Keystone Symposia: Structural Biology (Joint with "Structural Genomics")

January 8–13, 2010 • Beaver Run Resort • Breckenridge, Colorado • USA

Scientific Organizers: Alasdair C. Steven, Pamela J. Bjorkman and Andrej Sali

Program Faculty & Talks

Steven C. Almo◊, Albert Einstein College Of Medicine, USA
Sequence, Structure, Function, Immunity

Ad Bax◊, National Institute of Diabetes and Digestive and Kidney Diseases, NIH, USA
Combining Solution NMR with SAXS

Pamela J. Bjorkman*◊, California Institute of Technology, USA
Fc Receptors: From Molecules to Cells

Jamie H.D. Cate◊, University of California, Berkeley, USA
The Ribosome: New Structures, New Insights

Wah Chiu◊, Baylor College of Medicine, USA
Seeing Protein Backbone and Side-Chains in Molecular Machines by Cryo-EM

G. Marius Clore, National Institute of Diabetes and Digestive and Kidney Diseases, NIH, USA
Short Talk: Detecting and Visualizing Sparsely Populated Protein States

Angela M. Gronenborn, University of Pittsburgh, USA
Synergy between cryo-EM and NMR - Novel Findings for HIV capsid Function

Jay T. Groves, University of California, Berkeley, USA
Spatial and Mechanical Regulation of Signal Transduction in Cell Membranes

Albert Heck, Utrecht University, The Netherlands
Native Mass Spectrometry applied to Virus Structure and Assembly

Roger W. Hendrix†◊, University of Pittsburgh, USA
The Virome and Evolutionary Relationships

James H. Hurley, National Institutes of Health, USA
The ESCRT Complexes in Membrane Scission and Budding

Grant J. Jensen, California Institute of Technology, USA
Bacterial Cryotomography

John (Jack) E. Johnson, The Scripps Research Institute, USA
Virus Assembly and Evolution

Dorothee Kern, Brandeis University, USA
Short Talk: Panorama of a Signaling Protein: Excursions in silico and in proteo

Tanja Kortemme, University of California, San Francisco, USA
Prediction, Design and Engineering of Protein Interactions and Networks

Ohad Medalia, Ben-Gurion University, Israel
Structural Insight into the Nuclear Pore Complex by Cryo-Electron Tomography

Beat H. Meier, ETH Zurich, Switzerland
Amyloid and Prion Structure by Solid-State NMR: What Can We Learn?

Hartmut Michel♦◊, Max Planck Institute for Biophysics, Germany
Structural Genomics and Proteomics of Membrane Proteins

William E. Moerner♦◊, Stanford University, USA
Single Molecule Approaches to Biomolecular Dynamics and Imaging of Cellular Superstructures

Daniel J. Mueller◊, Technology University Dresden, Germany
Imaging and Sensing Living Cells to Molecular Resolution

Eva Nogales, HHMI – University of California, Berkeley, USA
Microtubule-Kinetochore Interactions

Andrej Sali◊, University of California, San Francisco, USA
Integrative Determination of Macromolecular Structures

Mark Sansom, University of Oxford, UK
Multi-Scale Simulations of Membrane Proteins

Gideon Schreiber, Weizmann Institute, Israel
Interfaces Controlling Protein-Protein Interactions

Alasdair C. Steven*◊, National Institute of Arthritis, Musculoskeletal and Skin Diseases, USA
Amyloid Polymorphisms from Cryo-EM

Natalie Strynadka†, University of British Columbia, Canada
Mechanisms of Bacterial Secretion

David I. Stuart◊, Oxford University, UK
Pushing the Envelope on Viruses

Joel Sussman, Weizmann Institute of Science, Israel
Natively Unfolded Proteins

Florence Tama, University of Arizona, USA
Getting it Together, EM and Crystal Structures

James A. Wells, University of California, San Francisco, USA
Talk Title to be Determined

Ian A. Wilson*◊, The Scripps Research Institute, USA

Cynthia Wolberger, Johns Hopkins School of Medicine, USA
Transcription Complexes by X-Ray Crystallography

Kurt Wüthrich*◊, ETH Zurich/The Scripps Research Institute, Switzerland

♦Keynote speaker. *Session Chair. † Invited not yet confirmed. ◊Speaker in a joint session.

Program subject to change. Current as of Sept. 8, 2009

Static depictions are appearing in ever-increasing numbers of the detailed structures of individual macromolecules. A key challenge for structural biology is how to parlay this reservoir of fundamental information into a comparably detailed understanding of how functional complexes assemble; what ranges of alternative conformations they may assume at successive stages of their functional cycles; how they recognize each other; how their propensities to bind small molecules, cofactors and other macromolecules are specified; and how they behave in cells. This meeting will explore ongoing developments in structural biology on several fronts including the following: the frontier between in vitro *and* in situ *observations; the frontier between traditional experimental approaches and newly emerging complementary ones; and the frontier represented by computational structural biology as a means to analyze, integrate and unify information emerging from diverse experimental sources.*

Program Plenary Sessions:

- Pushing the Limits of Structural Biology I: New and Innovative Methods (Joint)
- Interactions in Functional Complexes
- Unfolded, Misfolded and Alternatively Folded Proteins
- Computational Structural Biology I
- Pushing the Limits of Structural Biology II: Advances in Challenging Systems (Joint)
- Structural Biology of Prokaryotic Cells
- Macromolecular Complexes
- Computational Structural Biology II and Membrane Proteins

Deadlines:

Abstract & Scholarship: September 14, 2009
Late-Breaking Abstract: October 12, 2009
Early Registration: November 9, 2009

Registration Fee: US$665 Early/US$765 Regular
Student Discount: US$440 Early/US$540 Regular

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