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Molecular Biology of the Cell **The Phylogenetic Handbook** DNA'Protein Interactions **Protein-Nucleic Acid Interactions Genetic Manipulation of DNA and Protein** DNA-Protein Interactions **Protein-Based Inheritance Genetic Engineering of DNA and Protein Cell-Free Protein Synthesis DNA and Protein Sequence Analysis** Analytics of Protein-DNA Interactions **DNA Helicases and DNA Motor Proteins** *DNA* The Inside Story Sequence — Evolution — Function **Cell Biology by the Numbers Biophysics of DNA-Protein Interactions Establishment and Application of Methods for the Detection of DNA and Protein Adducts from Tobacco Specific Nitrosamines and Benzo(a)pyrene** TET Proteins and DNA Demethylation **Studies on DNA-protein Interactions of Phages P2 and P4 A Laboratory Guide to In Vitro Studies of Protein-DNA Interactions** *DNA-protein Interactions* **Progress in Nonhistone Protein Research** *Proteins Involved in DNA Replication* Introduction to Protein-DNA Interactions Biophysics of DNA-Protein Interactions **Biophysics of DNA-Protein Interactions Single Stranded DNA Binding Proteins Protein Bioinformatics** *The DNA, RNA, and Histone Methylomes* **Roles for the Drosophila Ku and DNA-dependent Protein Kinase in P Element Transposition Mapping Protein-protein and Protein-DNA Interactions Using a Cysteine-tethered Cleavage Probe (FeBABE) Electrophoresis in Practice A Laboratory Guide to in Vitro Studies of Protein-DNA Interactions** A Laboratory Guide for in Vivo Studies of DNA Methylation and Protein/DNA Interactions **Interaction of Adenoviral Core Proteins with DNA Fundmental Processes. DNA to RNA to Protein Association of DNA-bound Proteins in Controlling Initiation of Transcription The Double Helix Automation in Proteomics and Genomics**

DNA-protein Interactions Jan 07 2021 DNA-Protein Interactions describes methods for investigating how proteins interact with DNA. It should be especially useful for investigators studying gene expression and its relation to chromatin structure.

DNA'Protein Interactions Aug 26 2022 Dr. Tom Moss assembles the new standard collection of cutting-edge techniques to identify key protein-DNA interactions and define their components, their manner of interaction, and their manner of function, both in the cell and in the test tube. The techniques span a wide range, from factor identification to atomic detail, and include multiple DNA footprinting analyses, including in vivo strategies, gel shift (EMSA) optimization, SELEX, surface plasmon resonance, site-specific DNA-protein crosslinking, and UV laser crosslinking. Comprehensive and broad ranging, DNA-Protein Interactions: Principles and Protocols, 2nd Edition, offers a stellar array of over 100 up-to-date and readily reproducible techniques that biochemists and molecular, cellular, and developmental biologists can use successfully today to understand DNA-protein interactions.

DNA Oct 16 2021

Single Stranded DNA Binding Proteins Jul 01 2020 This volume provides a comprehensive set of protocols that can be used by any research lab to investigate diverse functional and structural properties of Single Stranded DNA Binding Proteins (SSBs) from eubacterial, archaeal, eukaryotic, mitochondrial and viral systems. 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. Authoritative and cutting-edge, Single Stranded DNA Binding Proteins aims to be a useful practical guide to researchers to help further their study in this field.

Interaction of Adenoviral Core Proteins with DNA Oct 24 2019

Automation in Proteomics and Genomics Jun 19 2019 In the last decade DNA sequencing costs have decreased over a magnitude, largely because of increasing throughput by incremental advances in tools, technologies and process improvements. Further cost reductions in this and in related proteomics technologies are expected as a result of the development of new high-throughput techniques and the computational machinery needed to analyze data generated. Automation in Proteomics & Genomics: An Engineering Case-Based Approach describes the automation technology currently in the areas of analysis, design, and integration, as well as providing basic biology concepts behind proteomics and genomics. The book also discusses the current technological limitations that can be viewed as an emerging market rather than a research bottleneck. Topics covered include: molecular biology fundamentals: from ‘blueprint’ (DNA) to ‘task list’ (RNA) to ‘molecular machine’ (protein); proteomics methods and technologies; modelling protein networks and interactions analysis via automation: DNA sequencing; microarrays and other parallelization technologies; protein characterization and identification; protein interaction and gene regulatory networks design via automation: DNA synthesis; RNA by design; building protein libraries; synthetic networks integration: multiple modalities; computational and experimental methods; trends in automation for genomics and proteomics new enabling technologies and future applications Automation in Proteomics & Genomics: An Engineering Case-Based Approach is an essential guide to the current capabilities and challenges of high-throughput analysis of genes and proteins for bioinformaticians, engineers, chemists, and biologists interested in developing a cross-discipline problem-solving based approach to systems biology.

DNA Helicases and DNA Motor Proteins Nov 17 2021 In recent years, a number of groundbreaking structural and mechanistic studies deepened our understanding of helicase mechanisms and established new approaches for their analyses. Many fundamental mechanistic questions ranging from the mechanism of force generation, mechanochemical coupling to distinct mechanisms by which the same enzyme translocates on DNA removing obstacles, unwinds DNA and/or remodels nucleoprotein complexes, however, remain to be answered. It is even less understood how the helicase motors are incorporated into a wide range of genome maintenance and repair machines. The field has reached a stage when the studies of molecular mechanisms and basic biology of helicases can and shall be integrated with the studies of development, cancer and longevity. The objective of this book is to provide the first systematic overview of structure, function and regulation of DNA helicases and related molecular motors. By integrating the knowledge obtained through the diverse technical approaches ranging from single-molecule biophysics to cellular and molecular biological studies the editors aim to provide a unified view on how helicases function in the cell, are regulated in response to different cellular stresses and are integrated into large macromolecular assemblies to form a complex and adaptive living system.

Genetic Engineering of DNA and Protein Mar 21 2022 This book provides readers with research works on worldwide discussions on the topic of latest molecular genetics. There are two approaches of every research work published in this book; first, to make the research chapters understandable to majority of readers and second, to describe the genetic tools and pathways used in research. The one fact mostly highlighted is the necessity of genetic insight in solving an issue. This book will prove to be an interesting read to those interested in genetic discoveries because of its structure, which has been made with a view point of attracting readers and familiarizing them with genetic approaches.

The Phylogenetic Handbook Sep 27 2022 Sample Text

Fundmental Processes. DNA to RNA to Protein Sep 22 2019 Research Paper (postgraduate) from the year 2014 in the subject Biology - Genetics / Gene Technology, , language: English, abstract: The biological living systems contain large number of fundamental processes that control the system. The components present in the system are interlinked and forms network of interactions. The molecules in the systems perform functional relationships that process the mechanisms based on the structural and functional aspects.

Introduction to Protein-DNA Interactions Oct 04 2020 One of the foundations of molecular biology is how the interactions of proteins with DNA control many aspects of gene expression. Since the mid-20th century discoveries of the lac repressor and operator and the competition between the cI and cro proteins for the same segment of DNA, we have learned an enormous amount about the interactions of proteins with DNA and their control

of fundamental processes in the cell. Introduction to Protein-DNA Interactions: Structure, Thermodynamics, and Bioinformatics describes what we know about protein-DNA interactions from the complementary perspectives of molecular and structural biology and bioinformatics and how each perspective informs the others. A particular emphasis is on how insights from experimental work can be translated into specific computational approaches to create unified view of the field and a fuller understanding of protein-DNA interactions.

Protein Bioinformatics May 31 2020 Features: --

Roles for the Drosophila Ku and DNA-dependent Protein Kinase in P Element Transposition Mar 29 2020

Analytics of Protein-DNA Interactions Dec 18 2021 With contributions by numerous experts

DNA and Protein Sequence Analysis Jan 19 2022 In recent years, the volume of nucleic acid and protein sequence generated by researchers has become a flood. Sequence databases have proliferated and good software for sequence analysis has become an absolute necessity. DNA and Protein Sequence Analysis: A Practical Approach provides clear and reasoned practical guidance in the analysis of sequence data and identifies the many pitfalls of interpreting data. The book begins with an overview of molecular biology databases and how to use them. The rest of the book is devoted to a critical appraisal of the software for sequence analysis, what software is available, and how to use it. DNA and Protein Sequence Analysis: A Practical Approach is an essential manual for all researchers in molecular biology and a valuable guide for advanced undergraduates. It will also be indispensable to computer scientists interested in bioinformatics.

Electrophoresis in Practice Jan 27 2020 This fifth edition of the successful, long-selling classic has been completely revised and expanded, omitting some topics on obsolete DNA electrophoresis, but now with a completely new section on electrophoretic micro-methods and on-the-chip electrophoresis. The text is geared towards advanced students and professionals and contains extended background sections, protocols and a trouble-shooting section. It is now also backed by a supplementary website providing all the figures for teaching purposes, as well as a selection of animated figures tested in many workshops to explain the underlying principles of the different electrophoretic methods.

Protein-Based Inheritance Apr 22 2022 This book covers a topic that has been neglected for years and has returned to the spotlight only recently. Until the genetic role of DNA was firmly established, many researchers suspected that proteins, rather than nucleic acids, could be carriers of heritable information. However, these models were completely forgotten with the triumphal march of the double helix and the development of a central dogma postulating that information flow occurs strictly from DNA, through RNA, to protein, making it seemingly impossible for the proteins to possess a coding potential. Proteins were downgraded to the role of simple perpetuators and executors of DNA orders. Taken together, data included in this book prove beyond a reasonable doubt that proteins and multiprotein complexes are able to control heritable traits, and that, at least in some examples, this control occurs in a template-like fashion, so that new structures strictly reproduce patterns of pre-existing structures that were not specifically coded in DNA. Thus, protein-based inheritance has left the area of speculation and has emerged as a new topic amenable to high-quality experimental analysis.

The Double Helix Jul 21 2019 The classic personal account of Watson and Crick’s groundbreaking discovery of the structure of DNA, now with an introduction by Sylvia Nasar, author of A Beautiful Mind. By identifying the structure of DNA, the molecule of life, Francis Crick and James Watson revolutionized biochemistry and won themselves a Nobel Prize. At the time, Watson was only twenty-four, a young scientist hungry to make his mark. His uncompromisingly honest account of the heady days of their thrilling sprint against other world-class researchers to solve one of science’s greatest mysteries gives a dazzlingly clear picture of a world of brilliant scientists with great gifts, very human ambitions, and bitter rivalries. With humility unspoiled by false modesty, Watson relates his and Crick’s desperate efforts to beat Linus Pauling to the Holy Grail of life sciences, the identification of the basic building block of life. Never has a scientist been so truthful in capturing in words the flavor of his work.

Biophysics of DNA-Protein Interactions Jun 12 2021 Depite the rapid expansion of the field of biophysics, there are very few books that comprehensively treat specific topics in this area. Recently, the field of single molecule biophysics has developed very quickly, and a few books specifically treating single molecule methods are beginning to appear. However, the promise of single molecule biophysics is to contribute to the understanding of specific fields of biology using new methods. This book would focus on the specific topic of the biophysics of DNA-protein interactions, and would include the use of new approaches, including both bulk methods as well as single molecule methods. This would make the book attractive to anyone working in the general area of DNA-protein interactions, which is of course a much wider market than just single molecule biophysicists or even biophysicists. The subject of the book will be the biophysics of DNA-protein interactions, and will include new methods and results that describe the physical mechanism by which proteins interact with DNA. For example, there has been much recent work on the mechanism by which proteins search for specific binding sites on DNA. A few chapters will be devoted to experiments and theory that shed light on this important problem. We will also cover proteins that alter DNA properties to facilitate interactions important for transcription or replication. Another section of the book will cover the biophysical mechanism by which motor proteins interact with DNA. Finally, we will cover larger protein-DNA complexes, such as replication forks, recombination complexes, DNA repair interactions, and their chromatin context.

Association of DNA-bound Proteins in Controlling Initiation of Transcription Aug 22 2019

Establishment and Application of Methods for the Detection of DNA and Protein Adducts from Tobacco Specific Nitrosamines and Benzo(a)pyrene May 11 2021

The Inside Story Sep 15 2021

Proteins Involved in DNA Replication Nov 05 2020 This book collects the Proceedings of a workshop sponsored by the European Molecular Biology Organization (EMBO) entitled "Pro teins Involved in DNA Replication" which was held September 19 to 23,1983 at Vitznau, near Lucerne, in Switzerland. The aim of this workshop was to review and discuss the status of our knowledge on the intricate array of enzymes and proteins that allow the replication of the DNA. Since the first discovery of a DNA polymerase in Escherichia coli by Arthur Kornberg twenty eight years ago, a great number of enzymes and other proteins were des cribed that are essential for this process: different DNA poly merases, DNA primases, DNA dependent ATPases, helicases, DNA liga ses, DNA topoisomerases, exo- and endonucleases, DNA binding pro teins and others. They are required for the initiation of a round of synthesis at each replication origin, for the progress of the growing fork, for the disentanglement of the replication product, or for assuring the fidelity of the replication process. The number, variety and ways in which these proteins inter act with DNA and with each other to the achievement of replication and to the maintenance of the physiological structure of the chromo somes is the subject of the contributions collected in this volume. The presentations and discussions during this workshop reinforced the view that DNA replication in vivo can only be achieved through the cooperation of a high number of enzymes, proteins and other cofactors.

Biophysics of DNA-Protein Interactions Aug 02 2020 Depite the rapid expansion of the field of biophysics, there are very few books that comprehensively treat specific topics in this area. Recently, the field of single molecule biophysics has developed very quickly, and a few books specifically treating single molecule methods are beginning to appear. However, the promise of single molecule biophysics is to contribute to the understanding of specific fields of biology using new methods. This book would focus on the specific topic of the biophysics of DNA-protein interactions, and would include the use of new approaches, including both bulk methods as well as single molecule methods. This would make the book attractive to anyone working in the general area of DNA-protein interactions, which is of course a much wider market than just single molecule biophysicists or even biophysicists. The subject of the book will be the biophysics of DNA-protein interactions, and will include new methods and results that describe the physical mechanism by which proteins interact with DNA. For example, there has been much recent work on the mechanism by which proteins search for specific binding sites on DNA. A few chapters will be devoted to experiments and theory that shed light on this important problem. We will also cover proteins that alter DNA properties to facilitate interactions important for transcription or replication. Another section of the book will cover the biophysical mechanism by which motor proteins interact with DNA. Finally, we will cover larger protein-DNA complexes, such as replication forks, recombination complexes, DNA repair interactions, and their chromatin context.

TET Proteins and DNA Demethylation Apr 10 2021 This volume explores the latest methods used to study various aspects of TET proteins and their

biology. Chapters in this book are divided into five parts. Part One describes technologies aimed at detecting and quantifying DNA methylation turnover using massively parallel sequencing, ELISA, and mass spectrometry approaches. Part Two looks at data analyses protocols for distinguishing acting versus passive DNA demethylation and estimation of 5mC and 5hmC levels. Part Three deals with a new topic that takes advantage of modified CRISPR/Cas9 genome editing systems to target DNA demethylation activity to genomic loci of interest. Part Four discusses protocols that detail how to purify TET proteins and unravel their protein interactions, and Part Five looks at the assessment of TET protein function and activity in vivo and in vitro. 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 thorough, TET Proteins and DNA Demethylation: Methods and Protocols is a valuable resource that aims to help research scientists at all levels working in the fields of DNA demethylation dynamics. Chapters 3, 7 and 17 are available open access under a Creative Commons Attribution 4.0 International License via link.springer.com.

Cell Biology by the Numbers Jul 13 2021 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

Cell-Free Protein Synthesis Feb 20 2022 Cell-free protein expression promises to narrow the technological gap between DNA and protein technologies and provide a platform for broad application of synthetic biology principles in the Life Sciences. It is a rapid and high throughput methodology for the conversion of DNA encoded genetic information into protein-mediated biochemical activities. Cell-Free Protein Synthesis: Methods and Protocols brings together the key opinion leaders of cell-free technology development and provides case studies and detailed protocols for the application of cell-free methodology. Chapters cover the main directions in the development of cell-free technologies including several recently developed cell-free systems, as well as a number of applications of cell-free systems ranging from discovery of biofuel enzymes to in vitro assembly of viruses. Written in the 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 protocols, and notes on troubleshooting and avoiding known pitfalls. Authoritative and easily accessible, Cell-Free Protein Synthesis: Methods and Protocols seeks to serve a wide variety of scientists with its well-honed methodologies.

A Laboratory Guide to in Vitro Studies of Protein-DNA Interactions Dec 26 2019

Protein-Nucleic Acid Interactions Jul 25 2022 The structural biology of protein-nucleic acid interactions is in some ways a mature field and in others in its infancy. High-resolution structures of protein-DNA complexes have been studied since the mid 1980s and a vast array of such structures has now been determined, but surprising and novel structures still appear quite frequently. High-resolution structures of protein-RNA complexes were relatively rare until the last decade. Propelled by advances in technology as well as the realization of RNA's importance to biology, the number of example structures has ballooned in recent years. New insights are now being gained from comparative studies only recently made possible due to the size of the database, as well as from careful biochemical and biophysical studies. As a result of the explosion of research in this area, it is no longer possible to write a comprehensive review. Instead, current review articles tend to focus on particular subtopics of interest. This makes it difficult for newcomers to the field to attain a solid understanding of the basics. One goal of this book is therefore to provide in-depth discussions of the fundamental principles of protein-nucleic acid interactions as well as to illustrate those fundamentals with up-to-date and fascinating examples for those who already possess some familiarity with the field. The book also aims to bridge the gap between the DNA- and the RNA- views of nucleic acid - protein recognition, which are often treated as separate fields. However, this is a false dichotomy because protein - DNA and protein - RNA interactions share many general principles. This book therefore includes relevant examples from both sides, and frames discussions of the fundamentals in terms that are relevant to both. The monograph approaches the study of protein-nucleic acid interactions in two distinctive ways. First, DNA-protein and RNA-protein interactions are presented together. Second, the first half of the book develops the principles of protein-nucleic acid recognition, whereas the second half applies these to more specialized topics. Both halves are illustrated with important real life examples. The first half of the book develops fundamental principles necessary to understand function. An introductory chapter by the editors reviews the basics of nucleic acid structure. Jen-Jacobsen and Jacobsen discuss how solvent interactions play an important role in recognition, illustrated with extensive thermodynamic data on restriction enzymes. Marmorstein and Hong introduce the zoology of the DNA binding domains found in transcription factors, and describe the combinational recognition strategies used by many multiprotein eukaryotic complexes. Two chapters discuss indirect readout of DNA sequence in detail: Berman and Lawson explain the basic principles and illustrate them with in-depth studies of CAP, while in their chapter on DNA bending and compaction Johnson, Stella and Heiss highlight the intrinsic connections between DNA bending and indirect readout. Horvath lays out the fundamentals of protein recognition of single stranded DNA and single stranded RNA, and describes how they apply in a detailed analysis of telomere end binding proteins. Nucleic acids adopt more complex structures - Lilley describes the conformational properties of helical junctions, and how proteins recognize and cleave them. Because RNA readily folds due to the stabilizing role of its 2'-hydroxyl groups, Li discusses how proteins recognize different RNA folds, which include duplex RNA. With the fundamentals laid out, discussion turns to more specialized examples taken from important aspects of nucleic acid metabolism. Schroeder discusses how proteins chaperone RNA by rearranging its structure into a functional form. Berger and Dong discuss how topoisomerases alter the topology of DNA and relieve the superhelical tension introduced by other processes such as replication and transcription. Dyda and Hickman show how DNA transposes mediate genetic mobility and Van Duyne discusses how site-specific recombinases cut and paste DNA. Horton presents a comprehensive review of the structural families and chemical mechanisms of DNA nucleases, whereas Li in her discussion of RNA-protein recognition also covers RNA nucleases. Lastly, FerrÚ-D'AmarÚ shows how proteins recognize and modify RNA transcripts at specific sites. The book also emphasises the impact of structural biology on understanding how proteins interact with nucleic acids and it is intended for advanced students and established scientists wishing to broaden their horizons.

Studies on DNA-protein Interactions of Phages P2 and P4 Mar 09 2021

A Laboratory Guide for in Vivo Studies of DNA Methylation and Protein/DNA Interactions Nov 24 2019 A Safety Considerations Genomie sequencing involves a number oj hazard ous steps, such as high eurrent, high voltage, radioaetive and highly toxie chemieals. It is, the- jore, absolutely essential that the instruetions oj equipment manu/aeturers bejollowed and that par tieular attention is paid to the loeal and jederal safety regulations. I Introduction 13 B Introduction Hypomethylation ofDNA has been positively correlated with thc activation of many eucaryotic genes. During the transition from inactive to active genes changes in the protein/DNA interaction pattern occur. Tran scriptional activation of eucaryotic genes is mediated by specific interac tions oftransacting factors with their respective DNA binding sites in Lhe control regions (promoters, enhancers) ofthe genes. This process is ofLen accompanied by changes in local chromatin strucLure, witnessed by the appearance of nuclease hypersensitive sites, as weil as by changes in protein-DNA interactions and, in the case of higher eucaryotes, alterations ofthe cytosine methylation pattern. The sole available experimental tech nique that permits the study ofthe latter phenomena at single nucleotide resolution is direct genomic sequencing/footprinting, pioneered by Church and Gilbert (1984). This method combines the chemical DNA sequencing procedure of Maxam amI Gilbert (1980) with thc detection 01' DNA sequences by electroblotting and indirect end-Iabeling by hybridiza tl0n. An alternative possibility is the novel procedure (Saluz and . lost, 1989), using Taq polymerase. The first steps 01' both meLhods are essen tially the same: total genomic DNA is digested wiLh a suilable restriction enzyme and the resulting DNA fragments are chemically sequeneed.

Biophysics of DNA-Protein Interactions Sep 03 2020 Depite the rapid expansion of the field of biophysics, there are very few books that comprehensively treat specific topics in this area. Recently, the field of single molecule biophysics has developed very quickly, and a few books specifically treating single molecule methods are beginning to appear. However, the promise of single molecule biophysics is to contribute to the understanding of specific fields of biology using new methods. This book would focus on the specific topic of the biophysics of DNA-protein interactions, and would include the use of new approaches, including both bulk methods as well as single molecule methods. This would make the

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DNA-Protein Interactions May 23 2022 Our understanding of the mechanisms regulating gene expression, which determine the patterns of growth and development in all living organisms, ultimately involves the elucidation of the detailed and dy namic interactions of proteins with nucleic acids - both DNA and RNA. Until recently the commonly presented view of the DNA double helix as visualized on the covers of many textbooks and journals - was as a monotonous static straight rod incapable in its own right of directing the processes necessary for the conservation and selective reading of genetic information. This view, although perhaps extreme, was reinforced by the necessary linearity of genetic maps. The reality is that the biological functions of both DNA and RNA are dependent on complex, and sometimes transient, three-dimensional nucleoprotein structures in which genetically distant elements are brought into close spatial proximity. It is in such structures that the enzymatic manipulation of DNA in the essential biological processes as DNA replication, transcription and recombination are effected - the complexes are the mediators of the 'DNA transactions' of Hatch Echols.

Genetic Manipulation of DNA and Protein Jun 24 2022 This diverse collection of research articles is united by the enormous power of modern molecular genetics. Every author accomplished two objectives: (1) making the field and the research described accessible to a large audience and (2) explaining fully the genetic tools and approaches that were used in the research. One fact stands out - the importance of a genetic approach to addressing a problem. I encourage you to read several chapters. You will feel the excitement of the scientists, and you will learn about an area of research with which you may not be familiar. Perhaps most importantly, you will understand the genetic approaches; and you will appreciate their importance to the research.

A Laboratory Guide to In Vitro Studies of Protein-DNA Interactions Feb 08 2021 A Safety Considerations Many techniques described here involve a number of hazards, such as high electrical current and voltage, radioactivity and highly toxic chemicals. It is absolutely essential that the instructions of equipment manufacturers be followed, and that particular attention be paid to the local and federal safety regulations. B Introduction The expression of prokaryotic and eukaryotic genes has been shown most often to be regulated at the level of mRNA synthesis. Thanks to the rapid development of methods for dissecting DNA sequences, cis-acting regulatory elements such as promoters and enhancers have been recognised. More recently, the widely expressed intuition that discrete sequences within these elements constitute binding sites for sequence-specific binding proteins has been confirmed, especially through the use of "footprinting" assays (for examples, Galas and Schmitz, 1978). This and similar assays have already resulted in the recognition, isolation and analysis of DNA-bind ing proteins for several genes. Excellent reviews exist of the structural studies on these transcription regulatory proteins and related DNA elements (for example, Glover, 1989 and Johnson and McKnight, 1989), to which the reader is referred for detailed information. To set the scene for applications of the techniques described in this volume, only the barest outline of previous studies is presented here. Protein-DNA interactions are dependent on very specific tertiary configurations of the binding protein which allow the closest contact with the DNA helix.

The DNA, RNA, and Histone Methylomes Apr 29 2020 This book reviews the chemical, regulatory, and physiological mechanisms of protein arginine and lysine methyltransferases, as well as nucleic acid methylations and methylating enzymes. Protein and nucleic acid methylation play key and diverse roles in cellular signalling and regulating macromolecular cell functions. Protein arginine and lysine methyltransferases are the predominant enzymes that catalyse S-adenosylmethionine (SAM)-dependent methylation of protein substrates. These enzymes catalyse a nucleophilic substitution of a methyl group to an arginine or lysine side chain nitrogen (N) atom. Cells also have additional protein methyltransferases, which target other amino acids in peptidyl side chains or N-termini and C-termini, such as glutamate, glutamine, and histidine. All these protein methyltransferases use a similar mechanism. In contrast, nucleic acids (DNA and RNA) are substrates for methylating enzymes, which employ various chemical mechanisms to methylate nucleosides at nitrogen (N), oxygen (O), and carbon (C) atoms. This book illustrates how, thanks to there ability to expand their repertoire of functions to the modified substrates, protein and nucleic acid methylation processes play a key role in cells.

Molecular Biology of the Cell Oct 28 2022

Progress in Nonhistone Protein Research Dec 06 2020 The purpose of this text is to encourage research on nonhistones and to stimulate the imagination of other investigators whose future efforts might result in new discoveries as to the significance of these proteins.

Sequence — Evolution — Function Aug 14 2021 Sequence - Evolution - Function is an introduction to the computational approaches that play a critical role in the emerging new branch of biology known as functional genomics. The book provides the reader with an understanding of the principles and approaches of functional genomics and of the potential and limitations of computational and experimental approaches to genome analysis. Sequence - Evolution - Function should help bridge the "digital divide" between biologists and computer scientists, allowing biologists to better grasp the peculiarities of the emerging field of Genome Biology and to learn how to benefit from the enormous amount of sequence data available in the public databases. The book is non-technical with respect to the computer methods for genome analysis and discusses these methods from the user's viewpoint, without addressing mathematical and algorithmic details. Prior practical familiarity with the basic methods for sequence analysis is a major advantage, but a reader without such experience will be able to use the book as an introduction to these methods. This book is perfect for introductory level courses in computational methods for comparative and functional genomics.

Mapping Protein-protein and Protein-DNA Interactions Using a Cysteine-tethered Cleavage Probe (FeBABE) Feb 26 2020