Arrest scenarios in concentrated protein solutions

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The occurrence of an arrest transition or glass transition in protein solutions with increasing volume fraction is a highly relevant property both physiologically as well as industrially. A prime example where this transition plays a crucial role are pharmaceutically relevant protein formulations, where a viscosity increase can inhibit the injection of effective doses. A typical physiologically relevant case is presbyopia, or age-related farsightedness, where the pathological stiffening of the eye lens can be related to such liquid-solid transitions of the protein mixtures inside the eye lens cells. Here we show results from a systematic investigation of the structural and dynamic properties of different concentrated protein solutions over a large range of time and length scales. We combine a characterization of the solution structure based on small-angle x-ray scattering with measurements of the zero shear viscosity and a determination of the short time dynamics at length scales comparable to the nearest neighbour distance with neutron spin echo experiments. The experimental data is compared with results from computer simulations using different schemes such as MC, MD as well as hybrid approaches that allow for an incorporation of hydrodynamic interactions. This allows us to assess and predict important parameters such as interparticle interactions, stability and flow behaviour of concentrated protein solutions. We in particular highlight the enormous influence of weak attractive interactions known to exist between many globular proteins, discuss the effects of attraction-induced self assembly, and demonstrate the dramatic effects of anisotropic contributions to the potential such as attractive patches often present in proteins on the dynamic properties.