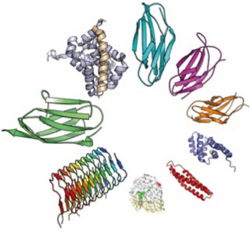
UNIVERSITY OF
CAMBRIDGE

Protein Folding Evolution Interactions

03 – 05 September 2017 | Cambridge, UK



Sun 3rd September 2017 - Opening Plenary Session

15:30 – 16:00	Registration
16:00 – 16:05	*Opening Remarks* Jane Clarke – University of Cambridge, UK
16:05 – 16:45	*From protein folding to membrane remodelling , Opening Plenary Lecture* Carol Robinson - University of Oxford, UK
16:45 – 17:10	*Protein Aggregation Energy Landscapes* Peter Wolynes - Rice University, USA
17:10 – 17:35	*How the proteasome selects its targets for degradation* Andreas Matouschek – University of Texas at Austin, USA
17:35 – 18:00	*Exploring allosteric pathways and interactions using native mass spectrometry* Amnon Horovitz – Weizmann Institute of Science, Israel
18:00 – 20:00	Drinks Reception

Mon 4th September 2017

Fundamentals of Folding

09:00 – 09:25	*Proteins as pH sensors and switches* Bertrand Garcia-Moreno – Johns Hopkins University, USA
09:25 – 09:50	*From MD simulations of all protein folds to the design of amyloid inhibitors* Valerie Daggett – University of Washington, USA

09:50 – 10:15	*Protein Folding and Dynamics* Thomas Kiefhaber – Martin Luther University of Halle-Wittenberg, Germany
10:15 – 10:40	*Modeling of unstructured and unfolded proteins interacting with their partners with multi-scale and multi-resolution methods* Charles Brooks III – University of Michigan, USA
10:40– 11:10	Coffee Break
11:10 – 11:35	*Metrics of Success in Protein Design* Elizabeth Meiering – University of Waterloo, Canada
11:35 – 12:00	*How to tie and untie protein knots* Sophie Jackson – University of Cambridge, UK
12:00 – 12:25	*Force-dependent upward curvature in Unfolding rate implies parallel pathways* Dave Thirumalai – University of Texas at Austin, USA
12:25 – 12:50	*Protein PIMPing: Elaboration of old scaffolds for new functions* Laura Itzhaki – University of Cambridge, UK
12:50 – 13:15	*Nearest-neighbor thermodynamic models applied to folding of tandem repeat proteins* Doug Barrick – Johns Hopkins University, USA
13:15 – 14:30	Lunch Break

Intrinsically Disordered Proteins

14:30 – 14:55	*Folding and unfolding of disordered proteins in cells* Philipp Selenko, FMP Berlin, Germany
14:55 – 15:20	*Coupled folding and binding reactions in transcriptional regulation* Sarah Shammas – University of Oxford, UK
15:20 – 15:45	*Kinetic control of competing IDP-protein interactions in gene regulation* Jacqui Matthews – University of Sydney, Australia
15:45 – 16:15	Coffee Break

Interactions and Dynamics

16:15 – 16:40	*Promiscuous protein assembly as a function of interface plasticity and protein stability* Gideon Schreiber – Weizmann Institute of Science, Israel
16:40 – 17:05	*Revisiting protein heat capacity and enzyme catalysis* Vic Arcus – University of Waikato, New Zealand
17:05 – 17:30	*The role of dynamics in the catalytic mechanism of ubiquitin E3 ligases* Mark Bycroft – MRC LMB Cambridge, UK
17:30 – 17:55	*Spatiotemporal organization of the bacterial outer membrane* Colin Kleanthous – University of Oxford, UK
18:00 – 20:00	Poster Session

Tues 5th September 2017

Single Molecules

09:00 – 09:25	*Location makes a difference in protein folding – the effects of the ribosome and "random" housing assignments at Coolfont* Susan Marqusee – University of California, Berkeley, USA
09:25 – 09:50	*Resolving differences between single-molecule and ensemble experiments using all-atom simulation* Robert Best – National Institutes of Health, USA
09:50 – 10:15	*Binding without folding: extreme disorder in a a high-affinity protein complex* Ben Schuler – University of Zurich, Switzerland
10:15 – 10:40	*Hidden in the structure: proteins that challenge paradigms* Emanuele Paci - University of Leeds, UK
10:40 – 11:10	Coffee Break

Aberrant Assembly

11:10 – 11:35	*How to Assemble a Fibril: A Feat of Folding* Sheena Radford – University of Leeds, UK
11:35 – 12:00	*Islet amyloid and the biophysics of beta-cell death* Daniel Raleigh – Stony Brook University, USA

12:00 – 12:25 *What small molecules teach us about big oligomers*
Andrew Miranker – Yale University, USA

12:25 – 12:50 *Using biophysics to find a drug for sickle cell disease*
William Eaton – National Institutes of Health, USA

12:50 – 14:15 Lunch Break

Evolution

14:15 – 14:40 *How do proteins evolve?*
Daniel Tawfik – Weizmann Institute of Science, Israel

14:40 – 15:05 *Evolution and dynamics of protein complexes*
Sarah Teichmann – Wellcome Trust Sanger Institute, UK

15:05 – 15:30 *Understanding evolution on multiple scales: from protein physics to population genetics and back*
Eugene Shakhnovich – Harvard University, USA

15:30 – 16:00 Coffee Break

Closing Plenary Session

16:00 – 16:45 *Protein Aggravation, Closing Plenary Lecture*
Alan Fersht - University of Cambridge, UK

16:45 – 17:10 *Exploring protein function: the convergence of structure based models and co-evolutionary information*
José Onuchic – Rice University, USA

17:10 – 17:40 *Keeping it in the Family*
Jane Clarke – University of Cambridge, UK

With thanks to our sponsors:

JBC | JOURNAL OF BIOLOGICAL CHEMISTRY

AstraZeneca

Sparrho

IPSEN
Innovation for patient care

AppliedPhotophysics