Effect of Crystal Packing on Protein Conformation and Dynamics

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X-ray crystallography has played the major role in structural biology, providing information on protein conformations. However, interpretation of this data is not always trivial. While proteins are flexible and adopt different conformations, X-ray structures represent only a single snapshot of the conformational ensemble. In addition, this static image may be subject to artificial forces such as crystal packing. It is especially important when several conformations of a protein are available – some conformations reflect their biological context (such as an allosteric effector), whereas others may be under the effect of crystal packing.

We have been studying several biological systems using molecular dynamics simulations and examining how experimentally determined structures correlate with the conformational ensembles to provide additional insight to the structural mechanism of their functions. We showed that, while the conformations of X-ray structures are energetically accessible, they are not always the most energetically favorable conformation. Thus, the X-ray structure itself is not sufficient to reveal the mechanism of protein function, and could even lead to inaccurate speculations.