

## Ancient Dna Methods And Protocols Methods In Molecular

A DNA barcode in its simplest definition is one or more short gene sequences taken from a standardized portion of the genome that is used to identify species through reference to DNA sequence libraries or databases. In *DNA Barcodes: Methods and Protocols* expert researchers in the field detail many of the methods which are now commonly used with DNA barcodes. These methods include the latest information on techniques for generating, applying, and analyzing DNA barcodes across the Tree of Life including animals, fungi, protists, algae, and plants. Written in the highly successful *Methods in Molecular Biology*™ series format, the chapters include the kind of detailed description and implementation advice that is crucial for getting optimal results in the laboratory. Thorough and intuitive, *DNA Barcodes: Methods and Protocols* aids scientists in continuing to study methods from wet-lab protocols, statistical, and ecological analyses along with guides to future, large-scale collections campaigns.

This book is intended to present current concepts in molecular biology with the emphasis on the application to animal, plant and human pathology, in various aspects such as etiology, diagnosis, prognosis, treatment and prevention of diseases as well as the use of these methodologies in understanding the pathophysiology of various diseases that affect living beings.

This fully updated second edition explores protocols that address the most challenging aspects of experimental work in ancient DNA, such as preparing ancient samples for DNA extraction, the DNA extraction itself, and transforming extracted ancient DNA molecules for sequencing library preparation. The volume also examines the analysis of high-throughput sequencing data recovered from ancient specimens, which, because of the degraded nature of ancient DNA and common co-extraction of contaminant DNA, has challenges that are unique compared to data recovered from modern specimens. 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, *Ancient DNA: Methods and Protocols, Second Edition* aims to serve both experts and beginners by presenting protocols in a manner that makes them easily accessible for everyday use in the lab. This topical volume in the respected *Encyclopedia* series is the first in many years to bring together all important aspects of developmental biology in one source, from morphogenesis and organogenesis, via epigenetic regulation of gene expression to evolutionary developmental biology. The editor-in-chief has assembled an outstanding team of contributors to review these topics, creating an authoritative work for many years to come. The result is a unique, top-level reference in developmental biology for researchers, students and professionals alike.

Genetics and the Past

Natural History Collections in the Science of the 21st Century

The Molecule Hunt

Recovery and Analysis of Genetic Material from Paleontological, Archaeological, Museum, Medical, and Forensic Specimens  
Strengthening Forensic Science in the United States

*This is the definitive source of information on techniques for the identification and sequencing of old DNA (pieces) and their use in biological and medical research and application. Application of aDNA techniques are useful tools for investigations reaching from evolutionary studies to law enforcement approaches. What brings them together is the interest in specific methods of handling aDNA, i.e. elaborated PCR and sequencing techniques and the interpretation of the results. This books serves as an ideal guideline for it demonstrates how problem-solving strategies can be applied in various areas.*

*This book is devoted to the knowledge of up to 250 years of collecting, organizing and preserving animals by generations of scientists. Zoological Collections are a huge resource for modern animal research and should be available for national and international scientists and institutions, as well as prospective public and private customers. Moreover, these collections are an important part of the scientific enterprise, supporting scientific research, human health, public education, and the conservation of biodiversity. Much of what we are beginning to understand about our world, we owe to the collection, preservation, and ongoing study of natural specimens. Properly preserved collections of marine or terrestrial animals are libraries of Earth's history and vital to our ability to learn about our place in its future. The approach employed by the editor involves not only an introduction to the topic, but also an external view on German collections including an assessment of their value in the international and national context, and information on the international and national collection networks. Particular attention is given to new approaches of sorting, preserving and researching in Zoological Collections as well as their neglect and/or threat. In addition, the book provides information on all big Public Research Museums, on important Collections in regional Country and local District Museums, and also on University collections. This is a highly informative and carefully presented book, providing scientific insight for readers with an interest in biodiversity, taxonomy, or evolution, as well as natural history collections at large. The untold story of the rise of the new scientific field of ancient DNA research, and how Jurassic Park and popular media influenced its development Ancient DNA research—the recovery of genetic material from long-dead organisms—is a discipline that developed from science fiction into a reality between the 1980s and today. Drawing on scientific, historical, and archival*

*material, as well as original interviews with more than fifty researchers worldwide, Elizabeth Jones explores the field's formation and explains its relationship with the media by examining its close connection to de-extinction, the science and technology of resurrecting extinct species. She reveals how the search for DNA from fossils flourished under the influence of intense press and public interest, particularly as this new line of research coincided with the book and movie Jurassic Park. Ancient DNA is the first account to trace the historical and sociological interplay between science and celebrity in the rise of this new research field. In the process, Jones argues that ancient DNA research is more than a public-facing science: it is a celebrity science.*

*Ancient DNA Methods and Protocols Humana Press*

*Method and Theory in Paleoethnobotany*

*Applied Uses of Ancient DNA*

*A Guide to Methods and Applications*

*The Grape Genome*

*Paleomicrobiology of Humans*

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.

How have humans colonised the entire planet and reshaped its ecosystems in the process? This unique and groundbreaking collection of essays explores human movement through time, the impacts of these movements on landscapes and other species, and the ways in which species have co-evolved and transformed each other as a result. Exploring the spread of people, plants, animals, and diseases through processes of migration, colonisation, trade and travel, it assembles a broad array of case studies from the Pliocene to the present. The contributors from disciplines across the humanities and natural sciences are senior or established scholars in the fields of human evolution, archaeology, history, and geography.

Double Helix History examines the interface between genetics and history in order to investigate the plausibility of 'new' knowledge derived from scientific methods and to reflect upon what it might mean for the practice of history. Since the mapping of the human genome in 2001, there has been an expansion in the use of genetic information for historical investigation. Geneticists are confident that this has changed the way we know the past. This book considers the practicalities and implications of this seemingly new way of understanding the human past using genetics. It provides the first sustained engagement with these so-called 'genomic histories'. The book investigates the ways that genetic awareness and practice is seemingly changing historical practice and conceptualisation. Linking six concepts - 'Public',

'Practice', 'Ethics', 'Politics', 'Self', and 'Imagination - Double Helix History outlines the ways that genetic information, being postgenomic, the public life of DNA, and the genetic historical imaginary work on the body, on collective memory, on the historical imagination, on the ethics of historical investigation, on the articulation of history, and on the collection and interpretation of data regarding the 'past'. This book will appeal to researchers and students alike interested in DNA, genetics, and historiography.

This volume discusses the oral microbiome, and oral and systemic health. The chapters in this book cover topics such as analytical techniques for identifying and measuring oral bacteria; strategies for controlling common sources of variability in oral microbiome methods for viral bacterial and fungal analysis; ways to study oral DNA and RNA samples to identify molecular pathways to disease; approaches to functional assays for oral bacteriophage, antibiotic purging of systemic bacteria; and metaproteomic analysis of various oral samples. 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 practical, The Oral Microbiome: Methods and Protocols is a valuable resource for any scientist or researcher looking to further study this exciting and developing field.

Diagnostic Molecular Biology

Zoological Collections of Germany

PCR Protocols

Wood in Archaeology

Ancient DNA Typing

**This book describes the current state of international grape genomics, with a focus on the latest findings, tools and strategies employed in genome sequencing and analysis, and genetic mapping of important agronomic traits. It also discusses how these are having a direct impact on outcomes for grape breeders and the international grape research community. While *V. vinifera* is a model species, it is not always appreciated that its cultivation usually requires the use of other *Vitis* species as rootstocks. The book discusses genetic diversity within the *Vitis* genus, the available genetic resources for breeding, and the available genomic resources for other *Vitis* species. Grapes (*Vitis vinifera* spp. *vinifera*) have been a source of food and wine since their domestication from their wild progenitor (*Vitis vinifera* ssp. *sylvestris*) around 8,000 years ago, and they are now the world's most valuable horticultural crop. In addition to being economically important, *V. vinifera* is also a model organism for the study of perennial fruit crops for two reasons: Firstly, its ability to be transformed and micropropagated via somatic embryogenesis, and secondly its relatively small genome size of 500**

**1 Mb. The economic importance of grapes made *V. vinifera* an obvious early candidate for genomic sequencing, and accordingly, two draft genomes were reported in 2007. Remarkably, these were the first genomes of any fruiting crop to be sequenced and only the fourth for flowering plants. Although riddled with gaps and potentially omitting large regions of repetitive sequences, the two genomes have provided valuable insights into grape genomes. Cited in over 2,000 articles, the genome has served as a reference in more than 3,000 genome-wide transcriptional analyses. Further, recent advances in DNA sequencing and bioinformatics are enabling the assembly of reference-grade genome references for more grape genotypes revealing the exceptional extent of structural variation in the species.**

**This volume mirrors the holistic feature of whole genome amplification (WGA) technology by combining reviews, detailed basic methods and advanced sample workflows. The first part of the book covers an overview of the development of WGA techniques throughout recent years including general considerations on bias in WGA, possible sample pre-enrichment strategies and how to run a single-cell lab. The second part focuses on major WGA methods and protocols that allow the assessment of WGA product quality. The final chapters contain advanced protocols and address issues such as sample preparation using laser-micro dissection; WGA from partially degraded DNA (formalin-fixed paraffin embedded samples); circulating tumor cells; and ancient samples.**

**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 thorough, Whole Genome Amplification: Methods and Protocols will serve as a rich source of detailed information and inspiration and will help researchers, both new and experienced, yield successful results.**

**Natural history collections have recently acquired an unprecedented place of importance in scientific research. Originally created in the context of systematics and taxonomy, they are now proving to be fundamental for answering various scientific and societal questions that are as significant as they are current. Natural History Collections in the Science of the 21st Century presents a wide range of questions and answers raised by the study of collections. The billions of specimens that have been collected from all around the world over more than two centuries provide us with information that is vital in our quest for knowledge about the Earth, the universe, the diversity of life and the history of humankind. These collections also**

provide valuable reference points from the past to help us understand the nature and dynamics of global change today. Their physical permanence is the best guarantee we have of a return to data and to information sources in the context of open science.

"In this book, Andy Baxevanis and Francis Ouellette . . . have undertaken the difficult task of organizing the knowledge in this field in a logical progression and presenting it in a digestible form. And they have done an excellent job. This fine text will make a major impact on biological research and, in turn, on progress in biomedicine. We are all in their debt." –Eric Lander from the Foreword Reviews from the First Edition "...provides a broad overview of the basic tools for sequence analysis ... For biologists approaching this subject for the first time, it will be a very useful handbook to keep on the shelf after the first reading, close to the computer." –Nature Structural Biology "...should be in the personal library of any biologist who uses the Internet for the analysis of DNA and protein sequence data." –Science "...a wonderful primer designed to navigate the novice through the intricacies of in scripto analysis ... The accomplished gene searcher will also find this book a useful addition to their library ... an excellent reference to the principles of bioinformatics." –Trends in Biochemical Sciences

This new edition of the highly successful *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* provides a sound foundation of basic concepts, with practical discussions and comparisons of both computational tools and databases relevant to biological research. Equipping biologists with the modern tools necessary to solve practical problems in sequence data analysis, the Second Edition covers the broad spectrum of topics in bioinformatics, ranging from Internet concepts to predictive algorithms used on sequence, structure, and expression data. With chapters written by experts in the field, this up-to-date reference thoroughly covers vital concepts and is appropriate for both the novice and the experienced practitioner. Written in clear, simple language, the book is accessible to users without an advanced mathematical or computer science background. This new edition includes: All new end-of-chapter Web resources, bibliographies, and problem sets Accompanying Web site containing the answers to the problems, as well as links to relevant Web resources New coverage of comparative genomics, large-scale genome analysis, sequence assembly, and expressed sequence tags A glossary of commonly used terms in bioinformatics and genomics

*Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Second Edition* is essential reading for researchers, instructors, and students of all levels in molecular biology and bioinformatics, as well as for investigators

**involved in genomics, positional cloning, clinical research, and computational biology.**

**Ancient DNA**

**Methods, Strategies and Applications**

**Forensic DNA Typing: Principles, Applications and Advancements**

**Microbial Environmental Genomics (MEG)**

**The Animal Kingdom in its Amazing Plenty at Museums and Universities**

Taxonomy is fundamental to understanding the variety of life forms, and exciting expansions in molecular biology are re- revolutionising the obtained data. This volume reviews the ma- jor molecular biological techniques that are applied in ta- xonomy. The chapters are arranged in three main sections: 1) Overviews of important topics in molecular taxonomy; 2) Case studies of the successful application of molecular methods to taxonomic and evolutionary questions; 3) Protocols for a range of generally applicable methods. The described techni- ques include DNA-DNA hybridization, DNA fingerprinting, RFLP analysis, and PCR sequencing.

The book explores the fundamental principles, advances in forensic techniques, and its application on forensic DNA analysis. The book is divided into three modules; the first module provides the historical prospect of forensic DNA typing and introduces fundamentals of forensic DNA typing, methodology, and technical advancements, application of STRs, and DNA databases for forensic DNA profile analysis. Module 2 examines the problems and challenges encountered in extracting DNA and generating DNA profiles. It provides information on the methods and the best practices for DNA isolation from forensic biological samples and human remains like ancient DNA, DNA typing of skeletal remains and disaster victim identification, the importance of DNA typing in human trafficking, and various problems associated with capillary electrophoresis. Module 3 emphasizes various technologies that are based on SNPs, STRs namely Y-STR, X-STR, mitochondrial DNA profiling in forensic science. Module 4 explores the application of non-human forensic DNA typing of domestic animals, wildlife forensics, plant DNA fingerprinting, and microbial forensics. The last module discusses new areas and alternative methods in forensic DNA typing, including Next-Generation Sequencing, and its utility in forensic science, oral microbes, and forensic DNA phenotyping. Given its scope, the book is a useful resource in the field of DNA fingerprinting for scientists, forensic experts, and students at the postgraduate level.

Biologists always need to grapple with integrating two explanatory approaches. On the one hand, there is

necessarily an effort to drill down to the lowest possible level to explain what is happening in whatever is being studied. That involves looking at how higher-level processes arise from lower level ones. On the other hand, there is a need to consider how the broader context influences bottom-up processes; that involves looking at how the whole influences the parts. Neither approach is satisfactory on its own. There is always a need to integrate the consideration of how parts influence wholes with how wholes influence parts. This book arises from a concern that in the public dissemination of biology the need to integrate these different perspectives is not coming across well. In popularisations, simplistic micro explanations always seem to arouse most interest and to capture the headlines. That risks distorting and simplifying the complexity of biological processes, and can mislead people. In this book we are urging a concerted attempt to come to grips with the interactive complexity of biology, and to find ways of conveying it to the public accessibly and effectively. We are particularly concerned with how biology is communicated to the public. Too often, what comes over to the public is a crude, out-of-date, simplistic, mono-causal, reductionist biology. Why so? Why is biology so misrepresented? Who is responsible? It is partly the media, of course, but we suggest that biologists themselves are often partly responsible. When it comes to communication with the public, they tend to over-simplify in a way that distorts.

Although all living beings modify their environment, human beings have acquired the ability to do so on a superlative space-time scale. As a result of industrialization and the use of new technologies, the anthropogenic impact has been increasing in the last centuries, causing reductions in the sizes or the extinction of numerous wild populations. In this sense, from the field of conservation genetics, various efforts have been made in recent decades to provide new knowledge that contributes to the conservation of populations, species, and habitats. In this book, we summarize the concrete contributions of researchers to the conservation of the Neotropical mammals using Molecular Ecology techniques. The book is divided into three major sections. The first section provides an up-to-date review of the conservation status of Neotropical mammals, the applications of the molecular markers in its conservation, and the use of non-invasive and forensic genetic techniques. The second and third sections present, respectively, a series of case studies in various species or taxonomic groups of Neotropical mammals.

Bioinformatics

A Sustainable Resource for Open Science

Rethinking Biology: Public Understandings

Double Helix History

Biochemical Applications

***Ancient DNA refers to DNA which can be recovered and analyzed from clinical, museum, archaeological and paleontological specimens. Ancient DNA ranges in age from less than 100 years to tens of millions of years. The study of ancient DNA is a young field, but it has been revolutionized by the application of polymerase chain reaction technology, and interest is growing very rapidly. Fields as diverse as evolution, anthropology, medicine, agriculture, and even law enforcement have quickly found applications in the recovery of ancient DNA. This book contains contributions from many of the "first generation" researchers who pioneered the development and application of ancient DNA methods. Their chapters present the protocols and precautions which have resulted in the remarkable results obtained in recent years. The range of subjects reflects the wide diversity of applications that are emerging in research on ancient DNA, including the study of DNA to analyze kinship, recovery of DNA from organisms trapped in amber, ancient DNA from human remains preserved in a variety of locations and conditions, DNA recovered from herbarium and museum specimens, and DNA isolated from ancient plant seeds or compression fossils. Ancient DNA will serve as a valuable source of information, ideas, and protocols for anyone interested in this extraordinary field.***

***Paleoethnobotany, the study of archaeological plant remains, is poised at the intersection of the study of the past and concerns of the present, including agricultural decision making, biodiversity, and global environmental change, and has much to offer to archaeology, anthropology, and the interdisciplinary study of human relationships with the natural world. Method and Theory in Paleoethnobotany demonstrates those connections and highlights the increasing relevance of the study of past human-plant interactions for understanding the present and future. A diverse and highly regarded group of scholars reference a broad array of literature from around the world as they cover their areas of expertise in the practice and theory of paleoethnobotany—starch grain analysis, stable isotope analysis, ancient DNA, digital data management, and ecological and postprocessual theory. The only comprehensive edited volume focusing on method and theory to appear in the last twenty-five years, Method and Theory in Paleoethnobotany addresses the new areas of inquiry that have become central to contemporary archaeological debates, as well as the current state of theoretical, methodological, and empirical work in paleoethnobotany.***

***An Indispensable Resource on Advanced Methods of Analysis of Human Skeletal and Dental Remains in Archaeological and Forensic Contexts Now in its third edition, Biological Anthropology of the Human Skeleton has become a key reference for bioarchaeologists, human osteologists, and paleopathologists throughout the world. It builds upon basic skills to provide the foundation for advanced scientific analyses of human skeletal remains in cultural, archaeological, and theoretical contexts. This new edition features updated coverage of***

***topics including histomorphometry, dental morphology, stable isotope methods, and ancient DNA, as well as a number of new chapters on paleopathology. It also covers bioarchaeological ethics, taphonomy and the nature of archaeological assemblages, biomechanical analyses of archaeological human skeletons, and more. Fully updated and revised with new material written by leading researchers in the field Includes many case studies to demonstrate application of methods of analysis Offers valuable information on contexts, methods, applications, promises, and pitfalls Covering the latest advanced methods and techniques for analyzing skeletal and dental remains from archaeological discoveries, Biological Anthropology of the Human Skeleton is a trusted text for advanced undergraduates, graduate students, and professionals in human osteology, bioarchaeology, and paleopathology.***

***After more than three decades of paleoecological research, the potential role of climatic and anthropogenic drivers on Easter Island's ecological and cultural change is still under discussion. This eBook aims to provide a synthetic view of the topic using evidence from different research fields such as paleoecology, archaeology, history and molecular phylogenetics. A holistic approach is provided to combine the results of these research fields into a comprehensive framework able to account for most of the available multidisciplinary evidence. This eBook is dedicated to the memory of John R. Flenley, the pioneer of paleoecological study of Easter Island, who passed away on June 22, 2018.***

***A Path Forward***

***Methods and Protocols***

***Molecular Plant Taxonomy***

***Experiments in Molecular Biology***

***Molecular Ecology and Conservation Genetics of Neotropical Mammals***

Scores of talented and dedicated people serve the forensic science community, performing vitally important work. However, they are often constrained by lack of adequate resources, sound policies, and national support. It is clear that change and advancements, both systematic and scientific, are needed in a number of forensic science disciplines to ensure the reliability of work, establish enforceable standards, and promote best practices with consistent application. Strengthening Forensic Science in the United States: A Path Forward provides a detailed plan for addressing these needs and suggests the creation of a new government entity, the National Institute of Forensic Science, to establish and enforce standards within the forensic science community. The benefits of improving and regulating the forensic science disciplines are clear: assisting law enforcement officials, enhancing homeland security, and reducing the risk of wrongful conviction and exoneration. Strengthening Forensic Science in the United States gives a full account of what is needed to advance the forensic science disciplines, including upgrading of systems

and organizational structures, better training, widespread adoption of uniform and enforceable best practices, and mandatory certification and accreditation programs. While this book provides an essential call-to-action for congress and policy makers, it also serves as a vital tool for law enforcement agencies, criminal prosecutors and attorneys, and forensic science educators.

A Research Strategy to Examine the Taxonomy of the Red Wolf provides independent guidance about taxonomic research on the red wolf, *Canis rufus*. Building from the 2019 report *Evaluating the Taxonomic Status of the Mexican Gray Wolf and the Red Wolf*, this report reviews and ranks research applications to determine the taxonomy of wild canid populations in southern Louisiana and other relevant locations. The report then develops a research strategy to examine the evolutionary relationships between ancient red wolves, the extant managed red wolf populations, and the unidentified canid populations.

A state-of-the-art collection of readily reproducible laboratory methods for DNA identity analysis, including Y chromosome haplotyping, mtDNA, and SNP typing. The book offers well-tested protocols for DNA quantification using real-time PCR on forensic samples and for the determination of the number of amelogenine gene copies. For forensic geneticists, there are readily reproducible methods for species identification, ancient DNA, and pharmacogenetics.

It considers research involving archaeological wood in all forms, ranging from fuelwood to ships' timbers, from sites around the globe.

Biological Anthropology of the Human Skeleton

Whole Genome Amplification

Human Dispersal and Species Movement

Cereal Genomics

Paleoecology of Easter Island: Natural and Anthropogenic Drivers of Ecological Change

The correct procedures you need for frustration-free PCR methods and applications are contained in this complete, step-by-step, clearly written, inexpensive manual. Avoid contamination--with specific instructions on setting up your lab Avoid cumbersome molecular biological techniques Discover new applications

In this new edition, the editors have thoroughly updated and dramatically expanded the number of protocols to take advantage of the newest technologies used in all branches of research and clinical medicine today. These proven methods include real time PCR, SNP analysis, nested PCR, direct PCR, and long range PCR. Among the highlights are chapters on genome profiling by SAGE, differential display and chip technologies, the amplification of whole genome DNA by random degenerate oligonucleotide PCR,

and the refinement of PCR methods for the analysis of fragmented DNA from fixed tissues. Each fully tested protocol is described in step-by-step detail by an established expert in the field and includes a background introduction outlining the principle behind the technique, equipment and reagent lists, tips on trouble shooting and avoiding known pitfalls, and, where needed, a discussion of the interpretation and use of results.

A revolution is underway in archaeology. For the first time the molecular record of past life, entombed for millennia in archaeological and geological material, has become widely accessible to science. Miraculous-seeming techniques now allow ancient remains to speak volumes about a past we thought lost.

Diagnostic Molecular Biology describes the fundamentals of molecular biology in a clear, concise manner to aid in the comprehension of this complex subject. Each technique described in this book is explained within its conceptual framework to enhance understanding. The targeted approach covers the principles of molecular biology including the basic knowledge of nucleic acids, proteins, and genomes as well as the basic techniques and instrumentations that are often used in the field of molecular biology with detailed procedures and explanations. This book also covers the applications of the principles and techniques currently employed in the clinical laboratory. • Provides an understanding of which techniques are used in diagnosis at the molecular level • Explains the basic principles of molecular biology and their application in the clinical diagnosis of diseases • Places protocols in context with practical applications

DNA Barcodes

Forensic DNA Typing Protocols

The Oral Microbiome

A Research Strategy to Examine the Taxonomy of the Red Wolf

The International Encyclopedia of Primatology, 3 Volume Set

In *Cereal Genomics: Methods and Protocols*, expert researchers provides modern protocols for the analysis and manipulation of cereal genomes. Techniques for isolation and analysis of DNA and RNA from both the vegetative tissues and from the more challenging seeds of cereals are described. Tools for the isolation, characterization and functional analysis of cereal genes and their transcripts are detailed. Methods for molecular screening of cereals and for their genetic transformation are also covered. 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 practical, *Cereal Genomics: Methods and*

Protocols provides a comprehensive resource for those studying cereal genomes. A state-of-the-art collection of readily reproducible laboratory methods for DNA identity analysis, including Y chromosome haplotyping, mtDNA, and SNP typing. The book offers well-tested protocols for DNA quantification using real-time PCR on forensic samples and for the determination of the number of amelogenine gene copies. For forensic geneticists, there are readily reproducible methods for species identification, ancient DNA, and pharmacogenetics. Additional chapters address new applications in the forensic genetics lab, such a species identification or typing of CYP polymorphisms for the analysis of adverse to drugs.

The International Encyclopedia of Primatology represents the first comprehensive encyclopedic reference focusing on the behaviour, biology, ecology, evolution, genetics, and taxonomy of human and non-human primates. Represents the first comprehensive encyclopedic reference relating to primatology Features more than 450 entries covering topics ranging from the taxonomy, history, behaviour, ecology, captive management and diseases of primates to their use in research, cognition, conservation, and representations in literature Includes coverage of the basic scientific concepts that underlie each topic, along with the latest advances in the field Highly accessible to undergraduate and graduate students in primatology, anthropology, and the medical, biological and zoological sciences Essential reference for academics, researchers and commercial and conservation organizations This work is also available as an online resource at [www.encyclopediaofprimatology.com](http://www.encyclopediaofprimatology.com)

Experiments in Molecular Biology provides a thorough introduction to recombinant DNA methods used in molecular biology and nucleic acid biochemistry. This unique laboratory manual is particularly appropriate for courses in molecular cloning, molecular genetics techniques, molecular biology techniques, recombinant DNA techniques, bacterial genetics techniques, and genetic engineering. Included is an especially helpful section to aid new instructors in avoiding potential pitfalls of specific experiments. Key Features \*

- \* Contains student-tested, easy-to-follow protocols
- \* Presents background information that reinforces principles behind the methods presented
- \* Includes questions at the end of

laboratory exercises \* Provides both detailed descriptions of experimental procedures and a theoretical support section \* Sequentially links experiments to provide a "project" approach to studying molecular biochemistry \* Includes student-tested, easy-to-follow protocols \* Background information reinforces principles behind the methods presented \* Includes questions at the end of laboratory exercises \* Advises new instructors on potential pitfalls of specific experiments \* Provides both detailed descriptions of experimental procedures and a theoretical support section \* Sequentially links experiments to provide a "project" approach to studying

A Practical Guide to the Analysis of Genes and Proteins  
Archaeology and the Search for Ancient DNA  
Polymerase Chain Reaction

### Frontiers in Developmental Biology

Only recently was it determined that two of the world's most devastating plagues, the plague of Justinian and the medieval Black Death, were caused by distinct strains of the same pathogen. Use of paleomicrobiological techniques led to this discovery. This work is just one example of the historical mysteries that this emerging field has helped to clarify. Others, such as when tuberculosis began to afflict humans, the role of lice in plague pandemics, and the history of smallpox, are explored and further illuminated in *Paleomicrobiology of Humans*. Led by editors Michel Drancourt and Didier Raoult, the book's expert contributors address larger issues using paleomicrobiology. These include the recognition of human remains associated with epidemic outbreaks, identification of the graves of disasters, and the discovery of demographic structures that reveal the presence of an epidemic moment. In addition, the book reviews the technical approaches and controversies associated with recovering and sequencing very old DNA and surveys modern human diseases that have ancient roots. Essentially, paleomicrobiologists aim to identify past epidemics at the crossroads of different specialties, including anthropology, medicine, molecular biology, and microbiology. Thus, this book is of great interest not only to microbiologists but to medical historians and anthropologists as well. *Paleomicrobiology of Humans* is the first comprehensive book to examine so many aspects of this new, multidisciplinary, scientific field.

This volume seeks to understand how organisms and gene functions are influenced by environmental cues while accounting for variation that takes place within and among environmental populations and communities. *Microbial Environmental Genomics (MEG)* guides readers through methods to analyse the diversity of different organism types (archaea, bacteria, fungi, protists and microfauna), interactions between fungi and trees, and methods to identify and characterize functions and functional diversity of

both pro- and eukaryotes. Written for the *Methods in Molecular Biology* series, 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 practical, *Microbial Environmental Genomics (MEG)* will serve as a primary research reference for researchers and research managers in environmental microbiology working in the expanding field of molecular ecology and environmental genomics.

In this volume expert researchers in the field detail the operations of microchip capillary electrophoresis. Chapters focus on small molecule, biomolecule applications, various detection modes, and sample preparation approaches are described. 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 key tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, *Microchip Capillary Electrophoresis Protocol* aids scientists in continuing to study microchip capillary electrophoresis.

Plant taxonomy is an ancient discipline facing new challenges with the current availability of a vast array of molecular approaches which allow reliable genealogy-based classifications. Although the primary focus of plant taxonomy is on the delimitation of species, molecular approaches also provide a better understanding of evolutionary processes, a particularly important issue for some taxonomic complex groups. *Molecular Plant Taxonomy: Methods and Protocols* describes laboratory protocols based on the use of nucleic acids and chromosomes for plant taxonomy, as well as guidelines for phylogenetic analysis of molecular data. Experts in the field also contribute review and application chapters that will encourage the reader to develop an integrative taxonomy approach, combining nucleic acid and cytogenetic data together with other crucial information (taxonomy, morphology, anatomy, ecology, reproductive biology, biogeography, paleobotany), which will help not only to best circumvent species delimitation but also to resolve the evolutionary processes in play. 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, *Molecular Plant Taxonomy: Methods and Protocols* seeks to provide conceptual as well as technical guidelines to plant taxonomists and geneticists.

The Making of a Celebrity Science

Microchip Capillary Electrophoresis Protocols

Molecular Techniques in Taxonomy