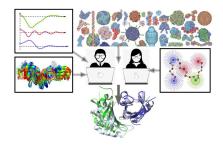
## **CANCELLED**: Algorithms for integrative structural biology



Contribution ID: 30 Type: Oral

## Current bottlenecks in protein assembly prediction

Protein-protein interactions play a central role in all biological processes. These processes result from the physical interaction of two or more protein molecules, forming a macromolecular assembly.

The CAPRI (Critical Assessment of PRedicted Interactions) experiment has been a proven catalyst of docking algorithms since its inception almost two decades ago. In recent years, the CAPRI experiment has diversified and now includes the prediction of multi-component assemblies, of protein-peptide, protein-nucleic acid and protein-polysaccharide binding, and of binding affinities and high-resolution prediction of interfacial water molecule positioning.

I will give an overview of the experiment and what it can do for you as computational or experimental biologist. In the context of the workshop, I will not only highlight its successes, but very specifically point out the current failures of protein docking and assembly prediction.

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**Presenter:** LENSINK, Marc (CNRS) **Session Classification:** Session 3