METHODS IN MOLECULAR BIOLOGY™ • 338
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Gene Mapping, Discovery, and Expression

Methods and Protocols

Edited by

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Completion of the sequence of the human genome and the development of high-throughput technologies have opened a new era of research in biology and medicine. In *Gene Mapping, Discovery, and Expression: Methods and Protocols*, a panel of researchers from around the world and from a variety of disciplines offer a unique blend of computational tools and experimental techniques for gene mapping, comparative genomics, and studies of the control of gene expression. On the computational side, for beginners in the field, the book describes web-based technologies to localize and map genes, to access and retrieve data from microarray databases, to conduct comparative genomics, and to discover the potential "codes" in genomic DNA that may control the expression of protein-coding genes. Detailed experimental techniques described include methods for studying chromatin structure and allele-specific gene expression, methods for high-throughput analysis and characterization of transcription factor binding elements, and methods for isolation and identification of proteins that interact with DNA. The protocols in the book follow the successful *Methods in Molecular Biology™* series format, offering step-by-step instructions, an introduction outlining the principles behind the technique, lists of the necessary equipment and reagents, and tips on troubleshooting and avoiding pitfalls.

Cutting-edge and interdisciplinary, *Gene Mapping, Discovery, and Expression: Methods and Protocols* offers a collection of DNA-sequence-based technologies for gene discovery, retrieval of gene expression data, discovery of regulatory elements, and discovery of transcription factors that interact with DNA.

FEATURES

- DNA-sequence-based technologies for solving research problems
- Web-based methods to discover genes in known vertebrate genomic DNA sequences
- Detailed experimental procedures for studies of allele-specific gene expression
- Web-based solution for retrieving data from microarrays
- miRNA expression vectors for studies of the control of gene expression
- Methods for large-scale characterization of transcription factor binding elements
- Web-based methods for comparative genomics
- A procedure for studies of chromatin structure
- Identification of the main components of *cis*-regulatory networks
- Help with conducting research in systems biology
- Step-by-step instructions for beginners in the field

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