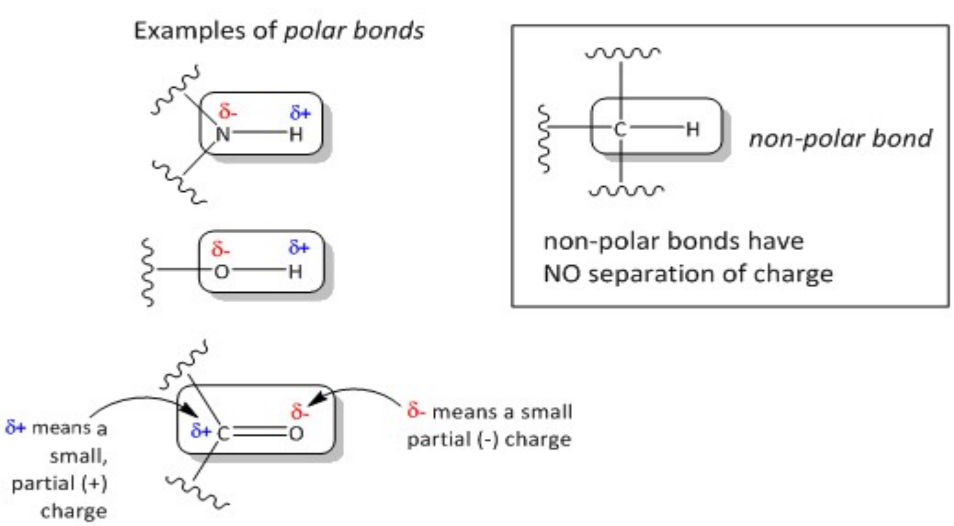
Higher order

PROTEIN DENATURING

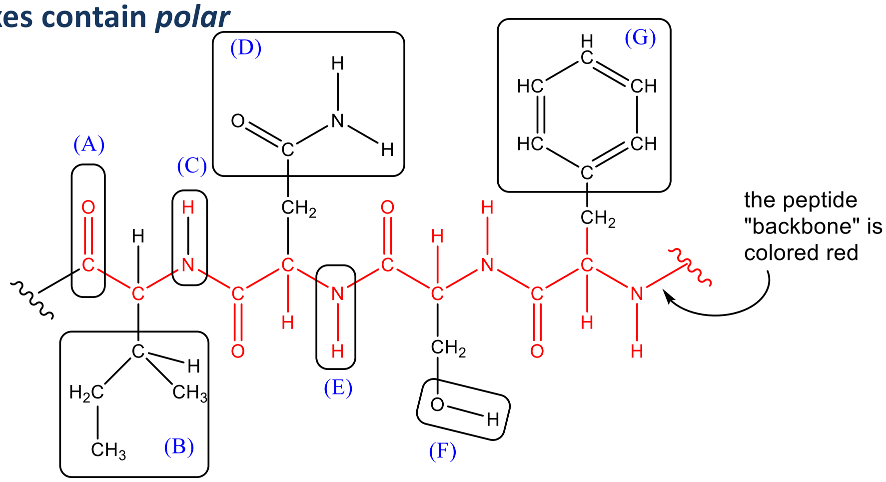
Polar bonds vs. Non-polar bonds



Polar bonds have a separation of charge due to unequal sharing of electrons in the covalent bond. The δ- atoms has "more" of the electrons and is therefore more negative (since electrons are negative)

Shown below is a drawing of a peptide.

Which labeled boxes contain *polar* bond(s).

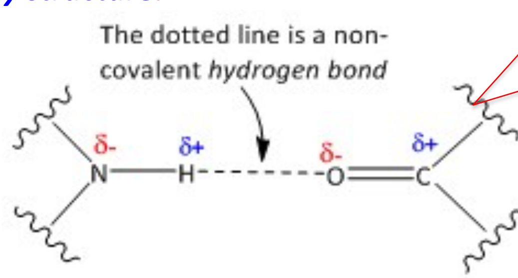


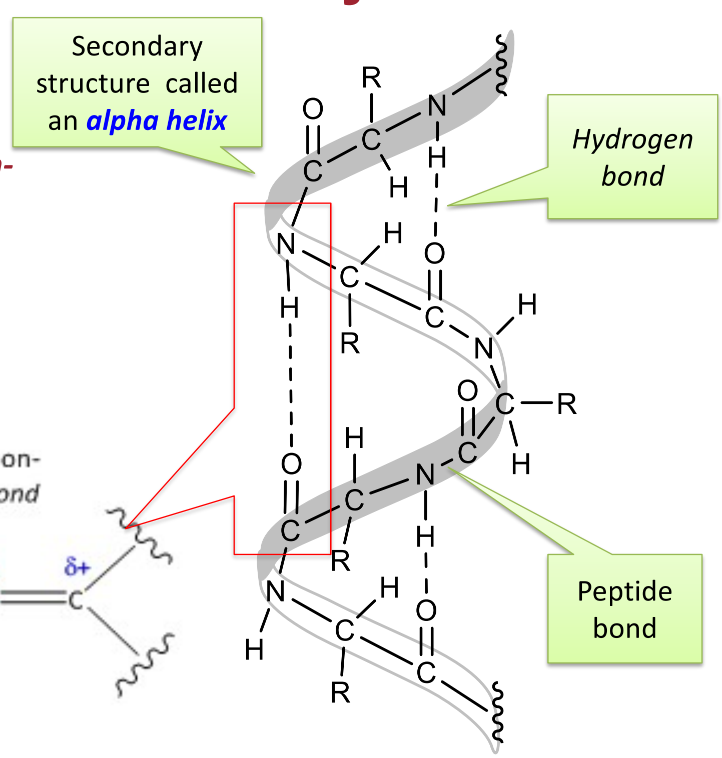
Which boxed areas of the peptide structure are *hydrophobic* (literally, “fears water”)

Hydrogen bonds stabilize protein secondary structure

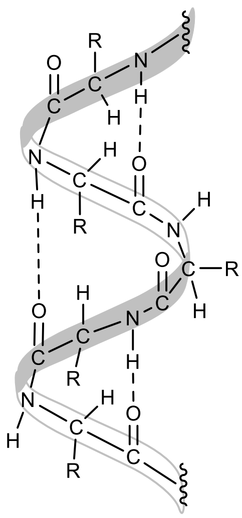
The N-H and C=O bonds of the *peptide backbone* engaging in ***non-covalent hydrogen bonds***.

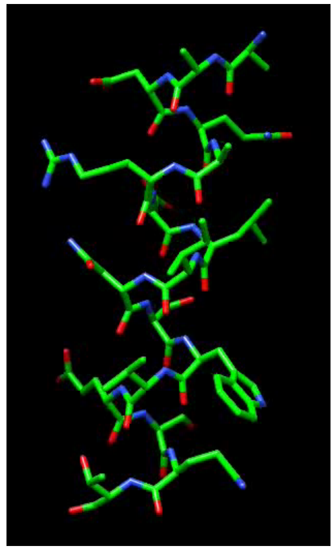
These stabilize 3-dimensional arrangements of amino acids residues in what is called ***secondary structure.***

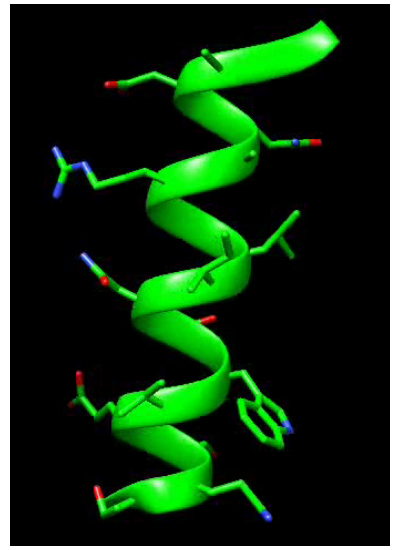




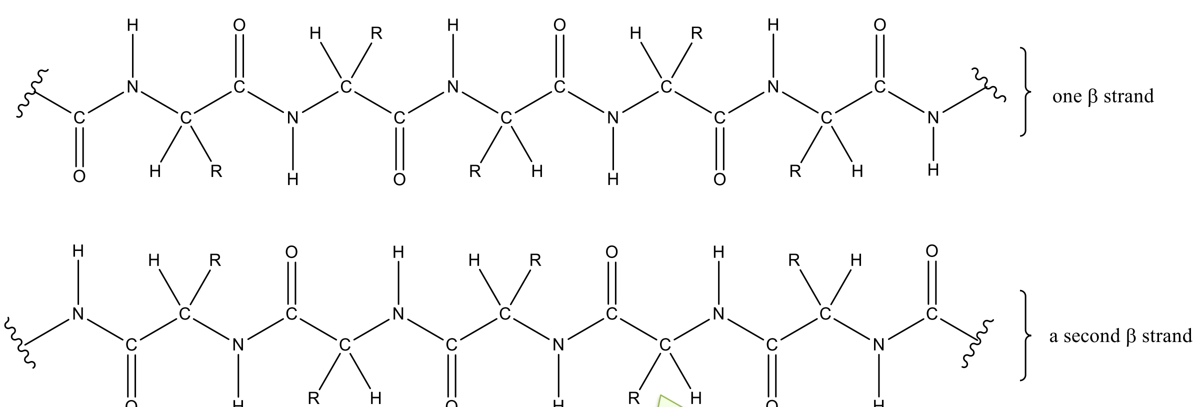
An **alpha helix** is the *shape* the *peptide backbone* takes





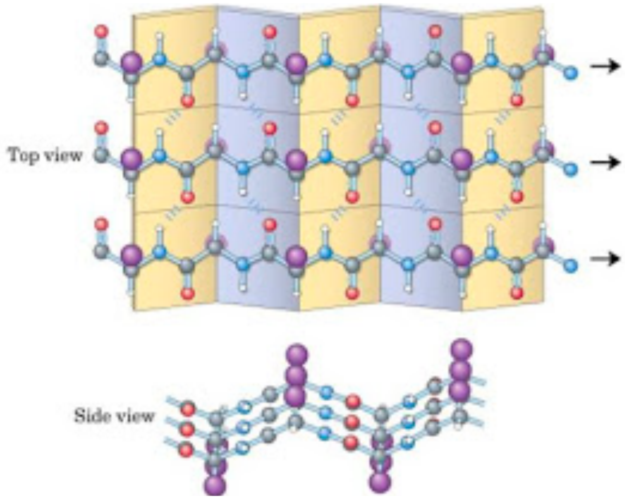


Beta (β) strands(sheets) are another type of protein secondary structure

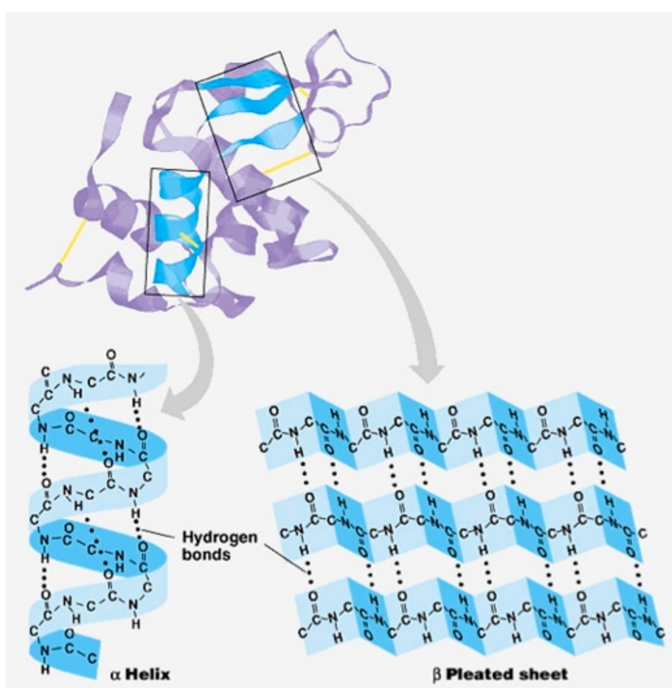


Where are the hydrogen bonds?

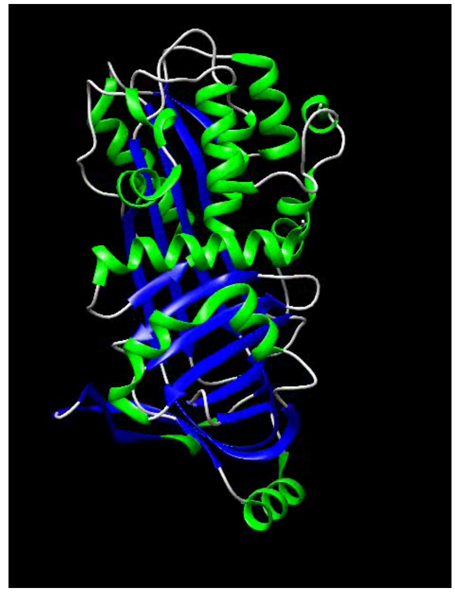
Beta (β) strands(sheets) are another type of protein secondary structure



Secondary Structures



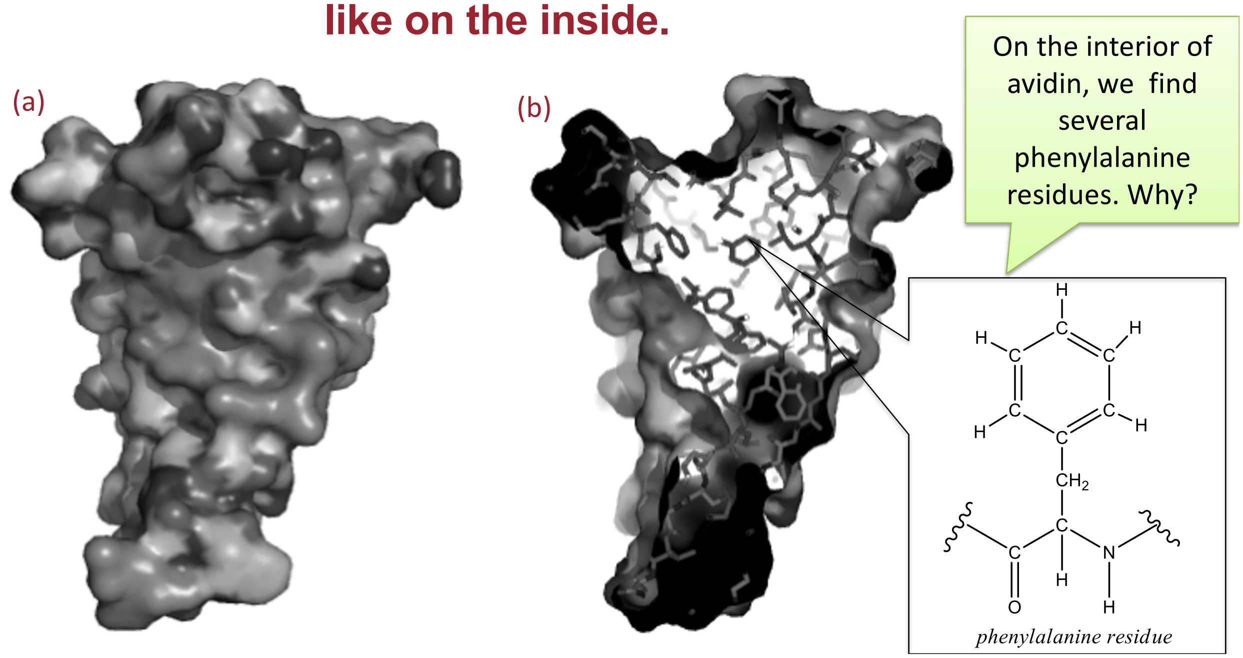
Proteins *fold* to bury the hydrophobic part and expose the hydrophilic parts



Proteins are *amphiphilic* molecules - they have both *polar* (*hydrophilic* = “loves water”) and non-polar (*hydrophobic* = “fears water”) parts. In nature, we find proteins in water based environments.

As not all parts of the protein love the water, the protein *folds* in a 3-dimensional way that buries the *hydrophobic* parts on the inside of the structure, and exposes the *hydrophilic* parts to the outside, where they can interact with the watery environment.

There are two representations of avidin below. The first (a) shows the overall globular protein in a “space filling” model. The second (b) is a slice right through the middle of avidin – so we can see what the protein looks like on the inside.



Time to Check-In

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