A. PRIMARY STRUCTURE

- This is the **number** and **order** of **amino acids** in a **polypeptide**.

B. SECONDARY STRUCTURE

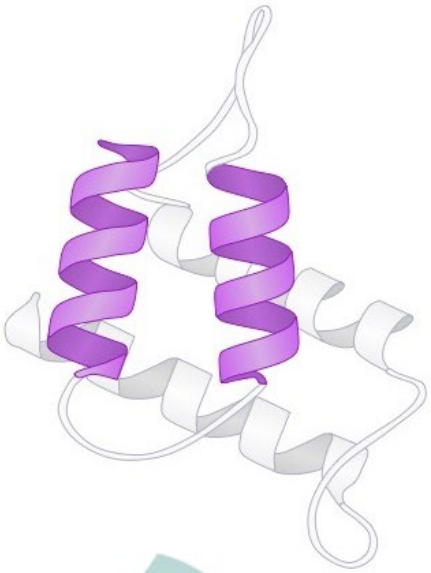
- The polypeptide **twists** and can form **two** different structures:

- Both of these result from **hydrogen bonds** forming between **non-adjacent amine** (NH_2) and **carboxyl** (**COOH**) groups.

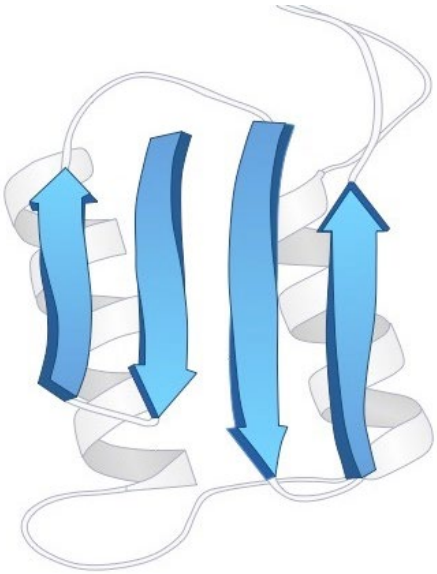
α-helices

The polypeptide folds into a **coil** or **spiral**

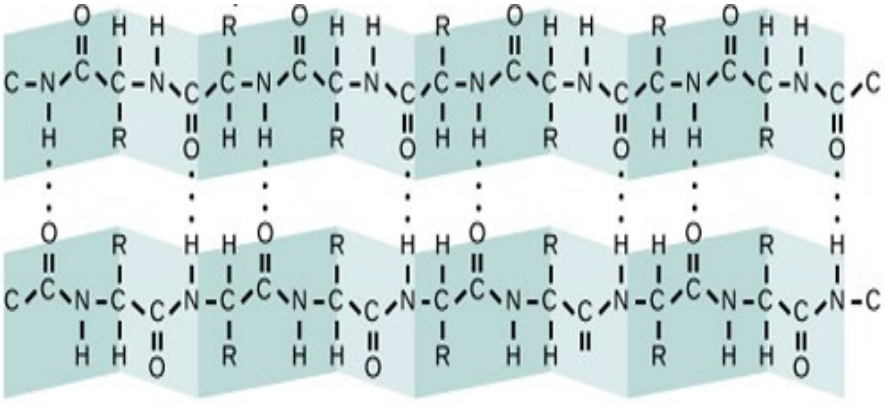
H-bonds form between **adjacent turns** of the **helix**



β-pleated sheets



Parts of the polypeptide run **parallel** and **H-bonds** form **between them**



C. TERTIARY STRUCTURE

- The polypeptide **folds** to give its **final 3-D shape**.
- It is determined by **interaction** of the **R-groups** of **non-adjacent amino acids**.
- **Different R groups** have **different charges**.
- They produce **different forces** of **attraction** and **repulsion**, which determine how the **polypeptide folds** to give its **final 3-D shape**.
- If the polypeptide is to be an **enzyme**, this will ensure that the **active site** is the **correct shape**.

The shape is stabilised by intramolecular bonds such as:

hydrogen bonds
ionic bonds
disulphide bridges (S-S)
hydrophobic interactions

The shape is not stabilised by peptide bonds as:

Peptide bonds connect adjacent amino acids (side-by-side)

Stability is caused by interaction of the R groups of non-adjacent amino acids

The DNA base sequence determines

The mRNA base sequence, which determines

The amino acid sequence of a protein, which determines

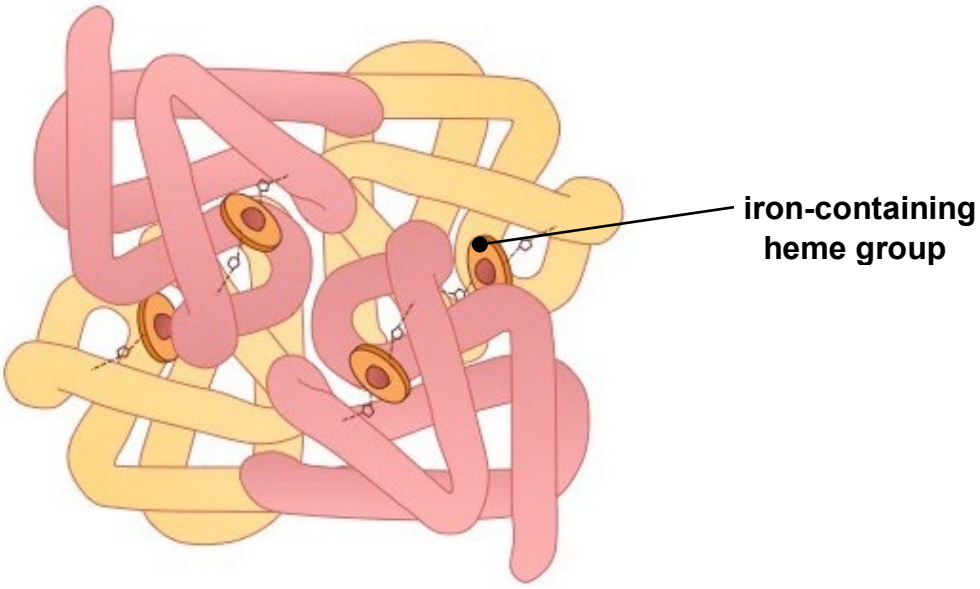
How the polypeptide folds, due to interaction of the R-groups, which determines

The tertiary structure of a protein

- In **water-soluble** proteins:
  - **polar** amino acids are on the **surface** where they **bond with each other** and come into **contact** with **water**.
  - **non-polar** amino acids are often in the **centre**, with **hydrophobic** interactions between them.

D. QUATERNARY STRUCTURE

- When **two** or **more polypeptides** are **joined together**.
- Only **some** proteins have a **quaternary** structure.
- **Hemoglobin** has a **quaternary** structure. It can **attach** to **O_2** and **release** it.



- Hemoglobin is composed of **four polypeptide** chains (**two alpha** chains and **two beta** chains)
- Each polypeptide is connected to an **iron-containing heme group**, which is responsible for **binding O_2**.
- Proteins with a **prosthetic group**, such as **heme**, are known as **conjugated proteins**.