Book Review

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Genome Analysis: A Laboratory Manual (*Vols. 1–4*). Edited by Bruce Birren, Eric D. Green, Philip Hieter, Sue Klapholz, Richard M. Myers, Harold Riethman, and Jane Roskams. Plainview, NY: Cold Spring Harbor Laboratory Press, 1997. Pp. 2,280 (total). $140.00 each set (paper); $230.00 each set (cloth).

The international collaboration that aims to map and sequence the entire human genome by the year 2003 will have a profound impact on biomedical research. DNA-sequence data are accumulating at a phenomenal rate, and we are acquiring tools that will allow us to manipulate the genome for therapeutic purposes. Meanwhile, molecular diagnostics, once thought to be a scientific fantasy, has become routine. As increasingly sophisticated techniques proliferate, numerous books and manuals are now being published to help researchers keep pace with the latest advances. *Genome Analysis,* perhaps the most comprehensive of these offerings, is a four-volume set that offers numerous step-by-step protocols, sensibly organized into several sections.

The editors of the series each contribute chapters in their own names, and they have assembled a distinguished group of scientists to author the remainder of the chapters. The protocols are well presented, allowing both new and experienced investigators to implement them with little or no help. The chapters all include a considerable amount of theoretical background information and extensive bibliographies. Although these volumes are user friendly, they do require a basic knowledge of molecular biology. The "troubleshooting" section is well presented and should be quite useful during trying times.

The first volume, entitled *Analyzing DNA,* begins with a compilation of techniques for isolating high-quality genomic DNA from a variety of sources and includes admirably complete protocols for Southern blotting, manipulation of high-molecular-weight DNA, and PCR. Three chapters are devoted to DNA sequencing, including strategies for "shotgun" sequencing of cosmid-sized or larger DNA segments, and the use of transposons in large-scale DNA sequencing projects. The final chapter, which covers computational analysis of DNA and protein sequencing data—also available in electronic format at http://clio.cshl.org/books/g-a/bklch7—should prove a useful guide to anyone who needs up-to-date information about the rapidly changing field of bioinfomatics.

Volume 2, *Detecting Genes,* covers strategies for gene discovery in mammalian systems, construction and screening of normalized cDNA libraries, direct cDNA selection, exon trapping, gene detection by the identification of CpG islands, and detection of DNA variation. Successful approaches for discovering genes, including functional and positional cloning, and the use of the candidate-gene approach with or without positional information are all clearly discussed and documented in this section.

Genomic cloning is the major theme of volume 3, *Cloning Systems,* which discusses a variety of *Escherichia coli*–based genomic DNA libraries that use cosmid, fosmid, P1, bacterial-artificial-chromosome, and plasmid-artificial-chromosome vectors. The final chapter provides detailed information on YACs, including an overview of YAC cloning, a primer on yeast genetics, library construction, screening, and characterization. Protocols are included for long-range restriction mapping, isolation of insert ends, and YAC manipulations, such as recombination-based modification, amplification, and transfer of YACs between yeast strains and into mammalian cells.

Human geneticists may find volume 4, *Mapping Genomes,* to be the most valuable part of the series. This final volume covers meiotic mapping in humans, genetic and comparative mapping in mice, identification and analysis of DNA polymorphisms, DNA markers for physical mapping, representational-difference analysis, and FISH. Five appendices include reference material on common reagents, basic procedures, safety precautions, useful facts about the genome, and valuable Web sites, e-mail addresses, and fax numbers.

Readers without an extensive background in laboratory science may find *Genome Analysis* difficult to follow at times, but both neophytes and experienced bench workers will discover a gold mine in each volume.

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