Preface

When microRNAs were first described in 1993 by the groups of Ruvkun (Wightman et al., 1993) and Ambros (Lee et al., 1993) or possibly even in 1976 by Heywood (Heywood and Kennedy, 1976), the scientific community was not yet ready to accept RNA as a general regulator of gene expression. Small non-coding prokaryotic RNAs were among the first to draw attention to their unusual structures and their potential to react rapidly to environmental stimuli and cellular changes by regulating genes on the post-transcriptional level (Mizuno et al., 1984). It is therefore appropriate to begin this volume with an update by Wagner and Darfeuille on small, non-coding RNAs in prokaryotes, that control cellular processes on many different levels.

More specifically, Söderbom describes approaches to identify regulatory RNAs *in silico* and *in vivo* and concentrates on snoRNAs. Though these are known to serve as guides for modification of rRNA and snRNAs, further targets are emerging.

The *in silico* search for non-coding RNAs is detailed in the contribution of Gräf et al. who describe programs to find non-coding RNAs in large databases.

Boutla and Tabler discuss the dual approach of bioinformatics and *in vivo* experiments to define and validate new microRNAs – a difficult task of great importance to understand this formerly unexpected network of regulation in eukaryotic development and differentiation.

Secondary structure, in particular dsRNA, has become a major focus in gene regulation. DsRNA is a processing intermediate and recruits diverse machineries that modify RNA, elicit enzymatic responses or guide RNA to specific targets. In this context, the proteins that interact with dsRNA have attracted increasing attention. The chapter by Hammann reviews the features of dsRBDs and discusses the problem how target dsRNAs are guided to one but not the other molecular pathway that coexist in the cell.

The following two chapters by Bleys et al. and Kuhlmann et al. concentrate on special aspects of the RNA interference pathway. In contrast to the basic RNAi mechanism, the spreading of dsRNA mediated gene silencing in an organism (systemic silencing) and along the gene or genome (transitive silencing) most likely involves the activity of RNA directed RNA polymerases. Models on how these enzymes may be involved in signal generation and amplification are

also presented in the latter chapter that evaluates differences and similarities between RNAi and antisense mediated gene silencing.

One branch of the RNA interference mechanism acts in the nucleus and confers transcriptional silencing by influencing chromatin structure. Dijk et al. review experiments that explain how small interfering RNAs prevent the proliferation of transposons in the genome of the model organism Chlamydomonas. Paulsen and co-workers extend the view on epigenetic regulation and summarize examples of chromatin remodelling at specific imprinted genes and in dosage compensation in the general context of RNA interference. Finally, Sano and Taira describe the application of small artificial riboregulators to identify gene functions in mammalian cells.

This volume can only provide a snapshot of the rapidly developing field of small RNA regulatory functions. New details are continuously emerging, nevertheless, we believe that the overviews, speculations, methods and models presented in this book will not only provide a summary of the current knowledge but also stimulate discussions and ideas how to further tackle this exciting area of research.

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