



University
of Basel

Department
Biozentrum



Basel Computational Biology Seminar

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NMR & Molecular Interactions

CNRS & Université de Lille

Lille, France

Coupled folding and binding of intrinsically disordered proteins to their partners: an interaction "filmed" by NMR spectroscopy

Intrinsically disordered proteins (IDPs) play important roles in biology, notably in signaling and regulation of key processes such as transcription and cell cycle control. They are consequently implicated in numerous types of disease, and their potential as drug targets is beginning to be recognized. In many cases, interaction with other proteins or assembly of protein complexes is key to their function, but their interaction mechanisms are still poorly understood. The interaction of the disordered C-terminal tail of Sendai virus nucleoprotein (NTAIL) with its folded partner, the PX domain of the phosphoprotein of this virus, can be considered an archetypical coupled folding and binding interaction of an IDP. We have studied this interaction in detail using NMR spectroscopy. We find that, during binding, a helical conformation of NTAIL already pre-configured in its free state is stabilized on the surface of PX in a dynamic encounter complex, before locating into its final binding site on PX at a rate coincident with intrinsic motions of its partner. Our study provides high-resolution structural and kinetic information about a complex folding and binding interaction and should help to understand the role of conformational disorder in biomolecular function.

Date: **Monday, March 04, 2019**

Time: **16:00 h**

Room: **Pharmazentrum, HS 2**

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