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	**AI-Based Characterization of Dynamic Proteins Using Transfer Learning**
Research Themes and questions	Proteins are the molecular machines of life, carrying out virtually all cellular processes, from signaling and metabolism to gene regulation. Understanding how proteins function is therefore one of the central challenges of modern biology. Recent advances in artificial intelligence have transformed this field, with large-scale foundation models trained on millions of protein sequences and structures now capable of capturing rich information about protein evolution, structure, and function. However, many proteins remain difficult to characterize because they do not adopt a single stable three-dimensional structure and instead exist as highly dynamic molecular ensembles. We are interested in how representations learned by state-of-the-art protein AI models can be adapted to predict functional and biophysical properties that remain difficult to characterize experimentally.
Methods and experimental approaches	The project combines machine learning, data science, and computational biology, using Python programming, modern deep-learning frameworks, and large-scale biological datasets. The student will gain hands-on experience with state-of-the-art AI approaches, including transfer learning and protein foundation models, while developing novel methods to address fundamental challenges in protein biology.
2-3 Publications	1. AIUPred - Binding: Energy Embedding to Identify Disordered Binding Regions. Erdős G, Deutsch N, Dosztányi Z. J Mol Biol. 2025 ;437(15):169071. 2. Deep learning for intrinsically disordered proteins: From improved predictions to deciphering conformational

	ensembles. Erdős G, Dosztányi Z. Curr Opin Struct Biol. 2024;89:102950. 3. AIUPred: combining energy estimation with deep learning for the enhanced prediction of protein disorder. Erdős G, Dosztányi Z. Nucleic Acids Res. 2024;52(W1):W176-W181.