# Preface

The aim of this book is to provide a comprehensive compendium of current methods and protocols to study posttranscriptional base modifications, in particular methylation, in RNA. The study of RNA methylation has emerged as an exciting new research area over the past few years not least due to the discovery that internal base methylation, such as N6-methyladenosine (m6A) and 5-methylcytosine (m5C), is widespread not only in abundant RNAs (tRNAs, rRNA) but also in mRNAs and in long noncoding RNAs (lncRNAs). Thus, it might represent an additional layer of gene regulation, leading to the coining of the terms "RNA epigenetics" and "epitranscriptomics." Although RNA methylation research is still in its early stages, disruption of RNA methylation has been linked to a number of disease conditions, including obesity, type 2 diabetes mellitus, Alzheimer's disease, cancer, and cardiovascular disease. Moreover, at least m6A is a reversible modification, which further underscores the regulatory potential of RNA methylation.

The protocols collected in this book represent the state-of-the-art methodology for investigating diverse aspects of RNA methylation on different types of RNA. Protocols include wet lab techniques for the detection of methylation, instructions for bioinformatics analyses of transcriptome-scale data sets as well as protocols for the functional examination of RNA modifications and enzymes. Thus, this laboratory manual may constitute a valuable source for biochemists and molecular biologists from different fields who wish to include the investigation of different types of RNA methylation in their studies.

*Innsbruck, Austria*                                                    *Alexandra Lusser*