

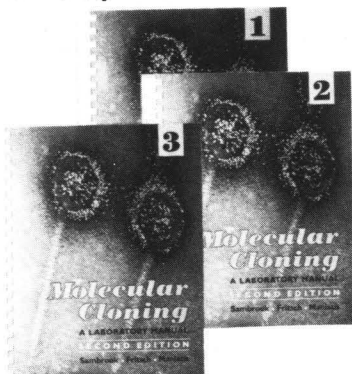
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J. Sambrook, University of Texas Southwestern Medical Center; **E.F. Fritsch**, Genetics Institute; **T. Maniatis**, Harvard University



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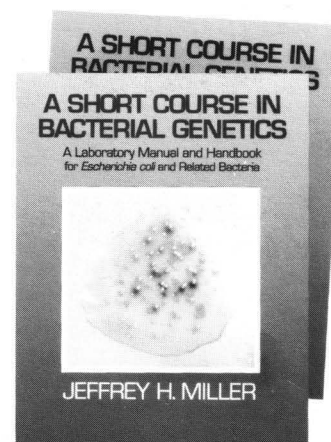
Jeffrey H. Miller, University of California, Los Angeles

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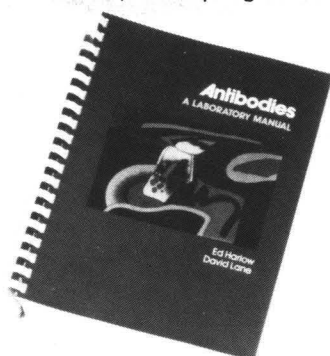
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1. Lundberg, K.S., et al. (1991) Gene 108: 1-6

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Ellson Y. Chen, Perkin Elmer Corporation
Richard Gibbs, Baylor College of Medicine
W. Richard McCombie, Cold Spring Harbor Laboratory
Richard K. Wilson, Washington University

Recent advances in the automation of DNA sequencing have opened new possibilities for the analysis of complex genomes at the DNA sequence level. This two week course will provide intensive training in this rapidly evolving field. The course will emphasize techniques and strategies for using automated sequencers to sequence large, contiguous genomic regions. Students will carry out all of the steps in the sequencing process from preparing cosmid DNA to computer analysis of the finished sequence. Topics will include subclone library generation, large-scale template purification, sequencing reactions, gel analysis on automated sequencers, sequence assembly, gap filling and conflict resolution. Students will work in groups to sequence a large region of DNA and through this process be trained in crucial project and data management techniques. A series of lecturers will discuss their applications of these techniques as well as alternate strategies for high speed automated DNA sequencing.

PROTEIN PURIFICATION & CHARACTERIZATION

March 30 - April 12

Richard Burgess, University of Wisconsin, Madison
James Kadonaga, University of California, San Diego
Sue-Hwa Lin, M.D. Anderson Cancer Center, University of Texas
Daniel R. Marshak, Cold Spring Harbor Laboratory

This course is intended for scientists who are not familiar with techniques of protein isolation and characterization. It is a rigorous program that includes laboratory work all day and a lecture with discussion session every evening. Each student will become familiar with each of the major techniques in protein purification by actually performing four separate isolations including: (i) a regulatory protein from muscle tissue; (ii) a sequence-specific, DNA-binding protein; (iii) a recombinant protein overexpressed in *E. coli*; and (iv) a membrane-bound receptor. A variety of bulk fractionation, electrophoretic, and chromatographic techniques will be employed including: precipitation by salts, pH, and ionic polymers; ion exchange, gel filtration, hydrophobic interaction, and reverse phase chromatography; lectin affinity, oligonucleotide affinity, and immunoaffinity chromatography; polyacrylamide gel electrophoresis, and electroblotting; and high performance liquid chromatography. Procedures will be presented for solubilizing proteins from inclusion bodies and refolding them into active monomeric forms. Methods of protein characterization will be utilized including immunological and biochemical assays, peptide mapping, amino acid analysis, protein sequencing, and mass spectrometry. Emphasis will be placed on strategies of protein purification and characterization rather than on automated instrumental analysis. Guest lecturers will discuss protein structure, modifications of proteins, methodologies for protein purification and characterization, and applications of protein biochemistry to cell and molecular biology. Guest lecturers have included: R. Aebersold, L. Gierasch, G. Hart, A. Kornberg, N. Pace, Y. Paterson, G. Rose, J. Rothman, B. Stillman, and N. Tonks.

CLONING & ANALYSIS OF LARGE DNA MOLECULES

March 30 - April 12

Hadi Abderrahim, Cell Genesys, Inc.
Bruce Birren, Whitehead / MIT Center for Genome Research
Douglas Vollrath, Stanford University

This course will cover the theory and practice of manipulating and cloning high molecular weight DNA. The course will focus on the use of yeast artificial chromosome (YAC), bacterial artificial chromosome (BAC) and bacteriophage P1 cloning systems for library construction and techniques of pulsed field gel electrophoresis (PFGE). Lectures and laboratory work will include an introduction to yeast genetics, the isolation and manipulation of high molecular weight DNA from a variety of sources, and preparative and analytical PFGE. Clones will be produced and characterized by several approaches, including library screening, contig assembly, long range restriction mapping, and recovery of YAC ends. Lectures by outside speakers on topics of current interest will supplement the laboratory work.

EARLY DEVELOPMENT OF *XENOPUS LAEVIS*

April 4 - 13

Robert Grainger, University of Virginia
Hazel Sive, Whitehead Institute

This course will provide extensive laboratory exposure to the biology, manipulation and use of embryos from the frog, *Xenopus laevis*. The course is suited both for investigators who have had no experience with *Xenopus*, as well as those who have worked with *Xenopus* and wish to expand their repertoire of techniques. All students should have a current training in molecular biology and some knowledge of developmental biology. The course consists of intensive laboratory sessions, supplemented by daily lectures and demonstrations from experts in both experimental and molecular embryology. Six areas will be covered: (i) care and handling of adults and embryo isolation; (ii) stages of embryonic development and anatomy; (iii) whole mount *in situ* hybridization and immunocytochemistry; (iv) microinjection of eggs and oocytes, including mRNA and antisense oligonucleotides; (v) micromanipulation of embryos, including induction and transplantation assays; and (vi) preparation and use of cell cycle extracts. Lecturers and co-instructors will include: Enrique Amaya, Rick Elinson, Janet Heasman, John Gurdon, Richard Harland, Ray Keller, John Newport, and Nancy Papalopulu.

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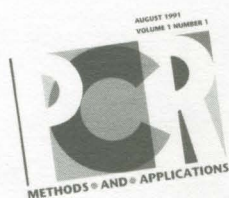
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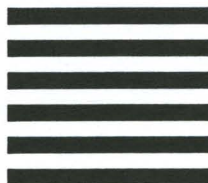
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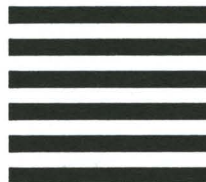
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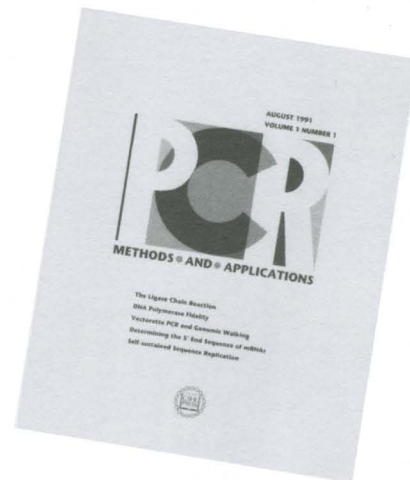
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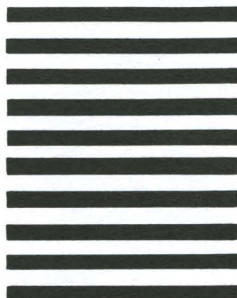
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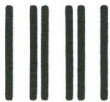
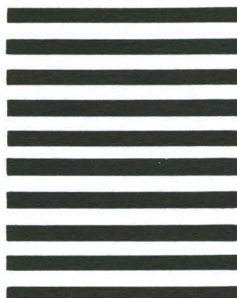
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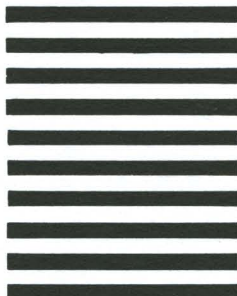
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