Soutenance

THESE

Vendredi 08 Octobre 2021 à 16h

Visioconférence

Institut de biologie structurale - 71 avenue des Martyrs CS 10090 38044 Grenoble Cedex 9 - T.+33 (0)4 57 42 85 00

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par **Wiktor Adamski**

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Groupe Flexibilité et Dynamique des Protéines par RMN

Investigating the relationship between intrinsic protein disorder and biological function: Mapping interaction trajectories at atomic resolution using nuclear magnetic resonance spectroscopy and molecular simulation

Thèse de Doctorat de l'Université de Grenoble

The Thesis describes the intricacy of unfolded proteins dynamics probed by 15N NMR relaxation with dominant contribution of three dynamic modes representing distributions of timescales of motions occurring on ps-ns timescales. While the experimental sensitivity sets the limit on the accuracy of estimation of dynamic modes from NMR relaxation rates following application of Model-Free analysis within the limits of adiabatic approximation, the heterogeneous and distinct dynamic profiles of the distributions of timescales of motions featured by peptide units of three unfolded proteins under investigation reaffirm previous assignment of the dynamic modes to librational motions in a flat potential well, local dihedral sampling of the backbone and correlated motions of several peptide units (segmental motions). Systematic modification of the composition of the medium by addition of viscogen allows to assess the influence of crowding on local backbone dynamics of three unfolded proteins, in turn revealing tight coupling of local backbone motions to the solvent dynamics on different length and timescales. The relative orthogonality of the analysis with the previously reported one allows to combine the expression relating relative deceleration of peptide units as a function of temperature and viscosity to a single Einstein-Arrhenius equation. Relating the relative changes in viscosity to the perturbation of solvent dynamics, rather than to viscogen concentration allows to predict changes in the local dynamics of unfolded proteins in complex macromolecular environments of different physicochemical nature, beyond the range of conditions studied, with application to prediction of intrinsically disordered protein NH-backbone fluctuations in condensed phases and in cell.

Lien pour suivre par visioconférence : *https://cnrs.zoom.us/j/95355871657?pwd=aVVJV3EwQmNWd1ZsWmgzR0RqNkoyUT09*

(Meeting ID: 953 5587 1657, Passcode: cC0Mf6)