

# BL41XU Structural Biology I

BL41XU is operated to extend the applicable range of biological macromolecular crystallography in two regions:

- (i) larger unit cells and smaller crystal size by taking advantage of the highly brilliant characteristics of the beamline
- (ii) wider range of anomalous scattering element for multiple wavelength anomalous dispersion (MAD) method with higher energy X-rays

The experimental station is equipped with a diffractometer with horizontal-axis goniometer and detectors. Two types of cryostream coolers, nitrogen gas and helium gas, are installed on the diffractometer for experiment under cryogenic condition. The imaging plate detector (RIGAKU R-AXIS V) and X-ray CCD detector (MAR USA marCCD165) are installed and available.

## Area of research

Macromolecular crystallography

## Keywords

*Scientific field*

Structural biology, Protein X-ray crystallography

*Equipment*

Large imaging plate detector, CCD detector, He-cryostream cooler

## Source and optics

This beamline employs the standard SPring-8 undulator as the light source, the rotated-inclined double-crystal monochromator as the monochromatizing device for the heat load removal function of the undulator beam. The two pieces of super mirrors are used to focus and eliminate the higher harmonics of the undulator beam. This combination, provides the X-rays of extremely high intensity focused to a 100 micron order at the sample position in the 6 ~ 38 keV energy range. The energy resolution is in the order of  $10^{-4}$ .

## X-rays at sample

Energy range      6.5 ~ 17.5, 19 ~ 37 keV  
 Energy resolution     $\Delta E/E < 2 \times 10^{-4}$   
 Photon flux         $10^{13}$  photons/s

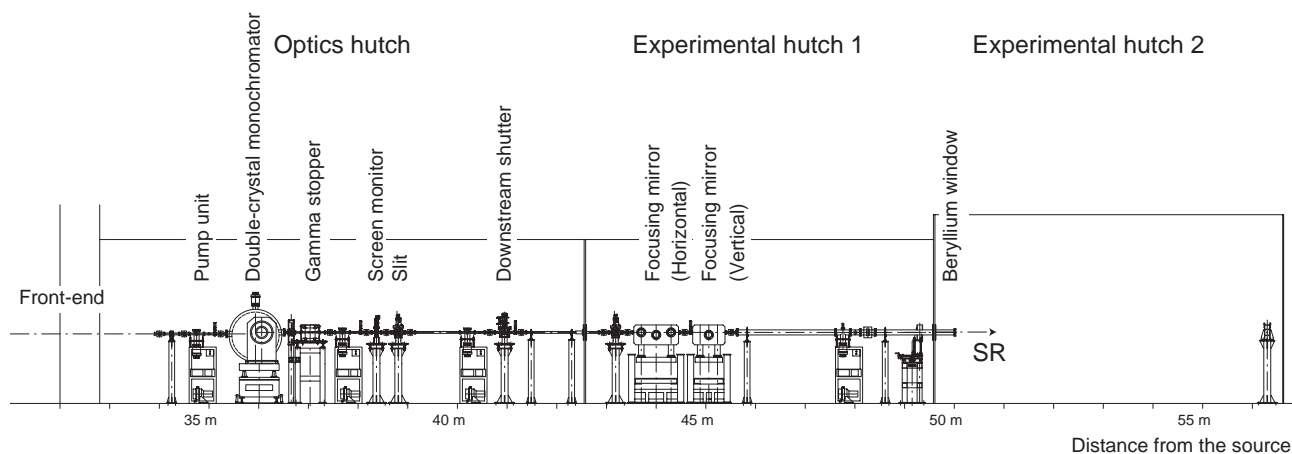
Beam divergence    0.1 mrad  
 Beam size            0.1 mm

## Experimental stations

### Protein crystal diffractometer

The diffractometer is designed for protein X-ray diffraction experiment. This diffractometer consists of three parts: X-ray beam shaper, dual-axes goniometer and detector base.

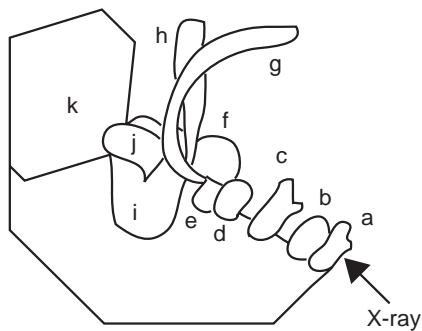
The X-ray beam shaper has two quadrant slits, rotary attenuator, collimator and shutter. The size and intensity of X-ray beam at sample position is changeable by using these components.



Schematic view of beamline

The dual-axes goniometer has a sample rotation axis ( $\omega$ ) and a sample alignment axis ( $\phi$ ). Three translation axes (X, Y and Z) are equipped in this goniometer for semi-automatic sample centering. Two types of cryostream coolers, nitrogen gas and helium gas, are installed on the diffractometer. These cryostream coolers are open-flow type, and the cryostream cooler using nitrogen gas can cool a sample to  $\sim 90$  K and the helium gas can do  $\sim 35$  K.

Two detectors (RIGAKU R-AXIS V imaging plate detector and MAR USA marCCD165 X-ray CCD detector) are installed on the detector base. This base has a function to change each position of detectors against X-ray beam. Users can choose either of the detectors depending on the experiments.



Schematic view of protein crystal diffractometer

- a : Quadrant slit
- b : Attenuator
- c : Quadrant slit
- d : Shutter
- e : Collimator
- f : Goniometer
- g : Cryostream cooler (Nitrogen)
- h : Cryostream cooler (Helium)
- i : Detector base
- j : X-ray CCD detector
- k : Imaging plate detector

#### Specifications of X-ray beam shaper

Collimator size : 0.05, 0.1, 0.2, 0.3, 0.5 mm

#### Specifications of dual-axes goniometer

Sample rotation axis ( $\omega$ ):  $\pm 177^\circ$

Sample alignment axis ( $\phi$ ):  $0 \sim 360^\circ$

Sample translation axis (X):  $\pm 3.0$  mm, (Y):  $\pm 3.0$  mm, (Z):  $\pm 10$  mm

Temperature of cryostream :  $300 \sim 90$  K (nitrogen gas)  $\sim 35$  K (helium gas)

#### Specifications of detector / RIGAKU R - AXIS V

Detector area :  $400 \times 400$  mm<sup>2</sup>

Pixel size :  $0.1 \times 0.1$  mm<sup>2</sup>

Read-out time : 50 sec.

Total turn-over time : 1 min

Camera length :  $150 \sim 950$  mm

#### Specifications of detector / MAR USA marCCD165

Detector area : 165 mm (diameter)

CCD size :  $4096 \times 4096$  pixel

Pixel size :  $0.08 \times 0.08$  mm<sup>2</sup>

ADC : 16 bit

Read-out time : 3.4 sec.

Total turn-over time : 10 sec. (without exposure time)

Camera length :  $100 \sim 300$  mm, tilt :  $0 \sim 40^\circ$

Peltier-cooled Si PIN photodiode

Multi-channel analyzer

Cryo-Xe-siter

Microscope

Incubator ( $4, 20^\circ\text{C}$ )

Cold room ( $5^\circ\text{C}$ )

Liquid nitrogen dewar vessel

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#### Contact information

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