High-Resolution Data Collection at the 17-ID Undulator Beamline at the APS

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Introduction

Third-generation synchrotron x-ray sources are playing an increasing role in macromolecular crystallography. In addition to providing the capability of performing multiwavelength experiments for initial phasing, third-generation sources offer brilliant x-ray beams that often enable collection of data to higher resolution than can be obtained elsewhere. Higher resolution data collection gives better electron density maps, and these in turn provide a more detailed understanding of molecular structure and function. We report high-resolution data collection from four crystalline proteins at 17-ID undulator beamline at the APS and a comparison with published structures derived from non-APS data.

Materials and Methods

Four commercially available proteins—bovine insulin, chicken citrate synthase, hen egg-white lysozyme, and horse myoglobin—were crystallized for this study. Bovine insulin cubic crystals have been formed from a solution of 0.4 M sodium potassium tartrate, 30% PEG3000. Chicken citrate synthase tetragonal crystals were grown from 1.1 M sodium citrate pH 6.0, and monoclinic crystals from the same well solution with 10 mM acetyl-CoA in the drop. Hen lysozyme tetragonal crystals were grown from 50 mM sodium acetate pH 4.72, 8.25% NaCl, 24% Ethylene glycol. Monoclinic hen lysozyme crystals were grown from 0.1 M sodium acetate pH 4.5, 2 % sodium nitrate. Horse myoglobin crystals were grown from 3.3 M sodium sulfate. X-ray data have been collected from cooled crystals at the 17-ID beamline of the Advanced Photon Source. All data were processed using X-GEN.

Results

Each of these proteins crystallized in the same space group and with unit cell parameters nearly identical to those found in the published crystal structures; this indicates that the crystals were approximately isomorphous with those studied previously. Bovine insulin cubic crystals diffracted to 1.45 Å, whereas the published structure is based on 1.9 Å data. Chicken citrate synthase tetragonal crystals diffracted to 2.3 Å instead of 2.8 Å,[2] and monoclinic crystals to 1.24 Å instead of 1.6 Å.[3] Hen tetragonal lysozyme crystals diffracted to 1.0 Å instead of 1.33 Å,[4] and monoclinic crystals diffracted to 1.1 Å instead of 1.6 Å. Horse myoglobin monoclinic crystals diffracted to 1.1 Å instead of 1.4 Å.[5] Refinements of these structures at or near these resolution limits are planned.

Discussion

High-resolution structures are always of interest to protein crystallographers. Several chemical and packing factors determine the resolution limit of a structure. The characteristics of the x-ray source and the detection method employed influence the resolution limit as well, and in obtaining data to higher resolution on these structures we are exploiting a variety of characteristics of the APS storage ring and IMCA-CAT's undulator facilities. Thus, the highly parallel character of 17-ID's beams provides for clear separation of spots and low backgrounds, both of which improve data quality near the limit of resolution, and the reliability and linearity of IMCA-CAT's charge-coupled device detector systems maintain the accuracy of the data.

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