The process of protein folding is highly dependent on the amino acid composition as well as on the solution condition, especially on the presence of denaturant. Our approach is to describe the dynamics and structure of the unfolded protein using polymer theory. Neutron scattering experiments have been performed as a function of denaturant type and denaturant concentration which has proved to be promising as demonstrated by single-molecule Förster resonance energy transfer FRET experiments[1,2].

Here, neutron spin-echo spectroscopy NSE is used to investigate the global and internal dynamics of proteins in solution in a time range up to 200ns. As a prerequisite small-angle neutron scattering SANS experiments have been performed to define the scattering strength of a respective sample. Furthermore, structural information of the protein in solution is obtained. Recently gained SANS results form Prothymosin alpha IDP at various solvent conditions will be presented.

SANS and NSE results of native and denatured Bovine Serum Albumin BSA in solution and at various concentrations of guanidine hydrochloride GndHCl and beta-mercaptoethanol will be presented as well. NSE studies of denatured BSA reveal a significant contribution of internal dynamics to the overall global diffusion that is clearly missing in the native state. We successfully showed that models from polymer theory are suitable for the interpretation of the observed motions. While BSA at 6M GndHCl follows quasi pure Zimm dynamics, dynamics of BSA at 4M GndHCl are best interpreted with a Zimm model including internal friction (ZIF) that reveals that an offset is required as contribution to all relaxation times.

References:

Date & time: Thursday, March 16, 2017 at 10:00 am
Location: Lecture Hall Y44-J-11, UZH Irchel

Contact: Prof. Ben Schuler, Email schuler@bioc.uzh.ch