# RIKEN Beamline

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## 1.Introduction

At SPring-8, RIKEN beamline has been designed and developed for structural biology by the Institute of Physical and Chemical Research (RIKEN)[1]. The structural knowledge upon biological macromolecules is essential for understanding cellular processes. Proteins, a major component of biological macromolecules, consist of 20 kinds of the amino acids, and many of them have been sequenced in the past few decades. However, functions of biological macromolecule have not been well understood in terms of three-dimensional structures. The compilation of the knowledge on three-dimensional structures at atomic resolution, could result in a remarkable breakthrough in protein engineering and drug design.

This beamline is the first branched beamline at SPring-8, and contains two experimental stations, one for protein crystallography (PX) and the other for small-angle scattering (SAXS). Both experiments can be carried out simultaneously with a multi-colour feature realized with serially arranged two undulators. The branched beams are generated by the transparent diamond monochromator. The PX-station is based on the "trichromatic concept"in order to optimize for multi-wavelength anomalous diffraction (MAD) method[2,3]. The main feature of this concept is to minimize systematic errors introduced in multi-wavelength measurements.

## 2.Beamline Design

As mentioned above, this beamline consists of two experimental stations: SAXS and PX. The undulator beam is provided so as to operate two stations simultaneously. The outline of the beamline is displayed in Fig.1 in the bird's-eye view. In order to provide beams with different energies to these stations, two undulators are arranged serially. These are the in-vacuum undulators[4], vertically polarized by the reason described below. Each undulator emits fundamental harmonics beam in the energy range from 6 keV to 14 keV.

Dichromatic synchrotron radiation emitted from these two undulators is branched into horizontal directions by a beam-splitter, which is a transparent diamond monochromator[5]. The beam-splitter functions as a first monochromator for the SAXS beamline. Since the glancing angles to the diamond crystal is often proximate to 45 degrees in this energy region, the polarization of the beam has to be vertical to obtain certain level of X-ray intensity. The SAXS station uses the monochromatized undulator beam, which enables us to obtain the data not only with high small-angule resolution but also with high flux as well. A micro-strip gas chamber (MSGC) is expected to be utilized for high-counting-rate scattering experiments[6]. The structures of proteins insolution under various conditions will be studied in this station.

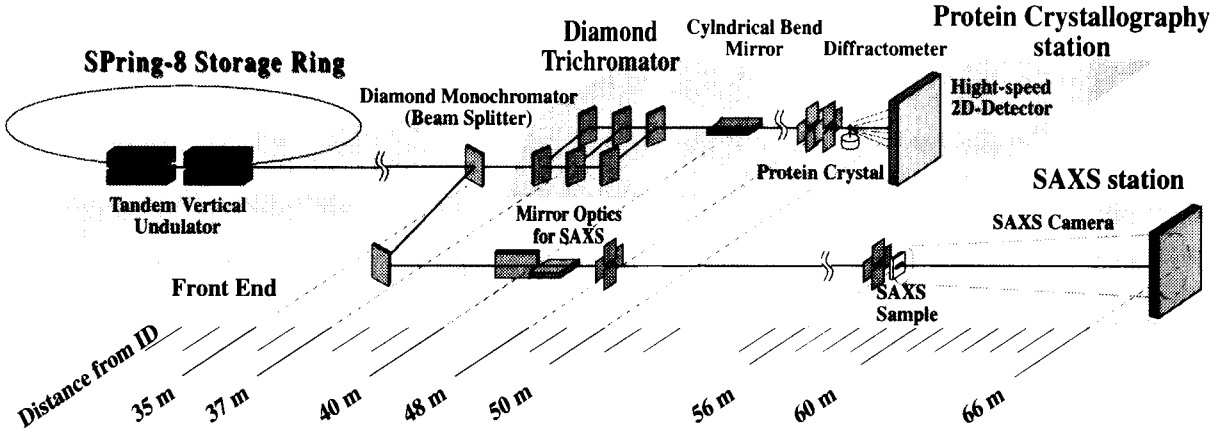


Fig.1. Brid's eye view of RIKEN beamline I for structural biology.

Passing through the beam-splitter, the beam is guided to the "trichromator" for protein crystallography.

### 3.Trichromatic Protein Crystallography

A goal of the PX-station is to accumulate a vast amount of information on three-dimensional structures. A problem in protein crystallographic analysis is, however, the "phase problem". Although with synchrotron radiation, MAD which determines the phases from a single anomalous scatterer, has been under development regarded as an elegant method, it is still not easy to apply. In general anomalous scattering contributes minimal so that the accuracy of multi-wavelength data collection constitutes central challenging problem in MAD. The PX-station has the "trichromatic concept" to optimize for MAD.

The "trichromatic concept" for MAD is that three independent data sets at three-wavelengths are taken quasi-simultaneously for the identical protein crystal without changing any beamline parameter. The "trichromatic concept" is summarized in Fig.2.

The "trichromator", consisting of three pairs of transparent diamond double crystal mono-chromators, collinearly introduces three monochromatized wavelengths on the identical beam direction.

These beams are sequentially supplied through a beam choppers. The data collection is sequentially performed with each wave-length to minimized the background generated by the other wavelengths.

The "trichromator" and the focusing mirror will be installed at 37 m and 40 m from the light source. The beam will be collimated to less than 0.1 x 0.1 $mm^2$ at 50 m back focal points. In the experimental station, a protein crystal will be aligned by a four-circle diffractometer. Detector is the other important device for MAD. A fast read-out two-dimensional detector is the most suitable for the high precision MAD. Multiple CCD X-ray detector (MCCDX) has been under development to record the diffraction patterns of protein crystal[7].

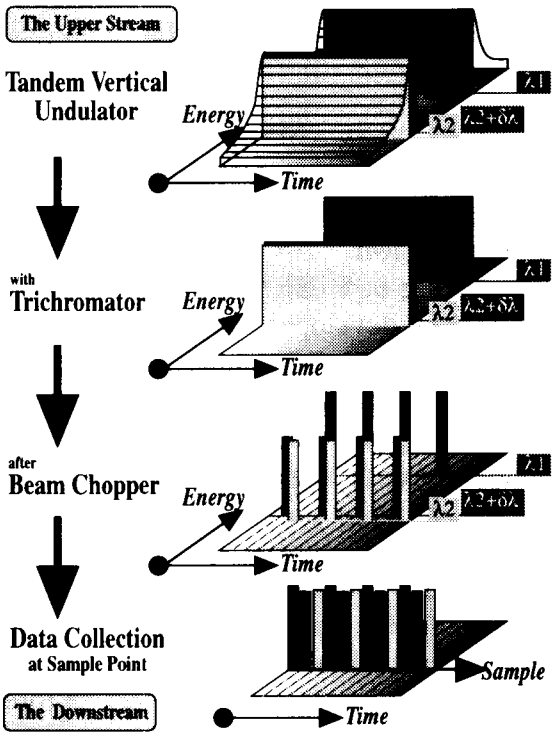


Fig.2.Summary of "trichromatic concept".

### 4.Summary

In the RIKEN beamline, protein crystallography station is a target for MAD-measurement, and SAXS studies will also be carried out on the structure of proteins in solution under various conditions. The operation of the RIKEN beamline will be started as soon as SPring-8 starts its initial beam operation.

### Reference


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