Gordon Research Conferences

Meeting Details

Proteins

Gordon Research Conference

Exploring the Role of Proteins as Cellular Organizers by Combining Experiment and Theory

Dates

June 18-23, 2017

Location

Holderness School Holderness, NH **Organizers**

Chairs:

Catherine A. Royer & Vijay S. Pande

Vice Chairs:

Charles L. Brooks & Elizabeth M. Meiering

Application Deadline

Applications for this meeting must be submitted by **May 21**, **2017**. Please apply early, as some meetings become oversubscribed (full) before this deadline. If the meeting is oversubscribed, it will be stated here. *Note*: Applications for oversubscribed meetings will only be considered by the Conference Chair if more seats become available due to cancellations.

Meeting Description

The 2017 Proteins Gordon Research Conference has been conceived with two underlying leitmotifs. The first is to highlight proteins as cellular organizers, while the second and equally central theme of the meeting is the interplay between experiment and theory and modeling in modern protein research. Recent major advances in electron and optical microscopy have revealed amazing structural and spatial organization at the level of protein complexes and protein interactions. These advances will be featured by Andre Hoelz of CalTech who will describe the structure of the nuclear pore complex in the opening Keynote address. Our closing Keynote speaker, Carol Post of Purdue University, will address a combined computational and experimental approach to understanding the regulation of a tyrosine kinase. Several sessions will follow up on the theme of proteins as cellular organizers. Session 3 will address new super-resolution imaging of nuclear organization, while Session 4 will speak to the dynamic aspects of proteins as organizers in vesicle sorting and membrane remodeling. Two other sessions, one on the role of intrinsically disordered proteins and the other on protein biogenesis and interactions in vivo will weave in this leitmotif, as well. Given the ever increasing level of integration of experimental and theoretical approaches in protein science, both theory and experiment have been included in each session. In several cases, individual invited speakers will address both experimental and computational aspects of protein research. In other sessions, a combination of talks, some theoretical and others experimental, will address similar topics. Of the 24 invited speakers, we have worked to achieve a near complete balance between theoretical and experimental protein science. The topics for each session correspond to very exciting areas of protein research, in which major advances are currently being achieved. We believe that the combination of these crucial topics and combined approaches, with outstanding scientists who will speak to their work in these areas will make for a very stimulating conference.

Related Meeting



This GRC will be held in conjunction with the "Proteins" Gordon Research Seminar (GRS). Those interested in attending both meetings must submit an application for the GRS in addition to an application

for the GRC. Refer to the associated GRS program page for more information.

Contributors







Preliminary Program

The topics and speakers for the conference sessions are displayed below (italics denote discussion leaders). The Conference Chair is currently developing their detailed program, which will include the complete meeting schedule, as well as the talk titles for all speakers. The detailed program will be available by **February 18, 2017**. Please check back for updates.

- Keynote Session: The Structure of the Nuclear Pore Complex (Catherine Royer / Andre Hoelze)
- Shape-Shifters Functional Mechanisms of Intrinsically Disordered Proteins
 (Julie Forman-Kay / Martin Blackledge / Joan-Emma Shea / Jane Dyson / Rohit Pappu)
- High Resolution Visualization of Nuclear Organization (Jacqueline Cherfils / Marcelo Nollmann / Elizabeth Villa)
- New Protein Functions by Design or Evolution
 (Joan-Emma Shea / Brian Kuhlman / Tanja Kortemme / Lynne Regan / Michael Harms)
- Vesicle Sorting and Membrane Remodeling
 (Lila Gierasch / Jacqueline Cherfils / Gregory Voth)
- Molecular Mechanisms Underlying Protein Dynamics and Allostery
 (K.C. Huang / Brian Kobilka / Rommie Amaro / Liskin Swint-Kruse / Joshua Wand)
- Structural Modeling and Sparse Data
 (Martin Blackledge / Julie Forman-Kay / Nikolas Sgourakis)
- Protein Biogenesis and Interactions In Vivo
 (Jane Dyson / Lila Gierasch / Berndt Bukau / K.C. Huang / Marina Rodnina)
- Keynote Session: Understanding Regulation of Syk Tyrosine Kinase Interaction with Receptor ITAM, from Solution NMR to Computer Simulation (Vijay Pande / Carol Post)