Tata Institute of Fundamental Research
Survey No. 36/P, Gopanpally Village, Serilingampally, Ranga Reddy Dist., Hyderabad – 500 046

Seminar

Structure and Dynamics of Biomolecules by NMR and Molecular Dynamics Simulations: The Beginning of a Wonderful Friendship

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Biomolecular function is based on a complex hierarchy of molecular motions. Here, we report an approach to construct the *dynamic landscape* of biomolecules, which describes the aggregate influence of multiple motions acting on various timescales and on multiple positions in the molecule. We use NMR relaxation and molecular dynamics simulation data for the characterisation of fully hydrated phosphatidylcholine bilayers. The approach yields site-specific amplitudes of motion, separated both by type and timescale of motion. This separation allows the detailed description of the dynamic landscape, which shows vast differences depending on molecular position. The method is applicable to a broad range of molecular systems, and can be adapted to other timescale-sensitive techniques. The approach is further demonstrated to investigate the dynamics of the GHS G protein-coupled receptor. The GHS receptor (GHSR) binds the peptide ghrelin. We analyse molecular dynamics simulation trajectories using detectors to compare dynamics of the apo and ghrelin-bound states. Differences are identified in the extracellular loop 2 and transmembrane helices 5-7. NMR of the GHSR histidine residues reveals chemical shift differences in these regions. Analysis of the correlation of motions yields a high degree of correlation for the first 8 ghrelin residues, but less correlation for the helical end.

Thursday, Mar 20th 2025

11:30 Hrs (Tea / Coffee 11:15 Hrs)

Auditorium, TIFRH