CRBM external seminar

BIOLuM

Thursday Dec 12th at Salle Marcel Dorée (CRBM) 11:00 am

Intrinsically Disordered Proteins: Bridging Sequence Features, Molecular Functions and Cellular Phenotypes

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Dr. Zsuzsanna Dosztányi is a group leader at the Department of Biochemistry, Eötvös Loránd University (ELTE), Budapest. Her research focuses on the structural and functional properties of intrinsically disordered proteins (IDPs) and their roles in various diseases. She is internationally known for development of innovative bioinformatics tools, including IUPred, for predicting disordered regions, and ANCHOR, for identifying disordered binding sites from amino acid sequences. Her work on IDPs has significantly advanced the understanding of this novel protein class, contributing to numerous high-impact publications and resources in the field. She is currently involved in three EU funded grants and actively participates in ELIXIR (Life Science Infrastructure for Europe), currently serving as the vice-chair of the ELIXIR Board.

Abstract: IDPs defy the classical structure-function paradigm, achieving function through dynamic conformational ensembles and transient, specific interactions. Central to signaling and regulatory networks, IDPs play critical roles in cellular processes, with their dysregulation linked to diseases like cancer and genetic disorders. Despite their significance, the experimental characterization of IDPs remains challenging, highlighting the importance of computational approaches in connecting sequence features to molecular functions and phenotypes. Recent advancements in deep learning, which have revolutionized structure prediction for globular proteins, also hold transformative potential for IDP research. This talk will explore how novel approaches can be used to identify functional regions within IDPs, predict their interactions, and map their involvement in disease processes, in order to deepen our understanding of how IDPs orchestrate complex cellular processes and contribute to disease biology.

Selected publications:

Erdős G, Dosztányi Z. (2024) Deep learning for intrinsically disordered proteins: From improved predictions to deciphering conformational ensembles. Curr Opin Struct Biol. 89: 102950.

Kurgan L, Hu G, Wang K, Ghadermarzi S, Zhao B, Malhis N, Erdős G, Gsponer J, Uversky VN, Dosztányi Z (2023). Tutorial: a guide for the selection of fast and accurate computational tools for the prediction of intrinsic disorder in proteins. Nat Protoc.;18: 3157-3172.

Szaniszló T, Fülöp M, Pajkos M, Erdős G, Kovács RÁ, Vadászi H, Kardos J, Dosztányi Z. (2022) The interaction between LC8 and LCA5 reveals a novel oligomerization function of LC8 in the ciliary-centrosome system. Sci Rep. 12: 15623.

Necci M, et al. (2021) Critical assessment of protein intrinsic disorder prediction. Nat Methods. 18: 472-481.

Erdős G, Pajkos M, Dosztányi Z. (2021) IUPred3: prediction of protein disorder enhanced with unambiguous experimental annotation and visualization of evolutionary conservation. Nucleic Acids Res. 49(W1):W297-W303.