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 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 in the end station, optional devices for room-temperature crystallography are provided. The temperature-controllable humid air and glue coating mounting method (HAG) 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 [6]. 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 RIKEN users.

2. Recent activities

By the end of the last fiscal year, an 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 (Fig. 1). 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 60 μm to 200 μm. Utilizing this apparatus, the structural changes accompanying catalysis corresponding to the change of the redox states at the active site of metalloenzyme, caused by X-ray irradiation to a single crystalline sample, were investigated [7].

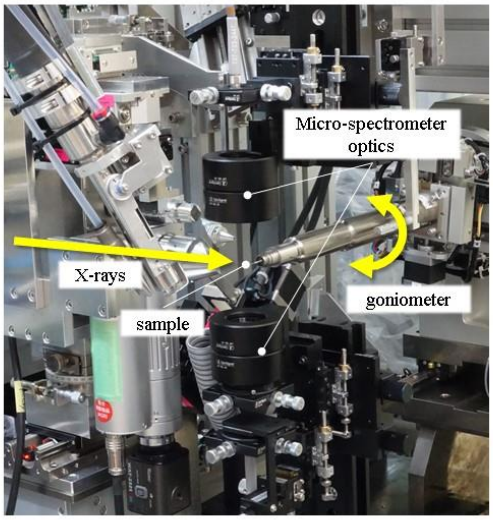

Fig. 1. Online micro-spectrometer installed at the BL26B1 end station.

Moreover, to expand the range of target samples for the HAG method, the development of a new system to cover high temperatures ranging from 20 to 70 °C has been continued. This fiscal

year, a test bench equipped with improved sheath gas piping to avoid condensation caused by high-temperature humid gas was developed. The applications to studies of the structural dynamics of macromolecules derived from, for example, thermophilic bacteria are expected.

In addition, 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.

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