



**BRAINSTRUC**

## Mini-symposium on Protein design, structure determination and intrinsic structural disorder

*Copenhagen Biocenter, Ole Maaløes Vej 5, Seminar room 1-2-03*  
**Monday Sept 16<sup>th</sup> 13:00-16:00**

The Department of Biology and the REPIN, BRAINSTRUC and PRISM centres are pleased to invite you to a mini-symposium on a range of current and important topics in protein science. *No registration is required, and the symposium is open to all.*

### Programme

13:00-13:45 **Ingemar André**, Lund University  
Computational design of protein and peptide self-assembly

13:55-14:40 **Frank DiMaio**, University of Washington,  
Improving protein structure determination through data-driven forcefield optimization

15:00-16:00 **A. Keith Dunker**, Indiana University School of Medicine  
Intrinsically Disordered Proteins, Alternative Splicing, and Post-translational Modification (IDP-AS-PTM): A Toolkit for Developmental Biology

### About the speakers

**Ingemar André**, Department of Biochemistry and Structural Biology, Lund University  
Prof. André's research lies at the interface between computational and experimental protein science, and deals with, for example, designing protein assemblies, using computational structural biology to study evolution and developing and applying methods to study conformational ensembles in solution  
Web: <https://www.andrelab.org>  
Publications: <https://scholar.google.se/citations?user=gFPAWgMAAAAJ>

**Frank DiMaio**, Institute for Protein Design and Department of Biochemistry, University of Washington  
Prof. DiMaio develops and uses computational methods to determine protein structure and design new protein sequences. He is part of the internationally renowned institute of protein design where he is part of the development of the Rosetta suite of tools. Recent research includes using Rosetta to refine CryoEM structures and developing improved methods for protein design  
Web: <https://dimaiolab.ipd.uw.edu>  
Publications: <https://scholar.google.com/citations?user=5t2eBF0AAAAJ>

**A. Keith Dunker**, Center for Computational Biology and Bioinformatics, Department of Biochemistry and Molecular Biology, Indiana University Schools of Medicine and Informatics  
Prof. Dunker is a pioneer in the study of intrinsically disordered proteins, and played a central role in defining the concept and demonstrating its many important roles in biology, evolution and disease. Key discoveries include defining sequence features for disorder and thereby developing prediction methods, and in demonstrating how intrinsic disorder is pervasive across all domains of life, and in regulating complex biological signaling networks.  
Web: <https://medicine.iu.edu/research/centers-institutes/computational-biology-bioinformatics/>  
Publications: <https://scholar.google.com/citations?user=4agt6FcAAAAJ>