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Short-Time Self-Diffusion of Salt- and Temperature-Dependent Protein Clusters

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Salt-induced charges in aqueous suspensions of proteins can give rise to complex phase diagrams including homogeneous solutions, large aggregates, and reentrant dissolution regimes. Moreover, depending on the temperature, a liquid-liquid phase separation may occur within the aggregation regime. Here, we systematically explore the phase diagram of the globular protein BSA via its dynamics as a function of temperature T and protein concentration c_p as well as of the concentrations c_s of trivalent salts YCl_3 and $LaCl_3$. By employing incoherent neutron backscattering spectroscopy at BASIS (SNS) with energy transfers up to 100 μeV, we unambiguously access the global and internal short-time self-diffusion of the protein clusters depending on c_p, c_s and T. We determine the cluster size in terms of effective hydrodynamic radii as manifested by the cluster center-of-mass diffusion coefficients D. For both salts, we find a simple functional form $D(c_p, c_s, T)$ in the parameter range explored. The master-curve observed previously [1] can be confirmed also for different temperatures and different salts. The salt- specific calculated binding probabilities and inter-particle attraction strengths, based on the short-time microscopic diffusive properties, increase with salt concentration and temperature in the regimes investigated and can be linked to the macroscopic behavior and to microscopy data.

[1] M. Grimaldo et al. J. Phys. Chem. Lett. 6 (2015)

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