Development of liquid interface spectrometer

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Soft matters, such as emulsion and lamella, have high ratios of interfacial area to total volume. Their structure, characteristics, and functions greatly depend on the structure of their liquid interfacial layer. So, it is essential to study the microscopic structure of the liquid interface in order to develop new, functional types of soft matter, both for fundamental science and for industrial applications.

X-ray analyses using synchrotron radiation, such as GIXD, XRF, and total reflection XAFS, are powerful techniques for obtaining the structural information of the liquid interface. In this study, we developed a multipurpose liquid interface spectrometer (Fig. 1) and tested its performance. The spectrometer was installed in an undulator beamline, BL37XU. The undulator beam having low divergence and high flux density is suitable for the reflectivity studies of the liquid interface, since the critical angle for the total reflection is lower than 1 mrad. This spectrometer consists of two main stages. A sample cell and detectors for the reflectivity measurement are mounted on the 0-2θ goniometer in a horizontal dispersion arrangement on the downstream stage, which is made of granite (1.5 x 1 x 0.2 m, 900 kg) and has an air bearing to reduce vibration to as low a level as possible. The incident angle of the beam on the sample interface is controlled by a deflection crystal, Si(111). The crystal is mounted on the three-axis goniometer on the upstream stage by adjusting the rotation angle along the incident beam axis.

We measured geometrical parameters of the spectrometer, such as accuracy of the incident beam angle on the sample and origin of the deflection angles of the crystal, which is necessary for the precise control of the spectrometer during reflectivity measurements. An automatic program for controlling the spectrometer, which includes adjustment of more than ten axes to identify the most accurate positions, is now under development.

![Diagram of Liquid Interface Spectrometer](image)

Fig. 1 Liquid interface spectrometer

X-ray crystallographic analysis of BAR domain proteins

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Membrane dynamics in a cell, such as membrane budding, tubulation, fission and fusion, is inevitably associated with vigorous changes in membrane curvature. The crystal structure of amphiphysin (Peter et al. Science 303, 409-499, 2004) provides a simple model to sense and to drive membrane curvature: the crescent-shaped BAR (Bin/Amphiphysin/Rvs-homology)-domain dimer impresses its concave surface on the membrane to form a positive-curvature membrane domain, for example tubules and vesicles. The endophilin BAR domain was reported to have lysophosphatidic acid acyltransferase (LPAAT) activity that might induce negative membrane curvature (saddle-shaped membrane). In order to understand molecular mechanism of membrane deformation by endophilin BAR domain at an atomic resolution, we have started structural analysis of human endophilin A1, an essential player in synaptic endocytosis.

The human endophilin-A1 BAR domain crystals were obtained by micro-dialysis method as well as by conventional vapor diffusion methods. The crystals belong to the space group \( P4_1 \), with the cell dimensions of \( a=b=126\text{Å}, c=101\text{Å} \). Diffraction data were collected to 3.2 Å resolutions at BL38B1. Structural analysis is now underway.