BL38B1 R&D (3)

This beamline is constructed as the third 'R&D beamline' which serves R&D's of the optics of the standard bending magnet beamline, the various applications of XAFS, monochromatic data collection for routine macromolecular crystallography, and technical R&D's for the novel experimental equipments.

Area of research

XAFS, R&D of optics and detector

Monochromatic data collection for routine macromolecular crystallography

Keywords

Scientific field

XAFS, R&D of optics, R&D of detector, Biological crystallography

Equipment

19-element Ge SSD, CCD detector (ADSC-Q4R), Imaging plate detector (RIGAKU RAXIS-V)

Source and optics

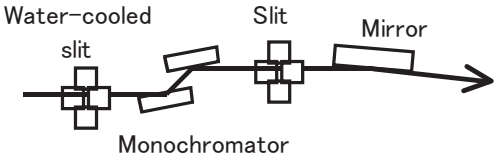
The optics consists of standard components for bending magnet beamline such as BL40B2. The designed glancing angle of the vertically bent cylinder mirror is from 0 to 5 mrad in a downward direction. The Rh-coated 1-m-long mirror focuses the beam at the experimental hutch with the glancing angle from 3 to 4 mrad, while the cut off energies in the angles are from 22 to 17 keV. The calculated horizontally acceptance of the beamline is about 1.5 mrad and that of the mirror is from 0.7 to 0.8 mrad.

X-rays at sample

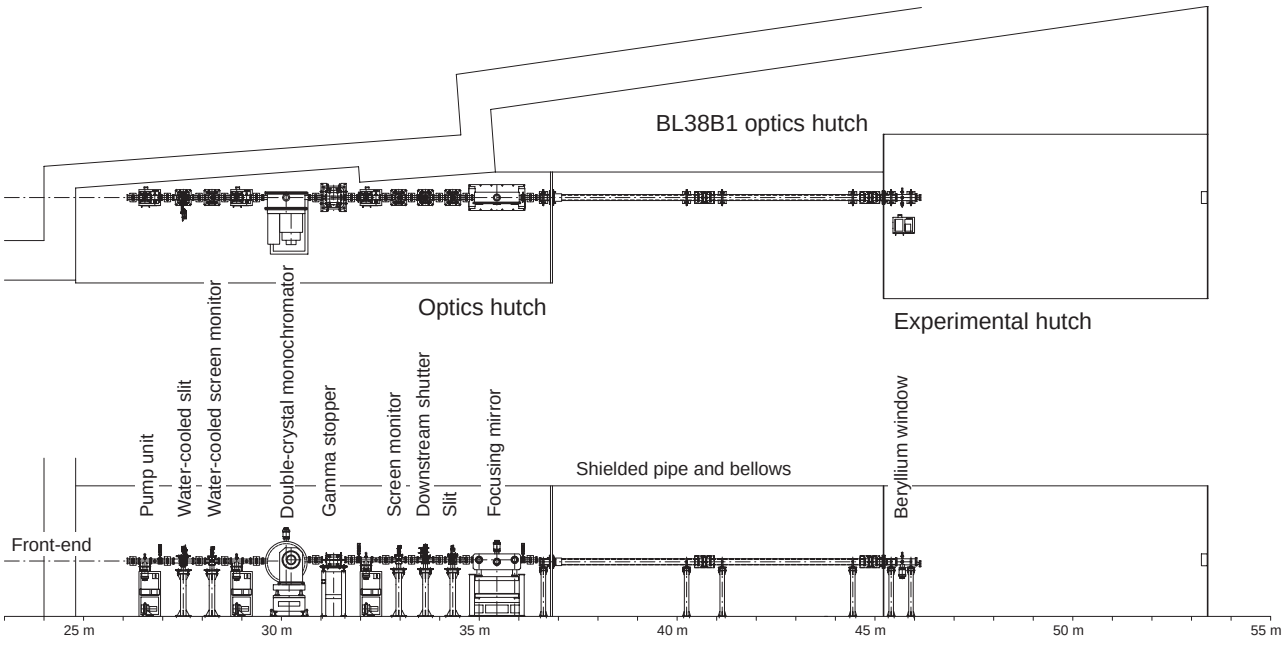
Energy range : 3.7~198 keV

Energy resolution : 10^{-5} ~ 10^{-4}

Photon flux : 10^{8} ~ 10^{11} photons/s



Outline of optics



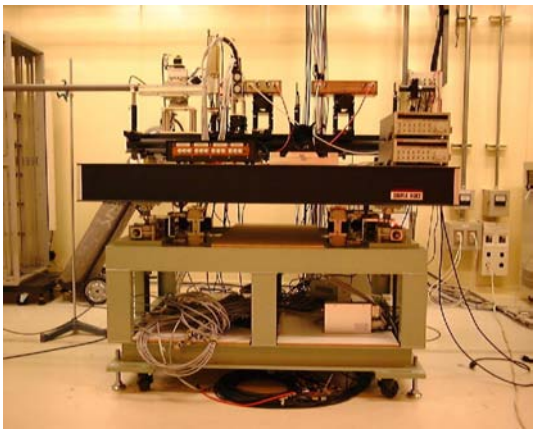
Schematic view of beamline

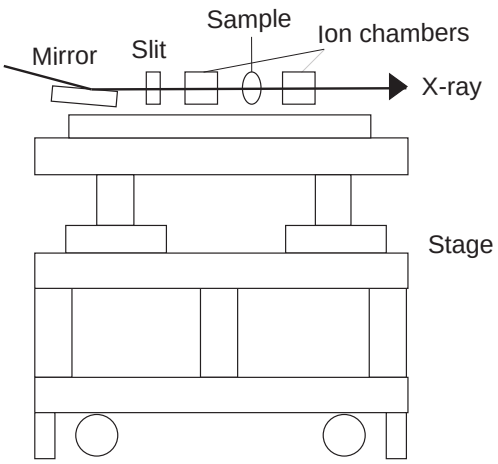
Experimental stations

XAFS

The standard XAFS measurements are available as well as BL01B1. The detectors for XAFS measurement are ionization chambers, a fluorescence detector (so-called Lytle detector), an electron-yield cell and a multi-element SSD. The new technique for XAFS method is to be developed.

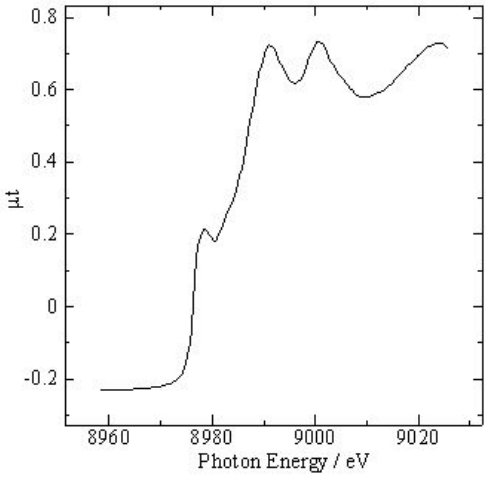
Stage is removal for user's R&D program with special large apparatuses. Si mirror is available for eliminating the higher harmonics and controlling the incident angle for samples. Sample is attached on the conventional holder, the fluorescence detector, electron-yield cell, the cryostat, the goniometer, or user's special holder. Continuous He flow cryostat for XAFS measurement in the temperature range of 3.5 ~ 320 K. Si PIN photodiode detector for fluorescence measurement is available.





Facilities

Slits (stepping motor driven)
Gas-flow type ionization chamber
Horizontal axis goniometer
Lytle detector
Conversion-electron-yield detector
Si PIN photodiode detector for fluorescence measurement
Energy resolution : 220 eV @ 5.9 keV of ^{55}Fe with 12 μs shaping time
Multi-channel analyzer of fluorescence measurement
Continuous He flow cryostat for XAFS measurement
Temperature range : 3.5 ~ 320 K
Ge single-element SSD for fluorescence XAFS measurement
Energy resolution :
150 eV @ 5.9 keV of ^{55}Fe with 6 μs shaping time, 1000 cps
250 eV @ 5.9 keV of ^{55}Fe with 0.25 μs shaping time, 100000 cps
Ge 19-element SSD for fluorescence EXAFS measurement
Energy resolution :
175 eV @ 5.9 keV of ^{55}Fe with 6 μs shaping time, 1000 cps
275 eV @ 5.9 keV of ^{55}Fe with 0.25 μs shaping time, 100000 cps



Typical data of photon energy

Protein Crystallography

Rapid data collection system for protein crystallography is installed at BL38B1. Two detectors, CCD (ADSC-Q4R) and imaging plate (RIGAKU RAXIS-V), are equipped on the experimental table and users can easily change these detectors depending on their experimental purpose (Fig. 1). Combination of the coaxial-microscope to observe crystal along x-ray beam path and the goniometer having motor driven x, y and z stage make centering of crystal very easy (Fig. 2). Data collection, including measurement of XAFS spectrum and automatic MAD (Multi-wavelength Anomalous Diffraction) data collection, is performed through controlling software BSS (Beamline Scheduling Software). Since BSS can control all of the instruments

required for data collection, switch of detector and change of camera length, wavelength are automatically performed at the beginning of measurement. Therefore, what beamline users have to do after crystal mounting and centering is to input measurement conditions to BSS.

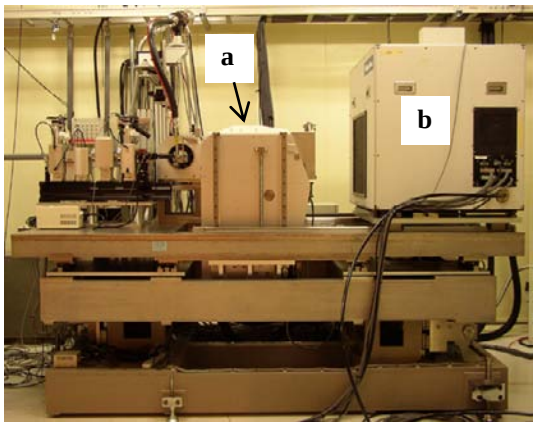


Fig.1. Overall view of the diffractometer for protein crystallography
(a : ADSC-Q4R, b : RIGAKU RAXIS-V)

When RAXIS-V is used, the CCD stage goes down into the experimental table and the IP stage can move toward the goniometer without any physical interference.

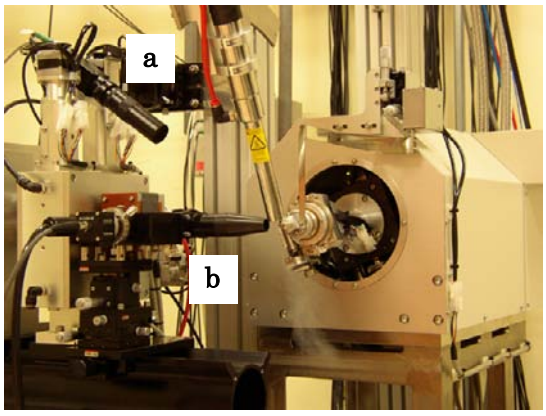


Fig.2. Magnified view around the goniometer
Two microscopes are used for crystal centering.
(a) low magnification microscope
(b) high magnification coaxial-microscope

X-rays at sample

Energy range	6 ~ 17.5 keV
Energy resolution	$\Delta E/E = 10^{-4}$
Spot size	horizontally 250 μm, vertically 200 μm (@ 12.4 keV (λ = 1.0 Å)) at detector position

Facilities

CCD detector (Quantum 4R (Area Detector System Corporation))

Detector area : 188 × 188 mm^2
Pixel size : 81.6 × 81.6 μm^2
No. of pixels : 2304 × 2304
Camera length : 135 ~ 340 mm

Imaging plate detector (RIGAKU RAXIS-V)

Detector area : 400 × 400 mm^2
Pixel size : 100 × 100 μm^2
No. of pixels : 4000 × 4000
Camera length : 195 ~ 1070 mm

Horizontal axis goniometer having motor-driven x, y, z stage
Cryostat : temperature control range 80 ~ 350 K
Gas-flow type ionization chamber
Si PIN photodiode detector for fluorescence measurement
Multi-channel analyzer of fluorescence measurement

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