

Correlated Motions from Protein Crystallography

Steve P. Meisburger¹, David A. Case², and Nozomi Ando¹

1. Department of Chemistry, Princeton University
2. Department of Chemistry & Chemical Biology, Rutgers University

Abstract:

The collective motions of proteins are important for function, yet these motions are a challenge to observe experimentally. Intriguingly, when such motions occur in protein crystals, they leave distinctive fingerprints in the scattering between the Bragg peaks. The nascent field of "crystallography beyond Bragg" aims to extract information of biological relevance from the diffuse signal. However, this goal has proven difficult to achieve. To interpret a diffuse pattern one must account for non-ideal aspects of protein crystals, such as solvent dynamics and lattice disorder. Although this has been demonstrated in a few pioneering studies, the phenomena remain poorly characterized in general because very few purposeful and accurate measurements of diffuse scattering have been reported. To address the paucity of data, we measured complete high quality maps of total scattering from several single-domain proteins of historical interest, at (or near) room temperature. We developed software and methods for data reduction, scaling and validation that are optimized for modern detectors. In addition, we are able to place both the diffuse and Bragg data on an absolute scale (electron units). To aid in interpretation, measurements are compared with all-atom MD simulations of one or more unit cells. These measurements and simulations highlight the variety of diffuse features that can be observed even in well-diffracting systems, and provide insight into the types of disorder that are likely common to all protein crystals.