

All eukaryotic messenger RNAs are derived from precursors, the pre-mRNAs, by an extensive series of nuclear modifications. Most notably, the removal of introns and the joining of the remaining exons in the process of pre-mRNA splicing is essential to generate mRNAs that are suitable templates for translation. The vast majority of human pre-mRNAs undergo alternative splicing, in which different RNA parts are either included or omitted in the mature mRNA. This process allows individual genes to generate multiple proteins and makes alternative pre-mRNA splicing a central element in gene regulation. Although pre-mRNA splicing occurs with high fidelity, an increasing number of diseases have been linked to defects that lead to mis-spliced mRNAs.

This book was written for graduate and medical students, as well as clinicians and postdoctoral researchers. It describes the theory of alternative pre-mRNA splicing in twelve introductory chapters and then introduces protocols and their theoretical background relevant for experimental research. These 43 practical chapters cover: Basic methods, detection of splicing events, analysis of alternative pre-mRNA splicing *in vitro* and *in vivo*, manipulation of splicing events, and bioinformatic analysis of alternative splicing.

A theoretical introduction and practical guide for molecular biologists, geneticists, clinicians and every researcher interested in alternative splicing.

Supplementary material is available at
www.wiley-vch.de/home/splicing



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