

GENOME ANALYSIS

A LABORATORY MANUAL

VOLUME 4

MAPPING GENOMES

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Mapping Genomes A Laboratory Manual

Paul Denny, Chittaranjan Kole



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Genome Mapping and Genomics in Laboratory Animals Paul

Denny, Chittaranjan Kole, 2013-01-13 Mapping of animal genomes has generated huge databases and several new concepts and strategies which are useful to elucidate origin evolution and phylogeny Genetic and physical maps of genomes further provide precise details on chromosomal location function expression and regulation of academically and economically important genes The series Genome Mapping and Genomics in Animals provides comprehensive and up to date reviews on genomic research on a large variety of selected animal systems contributed by leading scientists from around the world Laboratory animals are those species that by accident of evolution domestication and selective breeding are amenable to maintenance and study in a laboratory environment Many of these species are studied as models for the biology and pathology of humans Laboratory animals included in this volume are sea urchin nematode worm fruit fly sea squirts puffer fishes medaka fish African clawed frog mouse and rat

Genome Analysis Eric D. Green, 1997 A complement to the bible of recombinant DNA Molecular Cloning these manuals are essential for every laboratory in which genes are being studied

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Association Studies Pharmacogenetics Epigenetics Ethic and Insurance As with the second Edition the Handbook includes a glossary of terms acronyms and abbreviations and features extensive cross referencing between the chapters tying the different areas together With heavy use of up to date examples real life case studies and references to web based resources this continues to be must have reference in a vital area of research Edited by the leading international authorities in the field David Balding Department of Epidemiology Public Health Imperial College An advisor for our Probability Statistics series Professor Balding is also a previous Wiley author having written Weight of Evidence for Forensic DNA Profiles as well as having edited the two previous editions of HSG With over 20 years teaching experience he s also had dozens of articles published in numerous international journals Martin Bishop Head of the Bioinformatics Division at the HGMP Resource Centre As well as the first two editions of HSG Dr Bishop has edited a number of introductory books on the application of informatics to molecular biology and genetics He is the Associate Editor of the journal Bioinformatics and Managing Editor of Briefings in Bioinformatics Chris Cannings Division of Genomic Medicine University of Sheffield With over 40 years teaching in the area Professor Cannings has published over 100 papers and is on the editorial board of many related journals Co editor of the two previous editions of HSG he also authored a book on this topic **Genome Research** ,2000 **Genome Mapping and Genomics in Human and Non-Human Primates** Ravindranath Duggirala,Laura Almasy,Sarah Williams-Blangero,Solomon F.D. Paul,Chittaranjan Kole,2015-03-25 This book provides an introduction to the latest gene mapping techniques and their applications in biomedical research and evolutionary biology It especially highlights the advances made in large scale genomic sequencing Results of studies that illustrate how the new approaches have improved our understanding of the genetic basis of complex phenotypes including multifactorial diseases e g cardiovascular disease type 2 diabetes and obesity anatomic characteristics e g the craniofacial complex and neurological and behavioral phenotypes e g human brain structure and nonhuman primate behavior are presented Topics covered include linkage and association methods gene expression copy number variation next generation sequencing comparative genomics population structure and a discussion of the Human Genome Project Further included are discussions of the use of statistical genetic and genetic epidemiologic techniques to decipher the genetic architecture of normal and disease related complex phenotypes using data from both humans and non human primates

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