NEWS FROM THE PROTEIN SOCIETY
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Meeting report

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Methods in Protein Structural Analysis Conference (MPSA2000) took place in beautiful Charlottesville, Virginia, September 16–20, 2000, and was attended by 220 researchers from two dozen countries including Sweden, Germany, France, Spain, Italy, Greece, Japan, Australia, Cuba, and the United States. The MPSA conferences began in 1974 with a small workshop in Boston, Massachusetts, organized by Richard A. Laursen, Boston University, for the purpose of exchanging information on the newly developed automation of the chemistry for sequencing proteins by removing amino acids from the amino terminus one at a time. An automated sequencer had been developed by Pehr Edman, at the Rockefeller Institute; the University of Lund, Sweden; and finally at the St. Vincent School of Medical Research in Melbourne, Australia. Others, especially Dr. Laursen, had developed sequencing machines that operated on a different principle but still employed the basic Edman chemistry. Subsequent workshops were held approximately every two years and alternated between Europe, Japan, and the United States. Recent conferences were held in Snowbird (Salt Lake City), Utah, United States (1994); Annecy, France (1996); and Thessaloniki, Greece (1998). As new techniques for protein analysis were developed in the early 1990s, the workshops expanded in scope and size to emphasize additional aspects of protein structure analysis in addition to chemistries related to primary sequence analysis. The focus of the conferences has remained, however, on sharing cutting-edge techniques for protein analysis. To commemorate its origins and honor Pehr Edman, in 1988, MPSA began awarding at each meeting the Edman Award to individuals whose efforts had significantly advanced the field (Wittmann-Liebold, 1989). The first prize was awarded to Richard Laursen for his efforts in the development of solid-state protein sequencing methods.

Throughout the past 26 years, the MPSA conferences have been perpetuated by a small, international group of dedicated researchers; however, the need for a more formal organization increasingly was realized. To that end, the organizers of MPSA2000 undertook the establishment of the International Association of Protein Structure Analysis and Proteomics (IAPSAP, current website: Web site: http://www.med.virginia.edu/medicine/basic-sci/micr/fox/iapsap/iapsap.html), a not-for-profit organization chartered in the state of Virginia, to support MPSA2000 and subsequent international MPSA conferences. The purposes of IAPSAP are: to promote the discovery and exchange of new methods and techniques for the analysis of protein structure, to facilitate the application of methods in protein structure analysis in the pursuit of solutions to biological problems, and to support and foster the education of researchers in the techniques of protein chemistry, protein structure analysis, and proteomics. IPASAP is controlled by an 18–member international Board of Directors consisting of forefront research scientists from academia, government, and industry.

The rationale behind MPSA2000 was to explore the explosion of methodologies for protein structural analysis that extend from primary sequence analysis through secondary and tertiary structure analysis using both experimental and computational approaches, including methods for single–molecule analysis. Conference topics included conceptual and technological advances for protein structure analysis, proteomics, post-translational modifications, modeling and structural genomics, bioinformatics, protein engineering, protein–protein interactions, and single-molecule techniques. Plenary sessions consisting of three to four speakers were interspersed with poster session and workshop presentations by industry sponsors including Applied Biosystems, Agilent, ThermoQuest, Micromass, Amersham Pharmacia

Biotech, Genomic Solutions, Ciphergen, BIACORE, Beckman Coulter, LC Packings, and Bio-Rad, Inc.

The conference kicked off with a lecture by D. Hunt, University of Virginia, entitled "Proteomics: Automated Analysis of Peptides and Proteins at the Attomole Level in Complex Mixtures by Mass Spectrometry." This talk highlighted the rapid advances that have been made in instrumentation and software that, when coupled with rapidly expanding genomic sequence information, have pushed the envelopes of time, sensitivity, and resolution to levels only dreamed of a few years ago. The talk was illustrated with studies from Hunt's own laboratory, including work on proteins that allow a plant to synthesize its own fungicide, antigens presented on class II MHC molecules, proteins involved in the regulation of transcription and DNA repair, cell surface proteins, proteins secreted by tumors, and proteins involved in the acquisition of long-term memory. The technical themes were extended in the first session on mass spectrometry by M. Wilm, European Molecular Biology Laboratory (EMBL), Heidelberg, who spoke on the development of nanoelectrospray emitters as highly efficient electrospray ionization sources compatible with low capillary-electrophoresis flow rates. N. Kelleher, University of Illinois at Urbana-Champaign, described a top-down approach to the analysis of intact proteins using high high-resolution Fourier-Transform mass spectrometry. S. Patterson, Amgen Inc, spoke on the use of data-dependent chromatography and mass spectrometry for the identification and quantitative comparison of proteins in proteomic analysis. Advances in NMR that extend the technology to larger proteins and to the analysis of protein–protein interactions were described by T. Yamazaki, Institute for Protein Research, Osaka, Japan, who presented a protein autosplicing technique based on the use of inteins to isotopically label segments of large (200–300 amino acid) proteins. A. Bax, National Institutes of Health, then asked, "What can NMR tell about a protein?" and presented information on structural changes and domain rearrangements illustrated with studies on calmodulin.

Single-molecule techniques were emphasized by P. K. Hansma, University of California at Santa Barbara, who described experiments on protein unfolding using the cantilever of the atomic-force microscope to explore intra- and intermolecular forces. We learned, for example, that the abalone shell is 3000 times more fracture resistant than a single crystal of calcium carbonate, despite the fact that 97 percent of the shell's mass is calcium carbonate. A complementary talk on the mechanical unfolding of titin, an extremely large muscle protein kinase, was presented by J. Fernandez, Mayo Foundation, and Y. Ishii, Osaka, Japan, described the single-molecule biophysics of molecular motors, DNA transcription, and other problems, as explored using fluorescence techniques. In contrast to single-molecule techniques, R. Aebersold described the efforts of his laboratory to develop quantitative methods for analysis of the whole proteome using HPLC, mass spectrometry, and isotopic labeling methods. D. F. Hochstrasser, Central Clinical Chemistry Laboratory, Geneva, highlighted a new algorithm for identifying proteins by means of peptide mass fingerprinting and highly automated methods for generating fully annotated two-dimensional electrophoresis reference maps of eukaryotic subcellular compartments and organelles as well as for macromolecular structures and protein complexes. R. L. Jernigan, National Cancer Institute (NCI), described methods for inferring large-scale motions and functions from structures that were illustrated by his studies on HIV reverse transcriptase and the GroEL/GroES complex. Several companies have developed integrated packages for proteome analysis, and some of the issues were presented by M. R. Wilkins, Proteome Systems, Inc. Large-scale genome sequencing efforts and proteomic techniques now facilitate rapid protein identification; however, determining protein structure and function are still bottlenecks. An approach to protein structure prediction was presented by R. Sanchez from A. Sali's lab, Rockefeller University, who described their Modeller program. C. Nevill-Manning, Rutgers University, then presented an approach to function identification through the mining of information contained in small, conserved regions of proteins. Preliminary ideas for automating annotation of such motifs also were presented. F. Pearl, University College, London, described the CATH (Class Architechure, Topology or fold and Homologous superfamily) database and techniques for assigning structural families to genome sequences, which she illustrated using *Mycoplasma genitalium*. E. A. Komives, University of California at San Diego, beautifully illustrated the integration of NMR, mass spectrometry, and protein–protein measurements using surface plasmon resonance techniques with a description of her studies on the electrostatics, dynamics, and solvent accessibility of the thrombin–thrombomodulin interaction. These are but some of the key topics covered in the four days of scientific presentations. Highlighting the need for an integrated systems approach was the final banquet lecture by L. Hood, one of the two MPSA2000 Edman Award winners, who described his new Systems Biology Institute. The second recipient, M. Hunkapiller, Applied Biosystems, was unable to attend. K. Muller, University of Califormia, Berkeley, winner of a newly initiated MPSA Young Postdoctoral Fellow Award, described his working work on generating and linking protein binding domains of immunoglobulins.

The beauty of early fall in Virginia was not forgotten, and participants were treated to tours of the University of Virginia campus, a local winery, Monticello (home of Thomas Jefferson, 3rd third president of the United States), and a barbeque and bluegrass concert at Ashlawn-Highland (home of James Madison, 4th president of the United States). Participants left the rural setting of Charlottesville

with both practical information and an increased appreciation for the rapid speed of developments in both instrumentation and a wide range of techniques for protein structural analysis. Clearly, we have come a long way from the days of Pehr Edman, Fred Sanger, and manual stepwise protein degradation as a primary method of analysis, and certainly conference participants will be looking forward to the 14th MPSA conference, announced at the conclusion of MPSA2000, which will be held September 8–12, 2002 in Valencia, Spain.

Reference

Wittmann-Liebold, B. (Ed). 1989. Methods in protein sequence analysis, Springer-Verlag, Berlin, p. 575.

FASEB MARC travel awards

The FASEB MARC Program has travel awards available for faculty (and 2 underrepresented minority students) to attend The Protein Society national meetings. In addition, we now have funding to support travel awards for underrepresented minority students and/or postdoctoral fellows who have been selected to give poster or oral presentations at The Protein Society national meetings.

Each Faculty/Students Travel Award includes funding for 1 faculty member and 2 students. The maximum total for the Faculty/Students travel award is $2,400. The faculty award covers travel-related expenses up to $1,000. The students award covers travel-related expenses up to $700 per student. Each Poster/Oral Presenter Travel Award covers travel-related expenses up to $1,000. In addition, the meeting registration fee for all award recipients will be reimbursed at the advance registration rate. Our application deadline dates are included with the application forms which are available online (in Adobe Acrobat PDF format) at https://ns2.faseb.org/marc/forms/forms.htm.