

Alan Fersht - Gonville and Caius College, University of Cambridge, UK

From engineering mutations to study folding and stability to drugging

p53 oncogenic mutants

Ken Dill - Stony Brook University, USA

How protein folding may hold the key to origin of life

George Makhatadze - Rensselaer Polytechnic Institute, USA

Novel Tool for Biophysical Studies of Amyloidogenesis

Joan-Emma Shea - University of California, Santa Barbara, USA

Self-Assembly of the Tau Protein: Liquid-Liquid Phase Separation
and Fibrillization

Michele Vendruscolo - University of Cambridge, UK

Targeting protein aggregation in misfolding diseases

Gary Pielak - University of North Carolina at Chapel Hill, USA

Protein stability in living cells & under crowded conditions in vitro

Ellinor Haglund - University of Hawai'i at Mānoa, USA

The folding and function of proteins with a complex topology

Wim Vranken - Vrije Universiteit Brussel, BE

Defining and predicting conformational variability

Mihaly Varadi - EMBL-EBI, UK

Navigating the Flood of Predicted Protein Structures: Challenges and Opportunities for Understanding Disease

**Jiří Vondrášek - Institute of Organic Chemistry and Biochemistry
of the CAS, CZ**

Domain context determines function in chimeric multidomain proteins

Brian Baker - University of Notre Dame, USA

The structural biophysics of specificity in cellular immunity

Silvio Tosatto - Università di Padova, IT

CAID 2: lessons from the second critical assessment of protein intrinsic disorder prediction

Benjamin Schuler - University of Zurich, CH

Probing the dynamics and interactions of disordered proteins with single-molecule spectroscopy: From disordered complexes to phase separation

Gabriella Heller - University College London, UK

Drugging disordered proteins using NMR and MD

Virginia Burger - New Equilibrium Biosciences, USA

Targeting intrinsically disordered proteins with small molecule drugs

Paul Robustelli - Dartmouth College, USA

Molecular recognition mechanisms of intrinsically disordered proteins

Kamil Tamiola - Peptone Ltd., CH

Rational modulation of intrinsic disorder in cytokines using generative AI

Klára Hlouchová - Charles University, CZ

Towards artificial proteins and alternative alphabets

Konstantinos Tripsianes - Masaryk University, CZ

Order-disorder continuum in protein function and disease

Mikael Oliveberg - Stockholm University, SE

Functional optimisation of diffusive protein-protein interactions in live cells

List of posters

- 1. Molecular dynamic simulation study of multiple phosphorylations at the proline rich region of tau(210-240) peptide**
Krishnendu Bera - CEITEC MU, Department of Chemistry and National Centre for Biomolecular Research, Faculty of Science, Masaryk University
- 2. Simulation of oligosaccharide binding to HEV32 domain**
Jan Beránek - University of Chemistry and Technology, Prague
- 3. Predicting ion binding sites in proteins using machine learning**
Christos Feidakis - Charles University, Faculty of Science, Department of Cell Biology
- 4. Experiment Insight in Preferential Interactions in Bio-Soft Matter**
Jan Heyda - University of Chemistry and Technology, Prague
- 5. Unraveling Protein Patterns: The Unexplored Potential of Large Language Models**
Tomáš Honzík - University of West Bohemia
- 6. Engineering of a novel two-enzyme fusion system for PET degradation**
Jiraskova Katerina - Institute of Organic Chemistry and Biochemistry of the CAS
- 7. Protein substrate encapsulation in the GroEL/ES cage causes its destabilization due to a reduced hydrophobic effect**
Ilia Korobko - Weizmann Institute of Science, Israel
- 8. Using a Novel ANN to Design Artificial Promoter-Operator Constructs**
Lukáš Kuhajda - University of West Bohemia
- 9. Inhibitors of the mitochondrial rhomboid protease PARL modulate the PINK1/Parkin axis enhancing mitophagy**
Denise-Liu` Leone - Institute of Organic Chemistry and Biochemistry of the CAS
- 10. Specific ion effects on amino acid dissociation equilibria**
Varun Mandalaparthu - Technical University Darmstadt
- 11. New protein reactive centers against aspartic proteases**
Martina Mičková - Institute of Organic Chemistry and Biochemistry of the CAS; Faculty of Science, Charles University
- 12. Dances with enzymes: Multiscale simulation of glycolytic enzyme assembly formation**
Tom Miclot - Department of Computational Chemistry, J. Heyrovský Institute of Physical Chemistry

- 13. TRANSIENT OLIGOMERIZATION AND AGGREGATION OF HUMAN LEPTIN**
Grace Orellana - University of Hawaii at Manoa
- 14. Engineering of autocatalytic activity of HIV-1 protease**
Klára Poštulková - Institute of Organic Chemistry and Biochemistry of the CAS
- 15. Sequence fingerprint of structured and disordered proteins**
Patrícia Sotáková - Institute of Organic Chemistry and Biochemistry of the CAS
- 16. Protein tunnels, channels and pores, ChannelsDB & MOLEonline**
Anna Špačková - Placký University Olomouc
- 17. Dynamical allostery of multi-domain protein complexes**
Josef Šulc - Institute of Organic Chemistry and Biochemistry of the CAS
- 18. Analysis and Sampling of Molecular Simulations by adversarial Autoencoders**
Guglielmo Tedeschi - University of Chemistry and Technology, Prague.
- 19. Linking the Diffusive Dynamics of Bacterial Proteome to Cell Metabolism and Death**
Štěpán Timr - J. Heyrovský Institute of Physical Chemistry
- 20. To mistranslate or not to live**
Vjaceslav Tretjachenko - Weizmann Institute of Science
- 21. Proteolytic profiles of human AMBN by MMP-20 and KLK-4 proteases**
Veronika Vetýšková - Institute of Organic Chemistry and Biochemistry of the CAS
- 22. Accurate modeling of free energy landscapes enables “Unstructure”-based drug discovery for IDPs**
Bentley Wingert - New Equilibrium Biosciences