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Raising hopes for disease treatment and prevention, but also the specter of discrimination and "designer genes," genetic testing is potentially one of the most socially explosive developments of our time. This book presents a current assessment of this rapidly evolving field, offering principles for actions and research and recommendations on key issues in genetic testing and screening. Advantages of early genetic knowledge are balanced with issues associated with such knowledge: availability of treatment, privacy and discrimination, personal decisionmaking, public health objectives, cost, and more. Among the important issues covered: Quality control in genetic testing. Appropriate roles for public agencies, private health practitioners, and laboratories. Value-neutral education and counseling for persons considering testing. Use of test results in insurance, employment, and other settings.

Essential Cell Biology provides a readily accessible introduction to the central concepts of cell biology, and its lively, clear writing and exceptional illustrations make it the ideal textbook for a first course in both cell and molecular biology. The text and figures are easy-to-follow, accurate, clear, and engaging for the introductory student. Molecular detail has been kept to a minimum in order to provide the reader with a cohesive conceptual framework for the basic science that underlies our current understanding of all of biology, including the biomedical sciences. The Fourth Edition has been thoroughly revised, and covers the latest developments in this fast-moving field, yet retains the academic level and length of the previous edition. The book is accompanied by a rich package of online student and instructor resources, including over 130 narrated movies, an expanded and updated Question Bank. Essential Cell Biology, Fourth Edition is additionally supported by the Garland Science Learning System. This homework platform is designed to evaluate and improve student performance and allows instructors to select assignments on specific topics and review the performance of the entire class, as well as individual students, via the instructor dashboard. Students receive immediate feedback on their mastery of the topics, and will be better prepared for lectures and classroom discussions. The user-friendly system provides a convenient way to engage students while assessing progress. Performance data can be used to tailor classroom discussion, activities, and lectures to address students' needs precisely and efficiently. For more information and sample material, visit <http://garlandscience.rocketmix.com/>.

"In this book, Andy Baxevanis and Francis Ouellette . . . haveundertaken the difficult task of organizing the knowledge in thisfield in a logical progression and presenting it in a digestibleform. And they have done an excellent job. This fine text will makea major impact on biological research and, in turn, on progress inbiomedicine. 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 sequenceanalysis ... For biologists approaching this subject for the firsttime, it will be a very useful handbook to keep on the shelf afterthe 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 sequencedata." —Science "...a wonderful primer designed to navigate the novice throughthe intricacies of in scripto analysis ... The accomplished genesearcher will also find this book a useful addition to theirlibrary ... an excellent reference to the principles ofbioinformatics." —Trends in Biochemical Sciences This new edition of the highly successful Bioinformatics: A Practical Guide to the Analysis of Genes and Proteinsprovides a sound foundation of basic concepts, with practicaldiscussions and comparisons of both computational tools anddatabases relevant to biological research. Equipping biologists with the modern tools necessary to solvepractical problems in sequence data analysis, the Second Editioncovers the broad spectrum of topics in bioinformatics, ranging fromInternet concepts to predictive algorithms used on sequence,structure, and expression data. With chapters written by experts inthe field, this up-to-date reference thoroughly covers vitalconcepts and is appropriate for both the novice and the experiencedpractitioner. Written in clear, simple language, the book isaccessible to users without an advanced mathematical or computerscience background. This new edition includes: All new end-of-chapter Web resources, bibliographies, andproblem 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 genomeanalysis, sequence assembly, and expressed sequence tags A glossary of commonly used terms in bioinformatics andgenomics Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Second Edition is essential reading forresearchers, instructors, and students of all levels in molecularbiology and bioinformatics, as well as for investigators involvedin genomics, positional cloning, clinical research, andcomputational biology.

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This open access book, published under a CC BY 4.0 license in the Pubmed indexed book series Handbook of Experimental Pharmacology, provides up-to-date information on best practice to improve experimental design and quality of research in non-clinical pharmacology and biomedicine.

Marking the change in focus of tree genomics from single species to comparative approaches, this book covers biological, genomic, and evolutionary aspects of angiosperm trees that provide information and perspectives to support researchers broadening the focus of their research. The diversity of angiosperm trees in morphology, anatomy, physiology and biochemistry has been described and cataloged by various scientific disciplines, but the molecular, genetic, and evolutionary mechanisms underlying this diversity have only recently been explored. Excitingly, advances in genomic and sequencing technologies are ushering a new era of research broadly termed comparative genomics, which simultaneously exploits and describes the evolutionary origins and genetic regulation of traits of interest. Within tree genomics, this research is already underway, as the number of complete genome sequences available for angiosperm trees is increasing at an impressive pace and the number of species for which RNAseq data are available is rapidly expanding. Because they are extensively covered by other literature and are rapidly changing, technical and computational approaches—such as the latest sequencing technologies—are not a main focus of this book. Instead, this comprehensive volume provides a valuable, broader view of tree genomics whose relevance will outlive the particulars of current-day technical approaches. The first section of the book discusses background on the evolution and diversification of angiosperm trees, as well as offers description of the salient features and diversity of the unique physiology and wood anatomy of angiosperm trees. The second section explores the two most advanced model angiosperm tree species (poplars and eucalypts) as well as species that are soon to emerge as new models. The third section describes the structural features and evolutionary histories of angiosperm tree genomes, followed by a fourth section focusing on the genomics of traits of biological, ecological, and economic interest. In summary, this book is a timely and well-referenced foundational resource for the forest tree community looking to embrace comparative approaches for the study of angiosperm trees.

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Focusing on practical, patient related issues, this volume provides the basic concepts of Evidence Based Medicine (EBM) as they relate to Pathology and Laboratory Medicine and presents various practical applications. It includes EBM concepts for use in the identification of cost-effective panels of immunostains and other laboratory tests and for improvement of diagnostic accuracy based on the identification of selected diagnostic features for particular differential diagnosis. EBM concepts are also put forth for use in Meta-analysis to integrate the results of conflicting literature reports and use of novel analytical tools such as Bayesian belief networks, neural networks, multivariate statistics and decision tree analysis for the development of new diagnostic and prognostic models for the evaluation of patients. This volume will be of great value to pathologists who will benefit from the concepts being promoted by EBM, such as levels of evidence, use of Bayesian statistics to develop diagnostic and other rules and stronger reliance on "hard data" to support therapeutic and diagnostic modalities.

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