

## Let's take a spherical horse - a colloid physicists view of protein solutions

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Looking at globular proteins with the eyes of a colloid scientist has a long tradition, in fact a significant part of the early colloid literature was focused on protein solutions. However, it has also been recognized that proteins are much more complex than the typical hard sphere-like synthetic model colloids. Proteins are not perfect spheres, and their interaction potentials are in general not isotropic, and using theories developed for such particles are thus clearly inadequate in many cases. Here I will make an attempt to critically discuss the somewhat controversial exploitation of colloid science concepts to better understand protein solutions. I will not only consider classical applications aimed at understanding and predicting solution stability and phase behaviour, but also discuss new challenges related to the dynamics, flow behaviour and liquid-solid transitions found in concentrated or crowded protein solutions. I will in particular address the problem of enhanced self-association in high concentration antibody solutions and the concomitant high viscosities often experienced as an important problem in the formulation of future antibody-based drugs. In order to understand and predict the thermodynamic and flow properties of such formulations, I will demonstrate that we can achieve a quantitative description of antibody self-association and viscosity as a function of concentration by combining experiments (static and dynamic scattering and microrheology), theory and computer simulations using a model based on analogies to patchy colloids.