High resolution problems with biological samples

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Instead of “high resolution” I prefer “appropriate resolution” in a relevant time window. Biological samples are mostly aqueous solutions. Even with D_2O, there is a dominant water background scattering to be subtracted. The fraction of coherent to incoherent scattering varies with Q [1]. The resolution of protein internal dynamics is further limited by translational and rotational diffusion and the small accessible temperature range. These restrictions can be overcome, using hydrated samples: no diffusion, small water signals and a wide temperature range due to non-freezable water with stable structures and bio-activity [2]. Biological samples often come in small concentrations, mg/ml range, while reasonable inelastic signals and beam time require some 50 mg/ml. This problem can be partially overcome by focussing on the strong elastic component at variable resolution [3]. Merging data of several spectrometers in the time domain, reveals two dynamic components [4,5] as demonstrated with casein solutions [6,7]. The natively-disordered protein shows a third slow dynamic component, in excess to those of hydrated globular proteins.

References

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