

PREFACE

RNA helicases have fascinated and puzzled investigators for the three decades that have passed since the first report on a "protein involved in ATP-dependent binding of mRNA." Since then, it has become clear that RNA helicases are ubiquitous, highly conserved enzymes that participate in virtually all aspects of RNA metabolism from bacteria to human. In eukaryotic RNA metabolism, RNA helicases are the largest class of enzymes, and many of these proteins have emerged as central players in the regulation of gene expression at the RNA level.

Given the critical and diverse roles of RNA helicases in biology, detailed knowledge of molecular and cellular functions of these enzymes is important for delineating the molecular basis of RNA metabolism. The past decade has seen remarkable progress in our understanding of these essential enzymes on all fronts: several dozen RNA helicase structures have been solved, enzymatic mechanisms have been illuminated, and specific cellular roles of many of these enzymes have come into better focus. We have come to realize that RNA helicases use ATP not only to unwind RNA duplexes but also to remodel and assemble RNA structures and RNA-protein complexes. It is not yet clear how molecular mechanisms exactly translate into cellular functions for these enzymes. However, answers to this question may be within reach for many RNA helicases, given the available repertoire of biochemical, biophysical, molecular biological, and cellular approaches. This is an exciting time for research on RNA helicases.

Interest in these enzymes comes from all sides of the methodological spectrum of modern biology, from biophysicists to cell biologists. This volume thus aims to provide a reference for the diverse, powerful tools used to analyze RNA helicases. The wonderful work contributed to this volume covers the broad scope of methods in the research on these enzymes. Several chapters describe quantitative biophysical and biochemical approaches to study molecular mechanisms and conformational changes of RNA helicases. Further chapters cover structural analysis, examination of cofactor effects on several representative examples, and the analysis of cellular functions of select enzymes. Two chapters outline the analysis of inhibitors that target RNA helicases.

Investigators who are new to the field now have a focused collection of detailed protocols for an entire range of methods tailored toward RNA helicases. Investigators with previous experience in the field will find the volume useful for the perspective on complementary approaches and for the plethora of conceptual and practical tips that are often invaluable for a

successful examination of nucleotide-dependent enzymes that work on RNA. I am deeply grateful to the dedicated group of authors who have written a series of outstanding protocols and guides. It is my hope that this unique compilation encourages investigators and students to join the vibrant research on RNA helicases and that the volume inspires new angles of inquiry for investigators already in the field.

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