289, 290, 291
induction of, 292
Spo0A~P repression of, 293
sporulation mutants and, 297–298
virG regulation and, 380
PhoB protein, 4, 34, 35, 54, 173–174, 204, 205, 214, 291, 408
bacterial virulence factors and, 327, 329
catabolite control by acetyl phosphate and, 213
catabolite control by CreC and, 210
cross regulation and, 216, 217, 218
discovery of, 322
gene regulation by, 215
VanR compared with, 389
virG regulation and, 380
PhoB-P protein, 174
PhoE protein, 215
phoH gene, 322, 325, 329
PhoM protein, see CreC protein
phoN gene, 322, 325, 329
phoP gene, 290, 294
bacterial virulence factors and, 322, 323–324, 326, 327, 328–329, 330
discovery of, 322
induction of, 292
phylogenetic distribution of, 328–329
PhoP protein, 54, 289, 290–292, 300, 448
bacterial virulence factors and, 307, 319, 320, 322–323
discovery of, 322
phoPR induction and, 293
sporulation mutants and, 297–299
signal transduction during sporulation, 295–296
PhoP Q protein, 323, 325–326, 330
phoPR gene
autoregulated induction of, 292–293
induction during spore development, 295–296
sporulation mutants and, 297–299
phoPR protein, 293–294, 295, 300
phoQ gene, 322, 323–324, 326
PhoQ protein, 307, 320, 322–330
discovery of, 322
pathogenicity of, 322–323
signals transmitted by, 327–328
phoR gene, 2, 290, 294
catabolite control by acetyl phosphate and, 212–213
catabolite control by CreC and, 210, 211
cross regulation and, 217, 218
induction of, 292
PhoR protein, 203, 214, 242, 270, 289, 290–292, 300, 408, 448
bacterial virulence factors and, 329
catabolite control by acetyl phosphate and, 213
catabolite control by CreC and, 211
cross regulation and, 217, 218
Phosphatases, 44–45
kinase antagonism with, 137–139
kinase ratio to, see Kinase-phosphatase ratio
nitrogen regulator II regulated, 79–80
phosphorelay phosphatase regulation of, 135–137
protein II regulated, 44, 79–80, 81–82
in response regulators, 42–43
Phosphate, 203–204
Bacillus subtilis, 289–300
catabolite control by CreC and, 210–211
detection of environmental, 207–209
pathways of genes regulated by, 214–215
Pst system control of, 204–210
regulation of phosphorelay, 135–137
repression complexes of, 205–207
Phosphate regulon, see Pho regulon
Phosphoenolpyruvate-sugar phosphotransferase (PTS) system, 92–93
Phosphoramide, 43, 73
Phosphorelay system, 129–142
enzymatic activities of proteins, 133–134
kinase-kinase antagonism in, 137–139
nature of signals in, 140–141
quaternary structure of, 134–135
repressor-activator antagonism in, 139–140
signal input into, 132–133
transcriptional regulation of, 130–132
Phosphorus assimilation, 214–215
Phosphoryl group transfer, see Phosphotransfer
Phosphorylation, see also Autophosphorylation;
Dephosphorylation
of ArcA, 226
of BvgA, 342
of ComA, 457
of DegU, 451–454
of FixJ, 283, 453
of PrrZ, 427
of histidine protein kinases, 25–26, 29–31
of nitrogen regulator I, 35, 39, 41, 74, 80, 82–83, 150–151
of RcsB, 257–258
of response regulators, 35, 38–40, 41–43
transmitters and receivers in, 11
Phosphotransacetylase-acetate kinase (Pta-AckA), 204, 216–217
Phosphotransfer, 238–239
to BvgA, 342, 346
CheY and, 43–44, 110
NarL-NarX, 238–239
in VanR/VanS, 389
Photobacterium leiognathi, 432
Photobacterium phosphoreum, 432
phoU gene, 207
PhoU protein, 203, 270
catabolite control by CreC and, 211
cross regulation and, 216, 218
gene regulation by, 215
phosphate control of, 204–210
pilA gene, 310–311
PilA protein, 310–311
pilB gene, 310–311
PilB protein, 310–311, 355–356
pilE gene, 310, 311
PilR protein, 307
PilS protein, 307
Piston model, 93
Pivot model, 93
pksX gene, 450
Plant cell transformation, 367–381
pleC gene, 409
amino acid sequence analysis of, 405–406
cell division and, 407–408
pseudoreversion analysis of mutants, 404–405
PleC protein, 409, 414–415
catalytic activities of, 406
cell division cycle checkpoints and, 406–408
flagellar switch and, 410
pleD gene, 408–409
PleD protein, 408, 409, 414
pmtA gene, 321
PmrA protein, 320–321
pmtB gene, 321
PmrB protein, 320–321
PnifA protein, 284–285
Porin promoters, 116f, 120–122
Porin regulation, 105–124, 174, 307
response regulator in, 112–119
sensor in, 107–112
stimulus for, 106–107
transmembrane signal transduction in, 111–112
ppk gene, 213
pgB gene, 327
pgH gene, 326, 327, 329
PgrH protein, 326
proB gene, 454
Progression of division (DIVp), 404, 407
Promoters
activated by SpoOA, 164–166
in nitrogen fixation genes, 284–285
repressed by SpoOA, 166–167
in VanR/VanS, 389–390
Protein II (P\u208I), 2, 3, 69, 70, 270
ghL in nitrogen regulator II interaction, 78–79
mutations in histidine kinase C-terminal domain and, 76, 78
nitrogen regulator I phosphorylation and, 82
nitrogen regulator II autophosphorylation and, 76
phosphatase regulation and, 44, 79–80, 81–82
PhoU compared with, 206–207
purification and crystallization of, 79–80
redundancy of, 84–85
as sensor of carbon sufficiency, 83–84
uridylylation/deuridylylation of, 81
Protein II-uridine monophosphate (P\u208I-UMP), 69,
71, 81–82
Protein D, 149, 152
Proton motive force, 191
Pseudomonas, 306t, 308, 456
Pseudomonas aeruginosa, 449
virulence factors of, 306, 307–308, 312, 434
Pseudomonas fluorescens, 394
Pseudomonas solanacearum, 460
Pseudomonas syringae, 306t, 312
Pseudoreversion analysis, 404–405
psiD gene, 323, 326
psiE gene, 215
psiF gene, 215
psiH gene, see phoH gene
Pst system, 203, 204–210
catabolite control by CreC and, 211
cross regulation and, 218
PstA protein, 204, 206, 207, 211
psta2 gene, 206
PstB protein, 204, 206, 207, 211
PstC protein, 204, 206, 207, 211
psthI gene, 213
PstS protein, 204, 206, 207, 208, 209, 211
PstSCAB protein, 215, 216
pta gene, 73, 75
Pta-AckA, see Phosphotransacetylase-acetate kinase
PstG protein, 310
ptx gene, 338, 343–344
pur gene, 213
put gene, 71
Pyruvate, 73, 211, 226
Quenching, 17–18
Quorum sensing (luxR-luxI) system, 432–434, 442
Random walk, 91
rapA gene, 137
RapA protein, 137, 461
RapB protein, 137
raxA gene, 255, 258, 260
RcsA protein, 256–257, 260, 449
bacterial virulence factors and, 311
RcsB stimulation by, 258–259
rsB gene, 256, 257, 259, 312
RcsB protein, 255-257, 259-260, 271
bacterial virulence factors and, 311
phosphorylation of, 257-258
RcsA stimulation of, 258-259
rsC gene, 257, 258, 259, 312
RcsC protein, 257-258, 259, 260, 311
rsF gene, 258
RcsF protein, 256, 258
recA gene, 450, 461
Receivers, 10-11; see also specific receivers
phosphorylation activities of, 11
signaling properties of, 11-12
signaling transactions between transmitters and,
17-19
structure-function studies of, 19-22
Regulatory genes, 454-455
Regulatory site mechanism, 207, 208f, 210
resD gene, 295
ResD protein, 289, 294-295, 299, 300
resDE gene, 294-295, 299
resE gene, 295
ResE protein, 289, 294-295, 299, 300
Response regulators, 2, 10-11, 25, 34-43; see also
specific response regulators
autophosphatase activities in, 40-41
conservation in, 53-62
family relationships in, 54
historical perspective on, 53-54
modular design of, 54
mutant sites in regulatory domains of, 58-60
phosphatase kinetics in, 42-43
phosphorylation of, 35, 38-40, 41-43
in porin regulation, 112-119
SpoOA as model for, 173-175
structure-function relationships in, 35-38
thermodynamics and, 41-42
Reverse OA boxes, 164, 166
Reversion analysis, 22
gfb gene, 253
rhIR gene, 434
Rhizobium, 312, 403
Rhizobium leguminosarum, 371-372, 434
Rhizobium meliloti, 275-286, 405, 449
rmpA gene, 259
RmpA protein, 259, 449
rmpA2 gene, 311
RmpA2 protein, 311
RNA III, 309-310
RNA polymerase
bacterial virulence factors and, 344, 355
FixJ and, 282-283, 284
fliA and, 411
nitrogen assimilation and, 69, 70, 73
PhoB and, 204
phosphorelay and, 135, 140
porin regulation and, 117-118, 119
RteA/RteB and, 396
SpoOA and, 162, 166, 168-171, 173, 174, 175
VanR/VanS and, 389
VirG and, 375, 378
Rotors, 186-187
rpiA gene, 213
rpoA gene, 118, 119
RpoA protein, 344
rpoB gene, 458
rpoN gene, 411-412
rpoS gene, 123
RpoS protein, 322
rsC gene, 253
RscA protein, 253, 255
rscB gene, 253
RscB protein, 253
rscC gene, 253
RscC protein, 256
rscF gene, 258
RscF protein, 256, 258
Saccharomyces cerevisiae, 30, 328, 409, 447
sacXY gene, 450
Sad gene, 163, 164
Salmonella, 307, 308, 311, 319-330
pathogenesis biology in, 319-320
virulence phenotypes in, 323-325
Salmonella typhi, 320, 321, 324
Salmonella typhimurium, 150, 405, 439
chemotaxis in, 89-98
flagellar switch and, 181-196
nitrogen assimilation in, 67, 71
organophosphate transport systems of, 264, 265
response regulator of, 54
virulence factors of, 308, 319, 320, 321, 322, 323-324, 325, 328, 329, 363
sap gene, 297-299
sapA gene, 297, 299
sapB gene, 297
sasA gene, 206
Scissions, 15, 16-17
Φshl-lacZ, 223, 226, 227
Secondary structure conservation, 57-58
Selection schemes, 9, 13
Sensors, 2, 10-11; see also specific sensors
in porin regulation, 107-112
Sesbania rostrata, 284
Shielding, 19
Shigella flexneri, 306, 307, 308-309, 328
sigD gene, 462
Sigma factor-6, 123
Sigma factor-32, 355
Sigma factor-54, 2, 3–4, 147, 149f, 152, 154, 156, 173
bacterial virulence factors and, 311
fixJ and, 282, 284
nitrogen assimilation and, 69
fixJ and, 282, 284
nitrogen assimilation and, 69
VanR/VanS and, 389
Sigma factor-70, 4, 156, 173
bacterial virulence factors and, 311, 355
FixJ and, 282, 284
nitrogen assimilation and, 69
PhoB and, 204
VanR/VanS and, 389
Sigma factor-A, 130–132, 140, 162, 168
Sigma factor-F, 30
Sigma factor-H, 130–132, 140, 168, 169
Signaling pathways
chemotactic, 92–98
Signaling proteins, 15–19
sin gene, 458
Sin protein, 455, 458
sin1 gene, 139
Sinl protein, 139, 140
sinR gene, 140
SinR protein, 139–140
SLN1 protein, 409
Slow-switchers, 183
Smooth swimming, 91
sns gene, 458
sob gene, 163, 164
sodA gene, 228
sog gene, 163, 164
soxRS gene, 123
SosRS protein, 123
spac gene, 456
SpaK protein, 448
SpaR protein, 448
spoOA gene, 159–160, 164, 175, 293, 299
activation of, 166
res not dependent on, 295
transcriptional activation of phosphorelay components and, 131
SpoOA protein, 129, 133–134, 299, 300, 448, 460–461, 462
competence genes and, 455
domains of, 160–164
kinase-phosphatase antagonism and, 137, 139
phoPR during spore development and, 295–296
phosphorylation of, 39, 453
promoters activated by, 164–166
promoters repressed by, 166–167
quaternary structure of phosphorelay components and, 135
repressor-activator antagonism and, 140
signal input into phosphorelay and, 132
transcriptional activation of phosphorelay components and, 131, 132
transcriptional regulation by, 159–176
Spo0ABD protein, 160–162, 167, 171, 172f, 175
spoOF gene, 168
conversion of Spo0F–P to, 138f
kinase-phosphatase antagonism and, 137
phoPR during spore development and, 295–296
phoPR repression by, 293–294
repressor-activator antagonism and, 139, 140
ResD antagonism to, 295
transcriptional activation and, 168, 169, 170–171, 172f
transcriptional activation of phosphorelay components and, 130–132
transcriptional repression and, 168
spoOB gene, 132, 141, 163, 293, 295
Spo0B protein, 39, 133, 137, 141, 142, 299
Spo0B–P protein, 133
spoOE gene, 136
Spo0E protein, 136, 137, 139
spoOF gene, 163, 293
promotion activation in, 166
promotion repression in, 166
res not dependent on, 295
signal input into phosphorelay and, 132
transcriptional activation of phosphorelay components and, 131
Spo0F protein, 129, 133–134, 137, 141, 299, 448, 461
amino acid sequence analysis of, 406
kinase-phosphatase antagonism and, 138f
phosphorylation and, 39
quaternary structure of phosphorelay components and, 134
signal input into phosphorelay and, 132
transcriptional activation of phosphorelay components and, 131
spoOFp gene, 169
Spo0F–P protein, 133, 134, 136, 141, 142
conversion to Spo0A–P, 138f
kinase-phosphatase antagonism and, 137
spoOH gene, 168
Spo0K protein, 455, 457, 462
spo0K(opp) gene, 141, 457
spo0L gene, 136–137, 460–461
Spo0L protein, 136–137
spo0P gene, 136, 137
Spo0P protein, 136, 137
spoIIA gene, 130, 160, 162, 175
promotion activation in, 166
repressor-activator antagonism and, 139, 140
signal input into phosphorelay and, 132
sporulation APase and, 297
SpoIIAA protein, 30
SpoIIAB protein, 30
spoIIAp gene, 162, 166, 168, 169, 174
spoIIE gene, 139, 140, 166, 175, 297

spoIIG gene, 130, 160, 173, 175, 448

promotion activation in, 166
repressor-activator antagonism and, 139, 140
signal input into phosphorelay and, 132
SpoOA phosphorylation and, 453
sporulation APase and, 297
transcriptional repression in, 168

spoIIGp gene, 160, 174
promotion activation in, 164-166
transcriptional activation in, 169-173

SpoIIJ protein, 461

Sporulation
PhoP/PhoR and, 295-296
phosphorelay system in, 129-142
regulatory mutants of, 297-299
Sporulation APase, 297-299

SpoVR protein, 322

srfA gene, 448, 450, 455-456, 457-458, 460

SSE1 protein, 409

Staphylococcus aureus, 309-310, 312

Stentor, 186-187

Stoichiometric mechanism, 207, 208f, 209-210

Streptococci, 306t

Streptomyces griseus, 271

Streptomyces hygroscopicus, 449

Strong enhancers, 150, 154, 155f
Strong sites, 150, 155f

Structure-function relationships
in CheY, 35-38
in communication modules, 19-22
in histidine protein kinase domains, 26-29
in nitrogen regulator II, 75-79
in response regulators, 35-38

Succinyl-CoA synthetase, 29

suv-3 gene, 162

suv-4 gene, 162

tac gene, 361

Tap protein, 93, 212

tar gene, 90

Tar protein, 212
chemotaxis and, 93, 94
porin regulation and, 107-108
Ti plasmid and, 373-374
transplantations and, 17

Tax1 protein, 107-108, 111-112

Tax1tA protein, 112

tip gene, 360, 361

tipA gene, 363

TcpA protein, 361

TcpC protein, 363

T-DNA, 367-368, 369, 379

Teicoplanin, 387

Temperature
bacterial virulence factors and, 305
porin regulation and, 122, 123-124
Ti plasmid and, 374
Tertiary structure conservation, 57
tetQ gene, 393, 394, 395, 396-397, 398, 399
Tetracycline, 393-399

Thermodynamics, 41-42

Ti plasmid, 308, 367-381, 434
acidity and, 373-374, 375
monosaccharides and, 372-373
phenolic compounds and, 371-372
temperature and, 374

Tn916, 393

Tn1545, 393

Tn1546, 387-390

Tobacco, 371
toxA gene, 434

Toxin-coregulated pilus (TCP), 353-354, 360
toxR gene, 351, 353, 354, 360, 361
toxR protein, 307, 351, 362-363
cordinate gene expression controlled by, 360-361
dimerization of, 358-359
mutagenesis analysis and, 359-360
regulon of, 353-354
signaling by, 354-356

ToxS periplasmic interaction with, 356-358
toxT expression and, 361-362
transmembrane nature of, 354
toxR-phoA fusion gene, 355

ToxR-PhoA fusion protein, 354-355, 356, 359
toxRS gene, 361
toxS gene, 351

ToxS protein, 351, 356
periplasmic interaction with ToxR, 356-358
ToxR dimerization and, 358-359
ToxR DNA binding and, 360
toxT gene, 360-362

ToxT protein, 307, 351, 360-361, 363
tal gene, 434

Transcriptional activation
in FixJ, 282-283
by nitrogen regulator I, 147-157
by OmpR, 117-118
by SpoOA, 168-173
in ToxR/ToxS, 356-358

Transcriptional regulation
by bvg operon, 335
of phosphorelay components, 130-132
by SpoOA, 159-176

Transcriptional repression
by OmpR, 118-119
by SpoOA, 167-168

Transmembrane signal transduction, 308-310, 312

Transmitters, 10-11; see also specific transmitters
phosphorylation activities of, 11
signaling properties of, 11-12
signaling transactions between receivers and, 17-19
structure-function studies of, 19-22
Transplantations, of foreign domains, 15, 16f, 17
tnR gene, 434
tnY gene, 228
Trg protein, 17, 93, 94, 108, 212, 373
Trypanosoma brucei, 447
Trz1 protein, 108
tsr gene, 434
Tsfay gene, 228
Trg protein, 17, 93, 94, 108, 212, 373
Trypanosoma brucei, 447
Trzl protein, 108
tsr gene, 241
Tsr protein, 212, 370-371
bacterial virulence factors and, 358
chemotaxis and, 93, 94
jamming and, 18
shielding and, 19
signal-insensitive mutations in, 336
Tumbling, 13, 91–92, 97, 98
ubiD gene, 226
ugpAB gene, 327
UgpBAEC protein, 215
Uhp system, 263–273
complexity of signal transduction in, 270
genes of, 265
signal and response in, 265–266
uhpA gene, 265, 266, 267, 268, 271
UhpA protein, 265, 266, 268, 284
degrative enzyme synthesis and, 449
intracellular signal of, 270–271
sequence analysis of, 405
target of, 271–273
uhpABC gene, 268
uhpABCT gene, 265
uhpB gene, 267, 268, 270
UhpB protein, 242, 265, 266–267, 268, 270, 271
sequence analysis of, 405–406
uhpBC gene, 268
uhpC gene, 267, 268
UhpC protein, 265, 266–267, 268, 270, 271, 406
uhpT gene, 265, 266, 268, 270, 271–273
UhpT protein, 264–266, 267, 268, 273
uidA gene, 396–397, 398
URF–1 protein, 448
URF–2 protein, 448
Uridylylation, 81
Uridylyltransferase, 3
Uridylyltransferase/uridylyl (UTase/UR), 68–69, 70
nitrigen regulator I phosphorylation and, 82, 83
protein II uridylylation/deuridylylation by, 81
purification of, 80, 81
redundancy of, 84–85
Urococanase, 1
Urococanate, 1
UvrC2, 271
vanA gene, 390
VanA protein, 387, 389
Vancomycin resistance, 387–390
vanH gene, 390
VanH protein, 387
VanR protein, 387–390, 394
VanS protein, 387–390, 394
vanX gene, 390
VanX protein, 387
VanY protein, 387
VanZ protein, 387
Vibrio
bioluminescence in, 431–443
virulence factors of, 308
pathogenicity in, 352–353
transcriptional activation in, 356–358
Vibrio Fischeri, 362, 442, 443, 449
bioluminescence in, 431, 432–434
virulence factors of, 308
Vibrio harveyi, 431, 432, 439, 441, 442, 443
multichannel sensory circuit of, 434–438
Vibrio parahemolyticus, 306t
vir box, 375–376
vir gene, 344, see also bvg gene
monosaccharides in induction of, 372–373
VirA/VirG–ChvE model of, 376–379
virA gene, 368–369
VirA protein, 34
bacterial virulence factors and, 307
Lux compared with, 438, 439
monosaccharides and, 372
Ti plasmid and, 369–374, 375, 376–379, 380–381
vir regulation by, 376–379
virB gene, 368, 374, 380
virC gene, 368
virD gene, 368
virE gene, 368
VirF protein, 307
virG gene, 368–369, 375, 380
VirG protein, 54
bacterial virulence factors and, 307
monosaccharides and, 372
phosphorylation and, 35
Ti plasmid and, 369, 370, 371, 374–379, 380–381
vir regulation by, 376–379
virH gene, 368
virR gene, 312
VirR protein, 312
vpr gene, 450
Vsr protein, 460
Weak enhancers, 150
Xenorhabdus luminescens, 432
YecB protein, 394
Yersinia, 306, 307, 308, 325
Yersinia enterocolitica, 328
Yersinia pestis, 307, 328
YopN protein, 308