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Contributed talk 9 - Crowding-induced protein cluster formation

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Protein cluster formation plays an important role in some pathological pathways and in drug delivery applications. Studying protein diffusion allows to reliably monitor cluster formation, as exemplified in a study combining several scattering techniques to determine the cluster sizes in β-lactoglobulin [1]. By investigating the short-time self-diffusion with incoherent quasi-elastic neutron backscattering (QENS) on the example of ovalbumin (OVA), we investigate crowding-induced cluster formation of OVA in aqueous (D_2O) solutions. To this end, the obtained diffusion coefficients are compared with the theoretical diffusion coefficients determined from the pdb structure of different cluster sizes. A monotonously increasing cluster size can be observed with increasing protein concentration within the accessed protein concentration range. While for low protein concentrations, the solution predominantly contains monomers, clusters larger than tetramers are observed for the highest investigated protein concentration. Different fit algorithms with and without imposing the dependence of the employed models on the scattering vector are applied, resulting in consistent results.

Besides the global diffusion providing information on the cluster size, information on the internal dynamics of the proteins is obtained simultaneously by the analysis of the QENS spectra. The internal dynamics of OVA is compared with the internal dynamics of bovine serum albumin, β-lactoglobulin and immunoglobulin.

[1] M. Braun et al., J. Phys. Chem. Lett. 8, 12, 2590-2596

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