FROM SOLID TO SOLUTION: DYNAMICS OF PROTEIN SYSTEMS STUDIED BY FFC RELAXOMETRY

Paweł Rochowski, Danuta Kruk

University of Warmia and Mazury in Olsztyn, Faculty of Mathematics and Computer Science, 10-710 Olsztyn, Poland

Fast Field-Cycling Relaxometry is an NMR technique which provide the spin-lattice relaxation rates (R1) as a function of the resonant frequency (or, equivalently, the magnetic field strength). When studied over wide range of frequencies, the R1(ω) (relaxation dispersion profile) gives access to information on molecular dynamics of systems under investigation.

Dynamics of biomolecules is one of the key subjects of molecular science. The interest in revealing mechanisms of dynamical processes undergoing in biological systems is caused by the obvious relationship between dynamics of molecules and their functionality. To picturize dynamical behavior of proteins under diverse *biological* conditions we have performed series of experiments on model systems (based on bovine serum albumin - BSA): from solid state samples up to tissue-mimicking gels. Quantitative analysis of data, based on model-free approach, allowed us to point protein-proton and water-proton dynamics, and eventually estimate characteristic timescales of the motional processes (for example protein backbone dynamics ($\sim 10^{-6}$-10^{-7}s), modelular tumbling of dissolved protein or bound-water dynamics (10^{-8}s) etc.) contributing to the relaxation.

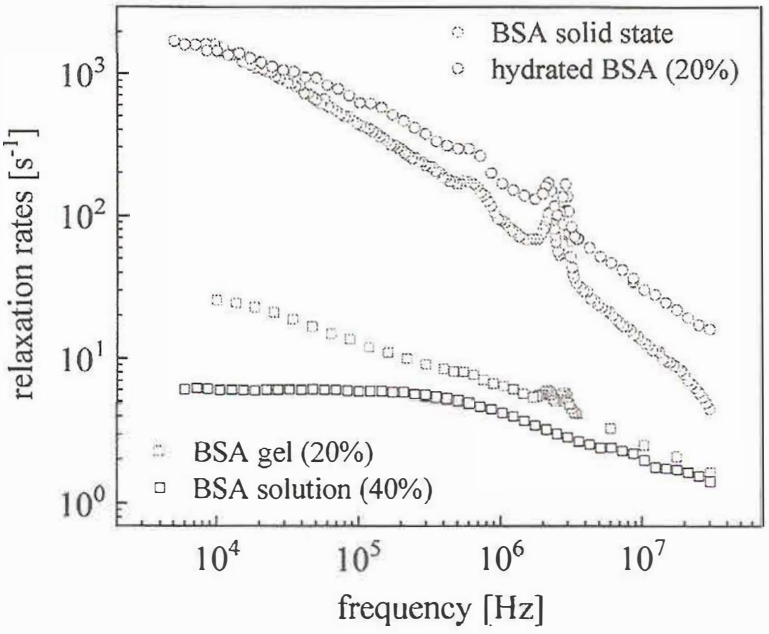

FIGURE 1. Exemplary dispersion profiles for Bovine Serum Albumin (BSA) systems at 20°C: from solid-state to protein solution.

Acknowledgements

This project has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 668119 (project "IDentIFY").