INVITED SPEAKER

ANALYSING THE CONFORMATIONAL LANDSCAPE OF IDPS BY INTEGRATED NMR AND SMFRET

S. MILLES [1]

[1]*Institut de Biologie Structurale - Grenoble (France)*

Intrinsically disordered proteins (IDPs) lack clearly defined structure and are therefore highly flexible and easily adaptable to different binding partners. This makes them important players in many biological processes, often with vital regulatory functions. Their dynamic features and broad range of interaction modes, however, render them difficult to study and their complexes often require integrated approaches. Exploiting the complementary nature and distance dependence of nuclear magnetic resonance (NMR) and single molecule fluorescence, in particular single molecule Förster Resonance Energy Transfer (FRET), allowed us to study the conformational landscape of IDPs. We present an integrated approach using FRET efficiencies and fluorescence lifetimes, NMR chemical shifts and paramagnetic relaxation enhancements (PREs), as well as small angle X-ray scattering (SAXS) to derive quantitative conformational ensembles in agreement with all experimental parameters. We demonstrate the predictive nature of the derived ensembles, underlining the potential of this strategy in integrative dynamic structural biology.