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Tracking the solution structures of membrane proteins by scattering and modeling

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SAXS and SANS combined with modeling have proved to be essential techniques in structural biology when the classical high-resolution methods are not appropriate. The “contrast matching” method in SANS is particularly suitable to specifically probe membrane proteins by contrast-matching their amphiphilic environment. I will illustrate this feature with TSPO translocator protein, a ubiquitous and functionally important membrane protein used as a pharmacological marker in neuroimaging.

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