

Protein Structure II

1. The sequence of amino acids in a protein is ultimately responsible for all of the properties a protein has. The sequence of amino acids of a protein is referred to as its primary structure.
2. Peptide bonds form resonance structures such that the bond itself behaves like a double bond. Double bonds cannot rotate (unlike single bonds) and thus they define a plane. Alpha carbons on either side of a peptide bond are generally arranged in a *trans* configuration (about 10,000 *trans* to one *cis*), except when proline is involved. Peptide bonds involving proline favor the *trans* by about a 100 to 1 ratio.
3. The bonds around the alpha carbon (the carbon bonded to both an amino group and a carboxy group) can both rotate, however, because they are single bonds. One can thus describe a polypeptide as a series of planes separated by an alpha carbon, with the planes each being rotated a certain number of degrees relative to the alpha carbon. If we think of the alpha carbon as being in between two planes, then the plane on the left can rotate (theoretically) 360 degrees and the plane on the right can also theoretically rotate 360 degrees. These angles of rotation of planes are referred to as phi and psi angles. Phi refers to the rotational angle around the single bond between the alpha amino group and the alpha carbon. Psi refers to the rotational angle around the single bond between the alpha carbon and the alpha carboxyl group.
4. The Indian scientist, Ramachandran, recognized that not all rotations of phi and psi would be theoretically feasible because steric hindrance would preclude some rotational positions. He plotted theoretical rotations of psi versus phi and calculated which of these angles would provide stable structures. The regions of stability turn out to be regions of known stability from protein structures that have been determined.
5. The secondary structure of a polypeptide refers to regular/repeating structure(s) arising from interactions between amino acids that are relatively close together in primary sequence. This means less than 10 amino acids away.
6. One protein secondary structure that is stable in both real proteins and theoretical ones (Ramachandran plots) is the alpha helix. Alpha helices are one type of secondary structure and form coils.
7. Hydrogen bonds are primary forces stabilizing secondary structures. In alpha helices, carbonyl oxygen from a peptide bond forms a hydrogen bond with an amine nitrogen of another peptide bond four amino acids distant.
8. Certain amino acids with simple side chains, such as alanine, are very favorable for formation of alpha helices, whereas bulky (tryptophan) or cyclic (proline) amino acids tend to disrupt alpha helices. Thus, one can reasonably accurately predict from an amino acid sequence which regions of a protein sequence will exist as alpha helices and which will not.
9. Another type of common secondary structure commonly found in protein is the beta strand (note that the term beta sheet refers to layering together of beta strands together), which consists of amino acid backbones in a V shape (like the pleats of a drape). A beta strand can be thought of as a helix in two dimensions though that is an over simplification. Again, specific amino acids favor the formation of this structure and others (proline again) favor its disruption.
10. Beta sheets arise from arrangement of beta strands. These arise from interactions (hydrogen bonds) between beta strands (parallel or antiparallel), such that the carbonyl oxygen of one side interacts with the

amine hydrogen with the other. Though I didn't mention it in class, beta strands can also orient their R groups such that they interact appropriately (hydrophobic-hydrophobic, for example). Beta sheets can be oriented in several ways.

11. Essential features of proteins that are essential for their overall structure are turns. Turns interrupt secondary structure (alpha helices and beta strands) and often involve proline and glycine residues.

12. Another type of fibrous protein is collagen, the most abundant protein in your body. It contains three intertwined helices comprised of abundant repeating units of glycine, proline, and hydroxyproline

13. Hydroxylation of proline is a post-translational modification (occurs after the protein is made) and the hydroxyls are placed there in a reaction that uses vitamin C.

14. The hydroxyls of hydroxyproline can react with other, forming covalent cross-links that make the collagen fibers more sturdy.