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Description of biological macromolecules

J Robinson*

Department of Health Sciences, Ostfold University, Halden, Norway

*Corresponding author. E-mail: Robinson@gmail.com

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DESCRIPTION

All biological functions depend on activities that occur onset of fundamental building blocks restricts the ultimate functional properties of proteins. These molecules includes protines, amino acids, lipids. These activities are directed, modulated, or detected through complex biological machines, which might be huge molecules or clusters of molecules. Included are proteins, nucleic acids, carbohydrates, lipids, and complexes of them. Many regions of biological science focus at the signals detected through those machines or the output from those machines. The area of structural biology is involved with the properties and behaviour of the machines themselves. The ultimate desires of this area are with a purpose to expect the shape, function, and behaviour of the machines from their chemical formulas, through using primary principles of chemistry and physics and information derived from research of other machines.

Much of biological studies still begin as descriptive science. A curious phenomenon in some living organism sparks our interest, perhaps due to the fact it is reminiscent of some previously known phenomenon, perhaps due to the fact it's far inexplicable in any terms currently available to us. The richness and diversity of biological phenomena have led to the danger of a biology overwhelmed with descriptions of phenomena and without any unifying principles. Unlike the rest of biology, structural biology is in the unique role of getting its unifying principles largely known. They derive from basic molecular physics and chemistry. Rigorous physical theory and effective experimental strategies already provide deep information of the properties of small molecules. The same principles, in large part intact, must suffice to explain and predict the properties of the bigger molecules. For example, proteins are composed of linear chains of amino acids, only 20 different kinds of which regularly occur in proteins. The properties of proteins must be determined by the amino acids they contain and the order in which they are linked. While these properties may become the complex and far removed from any property inherent in single amino acids, the existence of a limited. Nucleic acids are potentially simpler than proteins since they are composed of only 4 essential types of building blocks, known as bases, linked to each different through a chain of sugars and phosphates. The collection of those bases in the DNA of an organism constitutes its genetic data. This sequence determines all the proteins an organism can produce, all of the chemical reactions it can carry out, and, ultimately, all of the conduct the organism can screen in reaction to its environment. Carbohydrates and lipids are intermediate in complexity among nucleic acids and proteins. We currently know less about them, but this deficit is rapidly being eliminated.

The central focus in structural biology at present is the three-dimensional arrangement of the atoms that constitute a large biological molecule. Two decades ago this information was available for only several proteins and one nucleic acid, and each three-dimensional structure determined was a landmark in biology. Today such systems are determined routinely, and we have all started to see structures of not just individual large molecules, but complete arrays of such molecules. The first third-dimensional structures have been each consistent with our expectations based on fundamental physics and chemistry.

CONCLUSION

Biological functions depend on activities that occur on the molecular level. These activities are directed, modulated, or detected through complex biological machines, which might be huge molecules or clusters of molecules. Most of the structures determined subsequently, however, were completely unrelated, and a large body of descriptive structural data began to emerge as more and more structures were revealed by x-ray crystallography. From newer data, patterns of third-dimensional structures have all started to emerge; it is now clear that maximum if not all structures will eventually fit into rational categories.