Dynamics and Interactions of Intrinsically Disordered Proteins from Single-Molecule Spectroscopy Ben Schuler

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The functions of proteins have traditionally been linked to their well-defined threedimensional, folded structures. It is now clear, however, that many proteins perform essential functions without being folded. Quantifying the highly dynamic and conformationally diverse ensembles of such unfolded or 'intrinsically disordered' proteins (IDPs) is an important aspect of understanding their functional mechanisms. Single-molecule spectroscopy is a versatile approach for investigating these systems. I will focus on highly charged IDPs and illustrate how single-molecule techniques combined with theory and simulations can be used to probe their distance distributions, dynamics, and interaction mechanisms.

Heidarsson, P.O., Mercadante, D., Sottini, A., Nettels, D., Borgia, M.B., Borgia, A., Kilic, S., Fierz, B, Best, R. & Schuler, B. (2021) Disordered proteins enable histone chaperoning on the nucleosome. Nat. Chem., in press

Sottini, A., Borgia, A., Borgia, M.B., Bugge, K., Nettels, D., Chowdhury, A., Heidarsson, P.O., Zosel, F., Best, R.B., Kragelund, B.B., & Schuler, B. (2020) Polyelectrolyte interactions enable rapid association and dissociation in high-affinity disordered protein complexes. Nat. Commun. 11, 5736.

Schuler, B., Borgia, A., Borgia, M.B., Heidarsson, P.O., Holmstrom, E.D., Nettels, D. & Sottini, A. (2020) Binding without folding – the biomolecular function of disordered polyelectrolyte complexes. Curr. Opin. Struct. Biol. 60, 66-76.

Borgia, A., Borgia, M., Bugge, K., Kissling, V.M., Heidarsson, P.O., Fernandes, C.B., Sottini, A., Soranno, A., Buholzer, K., Nettels, D., Kragelund, B.B., Best, R.B. & Schuler, B. (2018) Extreme disorder in an ultrahigh-affinity protein complex. Nature 555, 61-66.