Structure dynamics and kinetics of folding and recognition in proteins by NMR

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Kinetics of protein dynamics will be discussed on examples of folded on unfolded proteins [1]. Protein recognition will be described with a new mathematical method to distinguish conformational selection and induced fit [2] which includes a concept for the measurement.

Further, the role of partially disordered proteins in droplet formation is investigated. The adaptor protein SLP65 which interacts with CIN85 [3]. The two proteins are essential for B cell activation. The protein is found to be mainly unstructured and its various segments entertain different functions or interact with membranes, SH3 domains and forming coiled coils. Based on the structures, a molecular lego will be described that reduces the SLP65/CIN85 interaction to its absolutely necessary essentials. The two proteins can perform phase separation which is related to function.

We are additionally interested in a class of IDPs that are important in neuro- and cellular degeneration, which form oligomers and fibrils. Interference with these aggregates specifically on the oligomer level proves to be a valid concept for treatment of devastating diseases such as Parkinson's, Alzheimer's, Creutzfeldt Jacob disease and Type II diabetes mellitus [4]. Suprising links to some cancers can be identified which will be also be discussed in the lecture [5].

References

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