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RNA—Protein Interaction Protocols

Second Edition

Edited by
Ren-Jang Lin

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Rnaprotein Interaction Protocols

Steven K. Chapman, Graeme A. Reid



Rnaprotein Interaction Protocols:

RNA-Protein Interaction Protocols Susan R. Haynes, 2008-02-03 The molecular characterization of RNA and its interactions with proteins is an important and exciting area of current research. Organisms utilize a variety of RNA-protein interactions to regulate the expression of their genes. This is particularly true for eukaryotes since newly synthesized messenger RNA must be extensively modified and transported to the cytoplasm before it can be used for protein synthesis. The realization that posttranscriptional processes are critical components of gene regulation has sparked an explosion of interest in both stable ribonucleoprotein (RNP) complexes and transient RNA-protein interactions. RNA is conformationally flexible and can adopt complex structures that provide diverse surfaces for interactions with proteins. The fact that short RNA molecules (aptamers) can be selected to bind many different types of molecules is evidence of the structural variability of RNA. RNA molecules are rarely entirely single or double stranded but usually contain multiple short duplexes interrupted by single stranded loops and bulges. In some RNAs, such as tRNAs, the short duplexes stack on each other. Further variability is generated by the presence of non-Watson-Crick base pairs, modified nucleotides, and more complex structures such as pseudoknots and triple-strand interactions.

RNA-Protein Complexes and Interactions Ren-Jang Lin, 2023-05-11 This second edition updates, complements, and expands upon the first edition by providing a collection of cutting-edge techniques developed or refined in the past few years, along with tried and true methods. Chapters explore the isolation and characterization of RNA-protein complexes, the analysis and measurement of RNA-protein interaction, and related novel techniques and strategies. Written in the highly successful *Methods in Molecular Biology* series format, the chapters include brief introductions to the material, lists of necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and a Notes section which highlights tips on troubleshooting and avoiding known pitfalls. Authoritative and cutting-edge, *RNA-Protein Complexes and Interactions: Methods and Protocols, Second Edition* aims to be a comprehensive guide for researchers in the field.

RNA-Protein Interactions : A Practical Approach Christopher W.J. Smith, 1998-07-09 RNA-protein interactions play a fundamental role in gene expression and protein synthesis. Recent research into the role of RNA in cells has elucidated many more vital interactions with proteins. This book provides an up-to-date and comprehensive guide to a wide range of laboratory procedures to investigate the interactions between RNA and proteins. RNA-protein interactions play a vital role in gene transcription and protein expression. Interactions such as the synthesis of mRNA by RNA polymerases, the essential modification of RNA by the proteins of the spliceosome complex, and the highly catalytic action of the ribosome in protein synthesis are established as being fundamental to the function of RNA. Recent research into, for example, the role of RNA as a catalyst has elucidated many more interactions with proteins that are vital to cell function. *RNA-Protein Interactions: A Practical Approach* provides a clear and comprehensive guide to the experimental procedures used in studying RNA-protein interactions. The approaches covered range from those initially used to detect a novel RNA-protein interaction to various

biochemical and genetic approaches to purifying and cloning RNA binding proteins through to methods for an in depth analysis of the structural basis of the interaction The volume includes a number of procedures that have not previously been covered in this type of manual These include the production of site specifically modified RNAs by enzymatic and chemical methods and in vivo screening for novel RNA protein interactions in yeast and E coli This is the first volume to gather in one place this wide array of approaches for studying RNA protein interactions As is customary for the Practical Approach series the writing is characterized by a clear explanatory style with many detailed protocols This informative book will be a valuable aid to laboratory workers in biochemistry and molecular biology graduate students postdoctoral and senior scientists whose research encompasses this field RNA-protein Interaction Protocols. 2nd Ed (9781588294197). Ren-Jang Lin,2008

Laboratory Methods in Enzymology: Protein Part B,2014-02-24 Laboratory Methods in Enzymology Protein Part B brings together a number of core protocols concentrating on protein carefully written and edited by experts Indispensable tool for the researcher Carefully written and edited by experts to contain step by step protocols In this volume we have brought together a number of core protocols concentrating on protein *Mass Spectrometry of Proteins and Peptides* John R. Chapman,2008-02-05 Little more than three years down the line and I am already writing the Preface to a second volume to follow Protein and Peptide Analysis by Mass What has happened in between these times to make this second venture worthwhile New types of mass spectrometric instrumentation have appeared so that new techniques have become possible and existing techniques have become much more feasible More particularly however the newer ionization techniques introduced for the analysis of high molecular weight materials have now been thoroughly used and studied As a result there has been an enormous improvement in the associated sample handling technology so that these methods are now routinely applied to much smaller sample amounts as well as to more intractable samples Again this particular community of mass spectrometry users has both increased in number and diversified And riding this wave of acceptance leaders in the field have set their sights on more complex problems molecular interaction ion structures quantitation and kinetics are just a few of the newer areas reported in Mass Spectrometry of Proteins and Peptides As with the first volume one purpose of this collection Mass Spectrometry of Proteins and Peptides is to show the reader what can be done by the application of mass spectrometry and perhaps even to encourage the reader to venture down new paths **Protein Interactions** Volkhard Helms,Olga V. Kalinina,2022-11-08 Protein Interactions A fundamental guide to the burgeoning field of protein interactions From enzymes to transcription factors to cell membrane receptors proteins are at the heart of biological cell function Virtually all cellular processes are governed by their interactions with one another with cell bodies with DNA or with small molecules The systematic study of these interactions is called Interactomics and research within this new field promises to shape the future of molecular cell biology Protein Interactions goes beyond any existing guide to protein interactions presenting the first truly comprehensive overview of the field Edited by two leading scholars in the field of protein bioinformatics this book covers all

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Flavoprotein Protocols Steven K. Chapman, Graeme A. Reid, 2008-02-03 As a scientist with an interest in proteins you will at some time in your career isolate an enzyme that turns out to be yellow or perhaps you already have Alternatively you may identify a polypeptide sequence that is related to known flavin containing proteins This may or may not be your first encounter with flavoproteins However even if you are an old hand in the field you may not have exploited the full range of experimental approaches applicable to the study of flavoproteins We hope that Flavoprotein Protocols will encourage you to do so In this volume we have sought to bring together a range of experimental methods of value to researchers with an interest in flavoproteins whether or not these researchers have experience in this area A broad range of techniques from the everyday to the more specialized is described by scientists who are experts in their fields and who have extensive practical experience with flavoproteins The wide range of approaches from wet chemistry to dry computation has as a consequence demanded a range of formats Where appropriate particularly for analytical methods the protocol described is laid out in easy to follow steps In other cases e g the more advanced spectroscopies and computational methods it is far more apt to describe the general approach and relevance of the methods We hope this wide ranging approach will sow the seeds of many future collaborations between laboratories and further our knowledge and understanding of how flavoproteins work

Post-transcriptional Regulation through Long Non-coding RNAs (lncRNAs) Michael Lodomery, Giuseppina Pisignano, 2021-08-18 This book is a collection of eight articles of which seven are reviews and one is a research paper that together form a Special Issue that describes the roles that long noncoding RNAs lncRNA play in gene regulation at a post transcriptional level

RNA Turnover in Eukaryotes: Analysis of Specialized and Quality Control RNA Decay Pathways Lynne E. Maquat, Megerditch Kiledjian, 2011-09-02 Specific complexes of protein and RNA carry out many essential biological functions including RNA processing RNA turnover and RNA folding as well as the translation of genetic information from mRNA into protein sequences Messenger RNA mRNA decay is now emerging as an important control point and a major contributor to gene expression Continuing identification of the protein factors and cofactors and mRNA instability elements responsible for mRNA decay allow researchers to build a comprehensive picture of the highly orchestrated processes involved in mRNA decay and its regulation Covers the nonsense mediated mRNA decay NMD or mRNA surveillance pathway Expert researchers introduce the most advanced technologies and techniques Offers step by

step lab instructions including necessary equipment and reagents

Differential Display Methods and Protocols Peng Liang, Jonathan Meade, Arthur B. Pardee, 2008-02-04 Since the first edition of this book dedicated to differential display DD technology was published in 1997 we have witnessed an explosive interest in studying differential gene expression The gene hunting euphoria was initially powered by the invention of DD which was gradually overtaken by DNA microarray technology in recent years Then why is there still the need for second edition of this DD book First of all DD still enjoys a substantial lead over DNA microarrays in the ISI citation data see Table 1 despite the hundreds of millions of dollars spent each year on arrays This may come as a surprise to many but to us it implies that many of the DNA microarray studies went unpublished owing to their unfulfilled promises 1 Second unlike DNA microarrays DD is an open ended gene discovery method that does not depend on prior genome sequence information of the organism being studied As such DD is applicable to the study of all living organisms from bacteria fungi insects fish plants to mammals even when their genomes are not sequenced Second DD is more accessible technically and financially to most cost conscious cottage industry academic laboratories So clearly DD still has its unique place in the modern molecular biological toolbox for gene expression analysis

Confocal Microscopy Stephen W. Paddock, 2008-02-03

HIV Protocols Vinayaka R. Prasad, Ganjam V. Kalpana, 2024-05-14 This fourth edition volume expands on the previous editions with discussions on the latest methodologies to study HIV live cell imaging HIV cure new modifications to the viral RNA that impacts HIV biology and new types of intracellular compartments The chapters in this book are organized into seven parts and cover topics such as HIV latency reactivation via single molecule RNA detection T cell responses new and efficacious anti HIV CAR T cells analysis of mucosal HIV infection analysis of 3D brain organoids to study neuro AIDS and the transfer of antibodies across the blood brain barrier Written in the highly successful Methods in Molecular Biology series format chapters include introductions to their respective topics lists of the necessary materials and reagents step by step readily reproducible laboratory protocols and tips on troubleshooting and avoiding known pitfalls Cutting edge and authoritative HIV Protocols Fourth Edition is a valuable resource for all preclinical HIV 1 researchers looking to learn more about this important and advancing field

Aptamers Selected by Cell-SELEX for Theranostics Weihong Tan, Xiaohong Fang, 2015-03-02 This edited volume describes cell SELEX as the fundamental tool used to generate aptamer molecules for a wide range of applications in molecular medicine bioanalysis and chemical biology Easily integrated into the natural heterogeneous cell matrix aptamers can be effectively used in theranostics bioanalysis environment detection and biomedical studies The book gathers reviews that reflect the latest advances in the field of aptamers and consists in fourteen chapters demonstrating essential examples of these aptamers and aptamer nanomaterial assemblies depending on the types of applications and biological systems It also includes a separate chapter on the utilization of aptamers in real clinics and what will be required to achieve this significant goal The book will be both appealing and useful to a broad audience including biologists bioscientists and clinicians whose interests range from chemistry and biomedical engineering

to cell and molecular biology and biotechnology Weihong Tan is a Distinguished Professor of Chemistry and Biomedical Engineering at Hunan University China and also a University of Florida Distinguished Professor and V T and Louis Jackson Professor of Chemistry at the University of Florida USA Xiaohong Fang is a Professor at the Institute of Chemistry Chinese Academy of Sciences China [Handbook of RNA Biochemistry](#) Roland K. Hartmann, Albrecht Bindereif, Astrid Schön, Eric Westhof, 2015-03-31 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 **Protein Structure, Stability, and Folding** Kenneth P. Murphy, 2008-02-04 In Protein Structure Stability and Folding Kenneth P. Murphy and a panel of internationally recognized investigators describe some of the newest experimental and theoretical methods for investigating these critical events and processes Among the techniques discussed are the many methods for calculating many of protein stability and dynamics from knowledge of the structure and for performing molecular dynamics simulations of protein unfolding New experimental approaches presented include the use of co solvents novel applications of hydrogen exchange techniques temperature jump methods for looking at folding events and new strategies for mutagenesis experiments Unique in its powerful combination of theory and practice Protein Structure Stability and Folding offers protein and biophysical chemists the means to gain a more comprehensive understanding of some of this complex area by detailing many of the major techniques in use today **Ribozymes and siRNA protocols** Mouldy Sioud, 2008-02-03 In this completely updated and expanded edition of a classic bench manual hands on experts take advantage of the latest advances in ribozyme DNAzyme hammerhead ribozymes and derivatives and RNA interference technologies to describe in detail the exciting and successful methods now available for gene inactivation in vitro and in vivo Their optimized techniques employ hairpin ribozymes DNAzymes hammerhead ribozymes and derivatives group I intron ribozymes RNase P ribozymes and siRNAs as well as general methods for RNA structure analysis delivery of oligonucleotides and gene therapy Also provided are novel methods for identifying accessible cellular mRNA sites group I intron and RNase P ribozyme protocols for effective design selection and therapeutic applications and the latest RNAi methods for sequence specific gene silencing in a wide variety of organisms Additional techniques cover the analysis of ribozyme structures and conformational transitions using nucleotide analog interference mapping and fluorescence resonance energy transfer the use of ribozymes in clinical and gene therapy and the use of ribozymes and DNAzymes in rodent models of human disease Each proven protocol includes a

background introduction outlining the principle behind the technique step by step instructions lists of equipment and reagents and tips on troubleshooting and avoiding known pitfalls Comprehensive and up to date Ribozymes and siRNA Protocols details for experienced and novice investigators alike the many exciting advances in our understanding of nucleic acid enzymes as well as demonstrating how they may be used to analyze gene function and target validation and to productively develop novel therapeutics for human diseases *Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing* Ana M. Aransay, José Luis Lavín Trueba, 2016-06-02 High throughput sequencing HTS technologies have conquered the genomics and epigenomics worlds The applications of HTS methods are wide and can be used to sequence everything from whole or partial genomes transcriptomes non coding RNAs ribosome profiling to single cell sequencing Having such diversity of alternatives there is a demand for information by research scientists without experience in HTS that need to choose the most suitable methodology or combination of platforms and to define their experimental designs to achieve their specific objectives *Field Guidelines for Genetic Experimental Designs in High Throughput Sequencing* aims to collect in a single volume all aspects that should be taken into account when HTS technologies are being incorporated into a research project and the reasons behind them Moreover examples of several successful strategies will be analyzed to make the point of the crucial features This book will be of use to all scientist that are unfamiliar with HTS and want to incorporate such technologies to their research *Structures of Large RNA Molecules and Their Complexes* ,2015-06-06 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 **RNA Processing** Steve J. Higgins, B. D. Hames, 1994 This two volume set provides detailed practical guidance on all major aspects of RNA processing Each procedure is clearly explained so that the reader can follow all of the key stages of a successful experimental investigation

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