ARREST TRANSITIONS IN PROTEIN SOLUTIONS – INSIGHT FROM COMBINING SCATTERING, MICRORHEOLOGY, AND COMPUTER SIMULATIONS

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The static and dynamic properties of concentrated protein solutions are essential ingredients for our understanding of the cellular machinery or formulating biopharmaceuticals. Here a combination of advanced characterization techniques such as light and x-ray scattering, neutron spin echo measurements [1] and microrheology experiments [2], combined with the theoretical toolbox from colloid physics and state-of-the-art computer simulations [3], considerably enhances our understanding of the link between protein interactions and the stability, dynamics and flow properties of these solutions up to high concentrations. We will address the enormous influence of weak attractive interactions known to exist between many globular proteins, and demonstrate the dramatic effect of an interaction potential anisotropy [1] such as attractive patches and shape anisotropy [3] on the dynamic properties. We will also discuss how we can combine interparticle interaction effects and the formation of (transient) equilibrium clusters in an attempt to understand and predict properties such as the concentration dependence of the zero shear viscosity of dense protein solutions [4].

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