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KEYNOTE 1 - Dynamics of intrinsically unfolded and partially folded proteins: Insights gained by quasielastic neutron scattering

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A general property of disordered proteins is their structural expansion that results in a high macromolecular flexibility. Quasielastic incoherent neutron scattering (QENS) is a well-suited experimental method to study protein dynamics from the picosecond to several nanoseconds and in the Ångström length-scale. In QENS experiments of protein solutions hydrogens act as reporters for the motions of methyl groups or amino acids to which they are bound. Neutron Spin-Echo spectroscopy (NSE) on the other hand, offers the highest energy resolution in the field of neutron spectroscopy and allows the study of slow collective motions in proteins up to several hundred nanoseconds and in the nanometer length-scale. In my presentation, I will summarize recent QENS and NSE results on the dynamics of the intrinsically disordered myelin basic protein (MBP) and the chemically denatured bovine serum albumin (BSA) (1,2,3). Using NSE experiments, we observed a high internal flexibility of the intrinsically disordered MBP and the denatured BSA in addition to centre-of-mass diffusion detected by dynamic light scattering. Internal motions measured by NSE were described using concepts based on polymer theory. The contribution of residue-solvent friction was accounted for using the Zimm model including internal friction (ZIF). Disulphide bonds forming loops of amino acids of the peptide backbone have a major impact on internal dynamics that can be interpreted with a reduced set of Zimm modes.

1. Stadler et al. 2014, Journal of the American Chemical Society 136 (19), 6987-6994
2. Ameseder et al. 2018, Physical Chemistry Chemical Physics 20 (7), 5128-5139
3. Ameseder et al. 2018, The Journal of Physical Chemistry Letters 9, 2469-2473

Author: Dr STADLER, Andreas (Forschungszentrum Jülich)

Presenter: Dr STADLER, Andreas (Forschungszentrum Jülich)

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