

Methods in
Molecular Biology 1351

Springer Protocols

Matthew McKenzie *Editor*

Mitochondrial DNA

Methods and Protocols
Third Edition

 Humana Press

Mitochondrial Dna Methods And Protocols

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Mitochondrial Dna Methods And Protocols:

Mitochondrial DNA Thomas J. Nicholls, Jay P. Uhler, Maria Falkenberg, 2023-02-20 This volume compiles a comprehensive range of methods to study key aspects of mitochondrial DNA including nucleoid structure and packaging replication genome integrity and disease Chapters are organized into eight methodological sections that cover in vitro and in vivo methods including for mtDNA isolation visualization deep sequencing gene editing and diagnostic aspects of mtDNA disease Written in the format of the highly successful Methods in Molecular Biology series each chapter includes an introduction to the topic lists necessary materials and methods includes tips on troubleshooting and known pitfalls and step by step readily reproducible protocols Authoritative and cutting edge Mitochondrial DNA Methods and Protocols aims to be useful and informative for researchers and clinicians with an interest in mitochondrial DNA **Methods in Molecular**

Biology: Mitochondrial DNA: methods and protocols John M. Walker, 1984 Ancient DNA Beth Alison Shapiro, Michael Hofreiter, 2012-01-01 Ancient DNA presents an overview of the many of the protocols commonly used to study ancient DNA These include laboratory instructions extraction protocols laboratory techniques and suggestions for appropriate analytical approaches to make sense of the sequences obtained **Liposome Methods and Protocols** Subhash C. Basu, Manju

Basu, 2008-02-04 In vitro utilization of liposomes is now recognized as a powerful tool in many bioscience investigations and their associated clinical studies e g liposomes in drug targeting liposomes in gene transport across plasma and nuclear membranes liposomes in enzyme therapy in patients with genetic disorders However before these areas can be effectively explored many basic areas in liposome research require elucidation including a attachment of liposomes to cell surfaces b permeation of liposomes through the plasma membranes and c stability of liposomes in cell or nuclear matrices None of these areas have been exhaustively explored and liposome researchers have ample opportunities to contribute to our knowledge The aim of Liposome Methods and Protocols is to bring together a wide range of detailed laboratory protocols covering different aspects of liposome biology in order to assist researchers in those rapidly advancing medical fields mentioned earlier With this goal in mind in each protocol chapter we have detailed the materials to be used followed by a step by step protocol The Notes section of each protocol is also certain to prove particularly useful since the authors include troubleshooting tips straight from their benchtops valuable information that is seldom given in restricted methods sections of standard research journals For this reason we feel that the book will prove especially useful for all researchers in the liposome field *Superantigen Protocols* Teresa Krakauer, 2008-02-05 Leading researchers in the biological chemical and physical investigation of superantigens describe in step by step detail their best experimental techniques to assess the physical characteristics and biological effects of superantigens Their protocols range from those for investigating the interactions of superantigens with cellular receptors to those for the analysis of their immunological and biological effects including methods for using BIOcore to determine binding kinetics and establishing various lymphocyte cell culture systems

There are also accounts of such methods as the RNase protection assay cytokine ELISA FACS analysis and cytokine production at the single cell level

DNA Methylation Protocols Ken I. Mills, Bernie H. Ramsahoye, 2008-02-05 DNA Methylation Protocols offer a set of readily reproducible protocols of the analysis of DNA methylation and methylases These powerful methods provide the tools necessary for studying methylation at both the global level and the level of sequence and include many techniques for identifying genes that might be aberrantly methylated in cancer and aging Additional methods cover genome wide analysis of abnormal DNA methylation and the isolation and measurement of demethylases and related proteins

Biostatistical Methods Stephen W. Looney, 2008-02-03 Leading biostatisticians and biomedical researchers describe many of the key techniques used to solve commonly occurring data analytic problems in molecular biology and demonstrate how these methods can be used in the development of new markers for exposure to a risk factor or for disease outcomes Major areas of application include microarray analysis proteomic studies image quantitation genetic susceptibility and association evaluation of new biomarkers and power analysis and sample size

Transgenesis Techniques Alan R. Clarke, 2008-02-05 The past decade has witnessed a spectacular explosion in both the development and use of transgenic technologies Not only have these been used to aid our fundamental understanding of biologic mechanisms but they have also facilitated the development of a range of disease models that are now truly beginning to impact upon our approach to human disease Some of the most exciting model systems relate to neurodegenerative disease and cancer where the availability of appropriate models is at last allowing radically new therapies to be developed and tested This latter point is of particular significance given the current concerns of the wider public over both the use of animal models and the merits of using genetically modified organisms Arguably advances of the greatest significance have been made using mammalian systems driven by the advent of embryonic stem cell based strategies and more recently by cloning through nuclear transfer For this reason this new edition of Transgenesis Techniques focuses much more heavily on manipulation of the mammalian genome both in the general discussions and in the provision of specific protocols

Aging Methods and Protocols Yvonne A. Barnett, Christopher R. Barnett, 2008-02-01 Aging is an almost universal process within biological systems one which leads to a decline in functional capacity disease onset and eventually death There has been much interest in recent years to elucidate the molecular mechanisms that underlie the aging process Many theories have been proposed since the last century that aim to explain the causes of aging There is no one theory that completely satisfies the phenotype of aging but genetics and environmental factors play an important role in the etiology of age related pathologies and the aging process However there is still much to be learned about the aging process which has been termed one of the last great frontiers in biology Demographic changes worldwide are leading to increased average life expectancies within our populations These changes in population characteristics will impact upon the economies of the supporting society with increasing healthcare and infrastructural costs arising from the prevalence of age related pathologies and other physical disabilities associated with advancing years Many

researchers worldwide are working in the attempt to identify key cellular processes through which it might one day be possible to slow down the aging process and thus increase the health span of humans. Numerous research projects from the cellular through to tissue organ and whole organism studies are currently underway to investigate the multifactorial aging process.

Transgenic Mouse Methods and Protocols Marten H. Hofker, Jan van Deursen, 2008-02-04 Marten Hofker and Jan van Deursen have assembled a multidisciplinary collection of readily reproducible methods for working with mice and particularly for generating mouse models that will enable us to better understand gene function. Described in step by step detail by highly experienced investigators these proven techniques include new methods for conditional induced knockout and transgenic mice as well as for working with mice in such important research areas as immunology cancer and atherosclerosis. Such alternative strategies as random mutagenesis and viral gene transduction for studying gene function in the mouse are also presented.

In Vitro Mutagenesis Protocols Jeff Braman, 2008-02-05 Hands on researchers with proven track records describe in stepwise fashion their advanced mutagenesis techniques. The contributors focus on improvements to conventional site directed mutagenesis including a chapter on chemical site directed mutagenesis PCR based mutagenesis and the modifications that allow high throughput mutagenesis experiments and mutagenesis based on gene disruption both in vitro and in situ based. Additional methods are provided for in vitro gene evolution for gene disruption based on recombination transposon and cassette mutagenesis and for facilitating the introduction of multiple mutations. Time tested and highly practical the protocols in *In Vitro Mutagenesis Protocols* 2nd Edition offer today's molecular biologists reliable and powerful techniques with which to illuminate the proteome.

GTPase Protocols Ed Manser, Thomas Leung, 2008-02-03 In the last 10 years researchers have firmly established key roles for Ras related GTPases in almost every aspect of cell biology. In the 1980s the proto-oncogene Ras itself was the focus of interest though in the 1990s this shifted to the increasing variety of Ras related proteins. In this new decade much yet needs to be done to establish the role for all the small GTPases now uncovered by the human genome project. In particular these GTPases need to be understood in the appropriate biochemical and cellular contexts. In the process of trying to uncover the role of these versatile proteins a variety of novel techniques and methodologies has been developed. These now enable investigators to move easily within a diversity of fields ranging from structural studies to real time in vivo analysis of a GTPase. In recognition of the need for access to key background methodologies *GTPase Protocols* The Ras Superfamily is devoted to techniques that are presently widely used and that will continue to be the standard for researchers worldwide. Each chapter is aimed at supplying detailed methodologies to allow reproduction in any laboratory while also providing the general principles on which the methods are based. Some of the techniques grouped in the first section apply broadly to small GTPases whereas others in Part II are more applicable within each GTPase subfamily.

Calcium-Binding Protein Protocols Hans J. Vogel, 2008-02-04 Calcium plays an important role in a wide variety of biological processes. This divalent metal ion can bind to a large number of proteins by doing so it modifies

their biological activity or their stability Because of its distinct chemical properties calcium is uniquely suited to act as an on off switch or as a light dimmer of biological activities The two books entitled *Calcium Binding Protein Protocols Volumes I and II* focus on modern experimental analyses and methodologies for the study of calcium binding proteins Both extracellular and intracellular calcium binding proteins are discussed in detail However proteins involved in calcium handling e.g calcium pumps and calcium channels fall outside of the scope of these two volumes Also calcium binding proteins involved in bone deposition will not be discussed as this specific topic has been addressed previously The focus of these two books is on studies of the calcium binding proteins and their behavior in vitro and in vivo The primary emphasis is on protein chemistry and biophysical methods Many of the methods described will also be applicable to proteins that do not bind calcium *Calcium Binding Protein Protocols* is divided into three main sections The section entitled *Introduction and Reviews* provides information on the role of calcium in intracellular secondary messenger activation mechanisms Moreover unique aspects of calcium chemistry and the utilization of calcium in dairy proteins as well as calcium binding proteins involved in blood clotting are addressed Mitochondrial DNA William C. Copeland, 2008-02-04 *MHC Protocols* Stephen H. Powis, Robert W. Vaughan, 2008-02-05 The aim of *MHC Protocols* is to document protocols that can be used for the analysis of genetic variation within the human major histocompatibility complex MHC HLA region The human MHC encompasses approximately 4 million base pairs on the short arm of chromosome 6 at cytogenetic location 6p21.3 The region is divided into three subregions The telomeric class I region contains the genes that encode the HLA class I molecules HLA A B and C The centromeric class II region contains the genes encoding the HLA class II molecules HLA DR DQ and DP In between is the class III region originally identified because it contains genes encoding components of the complement pathway The entire human MHC has recently been sequenced and each subregion is now known to contain many other genes a number of which have immunological functions The study of polymorphism within the MHC is well established because the region contains the highly polymorphic HLA genes HLA polymorphism has been used extensively in solid organ and bone marrow transplantation to match donors and recipients As a result large numbers of HLA alleles have been identified a process that has been further driven by recent interest in HLA gene diversity in ethnic populations The extreme genetic variation in HLA genes is believed to have been driven by the evolutionary response to infectious agents but relatively few studies have analyzed associations between HLA genetic variation and infectious disease which has been difficult to demonstrate

RT-PCR Protocols Nicola King, Joe O'Connell, 2008-02-04 Until the mid 1980s the detection and quantification of a specific mRNA was a difficult task usually only undertaken by a skilled molecular biologist With the advent of PCR it became possible to amplify specific mRNA after first converting the mRNA to cDNA via reverse transcriptase The arrival of this technique termed reverse transcription PCR RT-PCR meant that mRNA suddenly became amenable to rapid and sensitive analysis without the need for advanced training in molecular biology This new accessibility of mRNA which has been

facilitated by the rapid accumulation of sequence data for human mRNAs means that every biomedical researcher can now include measurement of specific mRNA expression as a routine component of his/her research plans. In view of the ubiquity of the use of standard RT-PCR, the main objective of RT-PCR Protocols is essentially to provide novel useful applications of RT-PCR. These include some useful adaptations and applications that could be relevant to the wider research community who are already familiar with the basic RT-PCR protocol. For example, a variety of different adaptations are described that have been employed to obtain quantitative data from RT-PCR. Quantitative RT-PCR provides the ability to accurately measure changes in mRNA expression between normal and diseased tissues.

Oxidative Stress Biomarkers and Antioxidant Protocols Donald Armstrong, 2008-02-04 The first protocols book *Free Radical and Antioxidant Protocols 1* was published in late 1998. Sections were divided into three parts covering selected biochemical techniques for measuring oxidative stress, antioxidant (AOX) activity and combined applications. In choosing the 40 methods to be included in that book, I realized there were considerably more of equal value than that which we could have presented in a single volume. To produce a comprehensive resource, this book and a third are being compiled to expand coverage of the field. A summary of papers published on this important subject emphasizes the continuing rapid growth in oxidative stress investigations relating to our understanding of biochemical reactions, their relevance to pathophysiological mechanisms, how disease may arise and how therapeutic intervention may be achieved. Although there is some overlap between the categories, the analysis shown below illustrates where current studies are concentrated and are almost evenly distributed between free radicals and AOX. Over the last 4 yr, there has been a 55% increase in the number of papers published in the area.

Functional Genomics Michael J. Brownstein, Arkady Khodursky, 2008-02-03 This collection of robust, readily reproducible methods for microarray-based studies includes expert guidance in the optimal data analysis and informatics. On the methods side, are proven techniques for monitoring subcellular RNA localization en masse, for mapping chromosomes at the resolution of a single gene and for surveying the steady-state genome-wide distribution of DNA-binding proteins in vivo. For those workers dealing with massive data sets, the book discusses the methodological aspects of data analysis and informatics in the design of microarray experiments, the choice of test statistic and the assessment of observational significance, data reduction and clustering.

Protein Sequencing Protocols Bryan John Smith, 2008-02-02 Determination of the protein sequence is as important today as it was a half century ago, even though the techniques and purposes have changed over time. Mass spectrometry has continued its recent rapid development to find notable application in the characterization of small amounts of protein, for example in the field of proteomics. The traditional chemical N-terminal sequencing is still of great value in quality assurance of the increasing number of biopharmaceuticals that are to be found in the clinic, checking processing events of recombinant proteins and so on. It is joined in the armory of methods of protein analysis by such techniques as C-terminal sequencing and amino acid analysis. These methods are continually developing. The first edition of *Protein Sequencing Protocols* was a

snapshot of methods in use in protein biochemistry laboratories at the time and this the second edition is likewise Methods have evolved in the intervening period and the content of this book has similarly changed the content of some chapters having been superseded and replaced by other approaches Thus in this edition there is inclusion of approaches to validation of methods for quality assurance work reflecting the current importance of biopharmaceuticals and also a guide to further analysis of protein sequence information acknowledging the importance of bioinformatics Tumor Suppressor Genes Wafik S. El-Deiry, 2008-02-03 It has become clear that tumors result from excessive cell proliferation and a corresponding reduction in cell death caused by the successive accumulation of mutations in key regulatory target genes over time During the 1980s a number of oncogenes were characterized whereas from the 1990s to the present the emphasis has shifted to tumor suppressor genes TSGs It has become clear that oncogenes and TSGs function in the same pathways providing positive and negative growth regulatory activities The signaling pathways controlled by these genes involve virtually every process in cell biology including nuclear events cell cycle cell death cytoskeletal cell membrane angiogenesis and cell adhesion effects Mutations in tumor suppressor genes have been identified in familial cancer syndromes and the same genes in many cases have been found to be mutationally inactivated in sporadically occurring cancers In their normal state TSGs control cancer development and progression as well as contribute to the sensitivity of cancers to a variety of therapeutics Understanding the classes of TSGs the biochemical pathways they function in and how they are regulated provides an essential lesson in cancer biology We cannot hope to advance our current knowledge and to develop new and more effective therapies without understanding the relevant pathways and how they influence the present approaches to therapy Moreover it is important to be able to access not only the powerful tools now available to discover these genes but also their links to cell biology and growth control

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