Announcing Keystone Symposia’s 2015 conference on:

Hybrid Methods in Structural Biology

March 4–8, 2015
Granlibakken Resort
Tahoe City, California, USA

Scientific Organizers:
Jens Meiler, Patrick Cramer and Ron A. Milligan

As we study the structure and dynamics of more and more complex systems to better understand their biological function, each individual technology in the structural biology toolbox approaches its limitations. Only at the intersection of several techniques does it become possible to distinguish information that is biologically relevant from perturbations introduced by any individual approach. Moving forward, hybrid methods and integrated methods in structural biology play a key role in studying complex systems verifying each other’s results. The objectives of this meeting are two-fold: 1) To discuss novel and potentially disruptive technologies and/or combinations thereof to be added to the hybrid methods toolbox; and 2) To illustrate and discuss application of hybrid methods to important biological systems.

Session Topics:
- New and Potentially Disruptive Technologies: X-Rays, Neutrons, Electrons
- Membrane Proteins
- New and Potentially Disruptive Technologies: Spectroscopy and Spectrometry
- Protein Transporters
- Supramolecular Assemblies
- New and Potentially Disruptive Technologies: Computation

Discounted Abstract/Scholarship Deadline: Nov 6, 2014
Abstract Deadline: Dec 9, 2014
Discounted Registration Deadline: Jan 8, 2015

To see the full program and for additional details, visit www.keystonesymposia.org/15C2.
KEYSTONE SYMPOSIA
on Molecular and Cellular Biology

Hybrid Methods in Structural Biology (C2)
March 4-8, 2015 • Granlibakken Tahoe • Tahoe City, CA, USA
Scientific Organizers: Jens Meiler, Patrick Cramer and Ron A. Milligan
Sponsored by Vertex Pharmaceuticals Incorporated


WEDNESDAY, MARCH 4
Arrival and Registration

THURSDAY, MARCH 5
Keynote Address

*Jens Meiler*, Vanderbilt University, USA
Ad Bax, NIDDK, National Institutes of Health, USA
When NMR Alone Is Not Enough

New and Potentially Disruptive Technologies: X-Rays, Neutrons, Electrons

Richard Neutze, University of Gothenburg, Sweden
Serial Femtosecond Crystallography and Time-Resolved Wide-Angle X-Ray Scattering Studies of a Photosynthetic Reaction Center at an X-Ray Free Electron Laser

Christian Betzel, University of Hamburg, Germany
Latest Methods to Grow, Prepare and Score Micro- and Nano-Crystals for Future Free-Electron-Laser and Synchrotron Radiation Sources

Osamu Miyashita, RIKEN, Japan
Short Talk: Hybrid Approach for X-Ray Free Electron Laser Single Particle Analysis of Biomolecular Systems

Basil J. Greber, University of California, Berkeley, USA
Short Talk: Insights into Structure and Function of the Mammalian Mitochondrial Ribosome

Stefan Rausner, Max Planck Institute of Molecular Physiology, Germany
How to Kill a Mocking Bug - Structural Insights into Tc Toxin Complex Action

Panel Discussion 1

*Andrej Sali*, University of California, San Francisco, USA
Charles H. Greenberg, University of California, San Francisco, USA
Bayesian Modeling of Macromolecular Structures Based on Electron Microscopy Density Maps

Abhishek Singharoy, Arizona State University, USA
Structure Determination with Data-Guided Molecular Dynamics

Stephan Niebling, University of Gothenburg, Sweden
Coarse-Grained Protein X-Ray Scattering Calculations for the Analysis of Time-Resolved X-Ray Scattering

Lam T. Nguyen, California Institute of Technology, USA
Coarse-Grained Simulations Reveal Mechanisms of Bacterial Cell Wall Synthesis

Steffen Lindert, University of California, San Diego, USA
CryoEM-Guided Iterative Molecular Dynamics - Rosetta Protein Structure Refinement Protocol Improves Protein Model Quality

Graham T. Johnson, University of California, San Francisco, USA
Towards Whole Cells Modeled in 3D Molecular Detail and Community Curated with cellPACK

Clarence Y. Cheng, Stanford University, USA
Consistent and Blind Inference of RNA Tertiary Folds from Multidimensional Chemical Mapping Experiments

**Michiel J. van de Waterbeemd**, Utrecht University, Netherlands
Structure and Activity of the RNA Polymerase II - Capping Enzyme Complex Probed by Native Mass Spectrometry and other Structural Biology Methods

Membrane Proteins

*Andre Hoelz*, California Institute of Technology, USA
Architecture of the Nuclear Pore Complex Coat

Matthew T. Eddy, University of Florida, USA
Short Talk: Conformational Dynamics of G Protein-Coupled Receptors Studied by 19F NMR and Novel Isotopic Labeling Approaches

Leo Sazanov, Medical Research Council, UK
Structure and Mechanism of Respiratory Complex I

*Lukas K. Tamm*, University of Virginia, USA
Hybrid Structural Approaches to Resolve the Build-Up of the Exocytotic Fusion Pore

Poster Session 1

FRIDAY, MARCH 6

New and Potentially Disruptive Technologies: Spectroscopy and Spectrometry

*Robert Kaptein*, University of Utrecht, Netherlands
Dorothee Kern, Brandeis University, HHMI, USA
Ancestor Resurrection as a Microscope into a Cancer Drug’s Mechanism

Mathias Ferber, Institut Pasteur, France
Short Talk: Integrating the Solvent Accessible Surface Distance with Cross-Links-Based Modeling Methods Improves the Conformational Sampling of Protein Assemblies

Thomas Huber, Australian National University, Australia
Protein Structure Determination from Sparse Pseudocontact Shifts

Gunnar Jeschke, ETH Zurich, Switzerland
Structure and Flexibility of Soluble and Membrane Proteins from Sparse Experimental Data

Florian Stengel, University of Konstanz, Germany
Short Talk: Chemical Cross-Linking/Mass Spectrometry and the Structural Biology Toolbox

Judy E. Kim, University of California, San Diego, USA
Resonance Raman and FRET Studies of a Beta-Barrel Membrane Protein

Workshop 1: Integrated Modeling with the Integrative Modeling Platform

*Andrej Sali*, University of California, San Francisco, USA
Benjamin Webb, University of California, San Francisco, USA
Dina Schneidman, University of California, San Francisco, USA
Charles H. Greenberg, University of California, San Francisco, USA
Seung Joong Kim, University of California, San Francisco, USA

Workshop 2: Protein Structure Determination Form Limited Experimental Data with Rosetta

*Jens Meiler*, Vanderbilt University, USA
Rocco Moretti, Vanderbilt University, USA

* Session Chair † Invited but not yet accepted  Program current as of December 17, 2019. Program subject to change. Meal formats are based on meeting venue. For the most up-to-date details, visit https://www.keystonesymposia.org.
Electron Microscopy

*Alasdair C. Steven, NIAMS, National Institutes of Health, USA
Elizabeth Villa, University of California, San Diego, USA
Opening Windows into the Cell: Cryo-Electron Tomography of Intact Cells for Structural Cell Biology

Melody G. Campbell, The Scripps Research Institute, USA
Short Talk: Automated Near Atomic Resolution Electron Microscopy

Frank DiMaio, University of Washington, USA
Toward Automatic Structure Determination from Near-Atomic-Resolution cryoEM Density Maps

Yifan Cheng, University of California, San Francisco, USA
Study Membrane Protein Structures by Single Particle cryo-EM

Poster Session 2

SATURDAY, MARCH 7

Supramolecular Assemblies

*Frank DiMaio, University of Washington, USA
Patrick Cramer, Max Planck Institute for Biophysical Chemistry, Germany
Integrated Structural Biology of Genome Transcription

Andrew B. Ward, The Scripps Research Institute, USA
Short Talk: Viral Glycoprotein Antibody Complexes

Andrea Graziadei, EMBL Heidelberg, Germany
Short Talk: Investigation of the Methylation Mechanism of the Box C/D Ribonucleoprotein Complex

Alasdair C. Steven, NIAMS, National Institutes of Health, USA
Mapping Components of Macromolecular Complexes in Two and Three Dimensions by Bubblegram Imaging

Juli Feigon, University of California, Los Angeles, USA
The Architecture of Tetrahymena Telomerase Holoenzyme

Martin Beck, European Molecular Biology Laboratory, Germany
Integrated Structural Analysis of the Human Nuclear Pore Complex

Panel Discussion 2

*Patrick Cramer, Max Planck Institute for Biophysical Chemistry, Germany
Philip Lössl, Utrecht University, Netherlands
FIRM – An Integrated Mass Spectrometric Approach to Study the Impact of Protein Phosphorylation on the Dynamic Interactions of Mitotic Regulators

Vladimir Svetlov, New York University Langone Medical Center, USA
Short Talk: Docking Model of E. coli RNA Polymerase Complex with Transcription Factor NusA Guided by in vivo Chemical Cross-Links Mapped by Mass Spectrometry

Carolina Sánchez-Rico, Technical University of Munich, Germany
Study of the Conformational Dynamics of the Splicing Factor of U2AF65

Sebastian Westenhoff, University of Gothenburg, Sweden
Signal Transduction in Phytochrome Photosensors Visualized by Time-Resolved X-Ray Scattering

Thomas U. Schwartz, Massachusetts Institute of Technology, USA
Atomic Structure of the Y-Complex of the Nuclear Pore

Audray K. Harris, NIAID, National Institutes of Health, USA
Characterization of Influenza Virus Subunit Vaccines by Electron Microscopy

Alexey Amunts, Stockholm University, Sweden
Structure of Human Mitochondrial Ribosome Determined by cryo-EM

Yuehan Feng, ETH Zürich, Switzerland
Global Analysis of Protein Structural Changes in Complex Proteomes

New and Potentially Disruptive Technologies: Computation

*Michael Nilges, Institut Pasteur, France
Sarah Teichmann, Wellcome Sanger Institute, UK
A Periodic Table of Protein Complexes

Nikolaos G. Sgourakis, University of California, Santa Cruz, USA
Modeling Supramolecular Assemblies Using NMR and cryoEM Data

Jens Meiler, Vanderbilt University, USA
Protein Structure Determination by Integrating Limited Experimental Data

SUNDAY, MARCH 8

Departure