BL38B1
RIKEN Structural Biology I

1. Introduction

BL38B1 is a small-angle X-ray scattering (SAXS) beamline for structural analysis of biological macromolecules such as proteins, nucleic acids, and their complexes mainly in solution using synchrotron radiation from a bending magnet as a light source. In FY2020, the activity of SAXS measurement of BL45XU was relocated to BL38B1, and the beamline became available for RIKEN users and the Basis for Supporting Innovative Drug Discovery and Life Science Research by AMED (BINDS) project. Since FY2021B, public use proposals, mainly for protein solution SAXS experiments, have been accepted.

2. Recent activities

The BL employs a standard transport channel of a bending magnet beamline, and it utilizes asymmetric crystals for monochromators to increase the X-ray beam intensity. Cylindrical mirrors with a length of 1 m realize a focused beam on the detector and eliminate higher order reflection from the monochromator crystals.

X-ray energy of 12.4 keV (flux: ~5 × 10^{10} photons/s/100mA) is used, which supports camera length settings of 2.5 m for SAXS and 0.3 m for Wide-angle X-ray Scattering (WAXS). We support size-exclusion chromatography coupled SAXS (SEC-SAXS) [Fig. 1(a)] for protein solution X-ray scattering experiments for public use and the BINDS project. The SEC system has an autosampler and a two-column system [Fig. 1(b)], allowing multiple preset solution samples to be measured by switching the columns. 1(c)] and analysis based on SAXS and UV/VIS output results.

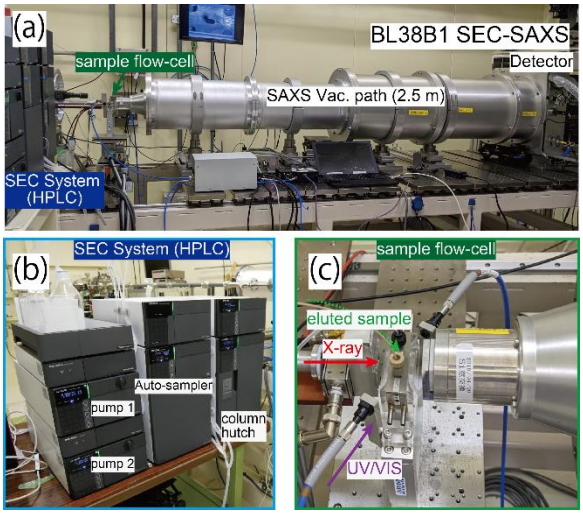

Fig. 1. SEC-SAXS system at BL38B1.

In FY2022, we improved the wiring of the X-ray transmittance monitor, updated the UV/VIS light source, mastered the two-column switching HPLC, and utilized the autosampler function for the purpose of efficient and reliable quantitative analysis for the SEC-SAXS system. Figure 2 shows a sample of commercially available bovine serum albumin dissolved in a buffer solution and eluted with the same buffer solution. While separating the dimer and monomer fractions [Fig. 2(a)], the respective scattering profiles are obtained [Fig. 2(b)]. The analysis of SEC-SAXS data, including X-ray scattering profiles and UV/VIS spectrum, was conducted with MOLASS software [1]. MOLASS is an analysis software for SEC-SAXS developed at KEK-PF and is a common software in BINDS SAXS support. The SEC-MALS (Multi-Angle Light Scattering) instrument (DAWN HELEOS II 8+, Wyatt Technology) has been installed in the ring building, and it is now a normal

practice to perform SEC-SAXS measurements in parallel with SEC-MALS measurements. SEC-MALS also provides important information for interpreting SEC-SAXS results because it can determine the molecular size and absolute molecular weight. In order to improve the efficiency of switching between SAXS and WAXS, a switching system has been introduced, in which the equipment around the sample for both SAXS and WAXS is unitized and inserted into and removed from the optical axis, respectively. This system has reduced the time required for switching from 3 hours to 0.5 hours.

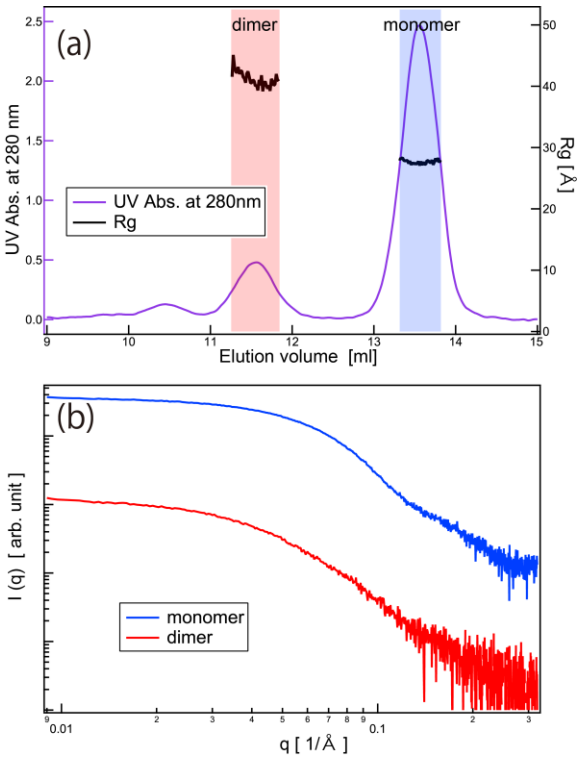

Fig. 2. SEC-SAXS results.

In FY2023, we plan to upgrade the X-ray focusing mirror, install a capillary-type flow cell for SEC-SAXS, and reorganize the system for high-throughput SAXS and WAXS measurements.

Authors

Sekiguchi Hiroshi[1], Masunaga Hiroyasu[1], and Yamamoto Masaki[2]

[1]Scattering and Imaging Division, JASRI

[2]Advanced Photon Technology Division, RIKEN SPring-8 Center

Reference:

[1] K. Yonezawa et al. (2023) *Biophys. Physicobiol.* **20**, e200001.