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## Preface

Since the discovery of catalytic RNA in 1982, for which the Nobel Prize was later awarded, RNA research has continued to experience an increasing attention. During the past decade, the RNA community has been intrigued by the discovery of hundreds of novel functional, noncoding RNAs. As a consequence, it has become increasingly evident that RNA is the driving force in the most essential processes in the cell—*RNA Regulates Biology*. Although these RNAs are quite diverse and fulfill very different functions, they share a common theme: their strict dependence on acquiring specific 3D fold(s) in order to be functional and to accomplish their cellular tasks. The process of RNA folding describes how an RNA molecule undergoes the transition from an unfolded, disordered state to the native, functional conformation. So far, RNA structure and folding has been almost exclusively studied in vitro. The in vitro refolding conditions differ, however, significantly from the intracellular folding environment. In the cell factors such as the directionality of transcription and translation, *trans*-acting noncoding RNAs as well as proteins are likely to influence folding of RNA molecules. Hitherto, very little is known about RNA folding in vivo, which is in part due to the complex nature of the cellular environment, but also to the limited availability of suitable methodologies. In these respects, the compilation of methodologies herein lies at the heart of the topical research focus of in vitro and intracellular RNA structure formation. The main purpose of the book is to provide a comprehensive collection of experimental protocols, which are suitable to dissect RNA folding pathways and to characterize the structure of RNA folding intermediates at nucleotide or even atomic resolution. This book will be equally useful for experienced researchers as well as PhD students and postdoctoral fellows new to the field. Presented techniques include powerful tools with a long tradition in RNA research as well as more advanced, novel methods. As such, the methods span multiple disciplines, including molecular biology, biochemistry, biophysics, and computational biology. I believe that this special issue on exploring RNA folding is timely in light of the everlasting boom of RNA research. With the vast expansion of known RNA molecules, I wish to share my fascination and passion for RNA with new researchers joining our efforts to gain insights into the secrets of this astounding macromolecule. At last, I want to acknowledge the extraordinary group of people who contributed high-quality chapters to this special issue on modern-day research in RNA folding.

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