INVESTIGATION OF LIPID MEMBRANES AND MEMBRANE-MIMETIC SYSTEMS BY SANS AT YUMO SPECTROMETER

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Small-angle neutron scattering (SANS) is one of the key methods for studying the structure of biological and materials science objects at the nanoscale (1-100 nm). In this work, we use it to study liposomes, vesicles from purple membranes, and detergent micelles.

Liposomes are microscopic vesicles consisting of one or more lipid bilayers that are used as model cell membranes for biophysical and biochemical studies of membrane proteins [1]. In our study, we present SANS results for azolectin liposomes containing the proton pumps MAR (marine actinobacterial rhodopsin) and *Mp*R (*Marinomonas posidonica* rhodopsin), as well as for empty liposomes. Based on the obtained data, conclusions are drawn regarding such liposomal properties as integrity, unilamellarity, and, where possible, overall size. In particular, it is shown that liposomes with incorporated protein are generally smaller than empty liposomes, as previously reported [2]. Verification of the above-mentioned characteristics is important for the subsequent use of liposomes in functional assays, for example, ΔpH and bilayer lipid membrane experiments. In turn, such assays will be applicable not only to proton pumps, but also to membrane proteins of other classes, for example, channelrhodopsins (ChR2, OLPVR1, etc.).

Purple membranes (PM) are specialized regions of the cell membrane of certain halophilic archaea and represent two-dimensional crystals of bacteriorhodopsin. This protein is a light-driven proton pump and is often used as a model system for studying the mechanism of proton transport [3]. Under certain conditions, PM can be transformed into spherical vesicles, which may subsequently be used to obtain bacteriorhodopsin crystals [4]. In our work, we present SANS data for such vesicles, which are used to determine their geometric dimensions.

We also use SANS to investigate the structure of detergent micelles, such as dodecyl maltoside and dodecyl phosphocholine. Previously, micelle models were obtained solely from SAXS data [5]; however, when their geometric parameters are fixed, it is not possible to fit the SANS data using any combination of scattering length densities (SLDs) of the individual model components. Therefore, obtaining accurate micellar models requires the simultaneous fitting of SAXS and SANS data. The experience gained from integrating these two methods may subsequently be applied to modeling the structure of protein-detergent complexes formed during the solubilization of membrane proteins.

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