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]. Also 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 (Fig.1) [6]. Eighty percent of the total beam time is assigned to public users and ten percent is assigned to BINDS (Basis for Supporting Innovative Drug Discovery and Life Science Research by AMED) project users.

2. Recent activities

In FY2021, the optional online micro-spectrometer was implemented at the diffractometer in the end station and a commissioning experiment and test use were conducted with collaborator groups. The optics for spectroscopy is set vertically to the X-ray incident beam online, and the available wavelength range for spectroscopy is from 250 nm to 650 nm, with the focal spot size designed to be adjustable from 10 µm to 200 µm.

Moreover, to expand the target samples for the HAG method, the development of the new system to cover high temperatures ranging from 20 to 70 °C has been started. The applications for structural dynamics of macromolecules derived from, for example, thermophilic bacteria are expected. Besides, further developments, such as an online temperature control system and the upgrading of the data collection control system for the crystallization plate scanner, are in progress.

Fig. 1. Plate-scan goniometer installed on the BL26B1 diffractometer.

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