In order to understand the workings of a living cell, we need to know the structures and dynamics of individual biological macromolecules, their complexes and networks, organelles and whole cells, thus interfacing structural biology with cell biology, systems biology, proteomics, chemical biology and biophysics. The accuracy, precision, completeness and efficiency of structural characterization are maximized by hybrid or integrative approaches that combine data from multiple types of experimental methods through the use of computational analysis and modeling methods. These experimental methods include X-ray crystallography, NMR spectroscopy, electron microscopy, small angle X-ray scattering, mass spectrometry, chemical cross-linking, super-high resolution optical microscopy, optical microscopy and others. The goal of this meeting is to highlight the strengths and limitations of the current hybrid approaches as well as to identify new promising advances in experimental methods for collecting the data and computational methods for converting the data to models. Finally, hybrid approaches will be demonstrated by their applications to important and challenging biological problems, spanning a wide range of length and time scales, from atomic structures of individual proteins to low-resolution representations of whole cells.

Session Topics
> Computation for Hybrid Approaches
> Hybrid Approaches to Studying Dynamic Systems
> Hybrid Approaches to Studying Macromolecular Structures
> Hybrid Approaches to Studying Cellular Organization
> Single Molecule Methods
> Latest Advances in Hybrid Methods

Abstract & Scholarship Deadline: November 5, 2012
Late-Breaking Abstract Deadline: December 3, 2012
Early Registration Deadline: December 19, 2012

Note: Scholarships are available to students and postdoctoral fellows and require a brief application and submission of an abstract. Short talk speakers will also be selected from abstracts. Early registration saves US$150 on later fee. Information shown is subject to possible change. Please visit meeting website for the most up-to-date program information.
SUNDAY, MARCH 3
Arrival and Registration

MONDAY, MARCH 4
Opening Remarks and Keynote Address
*Andreas Sali, University of California, San Francisco, USA
*David Baker, University of Washington, USA
*Brian T. Chait, Rockefeller University, USA
Peter Walter, HHMI/University of California, San Francisco, USA

The Unfolded Protein Response in Health and Disease

Computation for Hybrid Approaches
*Ian A. Wilson, The Scripps Research Institute, USA
Andreas Sali, University of California, San Francisco, USA
David Baker, University of Washington, USA
Klaus J. Schulten, University of Illinois at Urbana-Champaign, USA
Timothy O. Street, University of California, San Francisco, USA
Ines Chen, Max Planck Institute for Biophysical Chemistry, Germany
Zaida (Zan) Luthey-Schulten, University of Illinois at Urbana-Champaign, USA

Whole Cell Simulations

Hybrid Approaches to Studying Dynamic Systems
*Alasdair C. Steven, NIAMS, National Institutes of Health, USA
James R. Williamson, The Scripps Research Institute, USA
Bo Huang, University of California, San Francisco, USA
Timothy O. Street, University of California, San Francisco, USA
Klaus J. Schulten, University of Illinois at Urbana-Champaign, USA

Poster Session 1

TUESDAY, MARCH 5

Hybrid Approaches to Studying Macromolecular Structures
*David Baker, University of Washington, USA
Ian A. Wilson, The Scripps Research Institute, USA
Holger Stark, Max Planck Institute for Biophysical Chemistry, Germany

Combining Cryo-EM, X-Ray and MD Simulations to Study Dynamic Macromolecular Complexes

Alasdair C. Steven, NIAMS, National Institutes of Health, USA
Eva Nogales, University of California, Berkeley, USA
David Baker, University of Washington, USA
Andreas Sali, The Scripps Research Institute, USA
Gregory A. Voth, University of Illinois at Urbana-Champaign, USA

Hybrid Approaches to Antibody-Virus Systems
*Ian A. Wilson, The Scripps Research Institute, USA

Integrative Approach
Structure of the 26S Proteasome Holocomplex Determined by an Integrative Approach

Mary E. Matyskiela, University of California, Berkeley, USA

Short Talk: Molecular Mechanisms of Substrate Degradation by the 26S Proteasome Revealed by CryoEM
Helen M. Berman, Rutgers University, Center for Proteomics Research, USA

Short Talk: The Protein Model Portal – A Comprehensive Web Resource For Protein Structure Information

Panel 1: Key Issues in Measuring, Computing, Analyzing, Visualizing, Archiving, and Disseminating Hybrid Models
*Andreas Sali, University of California, San Francisco, USA
Frank Alber, University California, Los Angeles, USA
David Baker, University of Washington, USA

Panel 2: Reproducibility and Publishing of Hybrid Models
*Andrew Morin, Harvard Medical School, USA
Helen M. Berman, Rutgers University, Center for Proteomics Research, USA
Ines Chen, Springer Nature, USA
Daniel Russel, University of California, San Francisco, USA
Klaus J. Schulten, University of Illinois at Urbana-Champaign, USA

Hybrid Approaches to Studying Cellular Organization
*James R. Williamson, The Scripps Research Institute, USA
Benjamin Geiger, Weizmann Institute of Science, Israel

Supramolecular Structures Involved in the Scaffolding and Signaling Processes in Focal Adhesions
Frank Alber, University California, Los Angeles, USA

Exploring Parallel Genome Universes
Graham T. Johnson, University of California, San Francisco, USA
cellPack: A Virtual Mesoscope to Model and Visualize Structural Systems Biology
Wolfgang P. Baumeister, Max Planck Institute of Biochemistry, Germany

Structure of the 26S Proteasome Holocomplex Determined by an Integrative Approach

Poster Session 2

WEDNESDAY, MARCH 6
Single Molecule Methods
*Eva Nogales, University of California, Berkeley, USA
Stefan W. Hell, Max Planck Institute for Biophysical Chemistry, Germany

Nanoscopy with Focused Light

* Session Chair † Invited but not yet accepted  Program current as of May 22, 2020. Program subject to change. Meal formats are based on meeting venue. For the most up-to-date details, visit https://www.keystonesymposia.org.
Joseph D. Puglisi, Stanford University, USA
Hybrid Studies of the Ribosome Function

Scott C. Blanchard, Weill Cornell Medicine, USA
Allosteric Control of the Ribosome by Small-Molecule Antibiotics

Yujie Sun, Biodynamic Optical Imaging Center, China
Allostery Revisited

Alexander Leitner, ETH Zurich, Switzerland
Short Talk: Generating Spatial Restraints with an Integrated Chemical Cross-Linking-Mass Spectrometry Platform and their Use in Hybrid Methods

Robin E. Stanley, NIEHS, National Institutes of Health, USA
Short Talk: Architecture of the Atg17 Complex as a Scaffold for Autophagosome Biogenesis

Workshop: Software for Integrative Structure Determination
* Klaus J. Schulten, University of Illinois at Urbana-Champaign, USA
  High-Resolution Comparative Modeling with RosettaCM

Corey F. Hryc, Baylor College of Medicine, USA
  EMAN and Pathwalker

Robert Paul Rambo, Lawrence Berkeley National Laboratory, USA
  SAXS Suite at LBNL

Juan R. Perilla, University of Illinois Urbana-Champaign, USA
  VMD

Daniel Russel, University of California, San Francisco, USA
  IMP

Latest Advances in Hybrid Methods
* Brian T. Chait, Rockefeller University, USA
  Mass Spectrometry and Proteomics for Hybrid Structure Determination

Carolyn A. Larabell, University of California, San Francisco, USA
  Correlated Fluorescence and X-Ray Tomography of Intact Cells

Yifan Cheng, University of California, San Francisco, USA
  Short Talk: A New Electron Counting CMOS Camera Enables Routine Near Atomic Resolution Single Particle cryoEM

Michael Nilges, Institut Pasteur, France
  Inferential Structure Determination from Hybrid Data

Closing Remarks
Andrei Sali, University of California, San Francisco, USA
David Baker, University of Washington, USA
Brian T. Chait, Rockefeller University, USA

THURSDAY, MARCH 7
Departure