

THE STRUCTURE OF THE PROTEIN MOLECULE AND THE FORCES GENERATED IN IT

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ABSTRACT

In order for a protein to perform its biological function, its molecule must have a certain spatial configuration. There are four basic levels of organization of protein molecules - there are primary, secondary, tertiary and quaternary structures. Often, hydrogen bonds appear in one polypeptide chain between adjacent amino acid residues. The spatial structure of a protein determines its physicochemical properties and biological functions.

Key words: Protein, denaturation, hydrogen bond

АННОТАЦИЯ

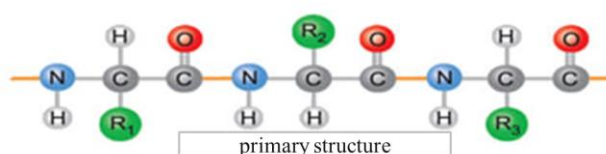
Для того чтобы белок мог выполнять свою биологическую функцию, его молекула должна иметь определенную пространственную конфигурацию. Различают четыре основных уровня организации белковых молекул — первичную, вторичную, третичную и четвертичную структуры. Часто водородные связи возникают в одной полипептидной цепи между соседними аминокислотными остатками. Пространственная структура белка определяет его физико-химические свойства и биологические функции.

Ключевые слова: белок, денатурация, водородная связь.

INTRODUCTION

Protein molecules contain many amino acid residues (up to several thousand), proteins are disordered biopolymers. They differ in the number, composition and sequence of amino acid units. In addition, each protein has a unique sequence of amino acids. In order for a protein to perform its biological function, its molecule must have a certain spatial configuration. There are four basic levels of organization of protein molecules - primary, secondary, tertiary and quaternary structures

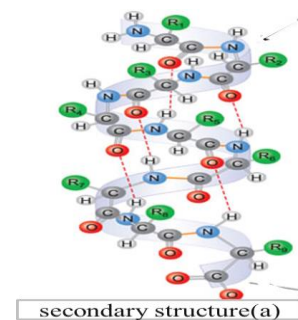
The primary structure of a protein is a fixed sequence of amino acid residues in a linear polypeptide chain. Each protein has a unique primary structure. Its presence is due to the



presence of strong peptide bonds between amino acid residues. All subsequent, more

complex structures are formed on the basis of primary structures. Therefore, a change in the primary structure leads to a change in the shape of the molecule, the properties and functions of the protein.

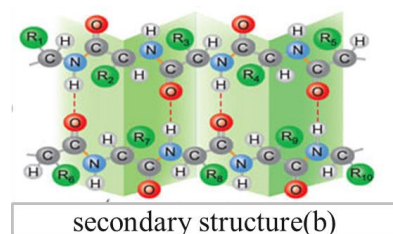
The secondary structure of the protein is formed due to the formation of a large number of hydrogen bonds between the hydrogen atoms of the NH groups and the oxygen atoms of the CO groups of various amino acid residues. Despite the fact that these bonds are weaker than covalent bonds, their number ensures the stability of the secondary structure.



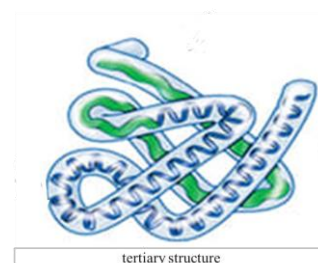
Often, hydrogen bonds occur in a single polypeptide chain between adjacent amino acid residues, causing the chain to twist into a so-called α -helix.

Only a few proteins have a secondary structure that is represented by only an α -helix or a β -fold.

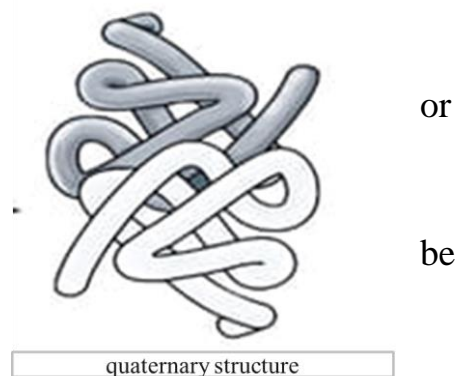
In the structure of many proteins, some sections have an α -helix shape, while others have a β -fold. The α -helix and β -structure sections of the protein molecule can interact with each other and form ordered structures (ensembles).



The formation of the tertiary structure is provided by hydrogen, ion and other bonds that appear between different atomic groups of the protein molecule. In an aqueous environment, the protein molecule is arranged in a special way in space and has a compact shape. In this case, hydrophobic amino acid radicals sink into the protein molecule and attract each other - this attraction is called hydrophobic interaction. The hydrophilic regions of the polypeptide, on the other hand, are located on the surface and interact with water molecules. The tertiary structure of each protein has a special, unique spatial configuration.



Many proteins are able to perform their biological functions with tertiary structure. But for some proteins, this requires the combination of two more molecules with a tertiary structure into a single complex. This is how the quaternary structure of the protein appears. The molecules that make it up can be the same or different. They are connected to each other due to various types of non-covalent bonds - hydrogen, ionic, hydrophobic interactions, etc.



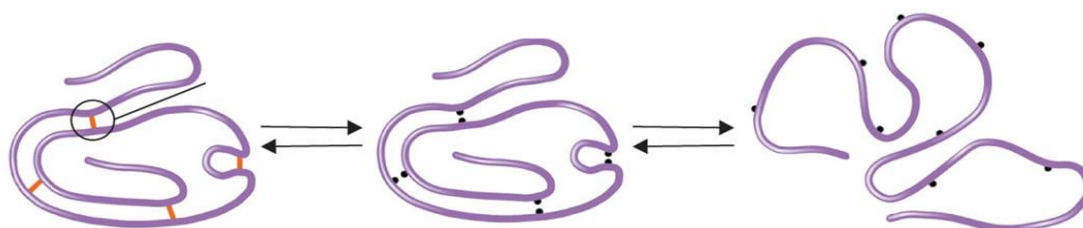
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According to the shape of the molecules, two groups of proteins are distinguished - fibrillar and globular.

DISCUSSION AND RESULTS

Many proteins are soluble in water, but there are also insoluble ones, globular proteins are mostly soluble in water, while fibrils are generally insoluble in water.

Proteins are sensitive to external influences: changes in the chemical composition of the environment, temperature and other factors lead to changes in their structure and properties. High and low temperatures, strong acids and alkalis, heavy metal ions, ultraviolet radiation, and radiation influence destroy bonds that stabilize the spatial configuration of proteins. Due to the breaking of hydrogen, ion, and other bonds, the protein can permanently lose its quaternary, tertiary, and even secondary structure. The process of breaking the natural structure of a protein under the influence of external factors without breaking its primary structure is called denaturation. The spatial structure of the protein determines its physicochemical properties and biological functions. Therefore, denaturation leads not only to changes in the size and shape of protein molecules, but also to its properties such as solubility. On its surface, non-polar hydrophobic groups located inside the molecule appear, and the protein becomes less hydrophilic. It is important that as a result of denaturation, proteins lose their ability to perform their functions. The degree of protein denaturation depends on the strength of the influence of various factors on it: the stronger their influence, the deeper the denaturation. In some cases, it becomes irreversible. However, if the factor that caused the denaturation is not affected for a long time, after its effect ends, the protein can restore its natural structure, properties and functions. This phenomenon is called renaturation. The spatial configuration of a protein is determined by its basic structure, that is, the sequence of amino acid residues. If the effect on the protein is too severe and leads to the breaking of the peptide bonds, it will be impossible for the protein molecule to return to its original structure. Denaturation of proteins can also occur with the addition of heavy metal ions to them.



Radicals of a number of amino acids that make up a protein molecule include basic and acidic functional groups. Thus, with an increase in acidity (that is, with an increase in the concentration of hydrogen ions), the dissociation of carboxyl groups in

the radicals of acidic amino acids is suppressed. At the same time, amino acids of basic amino acids bind an excess of H^+ ions. Due to this, at a certain pH value, the protein molecule receives a positive charge. A decrease in the acidity of the environment increases the dissociation of ^-COOH groups. In this case, additional hydrogen ions are released and the charge of the protein molecule becomes negative. Thus, proteins are able to maintain the pH level of the medium at a certain level.

At a certain pH value, the number of positively and negatively charged groups in a protein molecule is the same, and its total electric charge is zero. This pH value is called the isoelectric point of the protein. Each protein has its own isoelectric point, which is determined by the composition of amino acids. The isoelectric points of proteins dominated by acidic amino acid residues are in the $pH < 7$ region, and those dominated by basic amino acids are in the $pH > 7$ range. The more the pH value of the medium differs from the isoelectric point, the greater the charge of the protein. Therefore, there is an electrostatic repulsion between protein molecules that prevents them from sticking together (aggregation). At the isoelectric point, repulsive forces are minimal. Therefore, proteins are not the most stable in solution, their molecules easily stick together and precipitate.

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