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Combining NMR, SAXS and SANS in integrative structural biology to study dynamics and allostery in protein complexes

Friday, 11 June 2021 09:00 (30 minutes)

Most eukaryotic proteins are comprised of multiple structural domains connected by linkers of variable length and rigidity. We combine solution NMR spectroscopy and small angle scattering (SAXS, SANS) with crystallography and cryo-EM in integrative structural biology approaches to study the conformational dynamics of multidomain proteins and the roles of the connecting linkers. Studies with multidomain RNA binding proteins (RBPs) and the multidomain chaperone Hsp90, will be discussed.

The molecular functions of multi-domain proteins often rely on dynamic structural ensembles and can be controlled by population shifts between inactive and inactive conformations. This is not visible in static structures. The domains in these proteins are often connected or flanked by intrinsically disordered regions, where posttranslational modifications can further modulate the molecular interactions to regulate the biological activity. Integrative structural biology combining solution techniques, especially NMR spectroscopy, can help to unravel the molecular recognition, dynamics and regulation of protein complexes.

References

- [1] Kang H-S et al. PNAS 117, 7140–7149 (2020).
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- [3] Kooshapur, H. et al. Nature Commun 9, 2479 (2018).
- [4] Mackereth CD et al. Nature 475, 408–411 (2011).

Primary author: SATTLER, Michael (Helmholtz Center Munich & Technical University of Munich)

Presenter: SATTLER, Michael (Helmholtz Center Munich & Technical University of Munich)

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