

BioSANS for the Study of Membrane Protein

Content

An adequate membrane-mimicking environment is of first importance for the function of membrane protein. In recent years, several tools have been improved or developed to purify membrane protein in physiological-like conditions and enable their functional and structural study. I would like to present here the instrumental improvements that, together with adapted membrane mimicks and complementary techniques, allow us to probe the shape and dynamics of membrane protein in solution.

Using the example of the ABC transporter BmrA, I will show how SEC-SANS, together with invisible detergents or nanodiscs, provide the optimal experimental conditions to record low resolution structure and dynamics information on membrane protein. In combination with Cryo-Electron microscopy, H/D-exchange-mass spectroscopy and computing simulations, it reveals the conformational landscapes explored by BmrA through its enzymatic cycle. These tools are ideally suited for the study of protein-lipid interdependence.

References:

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