systems. The plastic strain distribution obtained in this way provides a general correlation between plastic deformation history and the properties of the observed diffraction peaks.

Keywords: strain scanning, synchrotron radiation, magnesium alloy

MS21.25.5

Acta Cryst. (2005). A**61**, C33

Depth-resolved Strain Measurements by Energy-variable X-ray Diffraction

Emil Zolotoyabko, *Department of Materials Engineering, Technion, Haifa 32000, Israel*. E-mail: zloto@tx.technion.ac.il

Characterization of the microstructure of materials with spatial resolution is one of key issues in materials related fields from nano-technology to non-destructive testing of manufactured articles. Depth resolved strain/stress measurements by diffraction methods are of particular interest. In order to improve depth resolution of x-ray diffraction, we are developing novel technique for synchrotron beam lines – energy-variable diffraction (EVD) [1]. The method is based on our ability to precisely change energy of synchrotron radiation and, in a result, to accurately control the x-ray penetration depth. Comprehensive analysis of x-ray trajectories, taking into account the instrument misalignment, change of the height of an incident x-ray beam with energy, and variable penetration of x-rays into the sample depth, allowed us to receive analytic expression for the diffraction profile measured by EVD and to show that the maximum diffraction intensity registered in the detector is coming from certain depth, which is energy-dependent [2]. This finding opens a way for measuring residual strains with high depth resolution by changing the x-ray energy in small enough steps.

Experimental examples taken with differently scaled metal/metal and metal/ceramic multilayers as well as structures from nature (seashells) demonstrate the capabilities of the method.

[1] Zolotoyabko E., Quintana J. P., *Rev. Sci. Instr.*, 2002, **73**, 1663. [2] Zolotoyabko E., Quintana J. P., *J. Appl. Cryst.*,2002, **35**, 594. [3] Zolotoyabko E., Quintana J. P., *Nucl. Instr. & Meth. B*, 2003, **200**, 382. [4] Zolotoyabko E., Pokroy B., Quintana J. P., *J. Synchr. Rad.*,2004, **11**, 309.

Keywords: residual strains, X-ray diffraction, multilayers

MS22 SINGLE PARTICLE X-RAY DIFFRACTION IMAGING

Chairpersons: Janos Hajdu, Henry Chapman

MS22.25.1

Acta Cryst. (2005). A**61**, C33

Diffraction Imaging of the Yeast Cell: First Results

David Shapiro[a], Pierre Thibault[b], Tobias Beetz[a], Veit Elser[b], Malcolm Howells[c], Chris Jacobsen[a], Janos Kirz[c], Enju Lima[a], Huijie Miao[a], Aaron M. Neiman[d], David Sayre[a], [a]*Department of Physics and Astronomy, Stony Brook University, USA.* [b]*Department of Physics, Cornell University, USA.* [c]*Advanced Light Source, Lawrence Berkeley National Laboratory, USA.* [d]*Department of Biochemistry and Cell Biology, Stony Brook University, USA.* E-mail: dshapiro@xray1.physics.sunysb.edu

We have developed an apparatus for soft x-ray diffraction microscopy (XDM) of dry or frozen hydrated biological specimens. The microscope, stationed at beamline 9.0.1 of the Advanced Light Source, can collect nearly complete three-dimensional diffraction data to 10 nm resolution. Diffraction patterns, from eight angular orientations of a whole and unstained freeze-dried yeast cell, were recorded with the microscope and phased using the difference map algorithm. The resulting images portray the natural complex refractive contrast of the cell to 30 nm resolution and their agreement provides confidence in the accuracy of the imaging technique. New techniques for handling noisy and incomplete diffraction data were developed and improved the convergence of the algorithm. The effects of large doses on the structure of the cell were also investigated and it is determined that dry specimens suffer from shrinkage while frozen hydrated cells are stable with doses as large as 5×10^9 Gray.

Keywords: X-ray diffraction, X-ray imaging, X-ray microscope

MS22.25.2

Acta Cryst. (2005). A**61**, C33

Imaging Magnetic Nanostructures by X-ray Holography

Stefan Eisebitt, *BESSY, Berlin, Germany*. E-mail: eisebitt@bessy.de

While holography has evolved to a powerful technique in the visible spectral range, it is difficult to apply at shorter wavelength as no intrinsically coherent (soft) x-ray laser is yet available as a light source. The progression from visible light towards shorter wavelength is motivated by the increase in spatial resolution that can be achieved. Of equal importance is the possibility to exploit special contrast mechanisms provided by scattering in resonance with transitions between electronic core and valence levels.

We demonstrate imaging of non-periodic objects by x-ray spectro-holography at 50 nm spatial resolution. Magnetic domain patterns forming in thin film Co-Pt multilayers with perpendicular anisotropy are imaged using x-ray magnetic circular dichroism contrast at 778 eV photon energy. The images are obtained by direct Fourier inversion of the coherent scattering pattern, without the need of phase retrieval or an iterative computing process. Holography at this wavelength was made possible by combining the sample with a nanostructured mask. [1] This approach is particularly valuable for future single shot and/or single molecule imaging experiments at free electron x-ray lasers. At such sources, the coherent x-ray flux will be sufficient to record a coherent x-ray diffraction snapshot using a single x-ray pulse with a duration of a few femtoseconds.

[1] Eisebitt S., Lüning J., Schlotter W. F., Lörgen M., Hellwig O., Eberhardt W., Stöhr J., *Nature*, 2004, **432**, 885.

Keywords: holography, coherent scattering, electronic structure and magnetism

MS22.25.3

Acta Cryst. (2005). A**61**, C33

Prospects for X-ray Diffraction Imaging of single Biological Molecules

Stefan P. Hau-Riege, *Lawrence Livermore National Laboratory, Livermore, CA 94539, USA.* E-mail: hauriege1@llnl.gov

Short x-ray pulses from x-ray free electron lasers (XFELs) may enable diffraction imaging of single biological molecules. This would allow the determination of the structure of many molecules that have, to date, resisted crystallization. Since the appropriate sources will not be available for a few years, experimental design currently has to be done through simulations and modeling. Various aspects of the models are tested through experiments on currently available light sources.

In this presentation we will discuss numerous issues of the injection, irradiation, and imaging process. We will present our plans to model all aspects of the diffraction imaging endeavor, and the progress that we have made to date. Specifically, we will present an analysis of the pulse length and photon energy requirements by combining results from a continuum damage model [1] with a fluence requirement model [2]. We will further discuss several means to alleviate the pulse requirements, and compare the requirements with parameters of two planned x-ray lasers. Finally, we will present results from recent 3D imaging experiments at a resolution down to 10nm.

[1] Hau-Riege S.P., London R.A., Szoke A., *Phys. Rev. E*, 2004, **69**, 051906. [2] Huldt G., Szoke A., Hajdu J., *J. Struct. Biol.*, 2003, **144**, 219.

Keywords: diffraction imaging of non-crystalline specimens, biological molecules, radiation damage studies

MS22.25.4

Acta Cryst. (2005). A**61**, C33-C34

Imaging of Atom Clusters by hard X-ray free Electron Laser Pulses

Zoltan Jurek, Gyula Faigel, Gabor Oszlanyi, Miklos Tegze, *Research Institute for Solid State Physisc and Optics,H-1525 Budapest, POB 49. Hungary.* E-mail: jurek@szfki.hu

We study the possibility of imaging a small cluster of atoms by

MS