Abstract Submitted for the MAR06 Meeting of The American Physical Society

Serial Crystallography: imaging single proteins at a synchrotron¹ DAVID SHAPIRO, Center for Biophotonics Science and Tech., JOHN SPENCE, R. BRUCE DOAK, DMITRI STARODUB, UWE WEIERSTAL, Arizona State University, HENRY CHAPMAN, STEFANO MARCHESINI, Lawrence Livermore Nat. Lab., MALCOLM HOWELLS, Lawrence Berkelev Nat. Lab. — A new method is proposed for the imaging of uncrystallized proteins at third generation x-ray sources. The method, serial crystallography, uses the diffraction pattern produced by a beam of hydrated proteins as they sequentially traverse a continuous x-ray beam after having been aligned by an intense laser field. Each particle is exposed to the x-ray beam so briefly that radiation damage is not a concern. The diffraction pattern is integrated as many identically aligned particles cross the beam and then the laser polarization is rotated to allow collection of other particle orientations. The diffraction pattern can then be phased by an iterative algorithm and the protein structure recovered with a Fourier transform. We are currently constructing a serial crystallography apparatus to be installed on beamline 9.0.1 of the Advanced Light Source at Lawrence Berkeley National Lab that will be operational by May, 2006. Preliminary experiments will use a 5 Watt CW IR laser to align particles of Tobacco Mosaic Virus and their soft x-ray diffraction patterns will be collected. We present the design of the serial crystallography apparatus and the current status of this project.

¹Supported by NSF funding SGER DBI-0429814 and CBST

David Shapiro Center for Biophotonics

Date submitted: 01 Dec 2005

Electronic form version 1.4