Rendering the dynamic static: examining how x-ray crystallography constructs investigation into protein function

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Abstract

In this paper I will examine the values and thought patterns embodied in the practices of x-ray crystallography and the ways this imaging method constructs a 'static' approach to protein functions.
In the late 1950s, X-ray crystallography revolutionized the way in which we visualize biological macromolecules. It allowed us to resolve and construct the image of the complex irregular structures of proteins captured within a crystal. This approach continues to influence our understanding of protein function and interaction fueling drug discovery. These crystal structure representations, however, construct a very specific concept of proteins. They encourage us to view proteins as static, rather than as the dynamic macromolecules they often appear in solution.
Specialists in more applied fields, such as chemical engineering, often treat these models as a black box, relying on the positions of the atoms in the model to investigate and/or engineer function. These structures, however, are visualizations of average positions and their 'static' appearance is an artifact of the technology. This project explores the values embedded in imaging technology that help shape the discourse of protein function in the wider scientific context. I will examine how the "static" methods of X-ray crystallography have shaped subsequent interpretations of what a protein is by addressing 1) how it has changed the way structural biologists interpret and resolve the spectrums produced to obtain a protein structure; 2) how these models are then applied not only by structural biologists but by the scientific and engineering community at large.

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