

of plates with the period of 2.3 micron is induced. It is shown, that the scattering of the relativistic electrons on such a stacks with the period of dielectric permittivity about a few microns in amorphous quartz leads to formation of intense transition radiation. Radiated photons have the intensity $\sim 10^7$ photon/second and the energy 1.3 KeV in a solid angle ~ 30 angular seconds with the energy spread $\Delta E/E \sim 10^{-5}$ [3]. The peak values of the energy E are coincide with $\gamma \omega_{pt}$, where γ is the Lorentz factor, and ω_{pt} is the plasma frequency of the melted quartz [2]. The theoretical evaluation and its comparison with the experiment shows that the maximal number of plates, which gives contribution to the intensity of the transition radiation is order to 20. The problem under consideration is theoretically solved using Maxwell's equations. Corresponding numerical calculations are carried out and conditions are found which yields to formation of the maximum number of photons. The obtained results are in good accord with the experiment [3].

[1] G.M. Garibyan and C. Yang.// Sov. Phys. JETP 36, p.631, 1973.

[2] L.Sh. Grigorian, A.H. Mkrtchyan, A.A. Saharian.// Nuclear Instruments and Methods B, pp. 197-202, 1998.

[3] A.R. Mkrtchyan, et al. // Physics Letters A, vol. 152, No 5,6, pp. 297-299, 1991.

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A monochromatic station for macromolecular crystallography at diamond light source

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The fixed wavelength monochromatic beamline will be situated next to the Phase I I04 MX beamline. The photon beam will be produced by two undulators placed in a canted formation, allowing I04 and I04-1 photon beams to be separated by 1 mrad. The beamline will provide rapid and extensive access to synchrotron radiation for a growing user community composed by both academic and industrial research groups. I04-1 will be dedicated to high-throughput data collection for rapid structure solution using MR method. As more structures are available in databases, MR is the most used method for the structure solution of proteins. The wavelength of the I04-1 beamline will be fixed at 0.9163 Å (energy of 13530 eV). The beamline will also be fully automated with a sample changer robot, automated crystal alignment, data collection and processing. Optionally, single anomalous diffraction (SAD) experiments will be possible since anomalous signal of several heavy atoms can still be measured at this wavelength. Finally, an X-ray fluorescence detector will be available to establish the metal ions footprint of the sample. I04-1 is currently in the construction phase and is planned to be ready for operation in late 2009.

Keywords: macromolecular crystallography, high-throughput data collection, fixed-wavelength

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Experience from operation and commissioning of the phase 1 MX beamlines at diamond light source

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Diamond Light Source [1] is the new UK third generation synchrotron located south of Oxford. In January 2007 Diamond welcomed first users. In Phase 1 seven beamlines are funded which includes three beamlines for macromolecular crystallography (MX) [2]. These are currently in a commissioning phase aimed for optimisation of operation. The beamlines are similar in design and take radiation from an in-vacuum undulator. A double crystal monochromator and a Kirkpatrick-Baez mirror arrangement are the main optical components. First experience from operation and results of the commissioning of the MX beamlines will be presented. This will include discussion of the beam properties, status and performance of the optical components and diagnostics in the optics hutch as well as results from commissioning of the equipment in the experimental end station. The software environment and results from data collections will also be discussed.

[1] <http://www.diamond.ac.uk>

[2] <http://www.diamond.ac.uk/MX>

Keywords: diamond Light Source, beamline commissioning, synchrotron

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Installation of high throughput protein crystallography data collection at SPring-8 BL12B2

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The SPring-8 Taiwan Contract Bending Beamline (BL12B2) has been dedicated to studies related to macromolecular crystallography in order to facilitate biological communities to explore all aspects of structural molecular biology. High-throughput protein crystallography using industrial automation technologies have significantly reduced the time needed to conduct protein structure experiments at many facilities around the world. At SPring-8, we are in the process of installing the new instruments of equipment stage, crystal goniometer, sample auto-changer robot SPACE and Beamline Control Software (BSS). The BSS software controls the entire beamline machinery such as pulse motors, counter control, equipment stage, automated sample changing, crystal centering and automatic data collection through the graphical user interface (GUI) communication protocol. The facility serves experts and non-expert crystallographers, who benefit in structural analysis from protein purification to three-dimensional structure determination. The upgrade of protein end station at SPring-8 Taiwan Beamline (BL12B2)