

## Preface

The Fifth International Conference on the Crystallization of Biological Macromolecules (ICCBM) in San Diego was combined for the first time with the National Institutes of Health (NIH) Membrane Crystallization Workshop. This provided the forum to expand on the practical aspects of the crystallization of membrane proteins. The conference has been since its inception, and remains, multidisciplinary and there is a demand for new areas of expertise, as exemplified by the molecular biology session.

The conference returned to California, where it had originated through the efforts of Robert Feigelson and Alex McPherson. The presidential address by Richard Giegé 'Crystallogensis of Biological Macromolecules: Facts and Perspectives' served as both reminder for us of the achievements made and, more importantly, of the many challenges remaining.

Hartmut Michel's session on membrane proteins consisted of presentations by Peter Timmins, Werner Kühlbrandt, Michael Garavito, Jürg Rosenbusch and Shinya Yoshikawa. This session provided not only an introduction for the practical membrane protein crystallization workshop, but celebrated some of the few achievements that have been made in this area of crystallization. It also exposed membrane protein crystallization as one of the major stumbling blocks on the road towards a structural understanding of biology.

Reuben Leberman, who, though not a strong advocate, is a knowledgeable critic of such studies, chaired the session which focused on crystallization in microgravity. Reports in this session were given by Lawrence DeLucas, Ruchang Bi, Jan Drenth, Naomi Chayen, Madeleine Riès-Kautt and A. Plaas-Link, who reminded us that many more improvements will be necessary in order to take advantage of what research in space has to offer.

While this session was underway, the membrane protein workshop encountered a few problems and the workshop participants learned how to re-solubilize protein that had precipitated during shipping from Germany to the United States. This was not a major setback, as the next day the workshop resumed and at the end of the week, the participants were able to obtain crystals of the *trans*-membrane protein LH-2 light harvesting complex of *Rhodospirillum mollischianum* with various precipitants and additives.

The session on molecular biology and protein crystallization was chaired by Janusz Sowadski and included the following speakers: Terese Bergfors, Stefan Gruenewald, Alec Tucker, Allan D'Arcy, Heather Baker, Axel Scheidig, Klaus Scheffzek and Bonnie McKinney. This session not only emphasized the fact that without high-

quality protein one has difficulties in crystallization, but also demonstrated the great potential in crystal growth offered through application of good diagnostics (light scattering), modification of protein and applying of cofactors.

Richard Giegé chaired the session on the physics of crystallization. Annette Tardieu and Madeleine Riès-Kautt gave presentations on small-angle X-ray scattering. Other scattering-method presentations were given by Magali Jullien and Mitsuo Ataka. The session ended with a computer simulation by Jos Tissen and a description by Michael Frey of the role of water in crystal contacts.

The poster session under the chairmanship of Ernest Villafranca consisted of over 70 posters including the award-winning poster by Gil Privé on engineering the *E. coli* lac permease for crystallization studies.

The new ICCBM president, Franz Rosenberger, chaired a session which included presentations by Bill Wilson, Roland Boistelle, Laurent Sibille, Arnaud Ducruix, Lisa Monaco, Alexander Malkin, Peter Vekilov, Marc Pusey, Keith Ward and Steve Durbin. While this session was a tour de force of physics, Wilson's lecture was perhaps the most rewarding for its presentation for the first time of the osmotic second virial coefficient  $B_{22}$  as a good diagnostic parameter for screening for crystallization conditions.

Alex McPherson's session focused on screening crystallization conditions. Presentations by Enrico Stura and Bob Cudney provided two opposing views of this field. The success of Crystal Screen 1 in obtaining crystals of 88 proteins is clear evidence of where development of fast-screening methods might lead. Charles Carter presented a statistically-based approach for evaluating different factors that effect crystallization and Shirley Tolley introduced the use of monomethyl ether polyethylene glycol 2000. Steve Sarfaty summarized the session with a discussion on random and not-so random matrices.

At the first open session, chaired by Charles Carter, Gene Scarborough presented large crystals that had not diffracted and discussed protein-detergent interaction in membrane crystallization. Lori Kohlstaedt convincingly demonstrated how a complete knowledge of the biological system is necessary in order to solve the problems associated with protein preparation and crystallization. A presentation on the results of seeding was given by Judy Dauberman. Brian Schick obtained an extension of the diffraction resolution of crystals of elongation factor EF-Tu-Ts complex from 6 to 2.7 Å.

Discussions extended well beyond the formal session hours. One memorable occasion was during the boat cruise banquet on the William B. Evans when Roger

Goody narrated the history of the time-resolved crystallography of p21<sup>H-ras</sup>.

Equally important to obtaining the crystals is having the powerful means to examine them and Nguyen-Huu Xuong described the landmark data-collection facilities at the multiwire area-detector facility at the University of California in San Diego. Åke Kvick gave a presentation about data-collection facilities at the European synchrotron radiation facility and Edwin Westbrook described synchrotron-based data-collection facilities for protein crystallography and the Advanced Photon Source under development at Argonne.

At the second open session, Gary Gilliland announced the new version of the biological macromolecule crystallization database version 3.0, Annie Hassell described new programming software for the ICN Biomedicals' protein crystallization robot and Anil Minstry presented a database for recording protein crystallization results. An additional presentation was made by Jean-Luc Eiselé on PIPEX - a computer-controlled motorized pipette system, which is based on the Rainin EDP-Plus motorized pipetter interfaced to the parallel port of a PC.

A round-table discussion on membrane protein crystallization, chaired by Hartmut Michel, summarized the practical results of 12 groups of workshop participants. It was followed by a session of hot results, chaired by Enrico Stura, which concluded the conference. Speakers at this session included Reuben Lebermann, Bill Boys, S.-X. Lin, Young Hee Ko, Noam Adir, Satoshi Ebina, Abel Cracamo and Kris Thiessen. In this session, crystallizations of two membrane proteins namely, human tissue growth factor receptor and cystic fibrosis transmembrane conductance regulator were presented by Bill Boys and Young Hee Ko, respectively. In both cases, the

strategy of the expression, purification and crystallization of the extra- and intracellular domains were presented as a viable alternative to the difficult task of crystallization of the entire receptor.

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Conference Organizers

JANUSZ M. SOWADSKI

*University of California, San Diego, USA*

ENRICO A. STURA

*The Scripps Research Institute, La Jolla, USA*