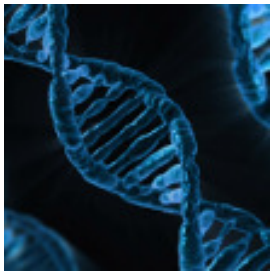

Contribution ID: **63** Type: **Oral presentation**

KEYNOTE 5 - Neutron Spinecho Spectroscopy: Protein internal dynamics, forces and friction

Tuesday 5 June 2018 08:30 (40 minutes)

The biological function of proteins is often related to large-scale domain motions, which are induced or suppressed by the binding of a substrate or due to cosolvents. Domain motions can be related to soft hinges, flexible linker regions or -as in the case of intrinsic unfolded proteins- be native to the unfolded protein structure. These large-scale domain motions in solution cannot be observed by X-ray crystallography or NMR spectroscopy. Small angle scattering by X-rays or neutrons in combination with neutron spin echo spectroscopy (NSE) in solution can be used to observe configurational changes and equilibrium dynamics between functional domains on 1-100 nanosecond timescale.
I present here examples for different types of motions related to the structure of proteins and bioconjugates. Thermal unfolded Ribonuclease A shows polymer like dynamics despite the 4 disulfide bonds restricting the degrees of freedom. Phosphoglycerate kinase shows a clear hinge motion between the main domains. PEGylation seems not to influence domain motion but adds additional internal dynamics in the protein-polymer complex. Immunoglobulin 1 (IGG1) presents a strong dynamics due to the short linkers connecting the Fc with the Fab domains.
Relevant forces and friction will be discussed in terms of the Ornstein-Uhlenbeck process.

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Session Classification: Antibody Dynamics and Internal Motion in Proteins

Track Classification: Antibody dynamics and internal motion in proteins