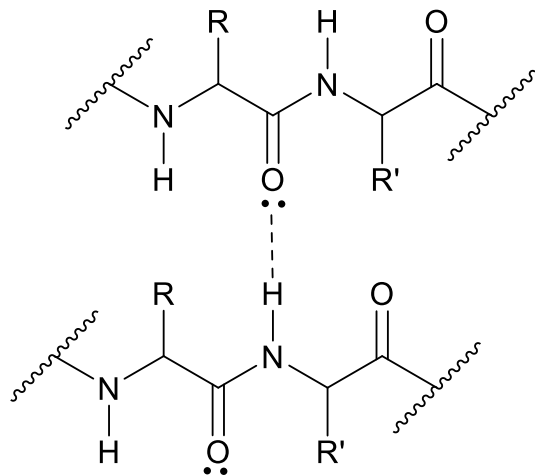


TA4 - Secondary Structures

The linear sequence of amino acids, its **primary structure**, can coil and fold upon itself to create 3D structures. Two important examples of these are **α -helices** and **β -sheets**, which are both held together by **hydrogen bonding** between the amino acids. This 3D organisation of the primary structure is called the **secondary structure**.



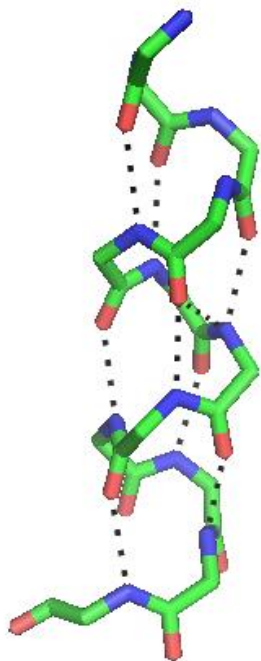
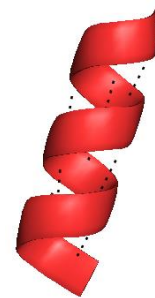
These hydrogen bonds occur between the oxygen lone pair of one residue, and the hydrogen attached to a nitrogen on another residue.

In proteins, the hydrogen bonding always occurs between C=O and N-H groups. Note that not every carbonyl group and amine group can hydrogen bond, such as the ones either side of the central H-bond.

The way in which these hydrogen bonds are arranged depends on the order of the amino acids in the primary structure. And this allows different types of secondary structures to form, such as α -helices and β -sheets.

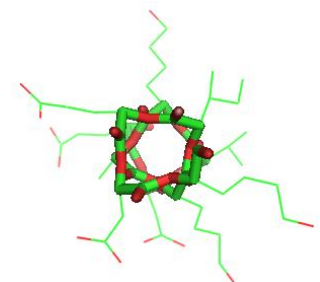
α -HELIX

The α -helix is a **rod-like structure**. The peptide main chain forms the inner part of the rod as shown in the figure on the left. Amino acid side chains are not shown for simplicity.



The coil is held together by hydrogen bonds between carbonyl oxygen, and the amine hydrogen **four residues ahead**. The hydrogen atoms aren't shown for simplicity. The red atoms represent oxygen, and the blue atoms nitrogen, which have the hydrogens attached which hydrogen bond to the oxygens.

If you look down the helix from the top, you can see it as a tube, with the amino acid side chains extending out from the rod as shown.



To simplify these 3D diagrams, the α -helices are simplified into cartoon helices. This makes it much easier to analyse the structure, as you can spot these common features much easier.

β-STRANDS, SHEETS, AND TURNS

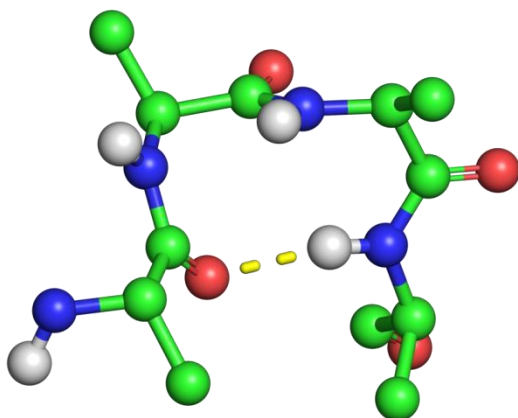
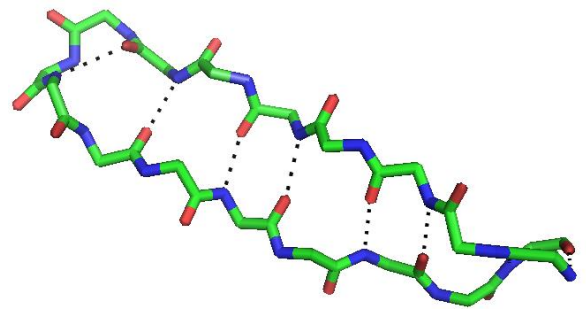
A **β-strand** is a section of the polypeptide chain which is almost fully extended. They can arrange alongside each other so that the sections of two or more strands can form hydrogen bonds and stabilise each other in a **β-sheet**.

Two strands can either run in the same direction to make a **parallel β-sheet**, or in the opposite direction to form an **anti-parallel β-sheet**.

In 3D images these β-sheets are often represented by long, flat arrows, pointing in the direction that the strand is running. This makes it easy to distinguish parallel and anti-parallel β-sheets. It also simplifies the diagrams a lot!

β-turns are regular structures which are commonly found in proteins. They allow the β-strands to **reverse direction**, and therefore are really useful when building a protein's overall structure. Each β-turn is made from four amino acid residues, and the C=O of residue 1 forms a hydrogen bond to the NH of residue 3. You can see the four residues as there are four nitrogen atoms in the main chain. The side chains are not shown for simplicity.

This small structure is key in protein folding and essential for proteins to form their complex structures and functions. The hydrogen bond which holds the loop together can be seen clearly below.



These 3D images show how the β-turn allows two β-strands to run in opposite directions. Notice the kinked shape of the turn, which is very common in protein structures.

