Centre de Recherche de Biologie cellulaire de Montpellier
CRBM / CNRS – Université de Montpellier
1919 Route de Mende, 34293 Montpellier Cedex 05

2027 Internship Offer

Master 1: YES – Duration: 5 months **Master 2**: YES – Duration: 6 months

Team, Contact	Zsuzsanna DOSZTANYI, CRBM, zsuzsanna.dosztanyi@crbm.cnrs.fr
Title	**Decoding protein disorder with novel machine learning tools**
Research Themes and questions	Intrinsically disordered proteins (IDPs) play central roles in cellular regulation, signaling, and biomolecular condensate formation. Unlike classical globular proteins, IDPs do not adopt a single stable three-dimensional structure but instead populate dynamic ensembles of conformations. Despite their abundance in the human proteome and their involvement in numerous diseases, including cancer and neurodevelopmental disorders, the relationship between sequence, conformational behavior, and function remains poorly understood. Recent advances in artificial intelligence have created unprecedented opportunities to study these proteins at scale. In this project, we aim to understand how the molecular properties of intrinsically disordered proteins determine their cellular functions and to identify sequence features associated with regulation, interaction networks, and disease using novel machine learning methods.
Methods and experimental approaches	The project involves the application of bioinformatics and machine-learning approaches to investigate the functional and conformational properties of intrinsically disordered proteins. State-of-the-art AI tools, including protein language models and protein structure prediction methods, will be used to identify functional regions, interaction motifs, conformational features, and phase-separation propensity directly from protein sequences. The work will integrate sequence, evolutionary, structural, and functional information to characterize protein disorder, predict biologically important regions, and assess how genetic variants may alter protein function.
2-3 Publications	1. Pathogenic variations illuminate functional constraints in intrinsically disordered proteins. Deutsch N, Erdős G, Dosztányi Z. iScience. 2026 ;29(4):115215. doi: 10.1016/j.isci.2026.115215.

	2. Uncovering the BIN1-SH3 interactome underpinning centronuclear myopathy. Zambo B, Edelweiss E, Morlet B, Negroni L, Pajkos M, Dosztanyi Z, Ostergaard S, Trave G, Laporte J, Gogl G. Elife. 2024;13:RP95397.