



Polymers under Multiple Constraints

Polymer and Soft Matter Seminar

Tuesday,

11th February
2013

at: 2.15 pm

VDP3 1.04,
Von-
Danckelmann-
Platz 3,
06120 Halle

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Folding and Dynamics of Proteins and Peptides

Protein function is often regulated by binding to specific partners, which leads to conformational changes that can range from subtle rearrangements in the native structure to folding/unfolding processes in major parts of the protein or of the whole protein. In recent years, a large number of proteins has been described that are unfolded in the absence of their binding partners (“intrinsically disordered proteins”; IDPs). Folding of these proteins is coupled to a specific binding process. The protein function is tightly coupled to the binding/folding process. Aim of our work is to elucidate the mechanism of these coupled binding and folding reactions, in particular to determine whether binding occurs to the small fraction of native molecules that are in equilibrium with the unfolded state in the absence of the binding partner (conformational selection) or whether an unfolded or partially folded state binds and folding occurs on the partner (folding-after-binding). Our experiments have revealed intra- and intermolecular backbone and side-chain interactions that are important for the folding/binding process and enabled us to test the importance of protein/ligand interactions for the mechanism and the rate-limiting steps of the investigated coupled binding and folding process.

In the second part investigations on the dynamics of loop formation in unfolded polypeptide chains and of local fluctuations in folded proteins will be presented. In these experiments we use triplet-triplet energy transfer (TTET) to gain information on the dynamics in different states of proteins on the nanoseconds to microseconds time scale. In addition, time-resolved FRET measurements are used to determine dimensions and intramolecular diffusion coefficients of polypeptide chains.