



plant cell systems. Rounding out the book, Lubienecki discusses the regulatory issues which face the producer of biopharmaceuticals from tissue culture systems.

This book provides a useful compendium of methods to produce mammalian cells in bioreactors. Since the contributors pose and answer basically the same questions, the book is reduced largely to a comparison (of-

ten by the company's own scientists) of commercial hardware used to grow the cells. The use of the term "large-scale" is somewhat misleading for several reasons. Some contributors clearly perceive large-scale to mean the commercial production of kilogram quantities of protein, whereas others view milligram to gram quantities as large scale. There is also a tendency to use "high-density" and "large-

scale" interchangeably. Nonetheless, this volume provides the reader with a collection of straightforward discussions on the growth of mammalian cells in various bioreactor systems.

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SEQUENCING AND SYNTHESIS: A UNIFIED APPROACH

Macromolecular Sequencing and Synthesis: Selected Methods and Applications. Edited by David H. Schlesinger. Pp. 282. ISBN 0-8451-4246-1. \$69.95 (Alan R. Liss, Inc., NY, NY: 1988).

In previous decades, sequence determination for proteins was difficult, relying on the same methods described in virtually all introductory biochemistry texts— isolation and sequencing of many peptide fragments, followed by piecing the entire sequence together by finding the overlapping fragments. Advances made in the 1980's in DNA sequencing, however, are the basis for modern protein sequencing techniques: once the gene itself for a particular protein is identified, the amino acid connectivity is read directly from the codon sequence determined from enzymatic or chemical protocols. A major limitation to these methods is that only the primary structure of a protein can be deduced. Any information on co- or posttranslational modifications must be obtained from protein chemical methods of structural determination before the protein can be synthesized.

Solid phase peptide synthesis (SPPS) has been the mainstay of peptide synthetic methodologies, but recent advances in genetic manipulations have allowed flexibility in the selection of a synthetic strategy. Since the techniques of DNA sequencing, protein chemical sequencing, and peptide synthesis are integrated procedures directed towards the laboratory preparation of functional proteins, they are worthy of a single publication devoted to their concerted use. *Macromolecular Sequencing and Synthesis* is this publication.

While the sequencing and synthesis of biopolymers are themselves topics of sufficient complexity to warrant their own book, a number of head-

ings were included that are related to the determination of protein structure. Consequently, sections describing protein purification, computer-assisted sequence analysis, and combined methodologies appear alongside those on peptide/nucleotide synthesis, peptide structural determination, and oligonucleotide sequencing. The inclusion of these related sections gives the book breadth and enhances its usefulness to a newcomer in the field.

The authors of the various chapters included in these sections reflect the broadened scope. They come from a wide variety of professional backgrounds, ranging from faculty in medical schools and biochemistry departments to industrial research positions. Their diversity is shown in the individual chapters, which vary in perspective from basic (deprotection reactions in peptide synthesis) to applied research (development of automated DNA sequencing protocols). The chapters, which are a mixture of literature reviews and research reports, reflect the entire spectrum of research in protein structural determination and synthesis. The combined methodology section is especially interesting. Readers can see the connections between apparently unrelated results.

Many books, by the time they reach the public, are years out of date; *Macromolecular Sequencing* is surprisingly up-to-date. The benefit to the reader is that individual chapters include topics of current interest such as applications of mass spectrometry to protein chemistry, the simultaneous synthesis of large numbers of peptides, and modern automated oligonucleotide sequencing. Each of these techniques can be applied to projects involving the quantitation of peptides, immunology, and sequencing the human genome; excitement

in the scientific community about these areas assures readership. Perhaps the greatest benefit is that many references are recent publications: many were published as late as 1987. Authors therefore provide contemporary leading references, saving interested investigators much of the tedium of an exhaustive literature search.

Macromolecular Sequencing and Synthesis, however, should not be used alone as a reference volume. While the book provides a useful overview of protein structure determination, and offers detailed chapters in selected topics, it does not contain specific information in all areas. For instance, the section on peptide synthesis contains chapters on acid deprotection reactions, methods for simultaneous synthesis, peptide cyclization reactions and automation of peptide synthesis. Each of these chapters is informative and well documented, but little information is to be found on vital topics such as methods for activation, racemization, or side chain protection. *Macromolecular Sequencing and Synthesis* would be used best as an updated supplement to an established references series such as *The Peptides* rather than an inexpensive replacement.

For the cost, however, *Macromolecular Sequencing and Synthesis* is an outstanding value. Diverse and readable, it provides an unusually accessible introduction to the field of protein structure determination and synthesis. Schlesinger, in the introduction, states that "it is truly an exciting time for science." Readers, after completing this volume, will understand why.

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