BL26B1
RIKEN Structural Genomics I

1. Introduction

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 automatically collected from a vast amount of cryo-cooled protein crystals with 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 were 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]. In the end station, optional devices for room-temperature crystallography are provided. The temperature-controllable HAG (humid air and glue coating mounting method) system [5] is capable of controlling 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. Eighty percent of the total beam time is assigned for public users and ten percent is assigned for BINDS (Basis for Supporting Innovative Drug Discovery and Life Science Research by AMED) project users.

2. Recent activities

In FY2020, the optional on-line microspectrometer was implemented at the diffractometer in the end station, and commissioning was begun with collaborator groups. The optics for spectroscopy is set vertical to the X-ray incident beam on-line, so that users can investigate an identical position in the crystal by rotating the spindle angle of the goniometer by 90° (Fig. 1). The available wavelength range for spectroscopy is from 250 nm to 650 nm, and the focal spot size is designed to be adjustable from 10 μm to 200 μm.

Fig. 1. On-line microspectrometer installed on the BL26B1 diffractometer.

Currently, further developments, such as an on-line temperature control system and the upgrading of the data collection control system for the crystallization plate scanner, are in progress.

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References:

[1] Ueno, G., *et al.* (2006). *J. Struct. Funct. Genomics.* **7**, 15–22.

[2] Murakami, H. *et al.* (2012). *J. Appl. Cryst.* **45**, 234–238.

[3] Ueno, G. *et al.* (2005). *J. Synchrotron Rad.* **12**, 380–384.

[4] Baba, S. *et al.* (2019). *AIP Conference Proceedings* **2054**, 060008.

[5] Baba, S. *et al.* (2019). *J. Appl. Cryst.* **52**, 699–705.