
Preface

The advent of next-generation sequencing revealed that the majority of the human genome is transcribed to noncoding RNAs. Recent studies on long noncoding RNAs (lncRNAs) suggest that they may represent another class of important, nonprotein regulators of various biological processes, including cell proliferation, differentiation, migration, apoptosis, and transformation. In this column of the *Methods in Molecular Biology* series, we assemble a broad spectrum of methods used in lncRNA research, ranging from computational annotation of lncRNA genes to molecular and cellular analyses of the function of individual lncRNA. Methods used to study circular RNAs and RNA splicing also are included. Given that many well-characterized lncRNAs exhibit important pathological functions, we also include a chapter to describe the most influential finding on lncRNA in human diseases. We would like to make this book a must-have for anyone who conducts lncRNA research. The intended audience includes molecular biologists, cell and developmental biologists, specialists who conduct disease-oriented research, and bioinformatics experts who seek a better understanding on lncRNA expression and function by computational analysis of the massive sequencing data that are rapidly accumulating in recent years. It is our hope that *Long Noncoding RNA Protocol* will stimulate the reader to explore diverse ways to understand the mechanisms by which lncRNAs facilitate the molecular aspects of biomedical research. We would like to acknowledge and thank all authors for their valuable contributions, particularly for sharing with readers all hints, tips, and observations that one learns from using a method regularly. We also thank Dr. John Walker for his technical guidance and support.

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Long Non-Coding RNAs

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