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Nucleic Acids Research Springer Science & Business Media
The study of RNA-protein interactions is crucial to understanding the mechanisms and control of gene expression and protein synthesis. The realization that RNAs are often far more biologically active than was previously appreciated has stimulated a great deal of new research in this field. Uniquely, in this book, the world's leading researchers have collaborated to produce a comprehensive and current review of RNA-protein interactions for all scientists working in this area. Timely, comprehensive, and authoritative, this new Frontiers title will be invaluable for all researchers in molecular biology, biochemistry and structural biology.

Journal of the National Cancer Institute CRC Press
Virus Structure covers the full spectrum of modern structural virology. Its goal is to describe the means for defining moderate to high resolution structures and the basic principles that have emerged from these studies. Among the topics covered are Hybrid Vigor, Structural Folds of Viral Proteins, Virus Particle Dynamics, Viral Gemone Organization, Enveloped Viruses and Large Viruses. Covers viral assembly using heterologous expression systems and cell extracts Discusses molecular mechanisms in bacteriophage T7 procapsid assembly, maturation and DNA containment Includes information on structural studies on antibody/virus complexes

RNA-protein Interactions Springer Nature
The second edition of a highly acclaimed handbook and ready reference. Unmatched in its breadth and quality, around 100 specialists from all over the world share their up-to-date expertise and experiences, including hundreds of protocols, complete with explanations, and hitherto unpublished troubleshooting hints. They cover all modern techniques for the handling, analysis and modification of RNAs and their complexes with proteins. Throughout, they bear the practising bench scientist in mind, providing quick and reliable access to a plethora of solutions for practical questions of RNA research, ranging from simple to highly complex. This broad scope allows the treatment of specialized methods side by side with basic biochemical techniques, making the book a real treasure trove for every researcher experimenting with RNA.

Official Gazette of the United States Patent and Trademark Office CRC Press
Ribozymes Provides comprehensive coverage of a core field in the molecular biosciences, bringing together decades of knowledge from the world's top professionals in the field Timely and unique in its breadth of content, this all-encompassing and authoritative reference on ribozymes documents the great diversity of nucleic acid-based catalysis. It integrates the knowledge gained over the past 35 years in the field and features contributions from virtually every leading expert on the subject. Ribozymes is organized into six major parts. It starts by describing general principles and strategies of nucleic acid catalysis. It then introduces naturally occurring ribozymes and includes the search for new catalytic motifs or novel genomic locations of known motifs. Next, it covers the development and design of engineered ribozymes, before moving on to DNAzymes as a close relative of ribozymes. The next part examines the use of ribozymes for medicinal and environmental diagnostics, as well as for therapeutic tools. It finishes with a look at the tools and methods in ribozyme

research, including the techniques and assays for structural and functional characterization of nucleic acid catalysts. The first reference to tie together all aspects of the multi-faceted field of ribozymes Features more than 30 comprehensive chapters in two volumes Covers the chemical principles of RNA catalysis; naturally occurring ribozymes, engineered ribozymes; DNAzymes; ribozymes as tools in diagnostics and therapy, and tools and methods to study ribozymes Includes first-hand accounts of concepts, techniques, and applications by a team of top international experts from leading academic institutions Dedicates half of its content to methods and practical applications, ranging from bioanalytical tools to medical diagnostics to therapeutics Ribozymes is an unmatched resource for all biochemists, biotechnologists, molecular biologists, and bioengineers interested in the topic.

RNA 3D Structure Analysis and Prediction John Wiley & Sons
This new volume of Methods in Enzymology continues the legacy of this premier serial with quality chapters authored by leaders in the field. This volume covers research methods in RNA folding and dynamics, RNA-protein interactions and large RNPs. Continues the legacy of this premier serial with quality chapters on structures of large RNA molecules and their complexes

Gene Quantification Springer Nature
Transfer RNA in Protein Synthesis is a comprehensive volume focusing on important aspects of codon usage, selection, and discrimination in the genetic code. The many different functions of tRNA and the specialized roles of the corresponding codewords in protein synthesis from initiation through termination are thoroughly discussed. Variations that occur in the initiation process, in reading the genetic code, and in the selection of codons are discussed in detail. The book also examines the role of modified nucleosides in tRNA interactions, tRNA discrimination in aminoacylation, codon discrimination in translation, and selective use of termination codons. Other topics covered include the adaptation of the tRNA population to codon usage in cells and cellular organelles, the occurrence of UGA as a codon for selenocysteine in the universal genetic code, new insights into translational context effects and in codon bias, and the molecular biology of tRNA in retroviruses. The contributions of outstanding molecular biologists engaged in tRNA research and prominent investigators from other scientific disciplines, specifically retroviral research, make Transfer RNA in Protein Synthesis an essential reference work for microbiologists, biochemists, molecular biologists, geneticists, and other researchers involved in protein synthesis research.

Double Helix John Wiley & Sons
Naturally occurring RNA always contains numerous biochemically altered nucleotides. They are formed by enzymatic modification of the primary transcripts during the complex RNA maturation process designated RNA modification. A large number of enzymes catalyzing the formation of these modified nucleosides or converting one canonical base into another at the posttranscriptional level have been studied for many years, but only recently have systematic and comparative studies begun. The functions of individual enzymes and/or the modified/edited nucleosides in RNA, however, have remained largely ignored. This book provides advance information on RNA modification, including the associated editing machinery, while offering the reader some perspective on the significance of such modifications in fine-tuning the structure and functions of mature RNA molecules and hence the ability to influence the efficiency and accuracy of genetic expression. Outstanding scientists who are actively working on RNA modification/editing processes have provided up-to-date information on these intriguing cellular processes that have been generated over the course of millions of years in all living organisms. Each review has been written and illustrated for a large audience of readers, not only specialists in the field, but also for advanced students or researchers who want to learn more about recent progress in RNA modification and editing.

RNA/Protein Interaction Protocols CRC Press
Biology for AP® courses covers the scope and sequence requirements of a typical two-semester Advanced Placement® biology course. The text provides comprehensive coverage of foundational research and core biology concepts through an evolutionary lens. Biology for AP® Courses was designed to meet and exceed the requirements of the College Board's AP® Biology framework

while allowing significant flexibility for instructors. Each section of the book includes an introduction based on the AP® curriculum and includes rich features that engage students in scientific practice and AP® test preparation; it also highlights careers and research opportunities in biological sciences.

Ribozymes Axolotl Academic Publishing
Concepts of Biology is designed for the single-semester introduction to biology course for non-science majors, which for many students is their only college-level science course. As such, this course represents an important opportunity for students to develop the necessary knowledge, tools, and skills to make informed decisions as they continue with their lives. Rather than being mired down with facts and vocabulary, the typical non-science major student needs information presented in a way that is easy to read and understand. Even more importantly, the content should be meaningful. Students do much better when they understand why biology is relevant to their everyday lives. For these reasons, Concepts of Biology is grounded on an evolutionary basis and includes exciting features that highlight careers in the biological sciences and everyday applications of the concepts at hand. We also strive to show the interconnectedness of topics within this extremely broad discipline. In order to meet the needs of today's instructors and students, we maintain the overall organization and coverage found in most syllabi for this course. A strength of Concepts of Biology is that instructors can customize the book, adapting it to the approach that works best in their classroom. Concepts of Biology also includes an innovative art program that incorporates critical thinking and clicker questions to help students understand--and apply--key concepts.

Concepts of Biology Oxford University Press, USA
This special volume of Progress in Molecular Biology and Translational Science focuses on catalytic RNA. Written by experts in the field, the reviews cover a range of topics, from hammerhead ribozymes to spliceosome catalysis to Varkud satellite and hairpin ribozymes. Contributions from leading authorities Informs and updates on all the latest developments in the field

An Interactive Introduction to Organismal and Molecular Biology Academic Press
Geneticists and molecular biologists have been interested in quantifying genes and their products for many years and for various reasons (Bishop, 1974). Early molecular methods were based on molecular hybridization, and were devised shortly after Marmur and Doty (1961) first showed that denaturation of the double helix could be reversed - that the process of molecular reassociation was exquisitely sequence dependent. Gillespie and Spiegelman (1965) developed a way of using the method to titrate the number of copies of a probe within a target sequence in which the target sequence was fixed to a membrane support prior to hybridization with the probe - typically a RNA. Thus, this was a precursor to many of the methods still in use, and indeed under development, today. Early examples of the application of these methods included the measurement of the copy numbers in gene families such as the ribosomal genes and the immunoglo bulin family. Amplification of genes in tumors and in response to drug treatment was discovered by this method. In the same period, methods were invented for estimating gene num bers based on the kinetics of the reassociation process - the so-called Cot analysis. This method, which exploits the dependence of the rate of reassociation on the concentration of the two strands, revealed the presence of repeated sequences in the DNA of higher eukaryotes (Britten and Kohne, 1968). An adaptation to RNA, Rot analysis (Melli and Bishop, 1969), was used to measure the abundance of RNAs in a mixed population.

RNA Spectroscopy Springer Science & Business Media
Vols. for 1963- include as pt. 2 of the Jan. issue: Medical subject headings.
RNA-Protein Complexes and Interactions Springer Science & Business Media
A Top 25 CHOICE 2016 Title, and recipient of the CHOICE Outstanding Academic Title (OAT) Award. How much energy is released in ATP hydrolysis? How many mRNAs are in a cell? How genetically similar are two random people? What is faster, transcription or translation?Cell Biology by the Numbers explores these questions and dozens of others provid

Cells: Molecules and Mechanisms Springer

"Microbiology covers the scope and sequence requirements for a single-semester microbiology course for non-majors. The book presents the core concepts of microbiology with a focus on applications for careers in allied health. The pedagogical features of the text make the material interesting and accessible while maintaining the career-application focus and scientific rigor inherent in the subject matter. Microbiology's art program enhances students' understanding of concepts through clear and effective illustrations, diagrams, and photographs. Microbiology is produced through a collaborative publishing agreement between OpenStax and the American Society for Microbiology Press. The book aligns with the curriculum guidelines of the American Society for Microbiology."--BC Campus website.

RNA Processing Springer Science & Business Media

This book examines a wide range of techniques on RNA extraction, detection, quantification, visualization, and genome-wide profiling, from conventional methods to state-of-the-art high throughput approaches.

Pre-mRNA Processing Academic Press

he past fifteen years have seen tremendous growth in our understanding of T the many post-transcriptional processing steps involved in producing func tional eukaryotic mRNA from primary gene transcripts (pre-mRNA). New processing reactions, such as splicing and RNA editing, have been discovered and detailed biochemical and genetic studies continue to yield important new insights into the reaction mechanisms and molecular interactions involved. It is now apparent that regulation of RNA processing plays a significant role in the control of gene expression and development. An increased understanding of RNA processing mechanisms has also proved to be of considerable clinical importance in the pathology of inherited disease and viral infection. This volume seeks to review the rapid progress being made in the study of how mRNA precursors are processed into mRNA and to convey the broad scope of the RNA field and its relevance to other areas of cell biology and medicine. Since one of the major themes of RNA processing is the recognition of specific RNA sequences and structures by protein factors, we begin with reviews of RNA-protein interactions. In chapter 1 David Lilley presents an overview of RNA structure and illustrates how the structural features of RNA molecules are exploited for specific recognition by protein, while in chapter 2 Maurice Swanson discusses the structure and function of the large family of hnRNP proteins that bind to pre-mRNA. The next four chapters focus on pre-mRNA splicing.

Structures of Large RNA Molecules and Their Complexes Garland Science

Gene expression in eukaryotes is regulated at different levels, which need to be coordinated to implement the information in the genome. Now it is clear that post-transcriptional regulation of gene expression such as pre-mRNA splicing, mRNA transport, editing, turnover and translation are as important as the control of transcription. In all aspects

RNA Abundance Analysis Humana Press

This volume is a timely and comprehensive description of the many facets of DNA and RNA modification-editing processes and to some extent repair mechanisms. Each chapter offers fundamental principles as well as up to date information on recent advances in the field (up to end 2008). They ended by a short 'conclusion and future prospect' section and an exhaustive list of 35 to up to 257 references (in average 87). Contributors are geneticists, structural enzymologists and molecular biologists working at the forefront of this exciting, fast-moving and diverse field of researches. This book will be a major interest to PhD students and University teachers alike. It will also serve as an invaluable reference tool for new researchers in the field, as well as for specialists of RNA modification enzymes generally not well informed about what is going on in similar processes acting on DNA and vice-versa for specialists of the DNA modification-editing and repair processes usually not much acquainted with what is going on in the RNA maturation field. The book is subdivided into 41 chapters (740 pages). The common links between them are mainly the enzymatic aspects of the different modification-editing and repair machineries: structural, mechanistic, functional and evolutionary aspects. It starts with two general and historical overview of the discovery of modified nucleosides in DNA and RNA and corresponding modification-editing enzymes. Then follows eleven chapters on DNA modification and editing (mechanistic and functional aspects). Two additional chapters cover problems related to DNA/RNA repair and base editing by C-to-U deaminases, followed by three chapters on RNA editing by C-to-U and A-to-I type of deamination. Discussions about interplay between DNA and RNA modifications and the emergence of DNA are covered in two independent chapters, followed by twenty chapters on different but complementary aspects of RNA modification enzymes and their cellular implications. The last chapter concerns the description of the present state-of-the art for incorporating modified nucleosides by in vitro chemical synthesis. At the end of the book, six appendicies give useful details on modified nucleosides, modification-editing enzymes and nucleosides analogs. This information is usually difficult to obtain from current scientific literature.

Fine-Tuning of RNA Functions by Modification and Editing Academic Press

With the dramatic increase in RNA 3D structure determination in recent years, we now know that RNA molecules are highly structured. Moreover, knowledge of RNA 3D structures has proven crucial for understanding in atomic detail how they carry out their biological functions. Because of the huge number of potentially important RNA molecules in biology, many more than can be studied experimentally, we need theoretical approaches for predicting 3D structures on the basis of sequences alone. This volume provides a comprehensive overview of current progress in the field by leading practitioners employing a variety of methods to model RNA 3D structures by homology, by fragment assembly, and by de novo energy and knowledge-based approaches.

Virus Structure Springer Science & Business Media

A version of the OpenStax text