Abstract Submitted
for the MAR07 Meeting of
The American Physical Society

Dose and exposure requirements for the protein x-ray serial crystallography. DMITRI STARODUB, Department of Physics, Arizona State University, Tempe, AZ 85287-1504 — We have proposed spraying proteins (aligned by a laser) across a synchrotron beam to solve proteins which cannot be crystallized.[1] A single-file stream of ice-jacketed proteins is considered. We compute diffraction patterns for the GroEL at the incident x-ray flux predicted for a new coherent scattering beamline at the Advanced Photon Source. Using iterative phasing of the data, we determine the relationship between the count rate at a reconstructed pixel (or 3D voxel) of a given size in the real-space charge-density map and number N of proteins in the 10-μm 2 kV x-ray beam at any instant. A modulation transfer function estimates resolution for various exposure times. With the incident flux of 10^6 photons/s/nm^2 and N=10, over 5,000 counts/s are distributed over the entire diffraction pattern, which is sufficient for a nm resolution with 200 s exposure. We compare the results of this numerical lensless imaging experiment with a simple theoretical treatment of image formation in the dark and bright field phase contrast. Supported by ARO, NSF and co-workers.[1] [1]J. Chem Phys. 123, 244304 .

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Date submitted: 20 Nov 2006 Electronic form version 1.4