PS01.02.21 X-RAY IMAGING OF POLYCRYSTALLINE AND AMORPHOUS MATERIALS. T. Wroblewski, HASYLAB at DESY, Notkestr. 85, D-22603 Hamburg

A novel method for obtaining position resolved information simultaneously from an entire plane of a polycrystalline or amorphous sample using the diffracted radiation or fluorescence has been developed. It makes use of a microchannelplate as a collimator in front of a position sensitive detector (CCD-camera). The resolution thus obtained is 30 μm with a field of view of 12*12 mm^2. Experiments may be performed either in transmission or in reflection geometry. In the first case a 'flat' parallel beam illuminates a slice through the sample while in the second case the surface of the specimen is illuminated by a broad beam. Typical fields of application are:

•non-destructive investigations of the distribution of polycrystalline components in composites

•reciprocal space mapping to determine the mutual influence of strain and orientation in adjacent grains in a polycrystalline material

•analysis of the distribution of chemical elements or even valence states (using the chemical shift of the absorption edges) via their fluorescence

The use monochromatized synchrotron radiation is recommended for two reasons: the diffraction experiments require high collimation, and for the selective excitation of fluorescence a source with tunable energy is needed.

PR01.02.22 THE PROPOSAL OF THE DIFFRACTION EXPERIMENT WITH NANO SECOND TIME RESOLUTION. THE FIRST TEST EXPERIMENTS WITH PROTOTYPE. Gennadiy N. Kulipanov, Svyatoslav I. Mishnev, *Boris P. Tolochko. Budker Institute of Nuclear Physics, M. Lavrentev st.11, Novosibirsk, 630090 Russia; *Institute of Solid State Chemistry, Kutateladze st.18, Novosibirsk-128, 630128 Russia

A history of the development of time-resolved diffraction experiment on the synchrotron in Novosibirsk INP started since 1975. There are two factors, which lies in the fundament of all time resolved experiments: 1) a powerful insertion devices and X-ray optic provided high intensity of the synchrotron radiation, 2) fast position sensitive and area detectors quickly collected diffraction data. There is no limits for improving the first one, but it will be a lot of problem with detectors, when you will try to do diffraction experiment with time resolution less then micro second. We think that it is impossible to use traditional diffraction scheme for the experiments in the nano second scale.

For the diffraction experiment with nano second time resolution we propose new scheme in which will be used the fast electron beam scanning in the ondulator. The scanning will be made by fast correctors of the electron beam trajectory in the ondulator only. The electron trajectory will not disturbed in the other part of the storage ring. New detector will be developed for this experiment, which will be synchronize with correctors.

The prototype of this experiment was realized at storage ring VEPP-3. The influence of the fast corrector on the behavior of the electron beam and synchrotron radiation was investigated. The prototype of new detector was used in this experiment.

PR01.02.23 THE FOUR CIRCLE DIFFRACTOMETER AT ELETTRA R. Spagna, L. Barba, M. Camalli, A. Cassetta, M. Catricala', C. Marciante, A. Pifferi, Istituto di Strutturistica Chimica, Area della Ricerca, CNR, C.P. 10, 00016 Monterotondo Stazione, M. Colapietro, G. Portalone, Dip. di Chimica, Universita' di Roma "La Sapienza", Pl. Aldo Moro, 00100 Roma

ELETTRA is a low emittance synchrotron radiation (SR) facility at Trieste. The radiation source of the beamline for X-ray diffraction is the 4.5m long, 57 poles permanent magnet wiggler which widens the range of wavelength available for experiments to a short wavelength limit of about 0.5Å. The SR can be monochromatized in the range 4-25keV (0.5-3.0Å) by means of a fixed-exit double-crystal monochromator containing two interchangeable pairs of Si(111) or Si(220) crystals in a nondispersive parallel setting. In order to obtain a higher flux on the sample a mirror collects 2.8 mrad horizontally and 0.23 mrad vertically and focuses X-rays up to 25keV with a demagnification factor of 1.5 (S.Bernstorff et al., Rev.Sci.Instrum. (1995) 66,1661-1664).

The experimental station is equipped with both a imaging plate detector system from Marresearch (180mm) and a Mod. 5020 Huber 4-circle diffractometer. The last instrument designed for operation with a vertical scattering plane is supported on a kinematic table to allow the alignment of the instrument with respect to the beam. The diffractometer is controlled by a personal computer through a plug-in board interface and the program system CS has been made to carry out single crystal diffraction experiments. A silicon crystal was used to plan the strategies to handle the very sharp diffracted beams. 19 reflections were located and centred. The rocking curves of these reflections show full widths at half-maxima of about 0.01. A first oriantation matrix gives a average value of the cell parameter a = 5.431(2) in very good agreement with the value of 5.43088(4) calculated by powder diffraction of NBS Standard Reference Material No. 640. Afterwards a spherical crystal of calcium fluride and then one of corundum, Al2O3, were mounted on the diffractometer and data collections were performed.

Results will be presented during the conference.

Synchrotron Radiation II Macromolecules

MS01.03.01 THREE-DIMENSIONAL DIFFUSE X-RAY SCATTERING FROM STAPHYLOCOCCAL NUCLEASE. Michael E. Wall and Sol M. Gruner (Department of Physics, Princeton University, Princeton, NJ 08544, USA), Steven E. Ealick (Section of Biochemistry, Cell and Molecular Biology, Cornell University, Ithaca, NY 14853, USA).

The first full three-dimensional map of diffuse x-ray scattering from a protein crystal has been obtained using a CCD detector at the Cornell High-Energy Synchrotron Source (CHESS). The map was characterized and used to study the nature of disorder in crystals of Staphylococcal nuclease. Simulations indicate a correlation between the Staph. nuclease diffuse map and the calculated unit-cell structure factor. This result is consistent with a number of models of disorder, the most plausible being liquid-like motions of the protein [Caspar et al., Nature 332 (1988) 659] and thermal excitation of crystalline normal modes, both of which involve internal dynamics of the protein. Unit-cell substitutions and unit-cell rigid-body displacements, though unlikely, cannot be ruled out as models describing the disorder.