Protein

An Introduction to
Protein Structure
and
Denaturation by Acidification
and Temperature

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Amino Acids and Protein Structure

A protein is a polymer of amino acids that obtains a unique configuration as it is assembled by a cell. It is this unique configuration that imparts to each protein a specific function. The function may be structural, enzymatic, hormonal, or immunological, to name a few. Clearly, proteins have an essential place in the anatomy and physiology of life.

The monomer of a protein is the amino acid. All amino acids have the same basic skeletal structure, shown at right, where an acid group (-COOH) and an amino group (-NH₂) are covalently bonded to a central carbon. Also of importance is the radical (R). This is essentially a "place holder"; as it is at this site that different side groups are attached. Variations in different types of amino acids are due to variations at the "R" and all amino acids with the same "radical" will have the same name. Six examples are shown below.

When two amino acids are covalently bonded together by a dehydration synthesis reaction, a peptide bond is formed. Additional amino acids may be added to lengthen the chain. As the linear sequence of amino acids expands, the primary structure is formed.
As the linear primary structure increases in size, it begins to take on a secondary structure, held together by hydrogen bonds. The secondary structure includes characteristic pleating and helical formations.

As the primary and secondary structure continues to grow, a complex irregular geometry develops as the protein repeatedly folds on itself. This third level of structural organization is called the tertiary structure. It is the unique configuration of the tertiary structure that frequently gives a protein its unique properties and functions.

The last level of structural organization that occasionally occurs is the quaternary structure. Here, more than one protein is bonded together. Hemoglobin is an example where four proteins are needed to create the protein foundation for this molecule.
Denaturation of Protein

When a protein is damaged due to a configuration change, the protein is said to be denatured. Denaturation may occur by several means, and two of the most important are covered here: denaturation due to a lowering of pH (acidification) or an increase in temperature.

In the case of a lowered pH, the introduction of positively charged hydrogen ions disrupts hydrogen bonds by competitive means. Here, the introduced hydrogen are attracted to the oxygen of the hydrogen bond, and the attractive force nullifies the previously existing bond. As this happens, the forces holding the unique structure are disrupted and the protein changes shape. And as the protein changes shape, it loses its functionality, and physiological stress ensues. Should the previous temperature be restored, the proteins will NOT return to their previous configuration, they are permanently damaged. The protein is said to be denatured.

If the complex structure of the protein has been totally disrupted, then the primary structure will result.
Elevated temperature may also denature proteins. Recall that temperature is a measurement of molecular movement (kinetic energy). Therefore, as the temperature increases, the hydrogen bonds may be inadequate to withstand the increased molecular bombardment from the water and other molecules around it.

However, at body temperature, the proteins within our body are stable because the hydrogen bonds adequately withstand this "moderate" bombardment of water molecules at body temperature.

As body temperature increases, the speed at which the adjacent molecules move may become sufficiently violent that the attractive forces that make up the hydrogen bond may not be adequate to withstand the bombardment. When this happens, the bond breaks and the protein structure is denatured. At very high temperatures, the protein structure may be radically altered.

If the temperature then decreases after denaturation has occurred, hydrogen bonds may once again form, but proteins never go back to their original configuration. In a random manner, wherever there is an adjacent oxygen and hydrogen, a hydrogen bond forms. As this happens, all the proteins may become cross-linked and become one solid protein mass.