**Disentangling the Structural Complexity of Disordered Biomolecular Assemblies**

Pau Bernadó
Centre de Biochimie Structurale, Montpellier, France

In the last decade Intrinsically Disordered Proteins (IDPs) have emerged as key actors in the vast majority of cellular events related with signalling, regulation and homeostasis. The inherent plasticity of IDPs, which lack of permanent secondary and tertiary structure, facilitates specific partner recognition. Importantly, interaction events are normally performed by short regions that rigidify upon binding and induce low affinity interactions. The structural characterization of these complexes is highly challenging due to the inherent flexibility of the non-interacting segments of the IDP and the thermodynamic equilibrium between bound and unbound species present in solution. The synergistic combination of SAS, Nuclear Magnetic Resonance (NMR) and advanced computational tools is the most adapted strategy to disentangle this complexity.
Examples of intrinsically disordered complexes involved in DNA repair and regulation of gene transcription will be presented. With these examples, new tools and strategies developed in the group to model disordered proteins and to study transient complexes will be described.