BL26B1
RIKEN Structural Genomics I

1. Introduction

The RIKEN Structural Genomics Beamline I consists of SPring-8 standard bending magnet beamline components and an end station dedicated to high-throughput protein crystallography [1]. Diffraction data can be sequentially collected from many cryo-cooled protein crystals using the auto–sample exchanger SPACE and the user interface BSS [2,3]. Asymmetric diffraction crystals (asymmetric angle of 4.4°) for the double-crystal monochromator are adopted, and the capillary focusing lens (Hamamatsu J12432) upstream of the sample is optionally available by switching the configuration on the user interface program [4]. Also, optional devices for room-temperature crystallography are provided at the end station. The temperature-controllable humid air and glue coating mounting method (HAG) system [5] can control the temperature and relative humidity of the sample environment in the ranges from 2 to 20 °C and from 40 to 100%, respectively. The crystallization plate scanner, plate stocker, and exchanger apparatuses with a dedicated interface program for users to rapidly exchange and address a position in an SBS 96-well crystallization plate are also installed [6]. Additionally, a new microfluidic device that enables the injection of crystal suspensions and the trapping of crystals aligned in pit patterns within the fluidic channel is being developed, eliminating the need to handle each crystal individually. Ligand–protein complex crystals are formed by replacing the content buffer with a ligand solution. The device is made of a transparent material, polydimethylsiloxane (PDMS), and is designed to be mounted on the plate scanner to collect diffraction data at room temperature [7].

Eighty percent of the total beam time is assigned to public users, and ten percent each is assigned to the Basis for Supporting Innovative Drug Discovery and Life Science Research by AMED (BINDS) project and to RIKEN users.

2. Recent activities

For the HAG system, development and commissioning with a user group to cover higher temperatures ranging from 20 to 70 °C have been conducted, expecting applications to studies of the structural dynamics of macromolecules derived from, for example, thermophilic bacteria. During the commissioning, a new anaerobic chamber for sample handling at room temperature was developed and is ready to be used beside the experimental hutch (Fig. 1). With a nitrogen gas flow system, the oxygen concentration inside the chamber is kept less than 0.1%. Compared with the existing sample handling chamber for low-temperature samples, it is not equipped with temperature control; however, it has higher anaerobic performance because of a compact housing and a separate side room for sample exchange.

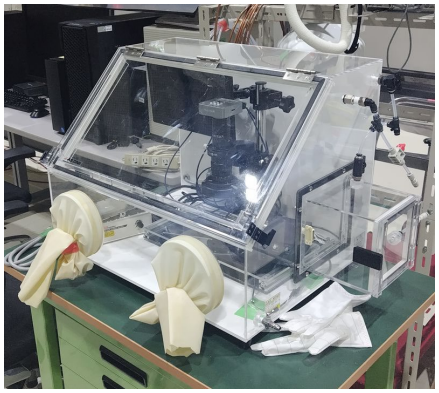

Fig. 1. Anaerobic sample handling chamber available aside the BL26B1 end station.

Also, for room-temperature in situ crystallography, a new low-profile, stable, leak-resistant 96-well crystallization plate manufactured by 3D printing has been developed and tested at BL26B1. Considering the limitation of the rotation range of the plate scanner, the new plate is designed to be separated into 12 goniometer-mountable 8-well strips (Fig. 2). Each well is designed to allow exposure over a rotation range of 110º. At BL26B1, high-quality data of bovine pancreatic trypsin, hen's-egg-white lysozyme, and rat transcobalamin were collected for room-temperature single-wavelength anomalous dispersion experiments using the native signal of sulfur, calcium (λ = 1.7Å), or vitamin B_{12} cobalt (λ = 1.5Å). Successful *ab initio* data collection and experimental phasing required up to 20 one-crystal wedges of around 40º. These are fewer than the strips that are capable of, but necessary to reduce radiation damage; the average per-wedge dose was approximately 50–100 kGy. Instead, for the molecular replacement data collection of monoclinic lysozyme, only two wedges of data were needed.

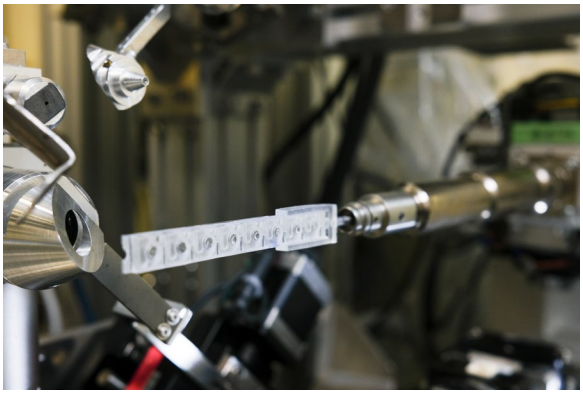

Fig. 2. 8-well strip of new plate mounted on the goniometer at BL26B1.

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