

Prokaryotic Metabolism and Physiology

Determination of the genome sequences for a wide range of bacteria and archaea has made an in-depth knowledge of prokaryotic metabolic function even more essential in order to give biochemical, physiological and ecological meaning to the genomic information. Clearly describing the important metabolic processes that occur under different conditions and in different environments, this advanced text provides an overview of the key cellular processes that determine prokaryotic roles in the environment, biotechnology and human health. Structure and composition are described as well as the means by which nutrients are transported into cells across membranes. Discussion of biosynthesis and growth is followed by detailed accounts of glucose metabolism through glycolysis, the TCA cycle, electron transport and oxidative phosphorylation, as well as other trophic variations found in prokaryotes including the use of organic compounds other than glucose, anaerobic fermentation, anaerobic respiration, chemolithotrophy and photosynthesis. The regulation of metabolism through control of gene expression and enzyme activity is also covered, as well as the survival mechanisms used under starvation conditions.

Professor Byung Hong Kim is an expert on anaerobic metabolism, organic degradation and bioelectrochemistry. He graduated from Kyungpook National University, Korea and obtained a PhD from University College Cardiff. He has carried out research at several universities around the world, with an established career in the Korea Institute of Science and Technology. Currently he is teaching at

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Professor Geoffrey Michael Gadd is an authority on microbial interactions with metals and minerals, their geomicrobial significance and applications in environmental biotechnology. He holds the Boyd Baxter Chair of Biology and leads the Geomicrobiology Group at the University of Dundee and was founding Head of the Division of Molecular Microbiology in the School of Life Sciences. He has published over 300 refereed scientific papers, books, chapters and reviews and has received invitations to speak at international conferences in over 30 countries. Professor Gadd has served as President of the British Mycological Society and is an elected Fellow of the Royal Society of Biology, the American Academy of Microbiology, the Linnean Society, the Learned Society of Wales, the Royal Society of Edinburgh and elected Member of the European Academy of Microbiology. He has received the Berkeley Prize and President's Award from the British Mycological Society, the Charles Thom Award from the Society for Industrial Microbiology and the Colworth Prize from the Microbiology Society for his research contributions to the microbiological sciences.

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Byung Hong Kim , Geoffrey Michael Gadd
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SECOND EDITION

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To our families
Hyungock Hong, Kyoungha Kim and Youngha Kim
and
Julia, Katie and Richard Gadd

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Preface for the second edition

Since the first edition of *Bacterial Physiology and Metabolism* was published in 2008, significant progress in many areas has been made, requiring extensive revision of the first edition. Furthermore, some important topics were not adequately covered in the first edition. These include the modified TCA cycles in cyanobacteria and obligately fermentative bacteria (Section 5.2.2), novel TCA cycle intermediate replenishment mechanisms (ethylmalonyl-CoA pathway, Section 5.3.3 and methylaspartate cycle, Section 5.3.4), archaeal pentose metabolism (Section 7.2.3), methane oxidation in anaerobic environments (Section 9.9.2), elucidation of novel CO₂ fixation cycles (the 4-hydroxybutyrate cycles, Section 10.8.5), bacterial immune systems (Section 13.5), toxin/antitoxin systems (Section 13.4.2) and competence (Section 13.6). Also included in this edition are accounts of the synthesis of the non-canonical amino acids, pyrrolysine and selenocysteine, and their codon usage. Analysis of bacterial genomes has led to

the identification of many novel mechanisms of metabolic regulation, including two-component systems and small non-coding RNAs (discussed in Chapter 12). Another intriguing discovery is the use of certain rare earth elements by methyloprotophytes (Section 2.1). The book title has also been amended to *Prokaryotic Metabolism and Physiology* to reflect the increasing content of archaeal processes. We hope this second edition is received as well as the first edition.

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Preface for the first edition

Knowledge of the physiology and metabolism of prokaryotes underpins our understanding of the roles and activities of these organisms in the environment, including pathogenic and symbiotic relationships, as well as their exploitation in biotechnology. Prokaryotic organisms include bacteria and archaea and, although remaining relatively small and simple in structure throughout their evolutionary history, exhibit incredible diversity regarding their metabolism and physiology. Such metabolic diversity is reflective of the wide range of habitats where prokaryotes can thrive and in many cases dominate the biota, and is a distinguishing contrast with eukaryotes that exhibit a more restricted metabolic versatility. Thus, prokaryotes can be found almost everywhere under a wide range of physical and chemical conditions, including aerobic to anaerobic, light and dark, low to high pressure, low to high salt concentrations, extremes of acidity and alkalinity, and extremes of nutrient availability. Some physiologies, e.g. chemolithotrophy and nitrogen fixation, are only found in certain groups of prokaryotes, while the use of inorganic compounds, such as nitrate and sulfate, as electron acceptors in respiration is another prokaryotic ability. The explosion of knowledge resulting from the development and application of molecular biology to microbial systems has perhaps led to a reduced emphasis on their physiology and biochemistry, yet paradoxically has enabled further detailed analysis and understanding of metabolic processes. Almost in a reflection of the bacterial growth pattern, the number of scientific papers has grown at an exponential rate, while the number of prokaryotic genome sequences determined is also increasing rapidly. This production of genome sequences for a wide range of organisms has made an in-depth knowledge of prokaryotic metabolic function even more essential in order to give biochemical, physiological and ecological meaning to the genomic information. Our objective in writing this new textbook was to provide a thorough survey of the prokaryotic metabolic diversity that occurs under

different conditions and in different environments, emphasizing the key biochemical mechanisms involved. We believe that this approach provides a useful overview of the key cellular processes that determine bacterial and archaeal roles in the environment, biotechnology and human health. We concentrate on bacteria and archaea but, where appropriate, also provide comparisons with eukaryotic organisms. It should be noted that many important metabolic pathways found in prokaryotes also occur in eukaryotes further emphasizing prokaryotic importance as research models in providing knowledge of relevance to eukaryotic processes.

This book can be considered in three main parts. In the first part, prokaryotic structure and composition is described as well as the means by which nutrients are transported into cells across membranes. Discussion of biosynthesis and growth is followed by detailed accounts of glucose metabolism through glycolysis, the TCA cycle, electron transport and oxidative phosphorylation, largely based on the model bacterium *Escherichia coli*. In the second part, the trophic variations found in prokaryotes are described, including the use of organic compounds other than glucose, anaerobic fermentation, anaerobic respiration, chemolithotrophy and photosynthesis. In the third part, the regulation of metabolism through control of gene expression and enzyme activity is covered, as well as the survival mechanisms used by prokaryotes under starvation conditions. This text is relevant to advanced undergraduate and postgraduate courses, as well as being of use to teachers and researchers in microbiology, molecular biology, biotechnology, biochemistry and related disciplines.

We would like to express our thanks to all those who helped and made this book possible. We appreciate the staff of Academy Publisher (Seoul, Korea) who redrew the figures for the book, and those at Cambridge University Press involved at various stages of the publication process, including Katrina Halliday, Clare

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