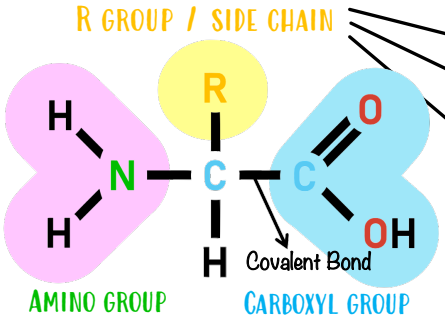
B1.2

Proteins (HL)

The 4 macromolecules

- Carbohydrates
- Lipids
- Nucleic acids
- Proteins

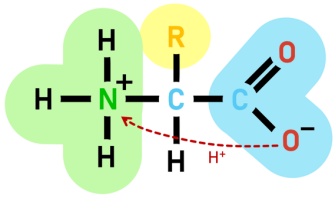


The 20 amino acids differ in their **R-group**

Can be **non-polar**, **polar** (not ionized), and **polar** (ionized).

Cause different types of **interactions**

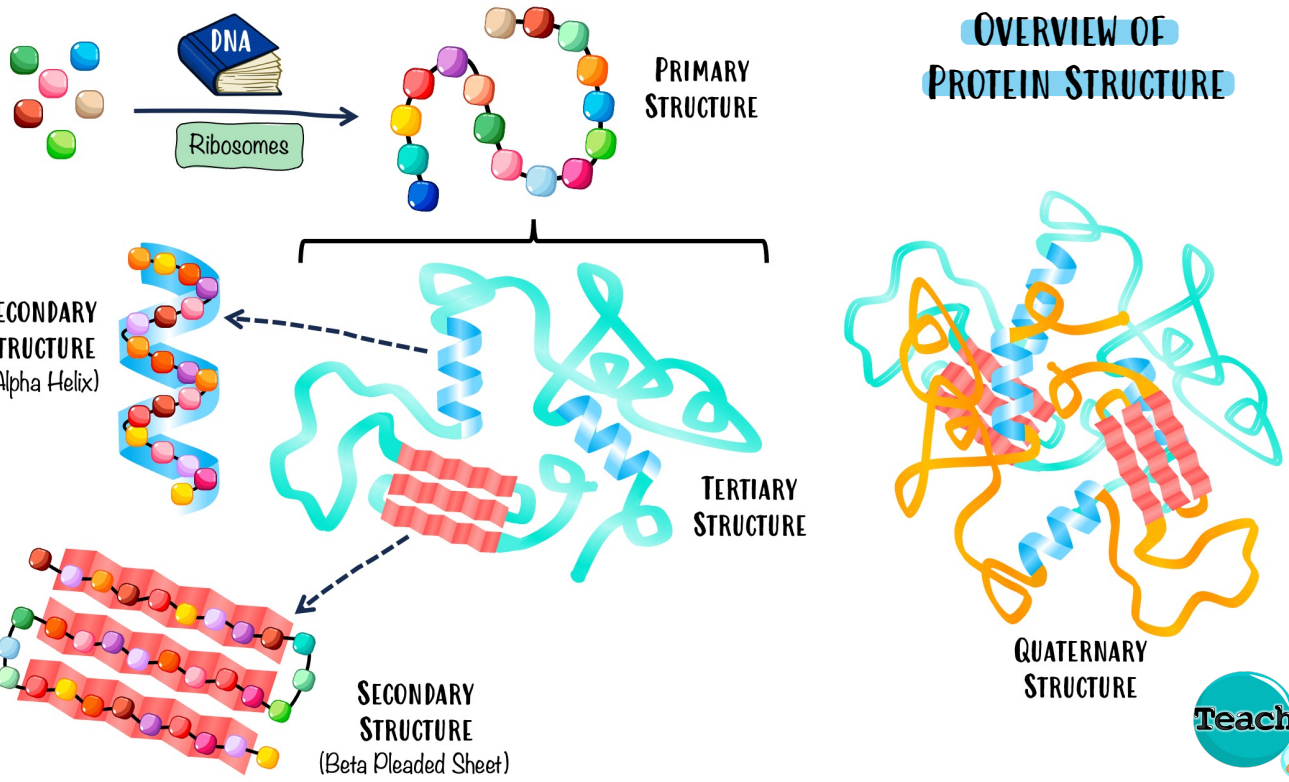
different folding -> different protein structure



Amino acid may be present in its ionized form

Category	Number of Amino Acids	Example & Explanation
Non-polar	9	R-group is Hydrocarbon
Polar	6	R-group has elements that form a polar covalent bond (oxygen, nitrogen or sulfur)
Polar due to (+) ionization charge	3	R-group is ionized to form a positive charge
Polar due to (-) ionization charge	2	R-group is ionized to form a negative charge

Overview of Protein Structure



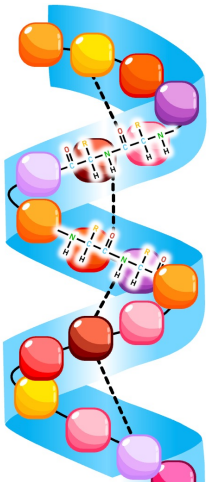
Proteins (HL)

1° Primary Structure*

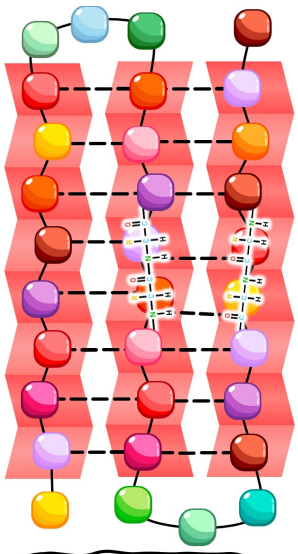
The **number and sequence of amino acids** in a protein, determined by your **DNA** (or gene). It controls the other levels of protein structure - folds into secondary, tertiary and quaternary structures.

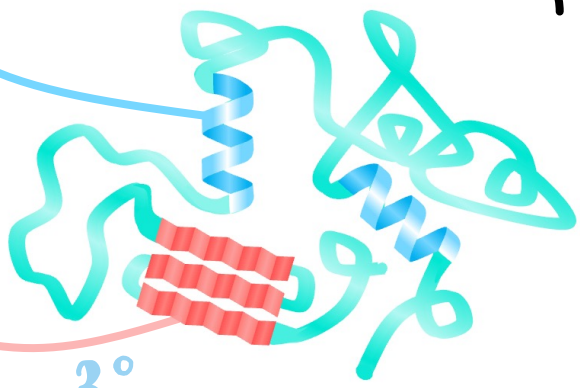
Amino acids

Alpha Helix



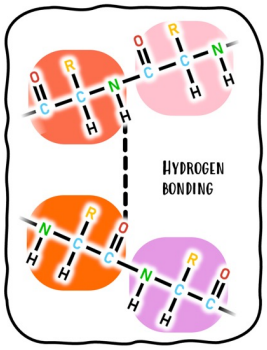
Beta Sheets

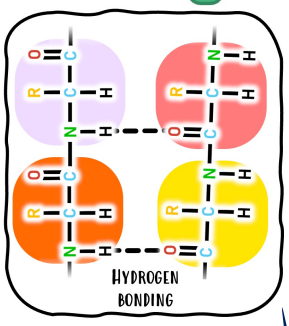




3° Tertiary Structure

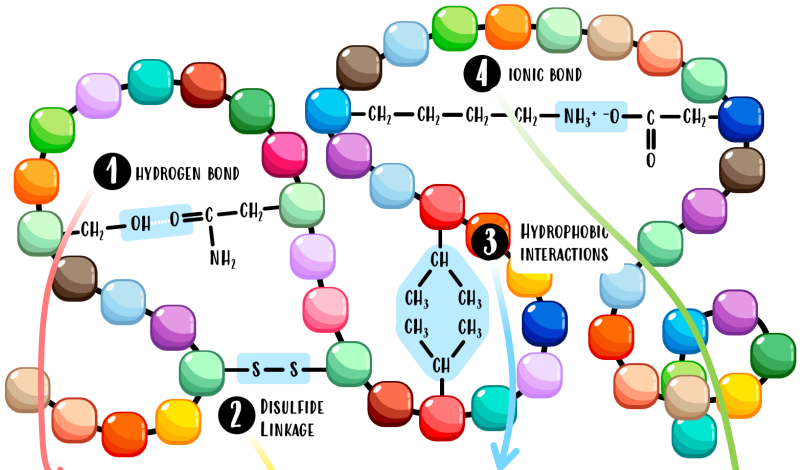
It is the complete **three-dimensional** arrangement of the entire protein molecule, folded into a specific, globular shape due to interactions between **R-groups** including hydrogen + ionic bonding, disulphide linkage & hydrophobic interactions.





2° Secondary Structure

Alpha helix & beta sheets form in the polypeptide (protein) where there are amino acids that have non-polar R-groups. **Hydrogen bonds** between the carboxyl group of one amino acid and the amino group of another: non-adjacent amino acids. These shapes maximize the number of hydrogen bonds.



Polar amino acids will form hydrogen bonds between **R-groups**, near the exterior of the polypeptide (hydrophilic), most numerous

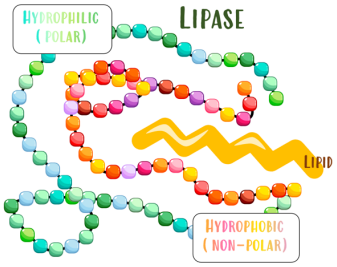
Non-Polar amino acids (R-groups) , being **hydrophobic**, will fold into an area within the interior of the polypeptide, to avoid the polar water molecules.

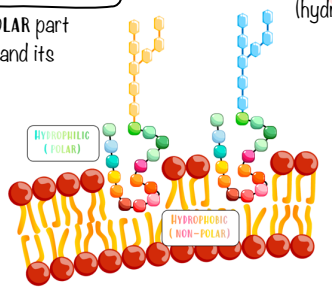
Pairs of cysteine amino acids form **covalent bonds** between themselves. **Disulfide bond (R-group**, the strongest of all bonding forces that influence polypeptide shape

Ionized R-groups (negative or positive) will align with each to form ionic bonds. Carboxyl group in R group loses hydrogen (become negative), amino group gains hydrogen (become positive). Opposite charges attract.

Protein Solubility

1. **Lipase** has both a **polar** and **non-polar** part to interact with the hydrophobic lipids and its hydrophilic environment: the intestines

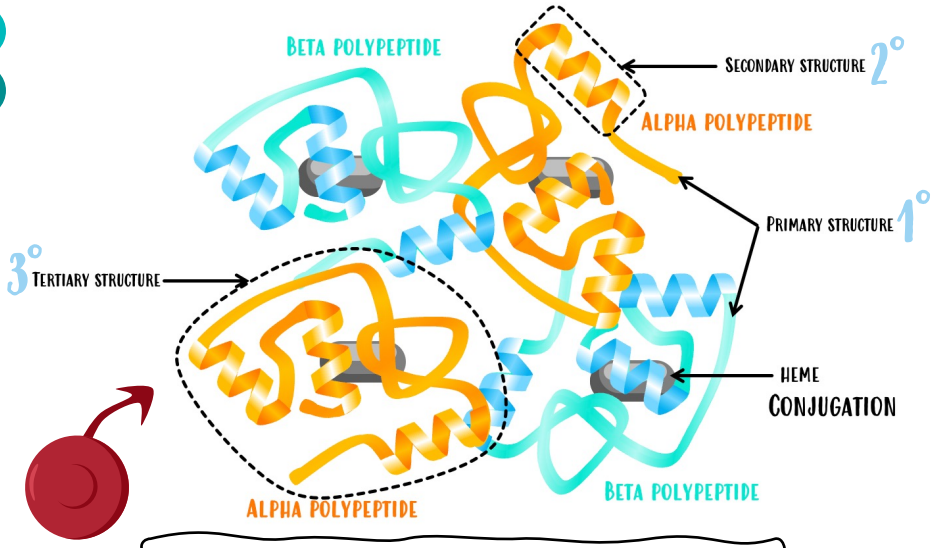




2. **Glycoprotein A and B**, present on red blood cells, have both a **polar** and **non-polar** part to interact with the hydrophobic lipid bilayer and its hydrophilic environment: the blood

*see "B1.2 Proteins (SL) " for structure of dipeptide & Polypeptide

Proteins (HL)



The quarternary structure of hemoglobin

4° Quaternary Structure

This is when **two or more** polypeptide chains bind together into one structure.

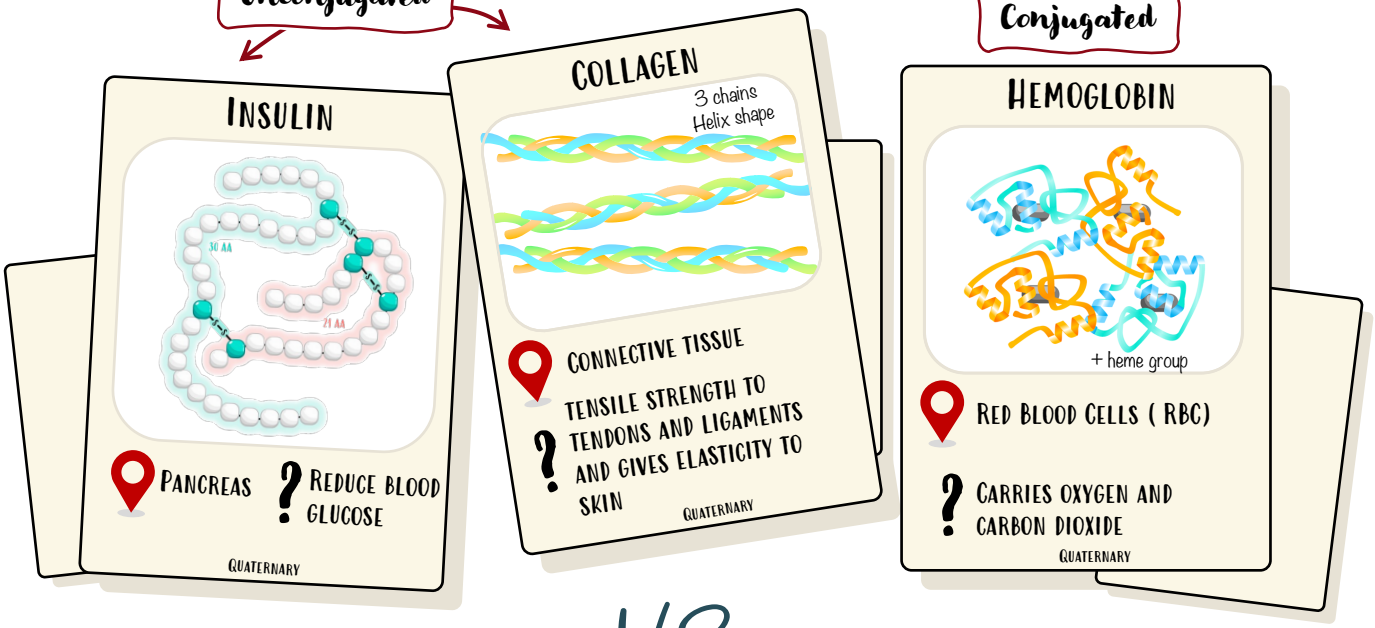
A **primary** structure forms the "backbone", polypeptide sequence.
Secondary structures form in regions of amino acids with non-polar R-groups.
Tertiary structure forms as the polypeptide chain folds into a 3D structure due to interactions with R-groups.

Quarternary strcutures can be **Unconjugated** or **Conjugated**

Protein NOT bound to other molecules

Protein bound to other molecules

Unconjugated



Conjugated

Globular VS. Fibrous

	Globular	Fibrous
Shape	Roughly spherical	Long strands (linear)
Function	Functional (specialized). E.g. Enzymes, antibodies, peptide hormones, cell signalling	Structural
Solubility	(Mostly) Soluble in water	(Mostly) Insoluble in water
Examples	Haemoglobin, enzymes, insulin, immunoglobulin	Collagen, keratin, myosin, actin, fibrin

notes