

1 Reading assignment 4. Section 1.2

Read Section 1.2 and answer the following:

1. What is a dihedral angle?

The dihedral angle is the angle between two planes. In practice, if there are four connected atoms and the dihedral angle around the central bond wants to be measured, the system has to be oriented in such a way that the two central atoms are superimposed and it's the resulting angle between the first and last atom.

2. What is the usual size of a dihedral angle in a peptidic bond?

180 degrees.

3. How many residues per turn has an alpha-helix?

On average, 3.6 amino acids residues per turn.

4. Why is a 3(10) helix less stable than an alpha-helix?

In the alpha helices, the peptide planes are approximately parallel with the helix axis. Because of this, there is a resulting dipole moment in the helix, and its side chains point outward and pack against each other. The dipoles of a 3 (10) helix are less well aligned and the side-chain packing less favorable, therefore it is usually less stable.

5. What kind of secondary structure would have several dihedral angles in "forbidden" regions of the Ramachandran plot?

Beta sheets.

6. Define the following: Supersecondary structure, Motif, Fold, Domain.

- **Supersecondary structure - Arrangements of two or three consecutive secondary structures (alpha helices or beta strands) present in different protein structures with different sequences.**
- **Motif - A term to describe some supersecondary structures, for example: the alpha-alpha unit, the beta-beta unit and the beta-alpha-beta unit.**
- **Fold - Relatively often observed combinations (of several and complex) supersecondary structural motifs in proteins.**
- **Domain - A portion of the polypeptide chain that folds into a compact semi-independent unit. It can be seen as "lobes" of the protein structure that seem to have more interaction between themselves than with the rest of the chain.**

7. What is the difference between architecture and topology of a protein?

The architecture means to the orientations of secondary structures and their packing pattern, regardless their sequential order. The topology also takes into account the nature of the connecting loops and the order of the secondary structures in the amino acid sequence.