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SEMINAIRE

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"Assessing the similarity of the residue pairing landscape in the interaction networks of protein complexes. "

In the cellular environment, several enzymes exhibit the ability to form dynamic assemblies. In particular, glycolytic enzymes coalesce into glycolytic enzyme assemblies (G-bodies). However, if there are hypotheses as to their regulatory role in glycolysis, the precise mechanisms governing the formation of these structures remain poorly understood.
This talk delves into enzyme assemblies and seeks to unravel the involvement of amino acid pairs in their formation. Using Molecular Dynamics (MD) simulations, we explore the effectiveness and limitations of the Martini 3 force field in elucidating protein assemblies. We are also developing a new analysis method to increase knowledge of the factors that contribute to the formation of residue-pair networks involved in protein-protein interactions. This tool represents a starting point for a comprehensive understanding of enzyme assemblies mechanisms.

Jeudi 19 octobre 2023

14h30

Salle des conférences