# Techniques in Protein Chemistry

Edited by

Tony E. Hugli

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# Foreword

At the first symposium of the Protein Society in August 1987, one of the exciting aspects of the meeting was the profusion of excellent posters and abstracts. How could all this current, fascinating information be brought rapidly to a larger audience? The new publications committee, under the chairmanship of George Rose considered this question, and the outcome is this volume of *Techniques in Protein Chemistry*.

The present volume is based on expanded abstracts from the second symposium of the society, held in August 1988, as well as several invited contributions. It represents only a fraction of the excellent work that was discussed at the symposium and is itself an experiment. There were more than 1000 participants in the symposium, and over 300 abstracts. If this volume of *Techniques in Protein Chemistry* proves useful, the series may be expanded to feature a larger fraction of the contributions at the 1989 symposium.

This first volume represents the vision and hard work of Tony Hugli. Tony welded the agreement between the society, Academic Press, the authors, and the industrial sponsors that has made rapid publication possible at a reasonable price. Then he selected the abstracts, identified associate editors, coordinated communication between the authors and the associate editors, and edited the volume. To the extent that the volume and the series proves useful, much of the credit belongs to Tony and the associate editors who gave of their time to complete the volume on schedule.

*David Eisenberg*
President
The Protein Society

# Preface

The Protein Society held its first annual meeting in San Diego in August of 1987. A commitment to excellence was apparent from the beginning, and the efforts of an enthusiastic membership have produced a highly successful organization. Meetings of the society have provided a forum for reporting major advances in the analysis of various aspects of protein architecture and function. The scientific programs at each meeting have featured dynamic leaders in the field, and attendance has always been greater than expected. The second annual meeting, in 1988, saw a marked expansion in size and sophistication over the inaugural meeting.

By 1988 it was clear that the society would continue to grow and prosper. Unfortunately, no formal mechanism existed to report details from the proceedings of these meetings to the society's membership and to scientists at large. The scientific sessions were already too extensive to be published in their entirety. It was suggested that a collection of reports of new methods and techniques, condensed into a single volume for rapid publication, could capture a significant aspect of the meeting for later reference. This idea was proposed to the publications committee and accepted on an experimental basis for the second annual meeting. For this first volume of *Techniques in Protein Chemistry*, topics were chosen that have both general interest and practical value to protein chemists; they emphasize new methods and applications in protein sequencing, highlight advanced applications of mass spectrometry and nuclear magnetic resonance technology, present a status report on limitations of amino acid microanalysis, and update advances in high-performance liquid chromatography. One chapter is also devoted to reports of general protein chemistry. As a bonus, participants in a special workshop organized to determine the structure of synthetic test peptide-3 (STP-3), a peptide designed to test the analytical limits of current technology in the field, reported their strategies in solving the structure of the "mystery" peptide.

Under the guidance of the eight associate editors, the six selected topics were integrated into sections that summarize recent and significant technical advances in protein chemistry. This information is timely and will be useful both to investigators actively involved in protein chemistry and to those just wishing to be informed of current trends in the field. Taken together, the articles in this volume provide an excellent review of

the analytical techniques currently available for the molecular characterization of proteins. We have attempted to select reports that reflect limitations as well as identify new procedures and advances in protein analysis. In this regard, the volume serves as an informative progress report of selected sessions from the annual meeting of the society. A small number of articles were also solicited from members not presenting abstracts in order to obtain a more general overview of specific areas of expertise. These articles provide the continuity needed for a more coherent documentation of each topic.

This volume is a direct result of the willingness of researchers who attended the second annual meeting of the Protein Society on August 13–17, 1988, to share their reports. It is a strong statement in support of the volume that so many participants were willing and even anxious to contribute articles to *Techniques in Protein Chemistry*. I thank all the authors for their contributions and the cooperative spirit in which they met the challenge of our rigorous deadlines.

*Tony E. Hugli*

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# Section I

# Introduction

## CHEMICAL MICROSEQUENCING TECHNIQUES

John E. Shively and David W. Speicher

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Keeping up to date on the latest techniques in protein chemistry is of prime interest to the protein chemist. The myriad problems encountered during the purification and structural analysis of minute amounts of protein of great biological interest continue to challenge protein chemists. Few current reference works exist in these areas despite continuing rapid changes and improvements to the methodology. The compilation of new or improved techniques in this section represent the current state of the art, and as such, will be open to close scrutiny and testing in many laboratories. The techniques which survive this scrutiny or go on to further iterations of improvement will certainly benefit the scientific community, since the need for improved and more sensitive methods of sequence analysis is apparent.

Protein sequencing techniques and the requisite sophisticated equipment are constantly evolving. The major driving force toward improvements in this field has historically been a continuing need for improved sensitivity and several articles in this section are focused on raising the sequencing sensitivity level beyond its already impressive low picomole level. In this context it is also critical for both sequence practitioners and investigators supplying proteins for analysis to have realistic concepts of the current capacities of available techniques and sequencing facilities. The article by Niece et al is an especially important contribution that describes the results of a well designed survey of 40 microchemistry core facilities. The data described can be used by participants to evaluate how their facility compares to other facilities. Other protein chemists can derive interesting suggestions concerning the relative capacities of different instruments as well as the need for cautious application of computerized sequence interpretation. Also, these data provide the investigator, that utilizes a core facility, with an accurate indication of the performance level of the average facility with a "real" unknown. In addition to the survey of core facilities, articles in this section cover most areas of recent progress in protein chemistry techniques as summarized below.