RIKEN Beamline

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The RIKEN beamline, a beamline for structural biology, is the first beamline for exclusive use by RIKEN scientists in biology, life science and related fields. It is presently under design and construction and will be commissioned by the first beam of SPring-8. It has been constructed by the RIKEN people in collaboration with beamline group of SPring-8 Project Team.

Basic Concept of the Beamline

The RIKEN beamline for structural biology has been designed with key words, small-angle scattering (SAXS) and structural biology, so that two experimental stations are simultaneously operated without time share-mode. More precisely, the second station is designed for use in macromolecular crystallography (PX). The simultaneous operation of several beamlines is not accomplished by beam branching in physical space but is able by energy splitting of the beam. The diamond crystals, recently crystallized by high pressure method as highly perfect crystals, are without appreciable defects and have been grown to several square millimeters. A diamond crystal with a few hundred micrometer thickness is quite transparent to hard X-rays, transmitting most of the X-rays after reflecting X-rays at a special wavelength. Thus, the RIKEN beamline is designed to operate two experimental stations simultaneously. The outline of insertion devices, the beam splitting by monochromator, arrangements of optics and experimental stations in two beamlines are be illustrated in Figure 1.

Beamline Design

As can be seen in Fig. 1, the beamline consists of undulators, front end components, beam transport channel including optics and experimental stations.

The X-rays are generated by two tandem undulators placed in a single straight section with normal length, called dichromatic source, providing two different energies.

These undulators are not the conventional type, but in-vacuum type, emitting vertically polarized X-rays by the reason described below. Each undulator emits X-rays with energies of 6 to 14 keV as fundamental harmonics.

The dichromatic synchrotron radiation is divided into two beams by a beam splitter, that is a transparent diamond crystal monochromator. The beam splitting is in the horizontal direction in the experimental hall so that two stations are easily accessible. This beam splitter is the first monochromator for the SAXS beamline. Since the Bragg angle on the diamond crystal is close to 45 degrees depending on the net plane and energy, vertical polarization of X-rays is essential to preserve intensity. The transmitted X-rays through the first thin diamond crystal are supplied to the PX beamline.

The Small-angle X-ray Scattering Beamline and Station

In the SAXS beamline, the horizontally reflected X-rays are restored their direction by the second diamond crystal, presumably the (111) net planes in both, employing the fixed-exit mechanism. The following mirrors focus X-rays in both directions to its backfocal plane, realizing small-angle resolution of 5,000 A. The scientific program in this experimental station is the small-angle X-ray scattering studies on complex biomolecular system as photo-systems and small-angle X-ray studies of biological macromolecules under high pressure typically, in addition to the program pursued in the past. For the high pressure system, time-resolved experiments are planned to understand behavior of oligomeric proteins in various conditions. The small-angle studies on giant macromolecules may lead to measurements in a very small-angle scattering region, requiring highly collimated optics as Bonse-Hart type.

The Protein Crystallography Beamline and Station

A goal of the protein crystallography is to accumulate a number of three-dimensional molecular structures of biological macromolecules to have a breakthrough in the field.

The need for structure analyses is immense in the Institute of Physical and Chemical Research (RIKEN) and is the principal motive force to construct PX beamline at its first stage of SPring-8 facility construction. To realize such a goal, we have to solve the "phase problem" that will save the period, money and man power in the analyses and will let the biochemists to familiarize and accomplish structure analyses of their biological systems. The PX beamline is designed to solve the phase problem by multiple wavelength anomalous diffraction (MAD) method, utilizing the anomalous scattering from heavy atoms.

Since the MAD method requires measurements of Bragg reflections at different wavelengths with high accuracy, there exist many problems in the experiments, as energy resolution of the beam, XAFS spectrum of crystal, absorption correction with different wavelengths, radiation damage in the course of measurements and others. Thus, the PX beamline has a concept of "trichromatic beam" to minimize systematic errors that may arise in MAD experiments.

The trichromatic concept is to realize measurements of intensities at three different wavelengths serially within a minimum period of time from a single crystal setting of the same crystal. Two wavelengths are supplied from one of the undulators and the third from the second undulator. The trichromator consists of three sets of double crystal monochromators with the fixed-exit mechanism, as seen in Figure 2. Thin diamond crystals are used as transparent monochromators, of which the conditions are investigated to give perfect and larger size under high pressure in collaboration with Sumitomo Electric Industry. Collinear three beams are chopped by shutters to give downstream diffractometer one wavelength at a time. Three sets of Bragg reflections are sequentially collected in the same crystal setting. This is to minimize the systematic errors from incident beams and the X-ray damage that is much more serious with SPring-8 undulator sources than the bending magnets X-rays in the second generation SR source.

The X-rays are focused to 52 m from the source, giving 100 micrometer squares. This may be very powerful in the structure analyses of proteins with small sizes.

The experimental station has a standard diffractometer with two-dimensional area detector with XAFS equipment and cryo-apparatus around the crystals.

The RIKEN beamline for structural biology will be completed by the time the storage ring to be commissioned in spring of 1997. The experimental stations will be in service by Fall, 1997. The second beamline for structural biology, XAFS and protein crystallography by Laue diffraction, and the third for R & D for the long straight section are in the stage of conceptual design.

Reference

[1] Hideo Kitamura, Synchrotron Radiation Calculation Program for PC98, *Spectra* V.20

[2] T. Tanaka, X. Marechal and K. Kitamura, these poceedings

[3] J. Karle, Int. J. Quant. Chem. 7, 375 (1980)

[4] W.A. Hendrickson, J.L. Smith, R.P. Phizackerley and E.A. Merritt, Proteins 4, 77 (1988)

[5] H. Yamaoka, K. Ohtomo and T. Ishikawa, these proceedings

[6] T. Uruga, H. Kimura, Y. Kohmura, M. Kuroda, H. Nagasawa, K. Ohtomo, H. Yamaoka, T. Ishikawa, T. Ueki, H. Ieasaki, S. Hashimoto, Y. Kashihara and K. Okui, these proceedings

[7] T. Tanimori, S. Minami, T. Nagase, T. Takahashi and T. Miyagi, SPIE Vol.1734, Gamma-Ray Detector, 68 (1992)

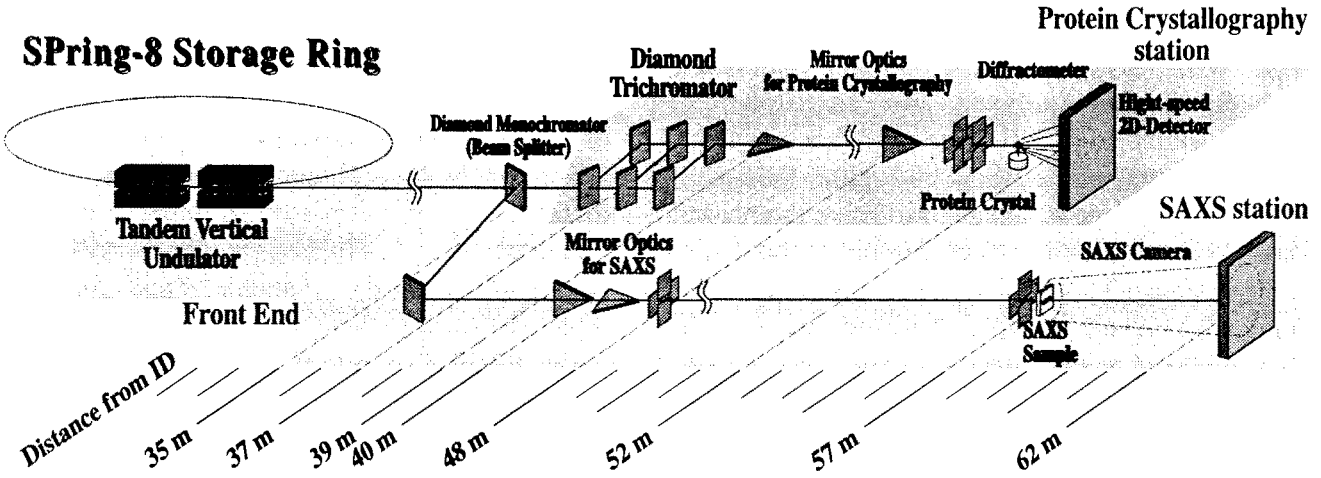

Figure 1

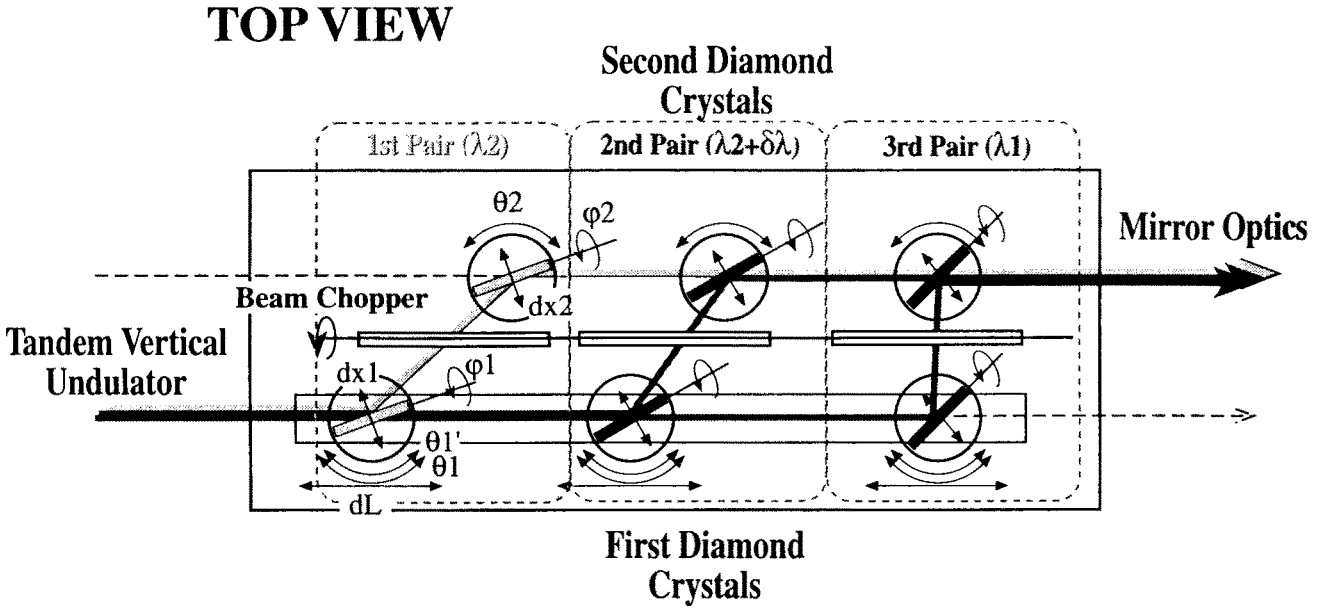

Figure 2