Preface

Why a second edition of the Handbook of RNA Biochemistry about eight years after release of the first edition? We see several profound reasons, the most fundamental one being that new biological and biochemical questions induce new technological advances, which in turn drives our research capabilities and opens up insights into novel RNA functions and mechanistic principles. For example, a multitude of novel non-coding RNAs (ncRNAs) have been uncovered, which entails a need not only for bioinformatic tools to predict their structure and to search for homologs, but also for further developments in biochemical tools for their functional analysis.

In the last decade, research in RNA biology, and here most notably global approaches, experienced an incredible boom, largely driven by new genome-wide and high-throughput technology, as well as RNA bioinformatics. Therefore, high-throughput and deep-sequencing approaches are covered by new chapters in this second edition (Chapters 34, 36–40), and contributions present already in the first edition have been thoroughly updated (Chapters 33 and 35) to keep pace with the fast evolution of these powerful methods.

Although unmodified RNA contains only four different nucleotides, the prediction of RNA secondary and tertiary structures and RNA homology searches are inherently sophisticated tasks of pivotal importance for RNA researchers. Chapters 26–32 are dedicated to these demands. There is also a need for protocols that enable experimental scientists to competently utilize bioinformatic, preferably web-based, tools. This aspect has been taken into account throughout this second edition.

All the chapters already present in the first edition have been updated, which concerns practical details (such as on company names, providers of enzymes and materials, web addresses), methodological details, and protocol streamlining. For example, the topics of RNA ligation or photoaffinity crosslinking to probe RNA structure, each previously represented by two separate chapters, are now consolidated in single chapters (Chapters 3 and 11). In addition, "old," but very informative, RNA techniques such as gel- or TLC-based approaches to identify modified nucleosides or temperature-gradient gel electrophoresis of RNA, currently out of fashion, have been described in even more detail (Chapters 9 and 21) in order to preserve this kind of more traditional knowledge, which may experience an unforeseen revival at some point in the future.

Methodology in the area of RNA interference is crucial for so many researchers in various fields and is not restricted to RNA specialists, but also essential for RNA-based biotechnology and application in molecular medicine. We have therefore included new chapters on vector-encoded siRNA or miRNA techniques (Chapter 55), miRNA analysis (Chapter 49), and the application of chemically modified siRNAs (Chapter 56).

In summary, we have expanded the number of chapters and protocols, all written by experts in their fields, included new methods and approaches, strengthened the ready-to-use-lab-protocol format, and eliminated some redundancies.

We wish all readers scientific success in the application of our protocols, as well as several *Eureka!* experiences when, or after, consulting this Handbook for experimental strategies to tackle their specific biological questions or problems in RNA research.

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