

Methods for the study of alternative splicing.

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Abstract Alternative splicing multiplies the coding capacity of genes, which provides unparalleled complexity to the transcriptome and proteome. This increased complexity has clear repercussions for the regulation of gene expression in many organisms and for the balance between human health and disease. This significance, which has only recently been fully understood, has led to a growing number of studies that address the mechanisms that control alternative splicing decisions and the biological consequences of alternative RNA and protein isoforms. These studies have adapted or developed new methods and protocols that span computational biology, the biochemical analysis of in vitro reactions, model tissue culture systems, and in vivo studies. Many of these methods have been assembled in this volume to assist a newcomer to the study of alternative splicing and to expand the methodologies of laboratories already in the field.

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