Protein as model colloid or the physics of dynamical arrest

T. Gibaud, F. Cardinaux, A. Stradner, P. Schurtenberger
Department of Physics, University of Fribourg
CH-1700 Fribourg, Switzerland
Email: thomas.gibaud@unifr.ch

We investigate the competition between spinodal decomposition and dynamical arrest using aqueous solutions of the globular protein lysozyme as a model system for colloids with short range attractions. For sufficiently deep quenches, below the tie line (Fig. 1), the spinodal decomposition becomes arrested as the composition of the dense phase crosses the glass line. The rheological properties of the resulting gels allow us to use centrifugation experiments to determine the local densities of both phases and to precisely locate the gel boundary and the attractive glass line close to and within the unstable region of the phase diagram [1]. By playing with the Coulombic repulsion due to the partially screened residual charges on the protein surface we show that for weakly charged particles the glass line position is fully determined by the short range attraction and independent of the repulsion [2]. We thus provide a new test ground for computer simulations and theoretical calculations in the current attempt to understand and generalize dynamical arrest in soft matter. Finally, I will discuss the rheological properties of the Gel.

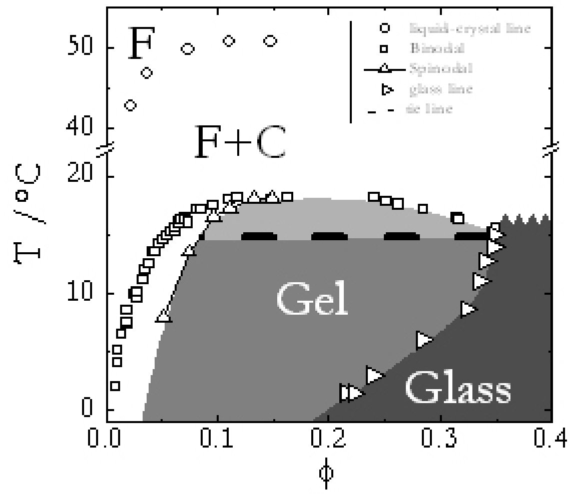

Fig1. *T-Φ* plane of the state diagram of aqueous lysozyme (20mM Hepes buffer, pH= 7.8, 0.5M NaCl. F: fluid, C: crystal.

[1] The interplay between spinodal decomposition and glass formation in proteins exhibiting short range attractions. F. Cardinaux, T. Gibaud, A. Stradner, P. Schurtenberger (submitted)
[2] Scaling of dynamical arrest and liquid-liquid phase preparation in proteins with short-range attraction. T. Gibaud, F. Cardinaux, J. Bergenholtz, A. Stradner, and P. Schurtenberger (in preparation)