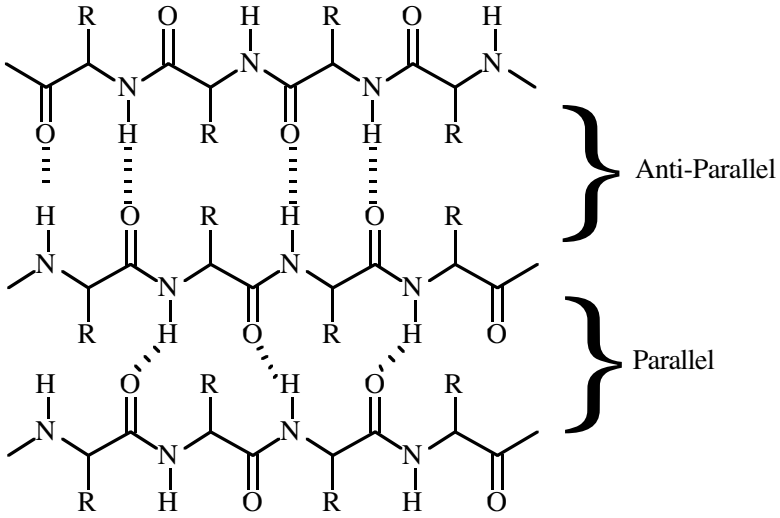
Secondary Structure: Alpha Helices, Beta Sheets and Turns - If there are 4 amino acids (**a.a.**) in a polypeptide, there is at least one conformation that allows the backbone to appear as a coil. If the coil is "just right", the C=O of the first a.a. is close enough to the N–H of the fourth a.a. to allow a H-bond to form. This is a very stable configuration, and can repeat for chains longer that 4. This structure, known as an **α-helix**, was deduced by Linus Pauling (and allowed him to win his first Nobel prize). The difference in the structures of the a.a.s make some more likely to form α-helices than others.

On the other hand, if the peptide chain is long enough so that two strands can line up next to each other, the backbones can make H-bonds with each other as well. This type of structure is called a **ß-(pleated) sheet**. The two strands are called ß-strands, and they can either be parallel or anti-parallel. In the case of **anti-parallel**, the first strand follows from N-term to C-term going from top to bottom, and the other strand is C-term to N-term from bottom to top. In the **parallel** case, both strands go from N- to C-term from bottom to top. The antiparallel sheet is more stable, since the C=O and H–N line up.



The two strands have to have a loop section of peptide between them. This region is called the **ß-turn**. Due to its rigid structure, proline is almost always found in a ß-turn. Collectively, these regions are called the **secondary structure** of the polypeptide.

Tertiary and Quaternary Structure - In a reasonably large polypeptide, you can have many regions, each of which have these structures. How these regions organize themselves relative to each other, i.e. the three dimensional structure of the molecule, is called the **tertiary structure**. ß-sheets tend to pack with each other, and α-helices tend to pack with each other. What holds them together?

Generally speaking, the side chains (a.k.a. **R-groups**) are responsible for this. Amino acids with nonpolar R-groups will stick together, and these R-groups also tend to stay away from the polar groups. The other categories of R-groups also interact with R-groups of the same ilk. In particular, if two cysteine **residues** are close to each other, they can form a disulfide bond.

Large polypeptides of biological importance are called **proteins**. Since most biological systems are water based, the a.a.s that are ionic tend to be on the outside of the protein. Occasionally, two oppositely charged residues are near each other and form an ionic bond to each other. This can occur between two separate polypeptides, each with its own tertiary structure. When this occurs, the overall structure is called the **quaternary structure**, and can be 2 or more polypeptides.

Proteins - There are many many proteins in our bodies, each with a very specific role. Some of them are **enzymes** (biological catalysts); some are structurally important; and others are needed for transporting materials through the body. Many proteins have non-amino acid content (known as conjugated proteins), and many are insoluble in water (known as fibrous). The structure of the protein often dictates its purpose. We will be discussing several of them in the next chapter.

The general characteristic of all proteins is that they are subject to **denaturation**. The normal tertiary or quaternary structure of a protein is referred to as the **native state**. More specifically, if the primary structure of the protein is the common one, and the shape is correct, it is a native protein. Often, one or two amino acids get switched, and the resulting protein is called a **mutant**. These mutations are often done on purpose (the field of genetic engineering is based on this), to change the property of the protein in some way. Other times, external forces (like cosmic rays, xrays, or some other nasty rays) cause the mutation. We will talk more about mutations when we discuss DNA.

On the other hand, a denatured protein is one where the primary structure is the same, but the tertiary structure is changed dramatically. This usually alters the action of the protein, so much that most denatured proteins are inactive. Denaturing occurs when the H-bonds and S-S bonds that hold the tertiary structure together are broken, and new ones form. This can be brought about by extreme changes in temperature, pH, ionic content of the solution, or combinations of them. The denaturation does not take place all at once. It is also not always irreversible. But, in many cases it is. For example, eggs white contains the protein **albumin**, which is a transport protein. We all know that when an egg is heated, the egg white hardens. This represents a denaturation process. We also know that there is no way to "uncook" an egg.

Another example is the practice of making straight hair wavy. Hair is made of the structural protein **keratin**, and contains many S-S bonds. In the "perm"ing process, the disulfides bonds present are broken (reduced) by adding the perming solution. Once the hair is set, the setting solution re-oxidizes the cysteines to form new disulfide bonds. This process is, thankfully, reversible. Otherwise, a "bad hair day" would be a life-long event!

Besides denaturing, proteins can also be **hydrolyzed**. In this process, the peptide bonds are broken (hydrolysis of the amide) to produce free amino acids. This requires fairly severe conditions as compared to normal denaturation. Boiling a protein in strong acid will do a nice job of destroying the protein!