NMR Studies of Hierarchical Protein Dynamics

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A fundamental challenge in biology is to understand the complex interaction between protein motion and function. Due to the complexity of this interaction and the wide range of timescales on which protein motion occurs, this task remains hard or even impossible. Recently, Lewandowski and coworkers have shown that temperature dependent magic angle spinning multinuclear solid state NMR relaxation measurements, at temperatures ranging from 105 to 280K, can provide a window into the hierarchy of dynamic processes in proteins.[1] Other available methods often focus only on a specific transition and are limited. In contrast, solid-state NMR allows simultaneous access to a wide range of observables (here we observe sixteen different probes (4 relaxations parameter for 4 different nuclei) within one protein).

We have reproduced those results[1] with a high accuracy, validated the previously proposed model and extended the method of this studies to a different system to conclude on the universalism of those dynamics.

The reproduced experiments allowed us to map the energies related to the “glass transition”. Similar transitions in the relaxation patern can be observed for different probes within the protein and the solvent. We propose that internal motion can be model as a two-component system, where the higher energy motion (20-30 KJ.mol$^{-1)}$ dominates the lower energy motion (5-10 KJ.mol$^{-1)}$ with rising temperature.

Quantitative description of motions occurring in the protein and the solvent are dependent on the applied magnetic fields. Thus, we have validated our previous model using different fields strength, in order to obtain field-independent data: 9.4, 11.7, 14.1 and 18.8 T (400, 500, 600 and 800 MHz). Our model accurately predicts the results found for all the used fields strength.

A different protein (SH3) has also been studied, in order to see if the proposed model can predict fundamental properties shared by all soluble peptides. Our results show similar (but not identical) behavior for both proteins. We thus conclude, that small soluble protein show several similar dynamical properties, which can be accurately described by the presented model.

[1] Lewandowski, Józef R, Meghan E Halse, Martin Blackledge, Lyndon Emsley, *Science,* **2015,** 348, 578-81.