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Restriction Landmark Genomic Scanning (RLGS)
A Study of the Cleavage of SV40 DNA by the Restriction Enzyme Alu, and a Determination of the Alu Recognition Sequence

SANTOS BRONSON

Technologies and Applications Cambridge Scholars Publishing
Genetic engineering is a rapidly growing field in the area of biological sciences. The driving forces behind this are the challenges encountered by health sectors, agriculture, the environment, and industry. As such, accurate and comprehensive knowledge about the philosophy, principles and application of genetic engineering is indispensable for students and researchers to harness maximum opportunities from this field of science. This volume gathers together comprehensive information regarding genetic engineering from recent studies, and presents it in a coherent manner. As such, it will be of interest to undergraduate and postgraduate students and researchers working in the biological sciences.
Methods and Applications Springer
Recent studies have indicated that epigenetic processes may play a major role in both cellular and organismal aging. These epigenetic processes include not only DNA methylation and histone modifications, but also extend to many other epigenetic mediators such as the polycomb group proteins, chromosomal position effects, and noncoding RNA. The topics of this book range from fundamental changes in DNA methylation in aging to the most recent research on intervention into epigenetic modifications to modulate the aging process. The major topics of epigenetics and aging covered in this book are: 1) DNA methylation and histone modifications in aging; 2) Other epigenetic processes and aging; 3) Impact of epigenetics on aging; 4) Epigenetics of age-related diseases; 5) Epigenetic interventions and aging: and 6) Future directions in epigenetic aging research. The most studied of epigenetic processes, DNA methylation, has been associated with cellular aging and aging of organisms for many years. It is now apparent that both global and gene-specific alterations occur not only in DNA methylation during aging, but also in several histone alterations. Many epigenetic alterations can have an impact on aging processes such as stem cell aging, control of telomerase, modifications of telomeres, and epigenetic drift can impact the aging process as evident in the recent studies of aging monozygotic twins. Numerous age-related diseases are affected by epigenetic mechanisms. For example, recent studies have shown that DNA methylation is altered in Alzheimer's disease and autoimmunity. Other prevalent diseases that have been associated with age-related epigenetic changes include cancer and diabetes. Paternal age and epigenetic changes appear to have an effect on schizophrenia and epigenetic silencing has been associated with several of the progeroid syndromes of premature aging. Moreover, the impact of dietary or drug intervention into epigenetic processes as they affect normal aging or age-related diseases is becoming increasingly feasible.
Medical Biochemistry Springer Science & Business Media
An essential resource for all scientists researching cellular responses to DNA damage. • Introduces important new material reflective of the major changes and developments that have occurred in the field over the last decade. • Discussed the field within a strong historical framework, and all aspects of biological responses to DNA damage are detailed. • Provides information on covering sources and consequences of DNA damage; correcting altered bases in DNA: DNA repair; DNA damage tolerance and mutagenesis; regulatory responses to DNA damage in eukaryotes; and disease states associated with defective biological responses to DNA damage.
Molecular Biology of the Cell Elsevier
This book is open access under a CC BY-NC 2.5 license. This book offers 19 detailed protocols on the use of induced mutations in crop breeding and functional genomics studies, which cover topics including chemical and physical mutagenesis, phenotypic screening methods, traditional TILLING and TILLING by sequencing, doubled haploidy, targeted genome editing, and low-cost methods for the molecular characterization of mutant plants that are suitable for laboratories in developing countries. The collection of protocols equips users with the techniques they need in order to start a program on mutation breeding or functional genomics using both forward and reverse-genetic approaches. Methods are provided for seed and vegetatively propagated crops (e.g. banana, barley, cassava, jatropha, rice) and can be adapted for use in other species.
Restriction Enzymes Springer Science & Business Media
Single Molecule Study of DNA Configuration on Restriction Enzyme Cleavage Rate Using Optical TweezersRestriction EndonucleasesSpringer Science & Business Media
Microbial Genome Program Report American Society for Microbiology Press
Many nucleases require cofactors (usually Mg2) for activity. Metal ions like Ca2, Mn2, Tb3+, Eu3+ etc., can bind at the active site and have varying effects on the enzymatic activity. In a crystal structure with DNA, two Ca2+ ions were bound to the active site of each PvuII monomer, and the metals share the ligands. Ca2+ ions promote DNA binding and not cleavage in many nucleases. We explored the role of Mg2+ and Ca2+ binding at the metal binding sites of PvuII to elucidate the role of each metal site. Ca2+ binding at the catalytic metal site would inhibit the cleavage activity, whereas its binding at the regulatory site can have varied effects. We monitored the cleavage kinetics of PvuII in presence of mixed metals. The cleavage kinetics data for Ca2+ and Mg2+ set were modeled using parameters from previous studies on PvuII. Our global analysis on single turnover cleavage kinetics datasets show best fit to a model in which mixed metal species are formed and active. The cleavage rate constants for the mixed metal species ranged from 0.01-0.08 sec-1, which is similar to the rate when only one metal is bound. From earlier work in our lab, Tb3+ was shown to have a tight (2 [mu]M) binding site and a weak binding site in PvuII. The difference in affinity allows one site to be filled with Tb3+ and the other with another metal. Indirect Tb3+ luminescence spectroscopy of the Tb3+ bound to enzyme in presence of other metals indicates that Ca2+ and Mn2+ displace Tb3+ from the enzyme. This was observed by the decrease in the luminescence intensity of E-Tb3+ complex with the addition of Ca2+/Mn2+ ions. Under similar conditions, the addition of Mg2+ ions to the E-Tb3+ complex results in an increase in the signal observed. This indicates the formation of the mixed species E-Tb3+-Mg2+ No enzymatic activity was

detected for the enzyme with the addition of Mg2+ to the E-Tb3+ complex, whereas with the addition of Mn2+ ions there was detectable activity. The observed activity with Mn2+ ion was due to the displacement of Tb3+ ions from the active site, forming the active EMn2+Mn2+ species. Although the E-Mg2+ Tb3+ species is catalytically inactive, it does bind the DNA as confirmed by fluorescence anisotropy using nonhydrolyzable phosphoramidate DNA.

Restriction Endonucleases Springer Science & Business Media

Restriction enzymes cleave DNA at specific recognition sites and have many uses in molecular biology, genetics, and biotechnology. More than 4000 restriction enzymes are known today, of which more than 621 are commercially available, justifying their description by Nobel Prize winner Richard Roberts as "the workhorses of molecular biology." This book by Wil Loenen is the first full-length history of these invaluable tools, from their recognition in the 1950s to the flowering of their development in the 1970s and 1980s to their ubiquitous availability today. Loenen has worked with restriction enzymes throughout her career as a research scientist, during which she came to know many of the leaders in this field personally and professionally. She is the author of several authoritative and widely appreciated reviews of the enzymes' biology. Her book was written with the close assistance of several of the field's pioneers, including Rich Roberts, Stuart Linn, Tom Bickle, Steve Halford, and the late Joe Bertani. The seed for the book was sown at a retirement party for Noreen Murray, to whom the book is dedicated, and its roots lie in a remarkable 2013 conference at Cold Spring Harbor Laboratory that celebrated the people and events that were vital to the field's development. Funding for the book was made possible by the Genentech Center for the History of Molecular Biology and Biotechnology at Cold Spring Harbor Laboratory.

Enzymology Primer for Recombinant DNA Technology Springer Science & Business Media

Insect Molecular Genetics, 2nd edition, is a succinct book that briefly introduces graduate and undergraduate students to molecular genetics and the techniques used in this well established and important discipline. The book is written for two converging audiences: those familiar with insects that need to learn about molecular genetics, and those that are familiar with molecular genetics but not familiar with insects. Thus, this book is intended to fill the gap between two audiences that share a common middle ground. * Up-to-date references to important review articles, websites, and seminal citations in the disciplines * Well crafted and instructive illustrations integral to explaining the techniques of molecular genetics * Glossary of terms to help beginners learn the vocabulary of molecular biology

A General Approach for Conferring Expanded Specificities on Restriction Endonucleases Academic Press

Restriction enzymes are highly specific nucleases which occur ubiquitously among prokaryotic organisms, where they serve to protect bacterial cells against foreign DNA. Many different types of restriction enzymes are known, among them multi-subunit enzymes which depend on ATP or GTP hydrolysis for target site location. The best known representatives, the orthodox type II restriction endonucleases, are homodimers which recognize palindromic sequences, 4 to 8 base pairs in length, and cleave the DNA within or immediately adjacent to the recognition site. In addition to their important biological role (up to 10 % of the genomes of prokaryotic organisms code for restriction/modification systems!), they are among the most important enzymes used for the analysis and recombination of DNA. In addition, they are model systems for the study of protein-nucleic acids interactions and, because of their ubiquitous occurence, also for the understanding of the mechanisms of evolution.

Cleavage of Nucleic Acids by Activated Diiron Complexes Academic Press

Gene-editing technologies (e.g., ZFNs, TALENs, and CRISPRs/Cas9) have been extensively used as tools in basic research. They are further applied in manufacturing agricultural products, food, industrial products, medicinal products, etc. Particularly, the discovery of medicinal products using gene-editing technologies will open a new era for human therapeutics. Though there are still many technical and ethical challenges ahead of us, more and more products based on gene-editing technologies have been approved for marketing. These technologies are promising for multiple applications. Their development and implications should be explored in the broadest context possible. Future research directions should also be highlighted. In this book, the applications, perspectives, and challenges of gene-editing technologies are significantly demonstrated and discussed.

Insect Molecular Genetics National Academies Press

The authors present a comprehensive collection of readily reproducible techniques for the manipulation of recombinant plasmids using the bacterial host E. coli. The authors describe proven methods for cloning DNA into plasmid vectors, transforming plasmids into E. coli, and analyzing recombinant clones. They also include protocols for the construction and screening of libraries, as well as specific techniques for specialized cloning vehicles, such as cosmids, bacterial artificial chromosomes, 1 vectors, and phagemids. Common downstream applications such as mutagenesis of plasmids and the use of reporter genes, are also described.

A Practical Guide to Molecular Cloning Springer Science & Business Media

Computational Epigenetics and Diseases, written by leading scientists in this evolving field, provides a comprehensive and cutting-edge knowledge of computational epigenetics in human diseases. In particular, the major computational tools, databases, and strategies for computational epigenetics analysis, for example, DNA methylation, histone modifications, microRNA, noncoding RNA, and ceRNA, are summarized, in the context of human diseases. This book discusses bioinformatics methods for epigenetic analysis specifically applied to human conditions such as aging, atherosclerosis, diabetes mellitus, schizophrenia, bipolar disorder, Alzheimer disease, Parkinson disease, liver and autoimmune disorders, and reproductive and respiratory diseases. Additionally, different organ cancers, such as breast, lung, and colon, are discussed. This book is a valuable source for graduate students and researchers in genetics and bioinformatics, and several biomedical field members interested in applying computational epigenetics in their research. Provides a comprehensive and cutting-edge knowledge of computational epigenetics in human diseases Summarizes the major computational tools, databases, and strategies for computational epigenetics analysis, such as DNA methylation, histone modifications, microRNA, noncoding RNA, and ceRNA Covers the major milestones and future directions of computational epigenetics in various kinds of human diseases such as aging, atherosclerosis, diabetes, heart disease, neurological disorders, cancers, blood disorders, liver diseases, reproductive diseases, respiratory diseases, autoimmune diseases, human imprinting disorders, and infectious diseases

The Influence of Divalent Metal Ions on DNA Binding and Cleavage by the Restriction Enzyme PvuII Endonuclease Elsevier
A wide range of microbiologists, molecular biologists, and molecular evolutionary biologists will find this new volume of singular interest. It summarizes the present knowledge about the structure and stability of microbial genomes, and reviews the techniques used to analyze and fingerprint them. Maps of approximately thirty important microbes, along with articles on the construction and relevant features of the maps are included. The volume is not intended as a complete compendium of all information on microbial genomes, but rather focuses on approaches, methods and good examples of the analysis of small genomes.
Isotope Labeling of Biomolecules – Applications BoD – Books on Demand
Enzymes are indispensable tools in recombinant DNA technology and genetic engineering. This book not only provides information for enzymologists, but does so in a manner that will also aid nonenymologists in making proper use of these biocatalysts in their research. The Enzymology Primer for Recombinant DNA Technology includes information not usually found in the brief descriptions given in most books on recombinant DNA methodology and gene cloning. Provides essential basics as well as up-to-date information on enzymes most commonly used in recombinant DNA technology Presents information in an easily accessible format to serve as a quick reference source Leads to a better understanding of the role of biocatalysts in recombinant DNA techniques
E. Coli Plasmid Vectors Elsevier
Calculations for Molecular Biology and Biotechnology: A Guide to Mathematics in the Laboratory, Second Edition, provides an introduction to the myriad of laboratory calculations used in molecular biology and biotechnology. The book begins by discussing the use of scientific notation and metric prefixes, which require the use of exponents and an understanding of significant digits. It explains the mathematics involved in making solutions; the characteristics of cell growth; the multiplicity of infection; and the quantification of nucleic acids. It includes chapters that deal with the mathematics involved in the use of radioisotopes in nucleic acid research; the synthesis of oligonucleotides; the polymerase chain reaction (PCR) method; and the development of recombinant DNA technology. Protein quantification and the assessment of protein activity are also discussed, along with the centrifugation method and applications of PCR in forensics and paternity testing. Topics range from basic scientific notations to complex subjects like nucleic acid chemistry and recombinant DNA technology Each chapter includes a brief explanation of the concept and covers necessary definitions, theory and rationale for each type of calculation Recent applications of the procedures and computations in clinical, academic, industrial and basic research laboratories are cited throughout the text New to this Edition: Updated and increased coverage of real time PCR and the mathematics used to measure gene expression More sample problems in every chapter for readers to practice concepts
A Guide to Mathematics in the Laboratory Academic Press
JACQUES S. BECKMANN & THOMAS C. OSBORN Extraordinary progress has been made in the analyses of the genetic structures of higher eukaryotic genomes. Only ten years elapsed between the initial proposals to use molecular DNA markers for the generation of a complete linkage map of the human genome [5, 17] and the first description of a 10 centimorgan map of one of its chromosomes [22], soon to be followed by others. The availability of molecular DNA markers, henceforth called genomic markers [for a review of their properties see 1, 2, 20], represents a milestone in genetics by providing the capacity for complete genetic coverage of all genomes. It is important to remember that the nature of the DNA polymorphism or of the specific method used to uncover it can be quite different for different marker loci. The genetic variation detected can be a result of a simple point mutation, a DNA insertion/deletion event, or a change in repeat copy number at some hypervariable DNA [11] or micro satellite [21] motif. Currently, the methods of detection can involve use of restriction endonucleases, nucleic acid hybridization, or DNA sequence amplification. Each of these sources of var iation and methods of detection can have utility for different applications. Furthermore, new approaches for the detection of DNA polymorphism are constantly emerging. The primary concern here is that the monitored poly morphism defines a genetic marker 'useful' for the desired application.
Molecular Biology, Pathogenicity, and Ecology of Bacterial Plasmids Academic Press
During the past few decades we have witnessed an era of remarkable growth in the field of molecular biology. In 1950 very little was known of the chemical constitution of biological systems, the manner in which information was trans mitted from one organism to another, or the extent to which the chemical basis of life is unified. The picture today is dramatically different. We have an almost bewildering variety of information detailing many different aspects of life at the molecular level. These great advances have brought with them some breath-taking insights into the molecular mechanisms used by nature for rep licating, distributing and modifying biological information. We have learned a great deal about the chemical and physical nature of the macromolecular nucleic acids and proteins, and the manner in which carbohydrates, lipids and smaller molecules work together to provide the molecular setting of living sys tems. It might be said that these few decades have replaced a near vacuum of information with a very large surplus. It is in the context of this flood of information that this series of monographs on molecular biology has been organized. The idea is to bring together in one place, between the covers of one book, a concise assessment of the state of the subject in a well-defined field. This will enable the reader to get a sense of historical perspective-what is known about the field today-and a description of the frontiers of research where our knowledge is increasing steadily.
Use of Plasmon Coupling to Reveal the Dynamics of DNA Bending AndCleavage by Single EcoRV Restriction Enzymes Springer
Molecular diagnostic procedures have been described in a number of recent books and articles. However, these publications have not focused on virus detection, nor have they provided practical protocols for the newer molecular methods. Written by the inventors or principal developers of these technologies, Molecular Methods for Virus Detection provides both reviews of individual methods and instructions for detecting virus nucleic acid sequences in clinical specimens. Each procedure includes quality assurance protocols that are often ignored by other methodology books. Molecular Methods for Virus Detection provides clinically relevant procedures for many of the newer diagnostic methodologies. Provides state-of-the-art PCR methods for amplification, quantitation, in situ hybridization, and multiplex reactions Goes beyond PCR with protocols for 3SR, NASBA, LCR, SDA, and LAT Covers important virus detection methods such as in situ hybridization; Southern, dot, and

slot blots; branched chain signal amplification; and chemiluminescence Includes quality control information crucial in research and clinical laboratories Most chapters are written by the inventors and principal developers of the methodologies Includes color plates, 77 figures, and 18 tables
DNA Repair and Mutagenesis Springer Science & Business Media
Restriction Landmark Genomic Scanning (RLGS) is a new multiplex method for simultaneous analysis of over 3,000 genome loci. Written by the inventor of RLGS, Yoshihide Hayashizaki, and his co-workers, this is the first manual on this method. RLGS is a powerful technique with enormous potential for biological (animal and plant sciences), and biomedical research. Yielding results much faster than conventional techniques, RLGS is particularly suited to the identification of the chromosomal location of the genes implicated in inherited diseases, and for the genetic disturbances present in cancerous tissue.
Vertically Intergrated Analysis of Human DNA . Progress Report, April 1, 1993--February 28, 1994 Springer Science & Business Media

DNA Modifications in the Brain: Neuroepigenetic Regulation of Gene Expression begins with an historical overview of the early discoveries surrounding DNA methylation in the mammalian brain and then explores the evidence supporting a role for this epigenetic mechanism in controlling gene expression programs across the lifespan in both normal and diseased states. Chapters describe new directions and technological advances, and provide an overview of what the future holds for this exciting new field. This book is ideal for medical, graduate and advanced undergraduate students, but is also a great resource for researchers who need a broad introduction to the dynamic nature of DNA that sheds light on evolving concepts of gene-environment interaction and their effects on adaptation and neuropsychiatric disease. Provides a comprehensive overview of the many facets of DNA modifications Discusses the impact of this dynamic epigenetic mechanism across brain development and lifespan at behavioral, cognitive, molecular and genetic levels Contains contributions by influential leaders in the field Edited by a Neuroscientist to further promote synthesis between epigenetics, neuroscience, and clinical relevance