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Opinion Article

Diffraction Structural Biology and Importance

Volker Langan*

Department of Chemistry, University of Manchester, Manchester, United Kingdom

ABOUT THE STUDY

Structural biology is the study of how biomolecules are constructed. Scientists use a variety of imaging techniques to observe molecules in three dimensions to see how they combine, function, and interact with each other. Structural biology is molecular biology, biochemistry, and biophysics, which includes biopolymers, especially proteins composed of amino acids, RNA or DNA composed of nucleotides, and the molecular structure of membranes composed of lipids. It deals with how they get the structure and how it changes. It affects their function in their structure. This topic is of great interest to biologists, as macromolecules perform most of the functions of cells and can only perform these functions when coiled into a particular three-dimensional shape.

This structure, which is the tertiary structure of a molecule, is complexly dependent on the basic composition or primary structure of each molecule. In recent years, high-precision physical molecular models have become possible to complement *in silico* investigations of biological structures. Examples of these models can be found in the Protein Data Bank. Computational techniques such as molecular dynamics simulations can be used in combination with empirical structure elucidation strategies to extend and scrutinize protein structure, conformation, and function.

The biological properties of a Protein molecule depends on its physical interaction with other molecules. Thus, antibodies attach to viruses and bacteria and mark them for destruction, the enzyme hexokinase binds to glucose and catalyze the reaction between them, and actin molecules bind to each other and assemble into actin filaments. In fact, all proteins attach or bind to other molecules. In some cases, this bond is very strong. For others, it is faint and short-lived. However, binding always shows great specificity. That is, each protein molecule can usually only bind to one or a few of the thousands of different types encountered. A substance, to which a protein binds, whether it is an iron, a small molecule, or a macromolecule, is called the ligand for that protein.

The ability of a protein to bind selectively and with high affinity to a ligand depends on the formation of a series of weak unshared hydrogen bonds, ionic bonds, van der Waals attraction, and favorable hydrophobic interactions. All single bonds are weak, so effective bond interactions require the formation of many weak bonds at the same time. This is only possible. If the surface contours of the ligand molecule match the protein very well and fit like a glove. The region of the protein that binds to the ligand, called the ligand binding site, is usually composed of cavities on the surface of the protein formed by specific arrangements of amino acids. These amino acids can belong to different parts of the polypeptide chain that come together when the protein is folded. Separate regions of the protein surface generally provide binding sites for different ligands that can regulate the activity of the protein, as will be seen later. And other parts of the protein can act as handles for placing the protein in specific locations within the cell. One example is the SH2 domain mentioned above. It is often used to move proteins containing it to the site of the plasma membrane in response to a specific signal.

Correspondence to: Noboru Akhtar, Department of Chemistry, University of Manchester, Manchester, United Kingdom, Email: voler@langan.edu

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