Methods for interpreting small-angle scattering scattering data from membrane proteins

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Membrane proteins are an important target for structural investigations by a broad range of experimental and computational methods. During the previous decade, several carrier systems for the reconstitution of membrane proteins have been developed and refined. Also, the experimental facilities and accesories for SAXS and SANS studies of such systems have improved tremendously. The interpretation of small-angle scattering data from membrane protein samples however remains a challenge that still to a large extent requires custom-fitted solutions on a case to case basis. This is in contrast to the more general methods that have been developed for the SAS analysis of soluble proteins and which has enabled a large user community to access these. In my talk, I will start by giving an overview of some of the initial work that has been done with respect to analysing SAS data from simple cases of membrane proteins by my own group and others. I will use this as a basis for discussing how the analysis of small-angle scattering data from membrane proteins and other samples could benefit from more systematic integration of data from complementary experimental or computational sources and give an example of how we are presently developing a combined SAXS/SANS/NMR and MD approach to extract more detailed information about nanodisc samples. The perspectives for generalising this approach to membrane protein samples will be discussed.