

Bacterial Regulatory Networks

Edited by

Alain A.M. Filloux

Centre for Molecular Microbiology and Infection
Division of Cell and Molecular Biology
Imperial College London
London
UK



Caister Academic Press

Copyright © 2012

Caister Academic Press
Norfolk, UK

www.caister.com

British Library Cataloguing-in-Publication Data
A catalogue record for this book is available from the British Library

ISBN: 978-1-908230-03-4

Description or mention of instrumentation, software, or other products in this book does not imply endorsement by the author or publisher. The author and publisher do not assume responsibility for the validity of any products or procedures mentioned or described in this book or for the consequences of their use.

All rights reserved. No part of this publication may be reproduced, stored in a retrieval system, or transmitted, in any form or by any means, electronic, mechanical, photocopying, recording or otherwise, without the prior permission of the publisher. No claim to original U.S. Government works.

Cover design adapted from Figure 6.4 and 12.7a

Printed and bound in Great Britain

Contents

List of Contributors	v
Preface	xi
1 σ^S-Controlling Networks in <i>Escherichia coli</i>	1
Eberhard Klauck and Regine Hengge	
2 Bacterial Virulence Gene Expression Contributed by the Alternative σ Factor, σ^{54}	27
Patricia C. Burrows, Simone C. Wiesler, Zhensheng Pan, Martin Buck and Sivaramesh Wigneshweraraj	
3 Extracytoplasmic Function Sigma Factors: From Stress Management to Iron Uptake	59
Karlijn C. Bastiaansen, Wilbert Bitter and María A. Llamas	
4 Quorum Sensing in Gram-negative Bacteria: Signals, Role and Networking	87
Zulma R. Suárez-Moreno, Juan F. González, Giulia Devescovi and Vittorio Venturi	
5 Cyclic di-GMP Signalling and Regulation in Bacteria	123
J. Maxwell Dow, Yvonne McCarthy, Karen O'Donovan, Delphine Caly and Robert P. Ryan	
6 RNA-mediated Regulation of Virulence Gene Expression: Another Layer of Complexity	143
Efthimia Liolou, Cédric Romilly, Thomas Geissmann, François Vandenesch and Pascale Romby	
7 H-NS, Global Regulator of Gene Expression and Organizer of the Bacterial Nucleoid	167
Charles J Dorman	
8 Two-component Regulatory Systems in Prokaryotes	191
David E. Whitworth	

9	Bacterial Chemotaxis	223
	Kathryn A. Scott, Elizabeth E. Jefferys, Benjamin A. Hall, Mark A.J. Roberts and Judith P. Armitage	
10	Regulation of Iron Homeostasis in Bacteria	261
	Pierre Cornelis and Simon C. Andrews	
11	Anaerobic Regulatory Networks in Bacteria	273
	Petra Tielen, Max Schobert, Elisabeth Härtig and Dieter Jahn	
12	Take It or Leave It: Mechanisms Underlying Bacterial Bistable Regulatory Networks	305
	Jeroen Siebring, Robin A. Sorg, Martijn Herber, Oscar P. Kuipers	
13	Evolution of DNA-binding Transcription Factors and Regulatory Networks in Prokaryotes	333
	Ernesto Perez-Rueda, Nancy Rivera-Gomez, Mario Alberto Martinez-Nuñez and Silvia Tenorio-Salgado	
	Index	347
	Colour plate	A1

Preface

Higher eukaryotic organisms, including humans, use vision, hearing, smell, touch or taste to promptly analyse the surrounding environment and react appropriately to avoid danger or take benefit of a favourable situation. In humans, perception of a danger or stress may result in adrenaline being released in the blood. Adrenaline contributes to increase speed and strength or to decrease pain sensitivity, thus making your body and brain ready to take quick decisions such as running away or fighting. Similarly, when you smell or see something that is likely to be good food, you will start to salivate and prepare your digestive organs to process the food that you will inevitably be tempted to swallow.

One may think that prokaryotic organisms do not have such sensory sophistication, but a closer look at their molecular equipment indicates that they have this capacity. In bacteria, the decision-making process is all about a quick change in gene expression. Such change starts with the synthesis of new determinants/molecules/proteins that will be more appropriate to cope with the newly encountered environment. This is combined with the arrest in synthesis of other molecules that became useless in the new context, since carrying on with their production will be nothing else than a waste of precious time and energy. For example, in an iron-limiting environment, and iron is an essential element of many key biological processes, bacteria will switch on the expression of genes that will allow synthesis and release of siderophores (Chapter 10). These molecules are scavengers that will actively hunt and trap iron wherever available in order to bring it back into the cells. This internalization procedure will also

involve receptors and transporters, the expression of which is also induced upon perception of low iron levels in the environment. The production of all the components involved in active iron capture is not required in other conditions than iron limitation and therefore a tight control in expression of dozens of genes prevents unnecessary waste of energy.

Iron limitation is only one of many other examples that are described in this book. The multitude and complexity of control events happening in one bacterial cell over its lifetime are tied into a hugely sophisticated ‘bacterial regulatory network’, which within seconds drastically change the transcription profile in the cell. The control events may involve master regulatory elements that sit on top of a hierarchical cascade, and which control global responses by affecting expression of hundreds of genes. These are for example alternative sigma factors that come into play to influence selectivity of the RNA polymerase in response to general stress situation (Chapters 1–3). Another example is the global regulator H-NS, a DNA-binding protein that keeps hundreds of genes silent (Chapter 7). These factors may in turn control expression of other regulators whose role will be more specific and that will induce change in expression of very few or even only one gene. A notorious regulatory system involved in responding to very specific changes in the environment is the two-component system (Chapter 8). This system involves a sensor protein whose role is to identify precisely what the environmental conditions are and in many cases it will be responsible for monitoring the presence/absence of only one specific stimulus. It is also important to highlight that in many cases the

bacterium would like to respond to environmental changes not only at a single cell level but would like to organize a coordinate change in the whole bacterial population. One such phenomenon has been known for years as quorum sensing (Chapter 4). This system is pinpointing to the fact that bacteria might not behave in a selfish manner but thanks to appropriate regulatory mechanisms and to the production of diffusible molecules have established their own communication/language skills. Quorum sensing has given a new vision of the microbiological world, and the Science behind this social behaviour was fancily quoted by Peter Greenberg (University of Washington) as 'sociomicrobiology'.

It is remarkable that in many cases some of the changes induce by bacterial regulatory network are hardly visible to the human eyes. However, in several cases these changes in bacterial behaviour are striking. One example is the series of regulatory events, in response to harsh nutritional stress, which leads to sporulation of bacteria such as *Bacillus subtilis*. Such drastically different state of the bacteria may cause the emergence of two distinct subpopulations, and has been linked to so-called bistable regulatory networks (Chapter 12). In other cases, bacteria may switch from a single cell and motility behaviour to a sessile lifestyle within a compact but organized and active bacterial population called biofilm. Sometimes, the morphotype of a bacterial colony primed to form a biofilm is clearly identifiable on agar plates. Such a colony may display a remarkable wrinkly aspect often associated with the production of an exopolysaccharide whose aim is to glue bacterial cells together. The switch between motile and sessile lifestyles is also the result of sophisticated regulatory networks, and in some cases these regulatory cascades result in the production of a simple secondary messenger, such as the c-di-GMP (Chapter 5), whose mechanism of action and impact on cell behaviour is yet far to be clearly understood. Finally, chemotactic networks sensing gradient of attractive nutrients or repelling toxic compounds guide mobility and directional movement of a single bacterium (Chapter 9). Observing bacteria swimming and tumbling is something that was earlier catch by the human eye looking through rudimentary microscopes and

whose mechanism and control are now understood with exquisite molecular details.

The regulatory networks are not necessarily linear and could be seen as trees or microchips with integrated circuits involving multiple routes and ramifications. Signalling into one branch will spread into many other routes that in a way or another have a connection with the initial input. Moreover, the signalling does not necessarily go exclusively into one direction but involves feedback loops control for example once the initial stimulus or signal is gone. These multiconnections and ramifications very often encourage scientists to present highly sophisticated diagram in which stimuli, regulators and effectors are connected by a multitude of arrows that challenge our analytical capacity. It is also important to realize that regulatory controls may not only be exerted at transcriptional levels and the importance of small regulatory RNA in post-transcriptional control of gene expression is nowadays a very fashionable field of investigation (Chapter 6).

The book that has been assembled here is far to be comprehensive but is meant to cover a wide array of examples, which hopefully will reflect this complexity while providing a useful tool to gain better grasp in understanding bacterial regulatory networks, how they have evolved (Chapter 13) and how they could further be studied and understood. One should be aware that there is probably a gap in between how these regulatory networks work and are inter-connected under circumstances that have been created in our laboratories, and how they really behave when the bacteria are thriving in their natural environment or host. This is certainly a challenge for further research to understand adaptive behaviour of bacteria in their natural niches, which may be of fairly higher complexity than our test tubes, not only in terms of nutrient or oxygen availabilities (Chapter 11) but also in terms of promiscuity with a multitude of other organisms.

I would like to thank the authors that have contributed to the writing of this book. They are all leaders in their field and their commitment to this task has been greatly appreciated. I also would like to thank all the colleagues, whose names are listed here below, that have helped to review the chapters and provided insightful suggestions to

the authors. Finally, I wish the owner of this book an enjoyable time reading it and hope he/she will recommend it to many colleagues in the field be it a microbiologist or any curious neophyte eager to broaden his/her vision of a microscopic but rich and sophisticated world.

Alain Filloux (pictured)

Acknowledgements

Thanks to Udo Bläsi, Emmanuelle Bouveret, Jeffrey Cole, Remus T. Dame, Elena Fabiano, Jörgen Johansson, Michael Hecker, John D. Helmann, Vincent Méjean, Helga Mikkelsen, Gabriel Moreno-Hagelsieb, Steven L. Porter, Gary Sawers, Eric Stewart, David Studholme, Tim Tolker-Nielsen, Gottfried Unden and Paul Williams.



Index

A

ABC transport(er) 72, 77, 261, Fig. 5.4
 Acetyl-phosphate 8–9, 18, 201, Fig. 11.2, Fig. 11.9
 Acetyl(acyl)-CoA 95, 109, 239, 293, Fig. 11.2, Fig. 11.9,
 Fig. 12.11
 Acetylation (acetylase) 239, 287, 293, Fig. 4.2, Fig. 11.2,
 Fig. 11.9, Fig. 12.11
 Acid shock 9
 Acid stress 13, 285
 Activator 2, 4, 14, 29–33, 45, 50, 62, 68, 95, 105, 128,
 151, 155, 156, 172, 173, 206, 207, 252, 265, 266, 284,
 287–290, 307–312, 338, Fig. 2.1, Fig. 5.1, Fig. 10.3, Fig.
 12.1, Fig. 12.2, Table 2.1
 Acyl-ACP 92–95
 Acyl-homoserine lactone (AHL) 87–89, 92–102, 106,
 110, 111, 291, Fig. 4.1, Fig. 4.2, Fig. 4.3, Fig. 4.4, Fig. 4.5,
 Table 4.1
 Adaptation 12, 46, 67, 68, 153, 160, 191, 195, 223,
 226–229, 232, 233, 236, 237, 243–253, 274–278, 282,
 285, 293–295, 315, 320, 340, 341, Fig. 9.2, Fig. 9.10, Fig.
 11.5, Fig. 11.6, Fig. 11.10
 Adaptive response 27, 50, 143, 147, 195
 Adaptor protein 123, 227, 237, 248, Fig. 8.1
 AdrA (GGDEF protein) 135, Fig. 5.5
 Aerobic/anaerobic 15, 207, 225, 261, 273–295, 335, Fig.
 11.4, Fig. 11.6, Fig. 11.8, Fig. 11.9, Fig. 11.10
 Agr system 151, Fig. 6.2, Table 6.1
 AHL synthase 92–94, 97–99, 102, 110
 AI-2 (autoinducer) 92, 106–110, 207, Fig. 4.1, Fig. 4.5,
 Fig. 6.2
 Alarmone 2–3, 5, 11, 14, 32, 178, 322
 Alginate 67–68, 195, Table 3.1
 AlgT (*sigma E P. aeruginosa*) 66, 68, Table 3.1, Fig. 3.3
 AlgU 62, 66
 Allosteric(ally) 14, 123–125, 128, 129, 146, 176, 206,
 208, 311, 226, 247, 321, 338, Fig. 12.11
 Amplification (signal) 67, 95, 226, 236, 237
 Anr (Oxygen responsive regulator) 155, 287–291, 295,
 Fig. 6.3, Fig. 11.3, Fig. 11.8, Table 6.1
 Anthranilate synthase 103
 Anti-sigma factor 8, 62–79, 211, 322, Fig. 3.2, Fig. 10.1
 Antifungal 45, 106
 Antimicrobial 50, 68, 69, 97, 146, 154
 Antisense 143, 146, 147, 153, 155, Fig. 6.2, Fig. 6.3, Fig.
 10.2, Table 6.1

Apo-form 75, 207, 230, 238, 262, 265, 267, 269, 276, 282,
 Fig. 3.4, Fig. 9.5, Fig. 10.3, Fig. 10.5
 Aptamer 132, 133, 145, 146
 AraC-like protein 172, 179

ArcA/ArcB (Two component system) 5–6, 15, 18, 198,
 276–282, 295, Fig. 1.1, Fig. 1.2, Fig. 1.4, Fig. 1.5, Fig.
 11.4, Fig. 11.5, Fig. 11.6

ArcZ (Small regulatory RNA) 6, 15, 273, 276, 280, Fig.
 1.1, Fig. 1.4, Fig. 11.5

ArgR (Arginine responsive regulator) 289, 291, Fig.
 11.8

asRNA (antisense RNA) 147, Table 6.1

ATP synthase 273, 275, 286

ATP-binding protein 282, 286, 290, Fig. 11.6

ATPase 29, 31, 137, 234, Fig. 5.3, Fig. 11.7

Attractant (chemo-) 195, 223, 225, 228, 229, 235–237,
 245–252, Fig. 9.1, Fig. 9.2, Fig. 9.10

Autoinducer 75, 87, 88, 92, 99–101, 110, 151, Fig. 4.1,
 Fig. 6.2

Autoregulation 12, 210, 287, 322, Fig. 10.1, Fig. 12.1

B

Bacterial community 106–108, 339, Fig. 12.8

Bacteriocin 49, 76

Bacteriophage 46, 147, 158, 159, 175, 177, 316–320, 326,
 Fig. 12.9, Fig. 12.10

BarA/UvrY (Two component system) 5, 156, Fig. 5.6,
 Table 6.1

Base-pairing 6, 144, 146, 147, 156, 159, 160

Biofilm 5, 13, 18, 45, 47, 67, 96, 98, 103, 107–111, 123,
 126, 128, 131–132, 135–136, 146–147, 151–159, 179,
 191, 251–252, 267, 311, 315, 323, 327, 339, Table 4.1,
 Fig. 4.6, Fig. 5.1, Fig. 5.4, Fig. 5.6, Fig. 9.12, Fig. 12.8

Bioluminescence 87, 153, 181, Table 4.1

Bistable/bistability 12, 305–306, 310–311, 320–322, 327
 Brownian motion 224

C

cAMP (5',3'-cyclic adenosine monophosphate) 2, 4, 5,
 14, 130, 177–178, 277, 282, 285, Fig. 1.1, Fig. 1.2, Fig.
 1.3

Carbapenem 50, 101, Table 4.1

Carbon metabolism 5, 156

CarQ (*Myxococcus* sigma factor) 62, 66, 69, Table 3.1

Catalase 261, 268, 278, Fig. 11.5

- Cell cycle 45, 132, 177, 178, 191, 205, 207, 234, 307, 324, Table 8.1
 Cell density 1, 3, 87, 88, 92, 106, 108, 110, 151, 155, 251, 252, 278, Fig. 1.1, Fig. 4.2, Fig. 6.2, Fig. 6.3, Table 6.1
 Cell division 100, 139, 207, 208, 233, 234, 313, Fig. 12.6
 Cell envelope 46, 59, 62, 65–70, 79, 103, 154, 224, Table 3.1, Fig. 3.3
 Cell pole 132, 207, 208, 232–234, 243, 249
 Cell surface signalling (CSS) 59, 72, Table 3.1, Fig. 3.2
 Cellulose 18, 123, 124, 126, 128, 134, 135, 195, Fig. 1.5, Fig. 5.5, Fig. 5.6
 CepI/CepR 98, 102, Table 4.1
 CheA (Kinase) 193, 202–208, 227–251, Fig. 9.2, Fig. 9.7, Fig. 9.9, Fig. 9.10, Table 8.1
 CheB (methylesterase) 193, 204, 208, 227–229, 233, 237, 240–242, 245–252, Fig. 9.2, Fig. 9.6, Fig. 9.10
 Checkpoint 27, 130
 Chemoreceptor (MCP) 195, 207, 226–237, 240–252, Fig. 8.1, Fig. 9.2, Fig. 9.3, Fig. 9.4, Fig. 9.6, Fig. 9.9, Fig. 9.10, Fig. 9.12
 Chemosensory 208, 209, 223–226, 229, 233, 234, 239–245, 249, 252, Fig. 8.1, Fig. 9.2, Fig. 9.6, Fig. 9.7, Fig. 9.9, Fig. 9.10
 Chemotaxis/Chemotactic 2, 45, 101–102, 110, 127–130, 192, 195, 205–208, 212, 223–253, 278, 282, 285, 326, Fig. 5.4, Fig. 9.1, Fig. 9.2, Fig. 9.11, Fig. 9.12, Fig. 11.5, Table 8.1
 CheW (adaptor protein) 227–229, 232–234, 237, 240, 246–252, Fig. 8.1, Fig. 9.2
 CheY-like regulator 124, 127, 193, 204–208, 227–229, 233–252, Fig. 9.2, Fig. 9.5, Fig. 9.8, Fig. 9.9, Fig. 9.10, Fig. 9.11
 Chromatin immunoprecipitation (ChIP) 168, 175, 180
 Circadian 324, Table 8.1
 Circuit(ry) 15–17, 92, 95–97, 112, 143, 151, 156, 158, 178, 207, 210, 211, 285, 295, 306, 317, 319, 323, 324, 333, 341, Fig. 4.5, Fig. 12.5
 Cis-acting 29, 144, 161
 Cleft 29, 61, 146
 Clockwise (counter-) 224, 228, 237, Fig. 9.2, Fig. 9.10
 ClpXP (Protease) 8–10, 66–69, 71, 132, 207, 276, Fig. 1.2, Fig. 3.3
 Cofactor 124, 126, 249, 278, 282, 285, 294, Fig. 10.3
 Cold shock 144, 176, 278, 284, 285, 336, Fig. 7.3
 Communication (cell–cell, inter-kingdom, inter-species, intraspecies) 87, 88, 104, 106, 107, 110, 111, 147, 161, 338, Fig. 5.6
 Comparative genomic 62, 198, 200, 211, 337
 Competence (for DNA uptake) 179, 315, 322, 324, Fig. 12.15, Table 6.1, Table 8.1
 Conformational change 8, 61, 73–75, 95, 110, 130, 143, 144, 205, 226–239, 245, 248, 263, 276, 282, 284, 338, Fig. 4.2, Fig. 8.4, Fig. 9.5, Fig. 9.10, Fig. 10.1
 Cooperative (cooperativity, cooperatively) 88, 170, 226, 236, 237, 263, 307–310, 322, Fig. 10.2
 CpxARP (two-component system) 195, 206, 207, Table 8.1
 CRISPR 143, 158–160, Fig. 6.5
 Crl (σ s binding protein) 10–11, 65, Fig. 1.1, Fig. 1.2
 Cross-regulation 102, 193, 210, 283
 Cross-talk 12, 110, 155, 159, 204, 210, 242, 250, 322
 CRP (c-AMP receptor protein) 2, 4, 5, 14, 50, 130, 177, 178, 277, 282, 285, 287, 293, 335, 340–342, Fig. 1.1, Fig. 1.2, Fig. 1.3, Fig. 11.3. *See also cAMP*
 CsgD (transcriptional regulator) 10, 18, 135, 339, Fig. 1.5, Fig. 5.5, Fig. 5.6
 CspA (cold shock protein) 176, 278, Fig. 7.3, Fig. 11.5
 CsrA (post-transcriptional regulator) 136, 156, 158, 161, Fig. 5.6, Table 6.1
 CsrB/C (small RNAs) 136, 156, Fig. 5.6, Table 6.1
 CtxAB (cholera toxin) 316, Fig. 12.9
 Cue (environmental, signal, regulatory) 27, 31, 45, 46, 50, 88, 92, 123–126, 130, 134, 138, 143, 144, 147, 160, 321, Fig. 5.5
 Curli 13, 18, 135, Fig. 1.5, Fig. 5.6
 Cyclic-di-GMP (c-di-GMP) 129, 130, 196, 205, 207, 252, Fig. 5.2, Fig. 9.12
 Cystic fibrosis (CF) 67, 285
 Cytochrome 207, 278, 280, 284–287, 294, Fig. 11.5, Fig. 11.7

D

- Deamidation 229, 246, 247, Fig. 9.10
 Decarboxylase 292, Fig. 11.9
 DegS 66–69, Fig. 3.3
 Dehydrogenase 274–280, 283–287, 292, 293, Fig. 11.2, Fig. 11.5, Fig. 11.9
 Denitrification 286, 287, 290, 291, Fig. 11.7, Fig. 11.8
 Developmental programme 45, 69
 DGC (diguanylate cyclase) 123, 124, 125, 126, 128, 132, 133, 135–137, 205, 252, Fig. 5.1, Fig. 5.2, Fig. 5.4, Fig. 9.12
 Diffusible signal 78, 87, 92, 108, Fig. 5.1
 Diguanylate cyclase *see DGC*
 DivJK (two-component system) 195, 206, 207, Table 8.1
 DksA (RNA polymerase binding protein) 7, 11, 65
 DMSO 273, 275, 284, 285, Fig. 11.1, Fig. 11.4, Fig. 11.5
 DNA damage 9, 319, Fig. 1.1, Fig. 1.2
 DNA looping 31, 319
 DNA-binding protein 30, 31, 88, 167, 172, 173, 175, 179, 262, Fig. 7.2
 DnaK chaperone 7, 10
 Dnr (NO sensor) 287–291, Fig. 11.8
 Dormant 317, 322
 DSF 92, 100, 108–110, 127, 135, 138, Fig. 4.1, Fig. 4.6, Fig. 5.1. *See also Diffusible signal*
 DsrA (small regulatory RNA) 6, 176–177, Fig. 1.1, Fig. 7.3
 DtxR (ferric uptake regulator family) 261, 266, 269, Table 10.1
 Duplex (RNA or DNA) 137, 151, 155, 171, Fig. 6.2, Fig. 6.5, Fig. 7.2

E

- EAL domain 123–138, Fig. 5.3, Fig. 5.4, Fig. 5.5, Fig. 5.6
 ECF 59–79, 262, 263, 339, Fig. 3.1, Fig. 3.2, Fig. 10.1, Table 3.1
 Effector domain 204, 205, 338, Fig. 13.2
 Efflux (pump or drug) 47, 96, 100, 138, 307
 Electromchemical gradient 224, 275
 Electron (transport, acceptor, donor) 15, 45, 266, 273–292, 295, Fig. 11.1, Fig. 11.7

Electron acceptor 15, 273–276, 282, 285, 290, 292, Fig. 11.1
 Enterobactin 262, 263, Fig. 10.1
 Environmental stimuli 3, 59, Fig. 11.4, Fig. 12.9
 EnvZ/OmpR (two-component system) 195, 201, 203, Table 8.1
 EPS (exopolysaccharide) 108, 110, 130, 131, Fig. 4.6, Table 4.1, Table 8.1
 Esal/EsaR 93, 94, Table 4.1
 Exotoxin A 75–78, 263, Fig. 10.1, Table 3.1
 Expression pattern 1, 32, 46, 143, 153, 160, 161, 178, 306, 310
 Extracytoplasmic 59–62, 203, 213, 262, 293

F

Fatty acid 70, 92, 93, 103, 108, 110
 Fe–S cluster 265–268, Fig. 10.5. *See also* Iron–sulfur cluster
 FecI (ECF) 62–65, 71–76, Table 3.1
 Feed-forward loop (FLL) 1, 12, 14, 151, 341, Fig. 1.3
 Feedback loop (FBL) 1–2, 12, 15, 17, 45, 67–70, 95–97, 105, 151, 306, 307, 310, 316–323, 327, Fig. 1.5, Fig. 12.9, Fig. 12.12
 Fenton (reaction) 261, 262, 268
 Fermentation 273–278, 285–294, Fig. 11.2, Fig. 11.4, Fig. 11.5, Fig. 11.8, Fig. 11.9, Fig. 11.10, Table 8.1
 Ferredoxin 265, 266
 Ferritin (bacterio-) 176, 262–268, Fig. 10.2, Fig. 10.3
 FhpR (NO sensor) 289, 291, Fig. 11.8
 Fimbriae 18, 127, 135, 168, 267, Fig. 5.6
 FimX (GGDEF/EAL protein) 125, 132, 134, 138
 Fine tune(ing) 9, 15, 17, 28, 102, 144, 158, 160, 273, 283–285, 294, 315
 FIS (factor for inversion stimulation) 4, 5, 12–14, 172–178, Fig. 1.3, Fig. 7.3
 Fitness 48, 49, 161, 177, 201, 314, 315, 322, 324, 327, Fig. 12.10
 FixJ (transcription factor) 97, 205
 Flagellum(a) 2, 11, 18, 45–49, 61, 100, 102, 129–130, 135, 205–208, 224–228, 234, 237–244, 249–252, 307, 336, 339, Fig. 5.2, Fig. 9.6, Fig. 9.9, Fig. 9.10, Fig. 9.12, Fig. 10.3, Table 8.1
 Flavin 103, 126
 Flavohaemoglobin 278, 284, 289, 291, 293, Fig. 11.5
 FleQ (flagellar gene master regulator) 48, 130, 131, 138, 252, Fig. 9.12
 FlgM (anti sigma factor) 47, Fig. 5.6
 FlhDC (master regulator of flagellar gene expression) 11, 18, 339, Fig. 2.2, Fig. 5.6, Fig. 13.2
 FliA 11, 16, 47, 48, 61, Fig. 3.1, Fig. 5.6. *See also* σ28
 FliM (flagellar switch component) 130, 205, 227, 238, 239, 244, Fig. 5.2, Fig. 9.5
 FliZ (negatively affects expression of many σS-dependent genes) 11, 18, 278, Fig. 5.6
 Fnr (fumarate nitrate reduction/regulator, redox regulator) 15, 266, 273, 276–280, 283, 287, 293–295, 335, Fig. 11.3, Fig. 11.4, Fig. 11.5, Fig. 11.10
 Folding/Unfolding 61, 66, 95, 146, 160, 161, 177, Fig. 3.3
 FpvA (ferric pyoverdine receptor) 74–76, 263, Fig. 10.1
 FRET (fluorescence resonance energy transfer) 138, 210, 236, 243

Fruiting body(ies) 45, 69, 87, 251, 252, 315, Fig. 9.12
 Frz (chemosensory pathway) 208, 250, 251, Fig. 9.11, Table 8.1
 Fumarate 273, 275, 276, 284, 285, 335, Fig. 11.1, Fig. 11.2, Fig. 11.4
 Fur (iron response regulator, ferric uptake regulation protein) 71, 72, 75, 77, 176, 261–269, 335, Fig. 7.1, Fig. 7.1, Fig. 10.1, Fig. 10.2, Fig. 10.3, Fig. 10.5, Table 10.1
 Fur box 78, 263

G

GacA/GacS (two-component system) 97, 156–157, 195, 204, Table 6.1, Fig. 6.4
 GAF domain 126, 203, 282, Fig. 11.6
 Genomic(s) 71, 102, 111, 146, 155, 191, 196, 198, 200, 211, 223, 337, Table 8.2
 GFP (green fluorescent protein) 316, 323, Fig. 12.14
 GGDEF domain 123–138, 252, Fig. 5.1, Fig. 5.3, Fig. 5.4, Fig. 5.5, Fig. 5.6, Fig. 9.12. *See also* DGC and diguanylate cyclase
 Gliding (motility) 45, 208, 224, 249, Table 8.1
 GlnY (small regulatory RNA) 32, Fig. 2.2
 Global regulator 97, 103, 167, 179, 261, 265, 335, 341, 342
 Glycerol-3-phosphate 275, 284, 285, Fig. 11.1, Fig. 11.5
 Glycolysis 273, Fig. 11.5
 Glyoxylate shunt 282, 285, Fig. 11.5
 Growth phase (exponential, stationary, mid-log etc) 1–11, 14–18, 28, 31, 46, 61, 65, 69, 87, 95, 102, 105, 125, 134, 135, 144, 158, 175–178, 180, 284, 307, 339, 341, Fig. 5.6, Fig. 7.3, Fig. 11.5
 Growth rate 2–5, 11, 178, 314–315, 320, 321

H

H-NS (Nucleoid structuring protein) 6, 10, 167–181, 263, 269, Fig. 7.1, Fig. 7.2, Fig. 7.3, Fig. 10.2
 Habitat 62, 229, 273, 285
 Haem (haemoglobin, haemopexin, haemophore) 71, 75–77, 126, 128, 261–266, 275, 278, 286, 288, 290, 294, Table 3.1, Fig. 10.4
 Haemolysin 102, 151, 155, 172, Table 6.1, Fig. 6.2, Fig. 13.2
 Haemophore 77, 262, Table 3.1
 Hairpin 144, 151, 153, 155, 156, 161, 229, 243, Fig. 6.1, Fig. 6.2, Fig. 6.3
 HAMP domain 203, 229–232, 235, 282, Fig. 9.3, Fig. 9.4, Table 8.2
 HapR (LuxR family) 151, 153, Table 6.1
 HasA/HasR 77
 HATPase domain 192, 196, 201, 202, 204, Fig. 8.1, Fig. 11.6, Fig. 11.10
 HD-GYP domain 109, 123–128, 132–138, Fig. 4.6, Fig. 5.1
 Heat shock 1, 10, 61, 65–66, 70–71, 280, Fig. 1.1, Fig. 1.2, Table 8.1
 Helix-turn-helix (HTH) 45, 61, 95, 99, 105, 131, 168, 251, 276, 277, 280, 283, 293, 294, 336, Fig. 4.2, Fig. 9.12, Fig. 11.6
 Hfq 6, 147, 151, 153, 160, 161, 176, 263, 277, Fig. 1.1, Fig. 6.2, Fig. 10.2
 HHQ(2-heptyl-4-quinolone) 102–105, Fig. 4.4

Histidine phosphotransfer (Hpt) 109, 156, 157, 192, 198, 202–206, 280, Fig. 8.1, Fig. 8.2, Fig. 8.3, Fig. 8.6
 HisKA domain 109, 192, 201–206, Fig. 8.1, Fig. 8.9, Fig. 11.6, Fig. 11.10
 Histidine sensor kinase 5, 15, 111, 289
 Histone(-like) 4–6, 167, 263
 HK 192–200, 203–213, Fig. 8.1, Table 8.2. *See also* Histidine sensor kinase
 Holoenzyme 1, 3, 10, 11, 14, 16, 29, 59–62, 65, 312, Fig. 1.1, Fig. 1.5, Fig. 6.2. *See also* RNAP
 Homeostasis/Homeostatic 1, 6, 9, 13–17, 67, 71, 97, 154, 261–262, 265–269, Fig. 1.2, Fig. 10.4, Table 6.1
 Housekeeping (gene, factor) 1, 28, 32, 59, 158, 334
 HptB (histidine phosphotransfer) 156, 157, Fig. 6.4
 HrpL (sigma factor) 49
 HrpR/HrpS (AAA+) 49
 HtrA (protease) 69, 70
 Hybrid sensor 106, 280
 Hydroxyketone 106, 110, Fig. 4.1
 Hydrogen peroxide (H_2O_2) 9, 261, 276, Fig. 1.1, Fig. 10.5

I

IdeR (ferric uptake regulator family) 261, 266, 268, 269, Table 10.1
In silico 236, 324
 Inhibitor 17, 18, 62, 68, 206, 207, 211, 309, 310, 320, Fig. 12.1, Table 3.1, Table 6.1
 Initiation (transcription) 1, 5, 14, 27, 59–61, 172, 176, 312, 332, 334, Fig. 2.1
 Initiation (translation) 6, 151, 155
 Input domain 109, 110, 123–127, 194, 198, Fig. 8.1
 Integration host factor (IHF) 31, 267, 291
 Interface (protein) 73, 202, 203, 209, 230, 235, 236, 239, 245, 246, 283, Fig. 7.1, Fig. 8.8
 Intergenic region 143, 180
 Intracellular (bacteria) 47, 101, 102, 138, 172, 175, 337
 IraP (Anti-RssB protein with IraD and IraM) 9–10, 14, 18, Fig. 1.1, Fig. 1.2, Fig. 1.3, Fig. 1.5
 Iron uptake 59, 71, 72, 76, 78, 110, 261, 262, 265, 266, 269, Fig. 10.1, Fig. 10.3, Table 10.1
 Iron–sulfur cluster 266, 273, 276, 284, 293. *See also* Fe–S cluster

K

Kinase (auto, sensor) 5, 15, 18, 63–65, 71, 95, 106, 109, 111, 127, 128, 191, 192, 198–211, 225–229, 232–237, 241–252, 280, 282, 287, 289, 293, 322, 340, Fig. 1.4, Fig. 3.2, Fig. 4.5, Fig. 5.1, Fig. 5.6, Fig. 6.2, Fig. 6.4, Fig. 8.2, Fig. 8.3, Fig. 9.2, Fig. 9.3, Fig. 9.4, Fig. 9.6, Fig. 9.9, Fig. 9.10, Fig. 9.11, Fig. 11.2, Fig. 12.13
 KinB/AlgB (two-component system) 193, 195
 Kinetic(ally) 12, 16, 31, 145, 201, 204, 228, 277, 283, 311, 325, 326

L

lac operon 317, 319, 320, 326, 327, Fig. 12.11
 LacI (repressor) 319, 320, 321, 323, 324, 326, Fig. 12.11
 Lactoferrin 71, 77, 261
 Lactonase 96
 Lactose 319–321, 326, 327, 338, Fig. 12.11

LadS (hybrid sensor) 195
 LapD (c-di-GMP binding protein) 132, Fig. 5.4
 LasI/LasR 94–99, 102, 105, 291, Table 4.1, Fig. 4.4
 LeuO (LysR-like regulator) 6, 177, Fig. 7.3
 Lifestyle 18–19, 28, 47, 146, 196, 198, 229, 273–276, 285, 337
 Lipopolysaccharide (LPS) 66, 103, 153, 154, 224, Table 6.1
 Locus of enterocyte effacement (LEE) 49, 172
 LRP (Leucine-responsive regulatory protein) 177, Fig. 7.3
 Luciferase 87, 106, Fig. 4.5, Fig. 6.2
 Lux box 92, 95, 98, 101, Fig. 4.2
 LuxI (AHL synthase) 87, 88, 92–102, Table 4.1, Fig. 4.2
 LuxM (AHL synthase) 92–95, 106
 LuxR 87, 88, 92, 95–102, 106, 111, 151, 153, 338, 339, Table 4.1, Fig. 4.2, Fig. 4.3, Fig. 4.5, Fig. 6.2
 LuxS (AI-2 synthase) 106, 107, Fig. 4.5, Table 6.1
 Lysogen/lysogenic 159, 317–319, 326, Fig. 12.10
 LysR-type regulator 6, 105, 177, 268, 294, 336–338, Fig. 4.4

M

Macrophage (survival in) 47, 70, 71, 102, 147, 172, 175, Table 6.1
 Matrix (extracellular, biofilm) 18, 130, 131, 252, 315, Fig. 12.8
 MCP *see* Chemoreceptor
 Methylation/demethylation 106, 196, 228, 229, 235–237, 245–252, 310, Fig. 9.2, Fig. 9.3, Fig. 9.10
 Methylesterase 205, 228, 229, 245, 246. *See also* CheB
 Microarray 46–49, 68, 76–79, 100–102, 143, 175, 290, 316
 Modelling 78, 130, 209, 210, 223, 295, 318, 319, 325–327
 Motility 2, 5, 18, 45–48, 98, 101–103, 110, 123, 126, 129, 131, 135, 138, 191, 195, 208, 223–224, 229, 239, 249–252, 307, Table 4.1, Table 8.1, Fig. 5.1, Fig. 5.2, Fig. 5.6, Fig. 9.11, Fig. 9.12
 Motor (flagellar) 45, 129, 130, 208, 224–228, 237–244, Fig. 9.2, Fig. 9.6, Fig. 9.9, Fig. 9.10
 MprA 70, 322, Fig. 12.13
 MS ring 47, Fig. 5.2
 MucA (RseA, anti sigma factor) 67, Fig. 3.3
 Multicellular(ity) 45, 69, 87, 135, 249, 253, 311, 315, 327, 338, Table 8.1
 MvaT 97, 179, 180, Table 7.1

N

NAD/NADH 103, 273–278, 285, 287, 294, Fig. 11.1, Fig. 11.2, Fig. 11.5, Fig. 11.6, Fig. 11.7, Fig. 11.9, Fig. 11.10
 NapAB (nitrate reductase) 278, 284–286, 289, 290, Fig. 11.1, Fig. 11.5, Fig. 11.7
 Nar family (two-component system) 197, 200
 NarXL (two-component system) 203, 273, 276, 282–285, 289–291, 295, Fig. 11.4, Fig. 11.5, Fig. 11.6, Fig. 11.8
 Negative regulation 31, 32, 99, 105
 Niche 88, 106, 153, 161, 228, 261, 274, 285, 341
 NirQ (NirS activator) 286–290, Fig. 11.8
 NirS (nitrite reductase) 286–291, Fig. 11.7, Fig. 11.8
 Nitrate respiration 276, 283, 284, 287, 292, 294, Fig. 11.8, Fig. 11.10

Nitric oxide 128, 276, 286, 287, 290, 291
 Noise (in gene expression) 12, 16, 193, 200, 204, 210, 305, 306, 311–314, 319–322, 326, 327, Fig. 12.4, Fig. 12.6
 NorBC (NO reductase) 287–291, Fig. 11.7, Fig. 11.8
 NosR (N₂O sensor) 287–291, Fig. 11.8
 Ntr family (Two-component system) 200, Table 8.2
 NtrC (transcriptional regulator) 50, 290
 Nuclease (endo, exo, ribo) 6, 136, 138, 153–159, 263, Fig. 6.3, Fig. 6.5
 Nucleoid 5, 6, 167, 175, 177, 180, 181, 267, 338

O

One-component system (OCS) 200, 201, 212, 225
 Osmolarity/Osmotic (chock, stress, response) 1–9, 16–18, 68, 71, 171, 177, 252, 285, 339, Fig. 1.2, Fig. 7.3, Fig. 11.5, Table 8.1
 Output domain 193, 196, 200, 204, 205, 208, 211, 212, 234, 237, 251, Fig. 9.12, Table 8.2
 Oxidation 65, 70, 92, 267, 273, Fig. 3.2
 Oxygen sensor 15, 273
 OxyR (LysR-like regulator) 9, 267–268, 276, Fig. 10.5
 OxyS (small regulatory RNA) 6, Fig. 1.1

P

P2CS (TCS database) 191, 196, 200, 212
 ParB (DNA-binding protein, plasmid partition system) 172, 233
 PAS domain 126, 249, 280, 293, Fig. 8.1, Fig. 11.6
 Pathogenicity island 98, 111, 141, 155, 161, 172, 173, 175, 178, Table 6.1, Table 7.1
 PchR (Arac-like) 263, Fig. 10.1
 PDE (phosphodiesterase) 123, 125, 126, 128, 129, 132, 133, 136–138, Fig. 5.2, Fig. 5.4, Fig. 5.5
 PDZ domain 66, Fig. 6.3
 Peptidoglycan 68, 151, 155, 224, Table 6.1, Table 8.1
 Peritrichous(ly) 208, 228, 234
 Permease 261, 262, 293, 319, 320, Fig. 12.11
 Persistence (bacterial) 305, 306, 321, 322, 327, Table 8.1
 Phase variation 168, 310
 Phenazine 99, Table 4.1
 PhnAB (anthranilate synthase genes) 105, Fig. 4.4
 Pho family (two-component system) 197, Fig. 8.8, Table 8.2
 PhoP/Q (two-component system) 9, 147, 154, 173, 177, 180, 195, Table 6.1
 Phosphatase 8, 78, 106, 111, 191, 192, 204–207, 210, 211, 248, 280–283, 322, Fig. 6.2, Fig. 9.2, Fig. 9.9, Fig. 9.10
 Phosphodiesterase 109, 123, 124, Fig. 4.6, Fig. 5.1, Table 6.1
 Photosynthesis 273, Table 8.1. *See also* PDE, EAL domain and HD-GYP domain
 PilZ domain 123, 128–130, Fig. 5.2, Fig. 5.3, Fig. 5.5, Fig. 5.6
 PleD (GGDEF-containing regulatory protein) 124, 134, 205
 Positive regulation 29, 78, 263
 Post-transcriptional(ly) 2, 11, 14, 15, 63, 128, 135, 136, 146, 147, 151, 156, 160, 161, 181, 263, 269, 277, 278, 280, Fig. 6.2, Fig. 10.5

Post-translational(ly) 128, 277, 286, 322, 323
 (p)ppGpp (5',3'-bisguanosine penta/tetraphosphate) 10–14, 18, 27, 65, 335, Fig. 1.1, Fig. 1.2, Fig. 1.3. *See also* Alarmone

PQS 92, 97, 102, 103, 105, 106, 291, Fig. 4.1, Fig. 4.4. *See also* quinolone
 PqsR 103, 105, 155, 291, Fig. 4.4, Fig. 6.3, Table 6.1
 PrfA (regulator, thermosensor) 144, Fig. 6.1
 PrhH (ECF) 78, Table 3.1
 Promoter recognition 1, 19, 59–62, 69, 74, 334, 335, Fig. 2.1

Promoter region 4, 11, 60, 68, 78, 92, 95, 98, 101, 263, 287–294, 312, 321, 342, Fig. 12.10

Promoter specificity 27, 28, 59, 62, 74, 76
 Proteolytic degradation 64, 70, 74, 75, 177, 276

Proton gradient 224, 275, Fig. 11.1

Proton motive force 47, 273, 286, Fig. 11.7

Protoporphyrin 69, 262, 265, 266, Fig. 10.4, Fig. 11.1

PrpL (protease) 75–78, 263, Fig. 10.1, Table 3.1

PrrF1/F2 (Small RNA) 263

Pseudogene 33, Table 2.1, Table 8.2

Psp response and PspA 46, 47, Fig. 2.2

PTS systems/components 7, 282, Fig. 11.5

PupI (ECF) 76, Table 3.1

PvdS (ECF) 75, 76, 263, Fig. 10.1, Table 3.1

Pyochelin 263, Fig. 10.1

Pyoverdine 50, 74–76, 262, 263, Table 3.1, Fig. 10.1

Pyruvate 275, 278, 280, 284–287, 290–292, Fig. 11.1, Fig. 11.2, Fig. 11.5, Fig. 11.8, Fig. 11.9

Q

Qrr (Small RNA) 151, 153, Fig. 6.2, Table 6.1

QscR 97–100, Fig. 4.3

Quenching 88, 96, 112

Quinolone 50, 92, 97, 100–106, 291

Quinone (Ubiquinone, menaquinone) 9, 15, 273–280, Fig. 1.2, Fig. 1.4, Fig. 11.1, Fig. 11.5, Fig. 11.7

Quorum sensing (QS) 45, 49, 87, 88, 97–99, 102, 110, 112, 135, 138, 147, 151–156, 161, 291, 307, 320, 321, 325, 326, 338, 339, Fig. 4.2, Fig. 4.5, Fig. 6.2, Fig. 6.3, Fig. 12.2, Table 6.1, Table 8.1

R

RBS (ribosome binding site) 133, 134, 151, 153, 155, 156, 178, Fig. 6.4, Fig. 7.3

RcsCBD (two-component system) 7, 195

Reactive oxygen species (ROS) 261

Receiver domain 71, 109, 192, 194, 198–211, Fig. 8.1, Fig. 8.4, Fig. 8.8, Fig. 8.9, Fig. 11.6

Recombinase 267

Redox

Potential 126, 228, 273, 275, Fig. 11.1

Sensing/Sensor/Regulator 69, 249, 266, 275, 276, 278, 280, 293–294 (Fig. 11.5)

State/status 15, 47, 126, Fig. 1.4

Stress 261, 267–268, 293

Reductase 261, 262, 265, 267, 275–280, 284–293, Fig. 11.2, Fig. 11.5, Fig. 11.7, Fig. 11.9

Reduction 70, 262, 266, 284–287, 290, 335, Fig. 11.7

Redundant (sequence, function, system) 151, 153, 158, 160, 172, Fig. 6.4

- Regulatory region 48, 153, 334, 335, 339, 340
 Regulon 12, 13, 18, 19, 28–32, 47–50, 66–71, 76, 79, 92, 97, 99, 100, 106, 110, 153, 167, 177–180, 195, 278, 282–295, 335, Fig. 2.2, Fig. 3.3, Fig. 4.3, Fig. 5.4, Fig. 7.3
 RelA/SpoT 5, 178
 Repellent (chemo-) 223, 225, 235
 Replication (DNA) 132, 137, 177, Table 8.1
 Reporter (gene) 278, 323
 Repressor 6, 14, 18, 29, 31, 69, 72, 95, 99, 101, 124, 128, 132, 147, 151, 155, 156, 169, 173, 176, 262–266, 269, 277, 293, 294, 312, 321–324, 335, 338, Fig. 6.2, Fig. 10.2, Fig. 10.3, Fig. 10.5, Fig. 12.11, Fig. 12.12, Fig. 13.2, Table 6.1
 ResDE (two-component system, anaerobic adaptation) 273, 293–295, Fig. 11.6
 Respiration 15, 207, 266, 273–287, 290–294, 335, Fig. 11.1, Fig. 11.4, Fig. 11.5, Fig. 11.8, Fig. 11.10, Table 8.1
 Respiratory chain 15, 282
 Response regulator 5, 8, 10, 15, 18, 63, 71, 106, 11, 150, 151, 172–176, 191, 202, 212, 227, 237, 241–245, 248–252, 265, 267, 280–284, 289, 293, Table 6.1, Fig. 6.2, Fig. 6.4, Fig. 8.1, Fig. 9.2, Fig. 9.6, Fig. 9.11, Fig. 10.1
 RetS (hybrid sensor) 156, 157, 195, 204, Fig. 6.4
 Rhamnolipid 103, 126, Table 4.1
 RhI/I/RhlR 93–99, 105, 291, Table 4.1, Fig. 4.4
 Ribosome 6, 10, 144, 146, 153, 155, 178, 311, Fig. 6.2
 Riboswitch 123, 128, 132, 133, 139, 144–146, 161, Fig. 6.1
 RirA (rhizobial iron regulator) 265, 268, 269, Fig. 10.2, Table 10.1
 6S RNA 11, 158
 RNA polymerase (RNAP, RNAP or RNAPc) 1–3, 8–14, 16–18, 27–30, 32, 49–50, 59–61, 65–69, 74, 79, 334–335, Fig. 2.1, Fig. 3.3, Fig. 6.2, Fig. 13.1
 RNAIII 151, 153, 155, 156, Fig. 6.2, Table 6.1
 RNase E 5–6, 136, 147, 160, 263, 280, 283, Fig. 10.2
 RNaseJ1 155–156, Fig. 6.3
 RNaseIII 5, 17, 151, 156, 159, Table 6.1, Fig. 6.2, Fig. 6.5
 RocSAR (two-component system) 127, 128, 134
 Rotor (flagellar) 130, 224
 RpfC (sensor kinase)/RpfG (response regulator) 109, 110, 126, 127, 138, Fig. 4.6, Fig. 5.1
 RpoE (ECF) 63, 66–69, Table 3.1
 RpoH 6, 61, 65 Fig. 2.2, Fig. 3.1
 RpoN (also σ 54) 10, 28, 33, 44–50, 97, 276, 289, 291, Fig. 2.3, Table 2.1
 RpoS/Sigma factor subunit S (σ S or E σ S) 1–18, 28, 46, 61, 65, 97, 167, 176–178, Fig. 1.1, Fig. 1.2, Fig. 1.4, Fig. 1.5, Fig. 3.1, Fig. 5.6, Fig. 7.3, Fig. 11.5, Table 4.1
 RprA (small regulatory RNA) 6–7, Fig. 1.1
 Rsd (anti- σ 70 factor) 10–11, 17–18, 65, Fig. 1.1, Fig. 1.2
 RseA (anti- σ E) 66–70, 322, Fig. 3.3, Fig. 12.3
 RseP (protease) 66–69, 74, Fig. 3.3
 RsmA (post-transcriptional regulator) 97, 101, 156, 158, Fig. 6.4, Table 6.1
 RsmE (post-transcriptional regulator) 156, Fig. 6.4
 RsmY/Z (small RNAs) 156, 157, Fig. 6.4, Table 6.1
 RssB (σ recognition factor, response regulator) 5–10, 13–18, 282, Fig. 1.1, Fig. 1.2, Fig. 1.3, Fig. 1.4, Fig. 1.5
 RyhB (small RNA) 263, 267, Fig. 10.2, Fig. 10.3
- S**
- σ 18 28
 σ 24 28, 32, 47
 σ 28 10, 16, 28, 47, 48, 61, Fig. 3.1. See also FliA
 σ 32 21, 61, Fig. 3.1. See also RpoH
 σ 38 28, 31, 32, 46, 47
 σ 54 10, 16, 27–33, 44–50, 60, 335, 339, Fig. 2.1, Fig. 2.2, Fig. 6.2, Fig. 13.3, Table 2.1. See also RpoN
 σ 70 (or E σ 70) 1, 4, 10–11, 14–18, 28–32, 47, 60–65, 158, 277, 334–335, 339, Fig. 1.5, Fig. 2.1, Fig. 3.1, Fig. 5.6
 σ E 10, 16, 32, 62, 65–71, 322, 335, 341, Table 3.1, Fig. 3.3, Fig. 12.13. See also AlgT
 σ H 70–71. See also RpoH
 S-adenosyl methionine (SAM) 92, 93, 106, 144, 245, Fig. 4.2, Fig. 6.1
Salmonella (enterica serovar Typhimurium) 4–5, 10, 47, 61, 100, 143–135, 145, 147, 167–168, 172, 175, 178–179, 228, Table 2.1, Table 7.1, Fig. 5.5
 ScbRA (quorum sensing system) 321, 325, Fig. 12.12
 SdiA 100, Fig. 4.3
 Second messenger 2, 14, 123, 134, 137, 146, 205, 252, Fig. 5.1
 Secondary metabolite 45, 156, 195
 Sensor(y) 5, 15, 18, 63, 71, 88, 95, 106, 109–111, 125–128, 143–145, 156, 191, 192, 195, 198, 203, 204, 207–212, 225, 227, 232, 236, 236, 242, 245, 249, 253, 262, 266, 273, 276, 280–284, 287, 289, 293, 322, 342, Fig. 1.4, Fig. 4.5, Fig. 5.1, Fig. 5.3, Fig. 5.4, Fig. 6.4, Fig. 9.4, Fig. 10.1, Fig. 11.3, Fig. 11.6
 Serine protease 68, 70, 111
 Shine-Dalgarno 144, 146, 156, Fig. 6.1, Fig. 6.3, Fig. 6.4
 Siderophore 71–79, 96–98, 106, 261–265, Table 3.1
 SigE 65, 70, Table 3.1, Fig. 12.13
 SigF 61, Fig. 3.1
 Sigma factor (σ) (anti- and anti-anti-) 1–3, 8, 10–11, 13–14, 16–19, 32, 47, 59–79, 135, 167, 171, 176–177, 211–212, 261–264, 280, 282, 291, 311, 322–323, 329, 334–335, Fig. 3.1, Fig. 3.2, Fig. 10.1, Fig. 12.3, Table 3.1
 Signal transduction 27, 59–62, 72, 78, 88, 109, 110, 127, 135, 160, 191, 201, 203, 208–212, 225–236, 252, 282
 Signalling pathway 27, 64, 65, 72, 74, 156, 157, 160, 191, 194, 196, 205, 211, 212, 225, 236, 239
 SigW 66–69, Table 3.1
 SigX 62, 66–69, 74, Table 3.1
 Silencing 169, 170–172, 175, 179, 180, Fig. 10.2
 Slime 45, 249
 SlyA (DNA-binding protein) 172, 173
 Small RNA 6, 32, 66, 132, 136, 159, 263, 267, 276, Fig. 1.2, Fig. 5.6, Fig. 10.5
 SoxR/S (oxidative stress regulator) 266, 268, 276
 SPI-1 or SPI-2 (*Salmonelle* pathogenicity islands) 155, 172, 175, Table 6.1
 Sporulation 45, 61, 202, 206, 249, 252, 305, 311, 322, 323, 327, 334, Fig. 8.1, Fig. 12.7, Table 8.1
 SreA (SAM riboswitch element) 144, Fig. 6.1
 SsrA/SsrB (two-component system) 7, 172
 Starvation 1, 3, 7–10, 14, 18, 69–72, 110, 130, 251, 315, 322, Fig. 1.1, Fig. 1.2, Fig. 1.3, Fig. 5.2, Fig. 9.12, Table 6.1
 Stator (flagellar) 130, 224

- Steady state 156, 308–310, Fig. 12.2
 Stem-loop 155, 158
 Stimulus(i) 64, 66, 69, 191, 192, 195, 200, 203–205, 210, 211, 213, 224, 237, 239, 245–249, 252, 316, 334, 336, Fig. 3.2, Fig. 8.1, Fig. 11.4, Fig. 11.5, Fig. 11.10, Fig. 12.9
 Stochastic/stochasticity 15, 233–234, 305–306, 311–314, 318–319, 325–326
 StpA (H-NS parologue) 167, 177–180, Fig. 7.3, Table 7.1
 Stress response 1–3, 28, 46, 59–62, 65–71, 101, 147, 160, 195, 207, 267, 278, 282, 285, 289, 322, 334, 339, 341, Fig. 11.4, Fig. 11.5, Fig. 12.13, Table 3.1, Table 10.1
 Stringent response 11, 32, 45, 178, 322
 Succinate 99, 239, 275, 276, 285, 287, Fig. 11.1, Fig. 11.2, Fig. 11.5
 Supercoiled(ing) 168, 171, 172, 176, 339
 Superoxide 70, 261, 276
 Superoxide dismutase 263, 267, 268, 278, 282, 284, Fig. 10.3, Fig. 11.5
 Swarming (motility) 47, 98, 103, 159, 249, 251, Table 4.1
 Swimming (motility) 129, 224, 227–229, 235, 247–252, Fig. 5.2, Fig. 9.1, Fig. 9.10, Table 4.1
 Switch complex (FliM/N) 224, 227, 228, 238
 Synthetic biology 195, 196, 210, 305, 323
 Systems biology 208, 210, 211, 295, 326
- T**
- TCA cycle 266, 282, 285, Fig. 11.5
 Temperature 3, 6, 7, 17, 18, 68, 100, 144, 171, 176, 178, 179, 228, Fig. 6.1
 Termination (transcription) 27, 59, 144, 145, Fig. 6.1
 TetR (tetracycline repressor) 323, 324, 337–339
 TF (transcription factor) 333–340, Fig. 13.1, Fig. 13.2, Fig. 13.3, Fig. 13.4
 Thermosensor 144, 160, 161
 TMAO (trimethylamine N-oxide) 207, 273, 275, 284, 285, Fig. 11.1, Fig. 11.5
 TonB 65, 72–79, Fig. 3.4
 Torque generation 130, 224
 TorS/R (two-component system) 198, 284
 ToxT (AraC-like protein) 172, 179, 316, Fig. 12.9
 TraI/TraR 95, 97, 99, 101, Table 4.1
 Trans-acting 29, 144, 146, 160, 161, 171, 312, Table 6.1
 Transcription(al) activator 29, 29–31, 46–50, 62, 95, 105, 172, 252, 265, 287, 290, 307, 309, Fig. 5.1, Fig. 13.2
- Transcription(al) repressor 14, 18, 29, 132, 169, 285, 266
 Transcriptome(ic) 28, 31, 97, 101, 103, 110, 169, 282, 283, 291, 294
 Transduction *see* Signal transduction
 Transferase 106, 205, 284, 287, 289, Table 6.1
 Transferrin 71, 261
 Translational coupling 155, 200
 Transmitter domain 191, 192, 196–207, 210, 211, 280, Fig. 8.1, Fig. 8.5
 tRNA 144, 311
 Tumbling 224, 229, 235, 237, 247
 Twin arginine translocation 70, 111
 Twitching (motility) 48
 Two-component system (TCS) 5, 6, 9, 62–66, 70, 95, 106, 109, 110, 125, 138, 143, 147, 154–160, 172, 191–212, 223–227, 237, 252, 262, 273, 280–283, 289–294, 322, 338, Fig. 1.4, Fig. 5.6, Fig. 6.4, Fig. 8.1, Fig. 8.2, Fig. 11.6, Table 8.1, Table 8.2
 Two-hybrid assay 210, 247, 252
 Type III secretion system (T3SS) 48, 49, 78, 158, Fig. 5.2, Fig. 6.4, Table 3.1
 Type IV pili 45, 48, 239, 249, Fig. 5.3, Fig. 9.11
 Type VI secretion system (T6SS) 49, Table 4.1, Table 6.1, Fig. 6.4
- U**
- 5' untranslated region (UTR) 6, 132, 143–144
- V**
- Vegetative 11, 16, 17, 69, 249, 321
 Versatile/Versatility 59, 62, 143, 160, 211, 239, 249, 274, 285, 340
 VpsT (c-di-GMP responsive regulator) 130, 131
 VqsR (FixJ family) 50, 97
- W**
- Winged helix–turn–helix 168, 280, 338, Fig. 13.2
 WspR (GGDEF-containing regulatory protein) 127, 252, Fig. 9.12
- Y**
- YcgR (c-di-GMP binding protein) 129, 130, Fig. 5.2, Fig. 5.6