Proteins

Proteins	Amino Acids	Amino acid have a **α-carbon** atom, covalently bonded to one **carboxyl** group, one **amino** group, one **H** atom and one **variable R group**. The R group can be a **polar**, **non-polar**, **acidic** or **basic** side group. Amino acids exist as **zwitterions** in solution, with a positive $-NH_3^+$ group and a negative $-COO^-$ group. They are able to act as **buffers** to **prevent sudden changes in pH**, accepting or donating H^+ to act as a base or acid respectively. Hence, they are **amphoteric**.
	Peptide Bonds	Amino acids are joined by a **peptide bond** via a **condensation reaction** with the **removal of one water molecule** with for every peptide bond formed to form polypeptides. The **-OH** group from the **carboxyl** group and the **H** atom from **amino** group contribute to the formation of water molecule.
	Structure	The **nucleotide sequence** in DNA determines the **amino acid sequence** in the polypeptide which determines the **types and location of R groups** will determine the **types and location of R group interactions** formed to maintain the **tertiary and quaternary structure** of the protein. This determines the **specific 3D conformation** and hence **functions** of the protein.
	Denaturation	Denaturation is the **loss of the 3D conformation** of the protein molecule which causes the protein to **lose its function**. This can be changed by heat, pH, inorganic ions, organic solvents or mechanical forces.
	Biuret Test	Describe how a test for proteins can be carried out. Add **$2cm^3$** of 5% **NaOH** solution to an **equal volume** of sample in a test tube. **Shake** the mixture well. Add two drops of 1% $CuSO_4$ solution, **shaking** well after each drop. If proteins are present, a **purple color** develops.

<table>
<tr><th colspan="4">Outline the structure of a protein molecule.</th></tr>
<tr><th>Definition</th><th colspan="3">Examples</th></tr>
<tr><td>Primary structure refers to the **specific number** and **sequence** of **amino acids** in a single polypeptide chain. It is maintained by **peptide bonds**.</td><td colspan="3">-</td></tr>
<tr><td rowspan="5">Secondary structure refers to the **regular coiling** or **pleating** of the polypeptide. It is held together by **hydrogen bonds** between **–CO and –NH groups** of the **polypeptide backbone**.</td><th>Comparison</th><th>α-helix</th><th>β-pleated sheet</th></tr>
<tr><td>Shape</td><td>Single polypeptide wound into a **coil.**</td><td>**Flat sheet**.</td></tr>
<tr><td>Location of Hydrogen Bonds</td><td>Turns linked by hydrogen bonds between the –CO group of one amino acid residue and the –NH group of another amino acid residue **four amino acids away** within a **single polypeptide backbone**.</td><td>Formed between the –CO group of one amino acid residue and the –NH group of another amino acid residue on **adjacent regions** of a **single polypeptide chain**.</td></tr>
<tr><td>Direction</td><td>Coiled in a **single direction**.</td><td>Amino acids in one segment can run **parallel** or **anti-parallel** relative to another segment.</td></tr>
<tr><td>Others</td><td>**3.6** amino acid residues per turn of the helix.</td><td>-</td></tr>
</table>

Outline the structure of a protein molecule.		
Definition	**Examples**	
	Interaction	**Formed Between**
Tertiary structure refers to the further **extensive folding and bending** of a **single polypeptide chain** giving rise to its **specific 3D conformation**. It is held in place by **hydrophobic interactions**, **ionic bonds**, **disulfide bridges** and **hydrogen bonds** between **R groups**.	Hydrophobic Interactions	**Non-polar** R groups cluster at the **core** of the protein where they are **shielded from water** in hydrophobic interactions.
	Ionic Bonds	**Oppositely charged acidic** and **basic** R groups attract each other.
Quaternary structure refers to the association of **two or more polypeptide chains**. It is held together by **hydrophobic interactions**, **ionic bonds**, **disulfide bridges** and **hydrogen bonds** between **R groups** of amino acid residues of **different polypeptides**.	Disulfide Bridges	**Sulfur** containing R groups of **cysteine** can form **covalent** disulfide bonds. They increase the **heat stability** of the protein.
	Hydrogen Bonds	**O** and **N** are electronegative and the **H** of **–NH** or **–OH** groups are electropositive. **Polar** R groups containing these groups attract each other.

Describe how the structure of haemoglobin is related to its function.	
Structure	**Function**
Secondary Structure: only **α-helices**. Tertiary Structure: only hydrogen bonds, ionic bonds and hydrophobic interactions, **no disulfide bonds**. Quaternary Structure: four polypeptide subunits: **two α-globin subunits** and **two β-globin subunits**.	Haemoglobin is a **globular transport** protein that transports **oxygen** in the blood.
Haemoglobin has a **quaternary structure** made up of **four polypeptide subunits**: **two α-globin subunits** and **two β-globin subunits**. Each subunit is arranged so that most of its **hydrophilic** amino acid side chains are on the **external surface** while its **hydrophobic** amino acid side chains are buried in the **interior**.	This makes haemoglobin **soluble** in an aqueous environment and allows it to be **transported** and **carry O_2** from lungs to tissues and vice versa.
Each subunit is made of a **globin polypeptide** and a **prosthetic haem group**, each consisting of a **porphyrin ring** and **Fe^{2+}**.	The **Fe^{2+}** of the haem group binds **temporarily** to O_2 so that one haemoglobin molecule can carry up to **four** O_2 at a time forming oxyhaemoglobin.
The 4 subunits held together by hydrogen bonds, ionic bonds and hydrophobic interactions between R groups and **not disulfide bonds**.	This allows **movement** of the haemoglobin subunits that influences its **affinity for oxygen**, allowing for **cooperative binding of oxygen** where as a result of the binding of one O_2 to one haemoglobin subunit, a **conformational change** is **induced** in the remaining three subunits, **increasing their affinity** for O_2.

Describe how the structure of collagen is related to its function.	
Structure	**Function**
Primary Structure: **glycine-X-Y** where X is usually proline and Y is usually hydroxyproline. Secondary Structure: **loose helix**. Tertiary Structure: **no** tertiary structure. Quaternary Structure: **three helical polypeptide** chains wound together to form a tropocollagen molecule.	Collagen is a **fibrous structural** protein in **connective tissues**.
A **tropocollagen** molecule consists of **three helical polypeptide chains** wound together.	This increases the **tensile strength** of the tropocollagen molecule.
Each chain contains a repeating tripeptide unit of **glycine-X-Y** where X is usually **proline** and Y is usually **hydroxyproline**.	The bulky and relatively inflexible **proline** and **hydroxyproline** residues confer **rigidity** to the molecule. The small **glycine** residues allow the formation of a **compact** triple helical structure, increasing **tensile strength**.
There are **numerous hydrogen bonds** formed between amino acids of **adjacent polypeptide chains** between –NH and –CO groups of the **peptide linkage** as well as between –OH groups of **hydroxyproline** residues.	This increases the **tensile strength** of the molecule. This makes the molecule **insoluble in water** since extensive hydrogen bonds are already formed between residues in different polypeptides, limiting interaction with water molecules;
Adjacent tropocollagen molecules are arranged in a **staggered** manner, and there are **covalent cross-links** between **lysine** residues of **adjacent** tropocollagen molecules, forming **collagen fibrils** which lie in **parallel** bundles to form **collagen fibers**.	The staggered arrangement **minimizes points of weaknesses** along the fibrils, and increases the **tensile strength**. The **large size** of the molecule makes it **insoluble** in water.

Compare fibrous and globular proteins.		
Point of Comparison	**Fibrous**	**Globular**
Shape	Long polypeptide chains forming **long straight fibers**.	Polypeptide chains folded into roughly **spherical** shape.
Solubility in Water	It is **large** and limited in its ability to form hydrogen bonds with water as **extensive hydrogen bonds** are already formed between **residues** in different polypeptides. Hence, it is **insoluble** in water.	**Polar** R groups are **exposed** to the aqueous environment and can form **hydrogen bonds** with water molecules. Hence, it is **soluble** in water.
Amino Acid Sequence	A **smaller variety** of amino acids is used to construct the protein, with a **repetitive regular sequence** of amino acids.	A **larger variety** of amino acids is used to construct the protein, with a **unique** amino acid sequence.
Length of Polypeptide	Length of polypeptide and sequence of amino acids **may vary slightly** between two samples of the same protein, yet protein will still be **functional**.	Length of polypeptide and sequence of amino acids are always **identical** between two samples of the same protein, or else the protein **may not be functional**.