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Editorial Note

# Development Editor Note: Biomolecular Structures

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The structure of biomolecules are three-dimensional shape that is formed by a molecule of protein, DNA, RNA and that is important to its function. They are classified into four levels of molecular structures called primary, secondary, tertiary, and quaternary.

The primary structure of a biopolymer is the atomic composition and the chemical bonds connecting those atoms (including stereochemistry) is the exact specification. The primary structure is equivalent to specifying the sequence of its monomeric subunits, such as amino acids or nucleotides for a typical unbranched, un-crosslinked biopolymer (such as a molecule of a typical intracellular protein, or of RNA or DNA). The primary structure of a protein will start from the amino terminal (N) to the carboxyl terminal (C), while the primary structure of DNA or RNA molecule will be from the 5' end to the 3' end.

The pattern of hydrogen bonds in a biopolymer is the secondary structure. These determine the general three-dimensional shape of the local biopolymer segments, but do not define the global structure of the unique three-dimensional space atomic positions that are called tertiary structures. The hydrogen bonds of the biopolymer formally describe the secondary structure. However, for proteins, the bonding of hydrogen is associated with other structural features, which has given rise to less formal secondary structure concepts. In some regions of the Ramachandran plot, for instance, helices can adopt backbone dihedral angles; hence, a section of residues with such dihedral angles is sometimes called a helix, regardless of whether it has the correct hydrogen bonds. Within one molecule or group of interacting molecules, the secondary structure of a nucleic acid molecule refers to the base pairing interactions. It is also possible to uniquely decompose the secondary structure of biological RNAs into stems and loops. Sometimes, it is possible to further classify these elements or combinations of them, such as tetraloops, pseudoknots, and stem loops.

Its three-dimensional structure, as described by the atomic coordinates, is the tertiary structure of a protein or any other macromolecule. Proteins and nucleic acids fold into complex three-dimensional structures that result in the functions of the molecules.

In a multi-subunit complex, the quaternary structure refers to the number and organization of several protein molecules. The term is less general for nucleic acids but can refer to the higher-level organization of DNA in chromatin, including its histone interactions, or to the interactions between separate ribosome RNA units or spliceosome units.

Using either nuclear magnetic resonance spectroscopy (NMR) or X-ray crystallography or single-particle cryo electron microscopy, protein and nucleic acid structures can be determined (cryoEM).

DNA conformations in a wide range of living cells occur at high levels of hydration. One of the most important goals sought by bioinformatics and theoretical chemistry is protein structure prediction. The prediction of protein structures is of great importance in medicine (for example, drug design) and biotechnology (for example, in the design of novel enzymes). In the Critical Assessment of protein structure prediction, the efficiency of current methods is evaluated every two years.