Internship 2018/2019
Master (M1/M2)

Multi-scale Molecular Modeling of the Dynamics of the Protein PIN1

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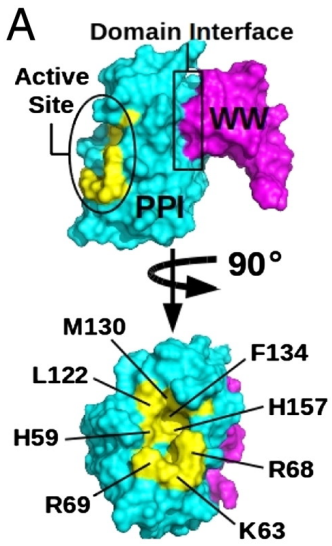

Motivations The protein called Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1) is an enzyme that isomerizes some prolines of peptides (or of other proteins), and regulates their activity. Since the activity of Pin1 is implicated in certain cancers, immune responses, or in Alzheimer's disease, understanding it may have therapeutic interests.

Objectives In collaboration with E. Miclet (Laboratoire des Biomolécules, Paris), this project aims at studying the dynamices of the PIN1 protein, both experimentally and theoretically. Thanks to Nuclear Magnetic Resonance and specific organic synthesis, it will possible to measure NMR chemical shifts and vicinal coupling $^3J\ H_N\text{-}H_\alpha$ within the protein. These data potentially contain information on the backbone dynamics of the protein, which is important for its enzymatic activity. The aim of the internship is to perform a multi-scale molecular modeling of the protein (first doing a dynamic at the coarse-grain level, and then to map the coarse-grain model into a all-atom model). The proton chemical shifts may then be calculated using empirical automated predictors.

Figure extracted from Namanja et al. PNAS, vol. 108 no. 30, 12289-12294 (2011) : Model of PIN1 with the two main domains called WW (violet) and PPI (light blue), with the chemical active site in yellow.

Candidate The student should be interested in biological molecules. She/he should have basic knowledge of protein structure, and of statistical physics. He/She should be willing to perform molecular modeling using computers (linux...).