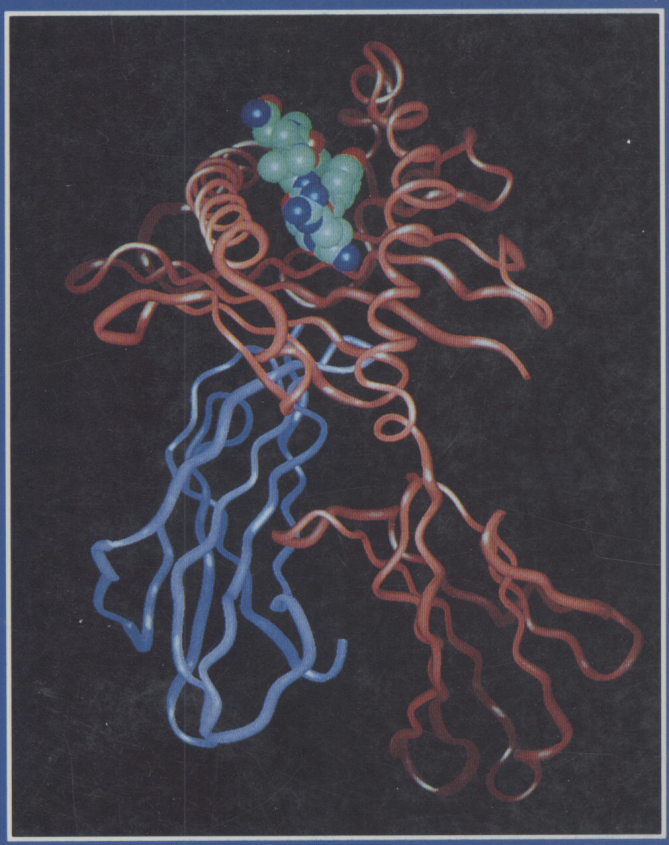
TECHNIQUES IN PROTEIN CHEMISTRY IV



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Edited by Ruth Hogue Angeletti

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Foreword

For most ventures it would be premature to assert that a fourth volume of the series "carries on a distinguished tradition," but a case can certainly be made for such a description of this volume. This is the fifth book based on abstracts selected from those presented at a Protein Society Symposium (the fourth to carry the title "Techniques in Protein Chemistry"). They were selected from an all-time record of 615 abstracts submitted to this Sixth Protein Society Symposium. The task of the associate editors was a difficult one indeed.

We would have been overwhelmed by the flood of abstracts had it not been for our friends in the Association of Biomolecular Resource Facilities (ABRF) who meet with the Protein Society Symposia. They volunteered to organize the poster sessions and did a superb job. All agreed that the posters were of very high quality. I am pleased that they have once again volunteered their services for next year.

The Seventh Symposium will be held July 24–28, 1993, in the Town and Country in San Diego. This site will not only increase poster space, but also the time in which they can be examined, so we look forward to an even bigger and more interactive meeting.

My most sincere thanks on behalf of the Protein Society to Ruth Hogue Angeletti and her associate editors for their dedicated work on this volume. Their efforts and the top quality contributions by the authors of the articles do indeed "carry on a distinguished tradition."

Mark Hermodson
President
The Protein Society

Preface

The president of the Protein Society has declared that this series of volumes is now a "distinguished tradition." However, this tradition has a dynamic quality, for the "Techniques in Protein Chemistry" series must embody change. In the first volume, advances in the organic chemistry of proteins—sequencing, fragmentations, separations—formed the core of the book. In this volume, the rapid developments in mass spectrometry of proteins dominate. Breakthroughs in technology enable new insights into protein structure and function. It is our job as editors and associate editors to put aside our parochial interests and continue to ensure that areas of rapid development are well represented.

The associate editors are at the forefront of identifying important contributions. This year they were John Crabb, Sheenah Mische, Al Smith, John Stults, Wesley Stites, and Leonard Spicer. Once again, the staff of Academic Press has ensured that the book will be published rapidly and as error free as possible. The members of the society are responsible for the continued high quality of this volume.

Ruth Hogue Angeletti

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The Protein Society acknowledges with thanks the following organizations who through their support of the Society's program goals contributed in a meaningful way to the sixth annual symposium and thus to this volume.

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SECTION I

Mass Spectrometry of Proteins and Peptides

Mass Spectrometry in Protein Sequence and Structural Investigations

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I. Overview

The growing realization of the importance of mass spectrometry in protein science is based upon quite recent recognition of the relative ease with which classically difficult or often intractable questions in protein biology may now be readily and successfully addressed. The progression of events which underpin the present state of the art was triggered by discoveries of revolutionary new ionization techniques, viz. LSIMS or FAB, electrospray and matrix-assisted laser desorption, able to handle polar, labile macromolecules mass spectrometrically and the subsequent development of new instruments utilizing these techniques. These methods are virtually ideally suited to deal effectively with the challenges of protein sequencing and structural analysis at the picomole level. Currently active "export" of some of this new instrumental capability to the biochemistry laboratories themselves is under way due to the burgeoning availability of more user-friendly, relatively low cost commercial instrumentation. The most recent examples are instruments designed to permit exploitation of the two newest ionization methods, namely electrospray (ES) (1) and matrix-assisted laser desorption (maLD) (2) techniques.

Over the last decade a number of mass spectrometry laboratories have been key participants in establishing the unique power and versatility of these techniques in solving previously tedious and often impossible problems. There is a growing literature of examples of questions which have been tackled successfully representing increasingly more difficult biological problems (See recent reviews 3-6). The present excitement about mass spectrometry in the protein biochemistry community is not due to any *recently* recognized need to have a better structural understanding of the machinery of cells, but rather to a growing awareness that the tools are now in hand with which to discover and dissect even minute structural details with high accuracy and fidelity through application of these mass spectrometric techniques. Indeed, the time is ripe to exploit these new methodologies, both to gain a deeper

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