Membrane protein scaffold systems and SAXS characterization

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Infrastructure needed for the solution characterization of reconstituted membrane proteins (MPs) has been designed and implemented at the iNEXT partner synchrotron facilities Petra-III (P12, **EMBL-HH)** and SOLEIL (SWING, **SOLEIL).** HT-SEC-SAXS systems are now optimized for purification and screening and rapid structural data collection of MPs. Feasibility studies, testing translational targets and the analysis of several MPs reconstituted in detergents have been conducted, including the newly developed saposin-lipid particles. An exhaustive assessment of the ability of the human saposin (Sap) proteins (A to D) to form nanoparticles (SapNPs) has been conducted including screening against a library of different detergent-solubilized lipids and lipid mixtures [1-2]. The SEC-SAXS data obtained demonstrates the typical lipid bilayer particle structure and modularity of the SapNPs. The mechanosensitive channel protein T2 has been successfully reconstituted in SapNPs and characterized by SAXS [2]. Work conducted using this infrastructure demonstrates the ready characterization of detergent solubilsed MPs and facilitated the establishment of generic protocols to be used as starting point to reconstitute any membrane protein in SapNPs. In addition, the work conducted in has provided the basis for further development on the automation of this HT-SEC-SAXS infrastructure.

References

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