Structural Biology Studies coupling SAXS with Crystallography and NMR

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Major cellular functions are performed by complexes involving multiple partners and modular proteins in which well-characterized domains are linked by fragments of unknown conformation. Such particles do not crystallize easily and their structural study requires complementary approaches. We present here two examples of systems studied by a combination of SAXS with high resolution (MX and NMR) approaches.

The interaction of the C-terminal domain of ribosomal protein L20 with its rRNA binding site was studied by NMR and SAXS. Scattering data show the existence of a dimer of the RNA/L20C complex in solution. Using the complex structure in the 50S context, NMR and SAXS data, a low resolution model is obtained [1].

$P47^{PHOX}$ is a soluble member of the NADPH oxidase complex of neutrophils. This modular protein comprises a PX domain and two SH3 domains together with fragments of unknown structure. Phosphorylation of Serine residues in the C-terminal part is the first step in the activation of the complex. A combination of rigid-body and *ab initio* modelling was used to model the conformation of the whole protein from the solution scattering pattern.

[1] Raibaud S., Vachette P., Guillier M., Allemand F., Chiaruttini C., Dardel F., *J. Biol. Chem*., 2003, 36522.

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