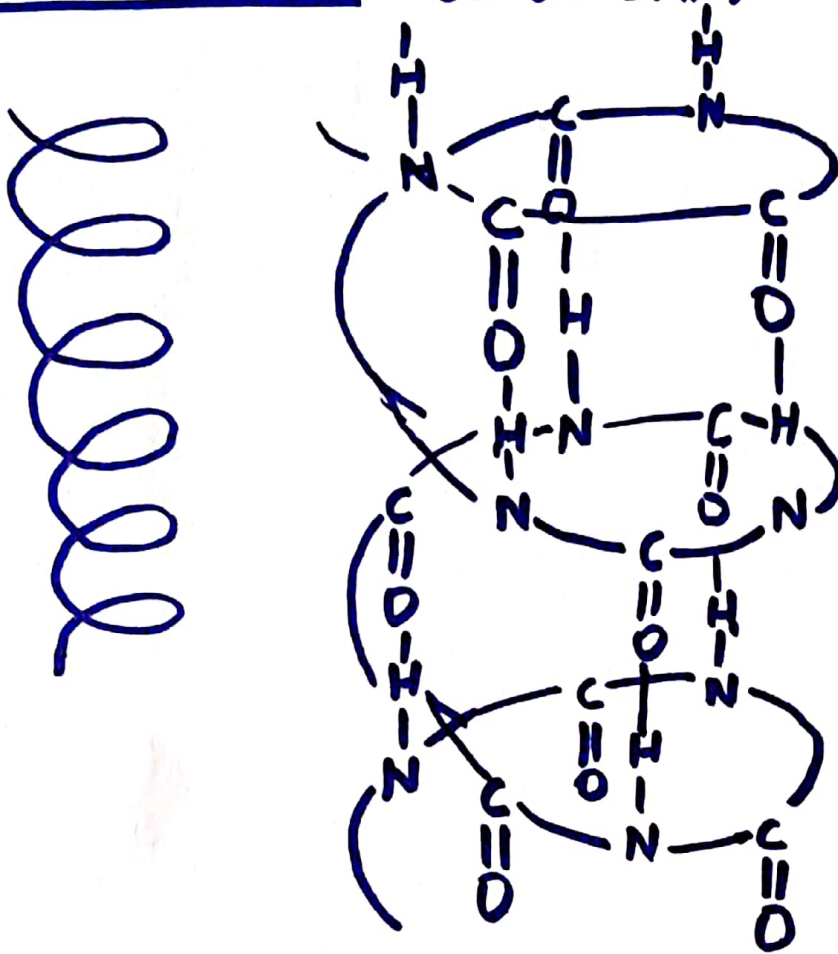


PROTEINS

SECONDARY STRUCTURE



Polypeptide chains assume a peculiar conformation as a result of H-bonding. This is  $\alpha$ -Helix structure (right handed)

R quite large, intramolecular H-bonds formed between the  $\text{C}=\text{O}$  of one amino acid residue and the  $\text{N}-\text{H}$  of the fourth amino acid residue in the chain causing it to coil up in a spiral.

## $\alpha$ -helix (contd.)

Each turn of the helix has approx. 3.6 amino acids and a 13-membered ring distance between 2 successive turns  
 $= 5.4 \text{ \AA}$

As amino acids (except glycine) are optically active, have L-configuration. For L-amino acids, right-handed helix is more stable than the left-handed helix. So helix is always right-handed due to stability reason.

Fibrous proteins like  $\alpha$ -keratin have  $\alpha$ -helix structure though globular proteins contain segments of  $\alpha$ -helix. Human hair are stretchable, elastic due to helical structure.