

Proteins – Summary

Components:

- Central α -carbon, with H-atom
- An amino group (-NH₂)
- A carboxyl group (-COOH)
- Variable R group (Side chain)

Are zwitterions/amphoteric

Can be classified according to R-groups

- Neutral
 - Hydrophilic
 - Hydrophobic
- Charged/Polar
 - Acidic
 - Basic

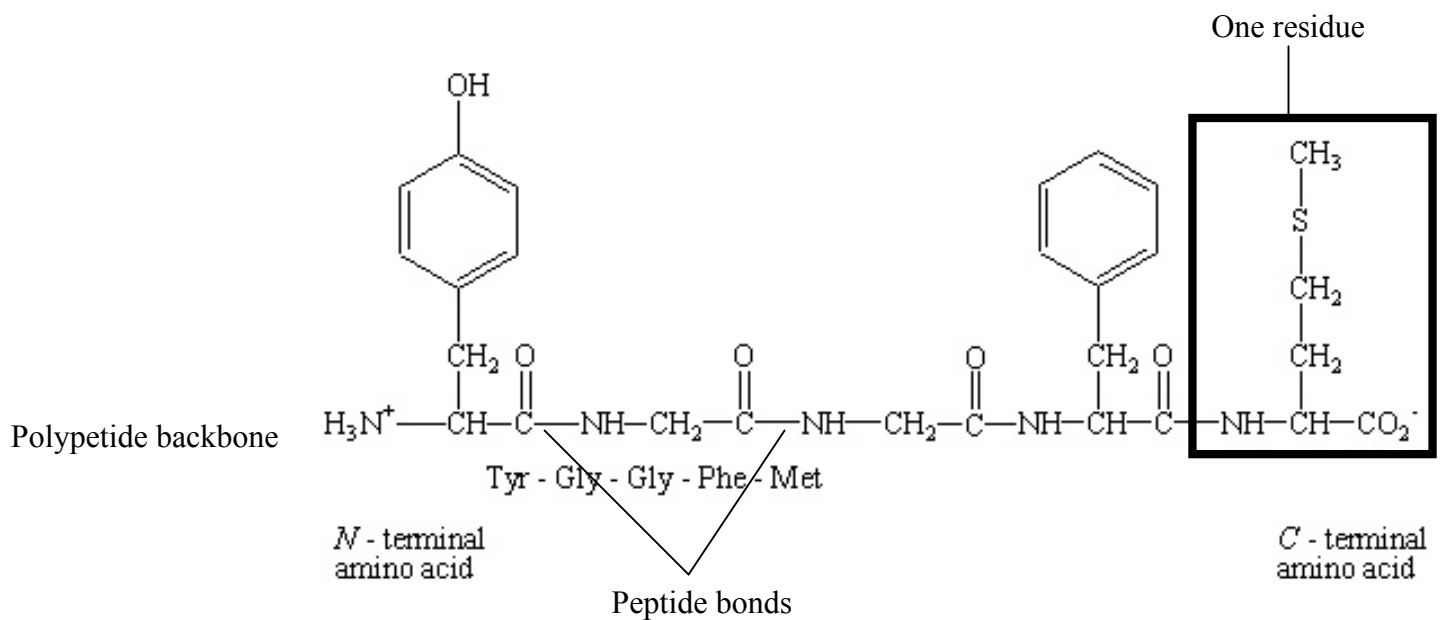
Humans – just 20 amino acids

A. Polypeptide



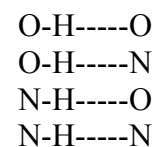
dehydration synthesis

- Peptide/amide bond
- Enzyme required for synthesis
- Water removed one molecule at a time (DEHYDRATION SYNTHESIS)
- Acid added one at a time
- Has direction (i.e. lys-cis-arg \neq arg-cis-lys)
 - Start: amino terminal
 - End: carboxyl terminal



- FOUR BONDS
 - Hydrogen bonds
 - Ionic (or electrovalent) bonds
 - Between NH_3^+ and COO^-
 - Hydrophobic interactions
 - -SH groups – form S-S bonds
 - Disulphide Bridges

H-Bonding (usually):



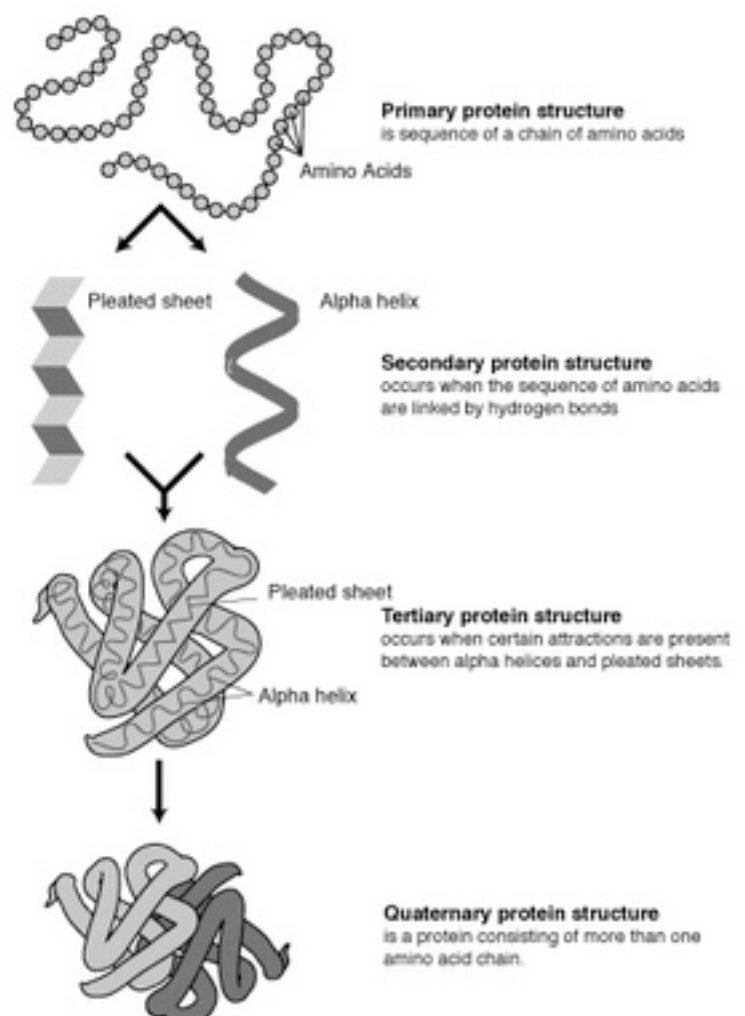
B. Structure:

Primary

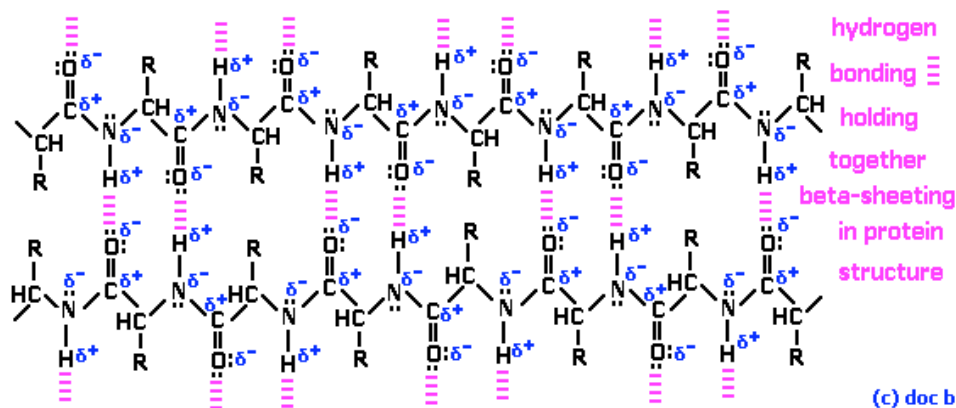
- Refers to sequence of amino acids in a polypeptide chain.
- Only covalent peptide bonds between successive amino acid residues

Secondary

- Refers to coiling and pleating of a polypeptide
- Maintained by:
 - H-bonds at regular intervals formed between CO and NH groups of backbone (intramolecular)



- *** R-GROUPS NOT INVOLVED
- A single protein can have both α -helix and β -pleated sheet
- α -helix
 - right hand screw rule
 - e.g. keratin (in hair)
- β -pleated sheet
 - when two or more regions of a single polypeptide lying side by side are linked together by H-bonds.
 - ***the entire sheet is one polypeptide (remember for diagrams)
 - high tensile strength
 - e.g. fibroin in silk worm silk



Tertiary

- Refers to the structure formed from extensive foldings/bendings of a single polypeptide chain, forming a compact chain.
- Maintained by 4 types of bonds between R-groups
 - Weak interactions: hydrogen bonds, ionic bonds, hydrophobic interactions
 - Strong covalent linkage: disulphide bonds
- Hydrophobic quantitatively most important

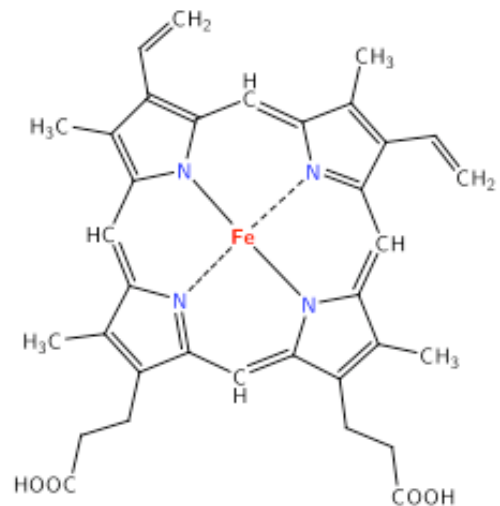
Quaternary

- Refers to the association of 2 or more polypeptide chains into one complex, functional protein.
- Each polypeptide – subunit
- Held together by hydrogen bonds, ionic bonds, hydrophobic interactions and disulphide bonds.
- E.g. collagen, haemoglobin

Fibrous Protein	Globular Protein
Structural support in cells	Various functions
Long polypeptide chains that form fibres or sheets	Polypeptide chains folded into spherical shape
Exists mainly as secondary proteins structures	Exist mainly as tertiary and quaternary structures
Length of polypeptide and sequence of amino acids may vary slightly between two samples of the same protein.	Length of polypeptide and sequence of amino acids are always identical between two samples of the same protein.
Insoluble in water <ul style="list-style-type: none"> Mainly hydrophobic R-groups on exterior 	Soluble in water <ul style="list-style-type: none"> Has hydrophilic R-groups on exterior
E.g. collagen, keratin	E.g. haemoglobin, enzymes, HIV protease

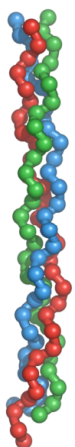
Haemoglobin (globular)

- Found in red blood cells
- Tetramer consisting of 4 polypeptide chains, known as globins, which are usually:
 - 2 α -chains, each 141 amino acids long
 - 2 β -chains, each 146 amino acids long
- Attached to each chain (subunit) is an iron-containing molecule known as haem (i.e. 4 haem molecule per haemoglobin molecule)
- Oxygen is transported in combination with the iron molecule of the haem group (this is an oxygenation reaction, not an oxidation)



Collagen (Fibrous)

- Collagen is the main protein of connective tissue in animals and the most abundant protein in mammals, making up about 25% of the total protein content.
- 3 polypeptide strands, each of which is a left-handed helix, not to be confused with the commonly occurring alpha helix, which is right-handed.
- These three left-handed helices are twisted together into a right-handed coiled coil, a triple helix, a cooperative quaternary structure stabilized by numerous hydrogen bonds



C. Denaturation

Agent	Cause of denaturation	Example
Acid	H^+ of acid attaches to COO^- of protein \rightarrow $COOH$ formed Disrupts <u>ionic bonds</u> formed by the COO^- within the protein.	Souring of milk by bacteria.
Alkali	NH_3^+ of protein loses a H^+ to neutralise OH^- Disrupts <u>ionic bonds</u> formed by the NH_3^+ within the protein.	
Heat	Kinetic energy of protein molecule increases Its atoms vibrate vigorously \rightarrow disrupting <u>hydrophobic interactions, ionic and hydrogen bonds</u>	Boiling of egg white.
Mechanical Force	Physical movement may break <u>hydrogen bonds</u> .	Hair styling – hydrogen bonds in keratin helix are disrupted.
Organic Solvents	Organic solvents form bonds with hydrophilic groups and disrupt <u>hydrophobic interactions</u> . Thereby disrupting <u>hydrogen bonds</u> .	Sterilisation with alcohol – denatures bacterial proteins.
Inorganic Chemicals	Uncharged inorganic ions form bonds with charged groups of proteins and disrupts <u>ionic bonds</u> .	Cytochrome oxidase (respiratory enzyme) is denatured by CN^- which combines with NH_3^+ of protein to disrupt ionic bonds.

D. Identification

Biuret Test

Steps:

1. 2 cm^3 of protein solution
2. Add equal volume of 5% KOH and mix.
3. Add 2 drops 1% CuSO_4 and mix.

Observation:

A purple colour develops slowly if proteins are present.

Explanation:

- A test for peptide bonds.
- In the presence of dilute CuSO_4 in alkaline solution, N atoms in peptide chain form a purple complex with copper (II) ions.
- Biuret is a compound derived from urea which also contains the $-\text{CONH}-$ groups and gives a positive result.