Diffraction from a Laser-aligned Beam of Hydrated Proteins

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The aim of this work is to solve proteins which cannot be crystallized. An apparatus is under construction at ASU physics (electrons) and at the Advanced Light Source in Berkeley (X-rays) to obtain diffraction patterns from a single-file submicron droplet stream [1]. Each water droplet contains, on average, one protein. The droplets freeze by evaporative cooling to vitreous ice, most of which is allowed to sublimate. The molecules are aligned by a 100 watt CW fiber laser. All three beams , laser, X-rays and droplets, run continuously, and diffraction data is aquired continuously by CCD camera until adequate signal-to-noise is achieved. The laser polarization is then rotated into a new orientation using a quarter-wave plate, allowing tomographic diffraction data collection for three-dimensional reconstruction. The phase problem for the continuous diffraction pattern is solved by novel iterative Gerchberg-Saxton-Fienup methods [2]. Waves scattered by different molecules don't interfere. The requirements of laser power and droplet temperature needed to achieve sub-nanometer resolution and so observe the secondary structure of proteins will be described in detail. Factors which affect the damping of oscillations in the laser beam and momentum transfer by elastic diffraction to a levitated molecule.

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Keywords: proteins, structure, laser alignment