PREFACE

The production and consumption of methane by microorganisms is central to the global carbon cycle. It has been 2 decades since a *Methods in Enzymology* volume focused explicitly on this field (Volume 188, *Hydrocarbons and Methylotrophy*). During that time, interest in methane metabolism has steadily increased in the context of dwindling petroleum reserves, increased greenhouse gas emissions, and environmental hydrocarbon pollution. A field previously dominated by microbiology and protein biochemistry has exploded in multiple directions. In particular, the advent of genomic and proteomic techniques has transformed the way methane metabolic pathways are studied. In these volumes, we cover both the generation (Part A) and utilization (Part B) of methane.

Part A describes recent developments that enable a wide variety of experiments with methanogenic Archaea, which seemed intractable two decades ago to all but those initiates who "grew up" studying anaerobes. Methods are presented to readily culture and to perform genetic experiments on these oxygen-sensitive microbes, as well as to characterize the remarkable enzymes and respiratory proteins that allow methanogens to generate energy for growth and produce as a byproduct a very important fuel that may be adopted as the "fuel of the future." Included is the state of the art in "biomethanation," the biotechnological use of methanogens to produce this important energy source. Finally, approaches are described for the deployment of "omics" technologies to understand how methanogens regulate metabolism.

The first methanotroph genome sequence was completed in 2004, and research has become progressively more "omic" in the past few years. Part B combines traditional approaches to methanotroph isolation and enzyme chemistry with state-of-the-art genomic and proteomic techniques. Novel methods have been developed and used to address challenging problems such as linking metagenomic data with environmental function or generating mutant forms of the methane monooxygenase enzymes. Moreover, whole new areas of research, such as the study of the copper chelator methanobactin, have been discovered. Taken together, we hope that the two volumes capture the excitement that pervades this rapidly developing field.

We thank an outstanding group of colleagues with diverse points of view for providing ideas on content and ultimately contributing a series of excellent chapters. The high level of enthusiasm in the community resulted in the

unexpected final production of two, rather than one, volumes. The methods and novel approaches described here should inspire and guide future research in the field as well as provide a central resource for researchers interested in methane metabolism.

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