

Protein Structure

As we discussed earlier, a protein's shape is critical to its function. For example, an enzyme can bind to a specific substrate at an active site. If this active site is altered because of changes in the protein shape, the enzyme may be unable to attach to the substrate. To understand how the protein gets its final shape or conformation, we need to understand the four levels of protein structure: primary, secondary, tertiary, and quaternary (Figure 3.29).

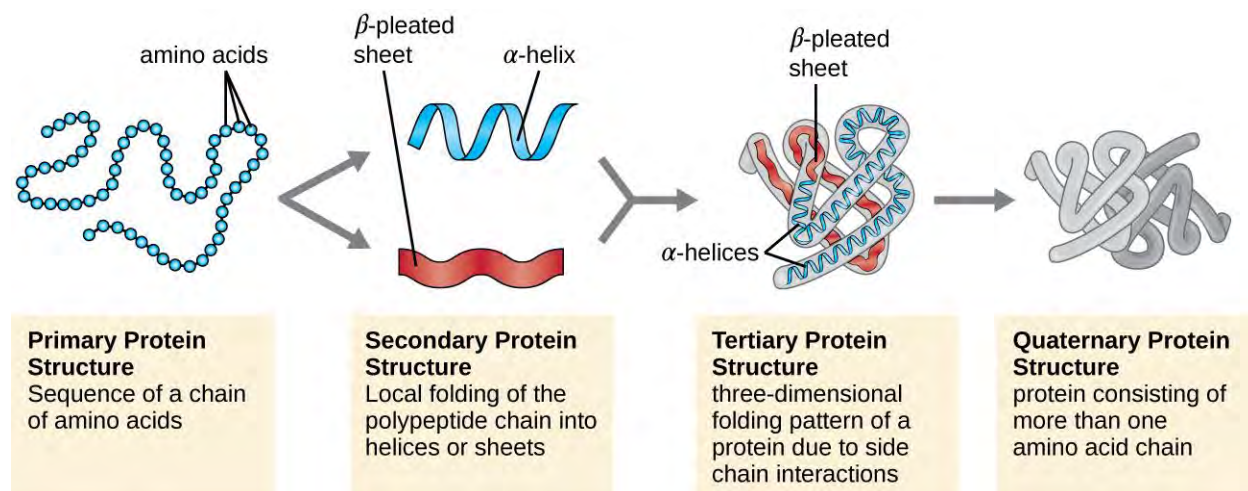


Figure 3.29 illustrates the four levels of protein structure (primary, secondary, tertiary, and quaternary). (credit: Parker et al. / [Microbiology OpenStax](https://openstax.org/))

Primary Structure

The **primary structure** is simply the polypeptide chain--the sequence of amino acids bonded together via peptide bonds. Figure 3.30 depicts the primary structure of a protein. A protein's primary structure is not rigid, but rather is flexible because of the nature of the bonds that hold the amino acids together.

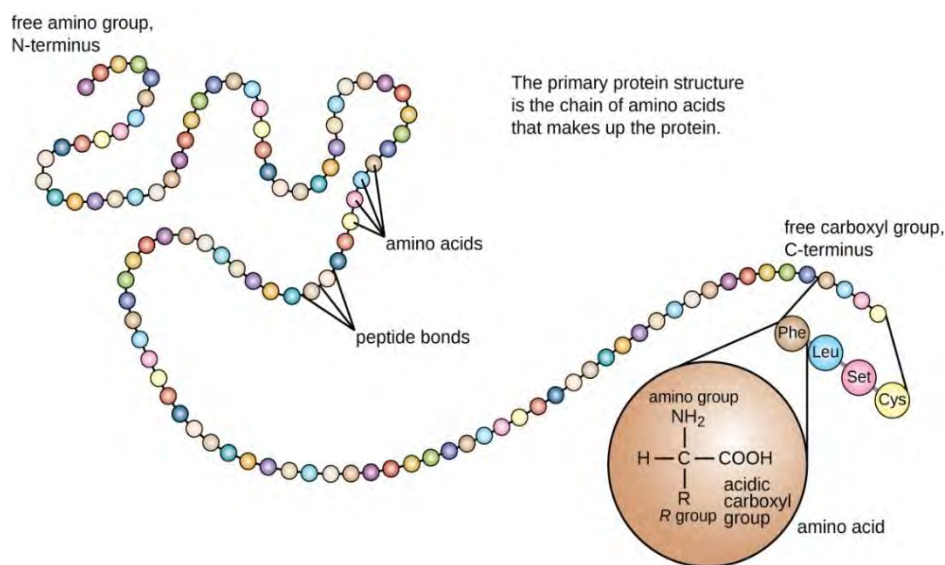
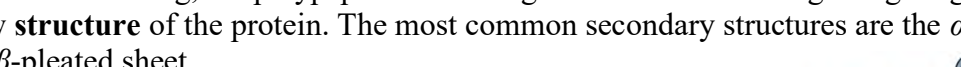


Figure 3.30 The primary structure of a protein is the polypeptide chain. (credit: modification of work by National Human Genome Research Institute / [Microbiology OpenStax](https://openstax.org/))

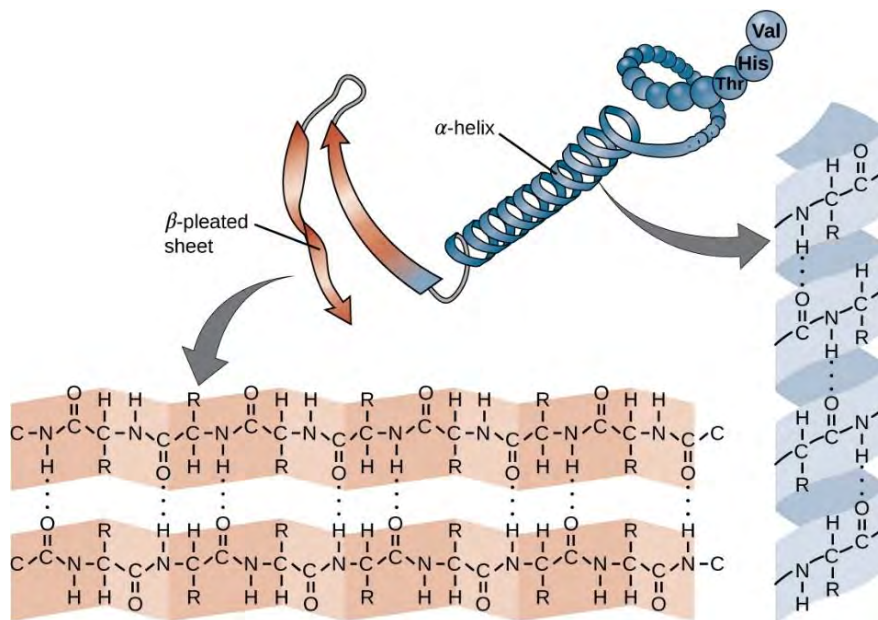
Secondary Structure

Due to chemical bonding, the polypeptide chain begins to fold in some regions giving rise to the **secondary structure** of the protein. The most common secondary structures are the α -helix and β -pleated sheet structures (Figure 3.31). Folding occurs because of hydrogen bonds that form between different amino acids within the chain.




The diagram illustrates two common protein secondary structures. On the left, a β -pleated sheet is shown as a zigzag structure with two orange arrows indicating the direction of the polypeptide chain. On the right, an α -helix is depicted as a blue coiled ribbon. A label points to the helix. To the right of the helix, three amino acids are shown as spheres: Val (Valine), His (Histidine), and Thr (Threonine). Further right, a chemical structure of an amino acid is shown, with labels for the amino group (N-H), the hydrogen atom (H), the side chain (R), and the carboxyl group (C=O).

Figure 3.31 The secondary structure of a protein may be an α -helix or a β -pleated sheet, or both. (credit: Parker et al. / Microbiology OpenStax)



Tertiary Structure

The polypeptide's unique three-dimensional shape is its **tertiary structure** (Figure 3.32). This structure is in part due to chemical interactions within the polypeptide chain. Primarily, interactions among different R groups create the protein's complex three-dimensional shape. It is only when the protein has folded into its three-dimensional shape is it considered to be functional. This assumes no additional modifications need to be made. When a protein loses its three-dimensional shape, it may no longer function properly.



The diagram shows a red, curved line representing the polypeptide backbone. A label 'Polypeptide backbone' points to this line. Below the backbone, a vertical line connects to a small circle, which is labeled 'O'.

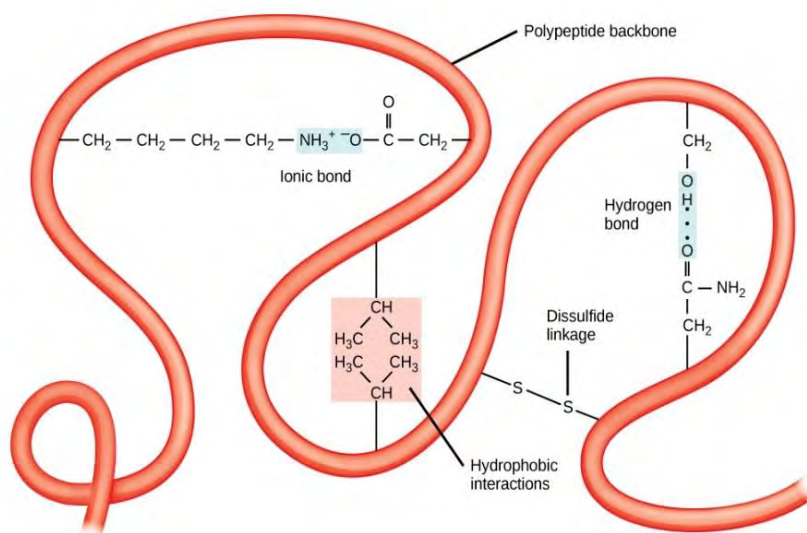
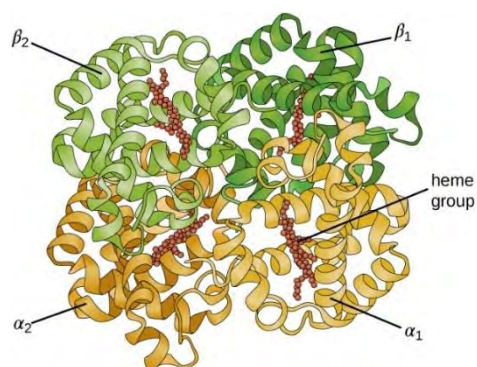


Figure 3.32 A variety of chemical interactions determine the proteins' tertiary structure. (credit: Parker et al. / [Microbiology OpenStax](#))

Quaternary Structure

Some proteins consist of several separate polypeptide chains. These proteins function only when all polypeptide chains are present and appropriately configured. The interactions that hold these subunits together leads to what is referred to as the **quaternary structure** of the protein.



Relatively weak interactions stabilize the overall quaternary structure. Hemoglobin, for example, has a quaternary structure of four globular protein subunits: two α and two β polypeptides. Each subunit contains an iron-based heme that will bond to an oxygen molecule (Figure 3.33).

Figure 3.33 A hemoglobin molecule has two α and two β polypeptides together with four heme groups. (credit: Parker et al. / [Microbiology OpenStax](https://openstax.org/))

Denaturation and Protein Folding

Each protein has a unique sequence and is held together by chemical interactions. These chemical interactions result in unique three-dimensional shapes that allow proteins to function. If the protein is subjected to changes in temperature, pH, salinity, harsh chemicals, etc. the protein shape may change. When a protein loses its three-dimensional shape and is no longer functional, the protein is said to be **denatured**. Denaturation is often reversible because the polypeptide's primary structure may be conserved during the process. If the denaturing agent is removed, and the primary structure was preserved, the protein can refold and resume its normal function.

Sometimes denaturation is irreversible. One example of irreversible denaturation is frying an egg. Liquid egg whites are rich in the protein albumin. When the liquid egg white is placed in a hot pan, the heat denatures the protein. As the protein is denatured, there is a structural change from the liquid clear egg into a semi-solid white substance. Once the semi-solid white substance has formed, it cannot revert to its original state.

It is important to keep in mind that each protein has its own optimal conditions under which it functions best. For example, not all proteins denature at high temperatures. Some bacteria that survive in hot springs have proteins that function at temperatures closer to boiling. Proteins that are produced and used in the stomach can tolerate and work under acidic conditions, whereas proteins that function in the blood operate at a pH closer to neutral.

Folding is critical to a protein's overall function. Scientists initially thought proteins themselves were responsible for the folding process. Recently researchers have discovered that often proteins receive assistance in the folding process from protein helpers, or chaperones (or chaperonins). These discoveries lead scientists to believe that there are still more exciting details to be learned on the process of protein folding.

CONCEPTS IN ACTION - For an additional perspective on proteins, view [this animation](#) called “Biomolecules: The Proteins.”