Integrated structural biology - reaching out to you!

M. Sunnerhagen

Department of Physics, Chemistry and Biology, Linköping University, SE-58183 Linköping, Sweden, maria.sunnerhagen@liu.se

Protein function relies on conformational dynamics on a wide range of time scales. In particular, grasping the molecular origins of allostery and conformational ensemble shifts in critical systems holds important keys to understanding protein interactions in health and disease. However, the width of time scales involved means that we run a severe risk of being too limited in our perspective if we restrict our use to the one or two experimental methods within our "safe zone". In this talk, I will present recent work in our group and thereby describe how we jointly use NMR, crystallography, small angle scattering and molecular simulations to analyse proteins involved in transcriptional regulation and ubiquitination and their interactions. By describing our recent work on the structural and functional characterisation of the oncoprotein Myc, the gene regulator MexR, and proteins involved in ubiquitination and deubiquitination (TRIM21, USP14), I will provide examples of how my fairly small group at a local Swedish university have leveraged the impact of our results and widened our competence by using national and international infrastructures.

References

- [1] M. Anandapadamanaban, R. Pilstål, C. Andresen, J. Trewhella, M. Moche, B. Wallner & M.
 Sunnerhagen (2016). Mutation-Induced Population Shift in the MexR Conformational Ensemble Disengages
 DNA Binding: A Novel Mechanism for MarR Family Derepression. Structure, 24(8), 1311-1321.
 [2] S. Helander, M. Montecchio, R. Pilstål, Y. Su, J. Kuruvilla, M. Elvén et al. (2015). Pre-Anchoring of
- [2] S. Helander, M. Montecchio, R. Pilstal, Y. Su, J. Kuruvilla, M. Elven et al. (2015). Pre-Anchoring of Pin1 to Unphosphorylated c-Myc in a Fuzzy Complex Regulates c-Myc Activity. Structure, 23(12), 2267-2279.
- [3] M. Anandapadamanaban, C. Andresen, S. Helander, Y. Ohyama, M.I. Siponen, P. Lundström et al. (2013). High-resolution structure of TBP with TAF1 reveals anchoring patterns in transcriptional regulation. Nature Structural & Molecular Biology, 20(8), 1008–1014.
- [4] A. Wallenhammar, M. Anandapadamanaban, A. Lemak, C. Mirabello, P. Lundström, B. Wallner & M. Sunnerhagen (2017). Solution NMR structure of the TRIM21 B-box2 and identification of residues involved in its interaction with the RING domain. PloS One, 12(7), e0181551.