TOPIC B: BIOMOLECULES

Learning Outcome

Candidates should be able to

Core Topic 1 – Cellular Functions

- (c) Describe the formation and breakage of a glycosidic bond.
- (d) Analyse the molecular structure of a triglyceride and a phospholipid, and relate these structures to their functions in living organisms.
- (e) Describe the structure of an amino acid and the formation and breakage of a peptide bond.
- (f) Explain the meaning of the terms primary structure, secondary structure, tertiary structure and quaternary of proteins, and describe the types of bonding (hydrogen, ionic, disulfide and hydrophobic interactions) which hold the molecule in shape.
- (g) Analyse the molecular structure of a protein with a quaternary structure e.g. haemoglobin, as an example of a globular protein, and of collagen as an example of a fibrous protein, and relate these structures to their functions.

Core Topic 6 – Cellular Physiology and Biochemistry

(f) Compare the storage and structural forms of starch, glycogen and cellulose and their roles in plants and animals.

Content Outline

- 1. Introduction
- 2. Carbohydrates
 - (a) Monosaccharides
 - (b) Disaccharides
 - (c) Polysaccharides
- 3. Lipids
 - (a) Triglycerides
 - (b) Phospholipids
 - (c) Steroids and Sterols
- 4. Proteins
 - (a) Amino acids
 - (b) Structure of protein
 - (c) Types of protein
 - (d) Denaturation

References

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1. Introduction

Cells and their contents are built up by many biomolecules. The structure and function of these molecules are essential to the working of the cell and life itself.

Some important biomolecules and their functions are:

- Carbohydrates: main energy source and storage
- Lipids: main component of cell membrane and energy storage
- Proteins: structural and enzymatic function
- Nucleic acids: store and transmit hereditary information

The monomers (basic units) of important biomolecules

Biomolecules	Monomers (the basic units)	
Carbohydrates	Sugars (saccharides)	
Lipids	Fatty acids and glycerol	
Proteins	Amino acids	
Nucleic Acids	Nucleotides	

2. Carbohydrates

Carbohydrates are the most abundant class of biomolecules. They contain the elements carbon, hydrogen and oxygen in the ratio of <u>C:H:O = 1:2:1</u>. Their general formula is $(CH_2O)_n$, where n = number of carbon atoms.

There are three main classes of carbohydrates namely:

(a) Monosaccharides

- Glucose
- Fructose

(b) Disaccharides

- Maltose (glucose + glucose)
- Sucrose (glucose + fructose)
- Lactose (glucose + galactose)

(c) Polysaccharides

- Starch (monomer: α-glucose)
- Glycogen (monomer: α-glucose)
- Cellulose (monomer: β-glucose)



(a) Monosaccharides

Monosaccharides are simple sugars, which are the monomers that make up disaccharides and polysaccharides.

They are classified according to the **number of carbon atoms** such as trioses (3C), tetroses (4C), pentoses (5C), hexoses (6C) and heptoses (7C).

They function mainly as energy sources as they contain many carbon-hydrogen bonds (C—H), which release energy when they are oxidised. They also act as building blocks for the synthesis of larger molecules.

Biologically Important Monosaccharides

No. of C atoms	General Name	Chemical Formula	Examples	Functions
3	Triose sugar	C ₃ H ₆ O ₃	Glyceraldehyde	Intermediate compound in respiration and photosynthesis
5 Pentose sugar	Pentose	C ₅ H ₁₀ O ₅	Ribose	Component of RNA and ATP
	sugar		Deoxyribose	Component of DNA
	Hexose sugar	C ₆ H ₁₂ O ₆	Glucose	Main source of energy for cellular respiration.
6			Fructose	An energy source. Component of sucrose.
			Galactose	Component of lactose. Found in dairy products.

(i) Structure of monosaccharides

- General formula: $(CH_2O)_n,$ where number of C atoms present, n > 3. E.g. Glucose: $C_6H_{12}O_6$
- Has a carbonyl group (C=O) and multiple hydroxyl groups (-OH). The C=O group is part of the aldehyde group or ketone group.
- A monosaccharide is either an aldose (with aldehyde group) or ketose (with ketone group).



Structures of monosaccharides

Aldoses (aldehyde sugars): Carbonyl group at the end of carbon skeleton. Ketoses (ketone sugars): Carbonyl group within carbon skeleton.

(ii) Properties of monosaccharides

- Physical properties: Monosaccharides are sweet, soluble and have crystalline structures.
- Chemical Properties: All monosaccharides are <u>reducing sugars</u> meaning they can carry out a chemical reaction called reduction.
 - They contain either a free aldehyde or ketone group that donates electrons to reduce Cu²⁺ to Cu⁺ in the Benedict's test.
 - Carbonyl carbon is oxidized to carboxyl group.

Ionic equation: $Cu^{2+} + e^- \rightarrow Cu^+$

Blue solution Orange-red suspension



Sugars as reducing agents

Oxidation of the glucose and other sugars is the basis for Benedict's reaction. The copper (Cu^{+}) produced under alkaline conditions forms a red oxide precipitate. In the ring form, C-1 of glucose cannot be oxidised by Cu^{2+} . However, the open-chain form is in equilibrium with the ring form, and eventually the oxidation reaction goes to completion.

(iii) Benedict's test

- Add 2cm³ of Benedict's solution to 2cm³ of sample solution in a test tube and mix.
- Place test tube in a boiling water bath for 2 minutes.
- If reducing sugar is present, the blue solution turns varying from green, yelloworange, orange to **orange-red suspension** as the concentration of reducing sugar increases.
- By measuring the amount of oxidising agent reduced by a solution of a sugar, it is also possible to estimate the concentration of that sugar.
- Therefore, Benedict's test is both a qualitative and quantitative test.



Range of colours for the Benedict's test corresponding to the relative amounts of reducing sugar



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(iv) Examples of Monosaccharides

Glucose

It is the most abundant hexose sugar and the main respiratory substrate for all living things.

- > Structure
 - Chemical formula of $\underline{C_6H_{12}O_6}$
 - In solution, glucose alternates between straight chains and ring structures freely. It exists mainly in the ring structures (more stable) and only a small proportion of the molecules exist in the straight chain at any one time.
 - The ring structure is the form in which glucose molecules combine to form maltose (disaccharide) and starch or glycogen (polysaccharides).



Structures of the open chain form and α and β ring structures of glucose

The three forms exist in equilibrium in aqueous solution, with 0.02% open chain, 36% α glucose and 64% β glucose.



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> • There are two possible ring structures of glucose namely the <u>α-glucose</u> and <u>β-glucose</u>. The hydroxyl group on carbon-1 can project below the ring (α-glucose) or above the ring (β-glucose). These molecules are known as isomers as they have the same chemical formula but different structural arrangements. (Fig. 3)



Structures of α -glucose and β -glucose

- Function
 - It acts as a substrate for production of energy in the form of <u>adenosine</u> <u>triphosphate (ATP)</u> during cellular respiration.
 - The carbon skeleton also serves as raw material for synthesis of other types of small organic molecules like amino acids and fatty acids.

Sugar Isomers:

Glucose is not the only sugar with the molecular formula of $C_6H_{12}O_6$. Other sixcarbon sugars such as fructose and galactose also have this molecular formula, but their atoms are arranged in different ways, therefore their three-dimensional structures are different. This also accounts for functional differences between the isomers.

• Fructose

Fructose ($C_6H_{12}O_6$) is a structural isomer of glucose. It is the sweetest common sugar.

- Function
 - It is used as substrate for production of energy in the form of adenosine triphosphate (ATP) during cellular respiration.



Galactose .

Galactose (C₆H₁₂O₆) and glucose are called stereoisomers. Galactose has identical chemical groups bonded to the same carbon atoms as glucose. The only difference between galactose and glucose is the orientation of one hydroxyl group.

- ➤ Function
 - It is used as substrate for production of energy in the form of adenosine 0 triphosphate (ATP) during cellular respiration.
 - Required for the synthesis of lactose. 0



FIGURE 3.26

Isomers and stereoisomers. Glucose, fructose, and galactose are isomers with the empirical formula C6H12O6. A structural isomer of glucose, such as fructose, has identical chemical groups bonded to different carbon atoms, while a stereoisomer of glucose, such as galactose, has identical chemical groups bonded to the same carbon atoms but in different orientations.



(b) **Disaccharides**

A <u>glycosidic bond</u> is formed between two <u>monosaccharides</u> in a <u>condensation</u> reaction with the <u>removal of one molecule of water</u>.

In this case, the glycosidic bond is formed between the hydroxyl group on carbon-1 of one α -glucose and the hydroxyl group on carbon-4 of the other α -glucose. Therefore the bond is known as α -1, 4-glycosidic bond.



Formation of a disaccharide by condensation reaction

Two glucose molecules combine to form maltose in a condensation reaction involving the formation of a glycosidic bond and removal of water.

(i) Properties of disaccharides

- Physical properties: Disaccharides are sweet, soluble and have crystalline structures.
- Chemical properties: Most disaccharides are reducing sugars except sucrose.
 - In sucrose, the aldehyde group of glucose and the ketone group of fructose are linked together to form a glycosidic bond. Therefore, sucrose has no free aldehyde or ketone group to carry out reduction.



Condensation and hydrolysis reactions

The condensation and hydrolysis reactions involve the formation and breaking of glycosidic bond, respectively.



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(ii) Hydrolysis Reaction

The <u>glycosidic bond</u> is broken between two <u>monosaccharides</u> (in a disaccharide) in a <u>hydrolysis</u> reaction with the <u>addition of one molecule of water</u>, to form the <u>hydroxyl group</u> on two different monosaccharides.

There are two types of hydrolysis reactions:

- Acid hydrolysis
 - > High temperature and acid is needed to cleave the glycosidic bond.
 - Method:
 - 1. Add a few drops of dilute hydrochloric acid to 2cm³ of sample solution and mix.
 - 2. Place test tube in a boiling water bath for 2 minutes.
- Enzyme hydrolysis
 - > Maltose is hydrolysed into glucose by maltase.
 - > Sucrose is hydrolysed into glucose and fructose by sucrase.

(iii) Non-reducing sugar test

- Add a few drops of dilute hydrochloric acid to 2cm³ of the sample solution.
- Place test tube in a boiling water bath for 2 minutes.
- Allow mixture to cool and neutralise acid with sodium hydrogen carbonate.
- Conduct the Benedict's test for reducing sugar.

(iv) Examples of Common Disaccharides

Disaccharide	Components	Functions	Types of Bonds
Maltose	glucose + glucose	Maltose is an intermediate compound in the digestion of starch to glucose by an enzyme called amylase.	α-1,4- glycosidic bond
Sucrose	glucose + fructose	 Sucrose is the most abundant disaccharide. Carbohydrates are transported in plants in the form of sucrose. It serves as a good transport sugar: very soluble can be moved efficiently in high concentrations relatively unreactive 	α-1,2- glycosidic bond
Lactose	glucose + galactose	Lactose is the sugar found in milk. It functions as an energy source for young mammals.	β-1,4- glycosidic bond



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Formation of maltose, sucrose and lactose

The formation of different types of glycosidic bond in the condensation reactions to form maltose, sucrose and lactose.



(c) Polysaccharides

A polysaccharide is formed when many monosaccharides (usually hexoses) combine by condensation reaction, and are linked by glycosidic bonds. The number of monosaccharide units (monomers) in a polysaccharide can vary from 40 to over 1000. The chains can be folded or branched.

Polysaccharides can be classified into two groups according to their functions:

(i) Storage polysaccharides (e.g. starch and glycogen)

These molecules are good for storage because:

- They are <u>large</u> and thus <u>insoluble</u> in water. As a result, they exert <u>no osmotic</u> <u>effect</u> on cells when stored in large amounts and do not interfere with chemical reactions of the cells.
- They are large and unable to diffuse out of the cells.
- They fold into <u>compact</u> shapes and thus large amounts can be stored within a fixed volume.
- They are **<u>easily hydrolysed</u>** into monosaccharides when required by the cells.
- (ii) Structural polysaccharides (e.g. cellulose)

These molecules are good for structural functions because:

- They are unbranched polymers.
- They form long straight chains which are ideal for formation of strong fibres.



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(i) Storage Polysaccharides

• <u>Starch</u>

Structure

- Polymer consisting of α -glucose monomers.
- Consists of a mixture of two types of polymers, <u>amylose</u> and <u>amylopectin</u>.
- The two components of starch (amylose and amylopectin) fit together to form a complex three-dimensional structure in which the amylose helices are entangled in the branches of the amylopectin molecules.



Structure of amylose and amylopectin in starch

The different types of glycosidic bonds present in amylose and amylopectin in starch.

Amylose

- Consists of several thousand <u>α-glucose</u> residues.
- ο Linked by <u>α-1,4-glycosidic bonds</u>.
- o **<u>Unbranched chain</u>** polymer.
- Coils into a <u>helical</u>, <u>compact</u> structure stabilised by <u>hydrogen bonds</u>.
- <u>Hydroxyl (-OH) group</u> on carbon-2 of each glucose residue projects into the middle of the helix and hydrogen bonds are formed between the –OH group of adjacent glucose residues

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Amylopectin

- Consists of several thousand <u>α-glucose</u> residues (up to twice as many glucose residues as amylose).
- $\circ~$ Linked by <u>**a-1,4-glycosidic bonds**</u> and <u>**a-1,6-glycosidic bonds**</u> where branch points occur.
- **Branched chain** polymer (branching occurs at every 24-30 residues).
- Coils into a <u>helical</u>, <u>compact</u> structure stabilised by hydrogen bonds.
- <u>Hydroxyl (-OH) group</u> on carbon-2 of each glucose residue projects into the middle of the helix and hydrogen bonds are formed between the –OH group of adjacent glucose residues.

Structure of Amylose

Note the differences in structure and properties that result from α -1,4-glycosidic bonds in α -amylose as compared to β -1,4-glycosidic bonds in cellulose. The polysaccharide chain is helical in amylose, rather than linear in cellulose.

Function

- Main energy storage molecule in plants, but is absent from animals where the equivalent is glycogen.
- Accumulates to form <u>starch grains</u> in the <u>chloroplast</u> of plant cells.
- <u>Compact</u> structure allows many glucose molecules to be stored in a small volume within the cell.
- Can be readily converted back to glucose for use in respiration to produce ATP. When necessary, free sugars are released by hydrolysis of starch.

Enzyme hydrolysis: starch \rightarrow maltose \rightarrow glucose Acid hydrolysis: starch \rightarrow dextrin \rightarrow maltose \rightarrow glucose

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Iodine test

- Add a few drops of iodine-potassium iodide solution to 2cm³ of sample solution.
- o If starch is present, the solution turns from yellow to blue-black.
- A suspension of amylose in water gives a blue-black colour whereas a suspension of amylopectin gives a red-violet colour.
- $\circ~$ The common iodine test for starch works because molecular iodine inserts itself into these helices.
- The intense blue colour of a positive test comes from interactions between iodine molecule and the helically arranged glucose residues of the amylose.

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- <u>Glycogen</u>
 - > Structure
 - o Glycogen has a structure similar to amylopectin.
 - Consists of <u>α-glucose</u> residues.
 - Linked by $\underline{\alpha-1,4-glycosidic \ bonds}$ and $\underline{\alpha-1,6-glycosidic \ bonds}$ where branch points occur.
 - <u>More extensive branching</u> as compared to amylopectin which results in a <u>more compact</u> structure.
 - Coils into a <u>helical</u>, <u>compact</u> structure stabilised by hydrogen bonds.

> Function

- Main energy storage molecule in animals.
- Accumulates to form <u>glycogen granules</u> in <u>liver and muscle cells</u>.
- <u>Compact</u> structure allows many glucose molecules to be stored in a small volume within the cell.
- Each branch in glycogen ends with a nonreducing sugar unit, a glycogen molecule has as many nonreducing ends as it has branches.
- When glycogen is used as an energy source, glucose units are removed one at a time from the nonreducing ends. Degradative enzymes that act only at nonreducing ends can work simultaneously on the many branches, speeding up the conversion of glycogen to glucose-1-phosphate.
- Glycogen is converted to glucose when glucose level is low. Its conversion back to glucose is controlled by the hormone glucagon which is secreted in the pancreas.

Why is glucose stored in muscle and liver in the form of glycogen, not as individual glucose molecules?

Glycogen is large and insoluble; negligible contribution to the osmotic pressure of the cell. In contrast, each molecule of an equivalent number of glucose molecules contributes to osmotic pressure. If the glucose molecules were not linked to form glycogen, the cell would burst.

Presence of extensive branching therefore glycogen has a compact structure; allows for more glucose molecules to be stored within a small volume.

Presence of many nonreducing ends due to the presence of many branches; allow for more rapid mobilization of stored glucose when there is an increase in energy demand

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Structure and location of (a) starch and (b) glycogen

Starch grains are found within a chloroplast of a plant cell. Glycogen granules are found in the liver or muscle cells.

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Structure of amylopectin and glycogen at three levels (a) formation of one branch (b) several branches and (c) highly branched structure of whole molecule The 1,6 linkages cause branching and the 1,4 linkages cause the chains to turn and <u>coil</u>.

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(ii) Structural Polysaccharide

- <u>Cellulose</u>
 - Structure
 - Consists of β -glucose residues.
 - Linked by <u>β-1,4-glycosidic bonds</u>.
 - <u>Adjacent</u> glucose molecules are <u>rotated 180° with respect to each</u> <u>other</u>.
 - o **<u>Unbranched</u>** chain polymer.
 - Straight chains of β-glucose run parallel to each other with numerous hydrogen bonds.
 - Intra-chain hydrogen bonds occur between –OH and O of adjacent molecules.
 - Inter-chain hydrogen bonds occur between –OH groups projecting outwards from each chain and O of parallel chain. This cross-linking binds the chains rigidly together.
 - The cellulose chains associate in groups to form bundles called microfibrils.
 - Microfibrils are arranged in larger bundles to form macrofibrils.
 - Macrofibrils of successive layers are <u>interwoven and are embedded</u> in a gel-like matrix, thus having <u>high tensile strength</u>.

(a) Starch: α -1,4-glycosidic bonds between α -glucose monomers

(b) Cellulose: β -1,4-glycosidic bonds between β -glucose monomers

Structure of (a) starch in comparison to (b) cellulose

- > Function
 - Main component of cellulose <u>cell wall</u> of plants for <u>structural support</u>.
 - Large <u>intermolecular spaces</u> between macrofibrils cause the cell wall to be <u>permeable</u> because they allow <u>free movement</u> of molecules in and out of the cell.

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Structure of cellulose

The glucose residues are rotated 180° with respect to the each other for the formation of β -1,4-glycosidic bonds.

Arrangement cellulose chains into microfibrils in plant cell wall

Compare and explain the 1,4 glycosidic bonds formed between α -glucose units and that between β -glucose units.

Both 1,4-glycosidic bonds are formed between C1 of 1 glucose and C4 of the adjacent glucose unit.

 β -1,4-glycosidic bonds alternate between the upper and lower planes of the β -glucose units, whereas α -1,4-glycosidic bonds occur on the same side of the α -glucose units.

This is due to the –OH group of C1 of β -glucose which is found above the plane of the ring while the adjacent β -glucose monomer has –OH of C4 on the opposite side / below the plane.

Therefore adjacent β -glucose units have to be rotated 180° with each other so that the –OH on C1 is on the same plane as the –OH on C4 on the adjacent glucose unit.

The two –OH groups then react to form glycosidic bond during condensation reaction.

Therefore α -glucose units linked by α -1,4-glycosidic bonds coil into an α -helix, whereas carbohydrate chains with β -glucose units linked by β -1,4-glycosidic bonds have linear/straight chains (as glycosidic bonds occur alternatively on opposite sides).

3. Lipids

Lipids contain the same elements as carbohydrates: carbon, hydrogen and oxygen. They do not have a general formula but have proportionally less oxygen compared to hydrogen. One example is tristearin ($C_{57}H_{110}O_6$) [Recall carbohydrate general formula: (CH_2O_n].

Lipids are **<u>non-polar</u>** due to even distribution of charge. In general, lipids are formed by condensation reactions between fatty acids and an alcohol.

Lipids can be classified into three types:

- (a) Triglycerides (e.g. fats and oils)
- (b)_Phospholipids (e.g. phosphatidylcholine)
- (c)_Steroids and sterols (e.g. cholesterol)

(a) <u>Triglycerides</u>

(i) Structure of triglycerides

Triglycerides are the most common lipids in nature. They are made up of <u>3 fatty</u> <u>acid chains</u> and <u>1 glycerol</u> molecule.

• Fatty acid

- Consists of a <u>hydrophobic hydrocarbon chain</u> (only carbon and hydrogen atoms) and a <u>hydrophilic carboxyl group (-COOH)</u>.
- > Are relatively polar due to the carboxyl group.
- General formula of R-COOH, where R is the hydrocarbon chain.
- Vary in length depending on the number of carbon atoms present in the hydrocarbon chain. Most naturally occurring fatty acids have an even number of carbon atoms between 14 and 20.
- Two types of fatty acids:
 - <u>Saturated</u> fatty acids contain only carbon-carbon single bond (C-C) in the hydrocarbon chain.
 - <u>Unsaturated</u> fatty acids contain carbon-carbon double bond (C=C) in the hydrocarbon chain, resulting in <u>kinks</u> that prevent the tight packing of fatty acid chains.
 - Monounsaturated: One double bond
 - Polyunsaturated: More than one double bonds between carbon atoms

Structure of fatty acids (a) structural formula (b) simplified representation

Fatty acids consist of a long hydrocarbon chain and carboxyl group (-COOH).

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Structure of saturated and unsaturated fatty acids

Unsaturated fatty acids contain at least one carbon-carbon double bond.

Diagram showing the difference between saturated and unsaturated fats

(b) At room temperature, the molecules of a saturated fat, such as the fat in butter, are packed closely together, forming a solid. The straight chain allows the molecule to pack tightly with other molecules.

(c) At room temperature, the molecules of an unsaturated fat such as olive oil cannot pack together closely enough to solidify because of the kinks in some of their fatty acid hydrocarbon chains.

- Glycerol
 - Glycerol is an alcohol, which has 3 carbon, each attached to a hydroxyl group (-OH).

Structure of glycerol

- (ii) Formation of triglycerides
 - Triglycerides are formed from <u>3 fatty acid molecules</u> with <u>1 glycerol</u> <u>molecule</u> by <u>condensation</u> reaction. (This process is also known as esterification).
 - <u>3 ester bonds</u> are formed with the removal of 3 water molecules.
 - The resulting triglyceride is **<u>non-polar</u>**.
 - Each of the hydroxyl (-OH) groups in glycerol reacts with a carboxyl group (-COOH) in a fatty acid molecule to form an <u>ester bond or linkage</u>.
 - Ester bonds can be broken by <u>hydrolysis</u>.

(a) Formation of Triglyceride (b) Simplified representation of Triglyceride

A triglyceride is formed by a condensation reaction between 1 glycerol and 3 fatty acids with the removal of 3 molecules of water.

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What is the difference between condensation and esterification?

Condensation is the chemical reaction in which 2 molecules react and become covalently bonded to one another with concurrent loss of a small molecule, water.

Esterification is a chemical reaction in which 2 specific reactants (alcohol and carboxylic acid) to make ester.

(iii) Properties of triglycerides

- Physical Properties
 - Melting points: Triglycerides can be classified as <u>fats</u> or <u>oils</u>.
 - Fats are <u>solid at 20°C</u>.
 - Consist of long saturated fatty acid chains.
 - Presence of single bonds thus packed tightly and more compact.
 - More hydrophobic interactions between the fatty acid chains, resulting in higher melting points.
 - Oils are <u>liquid at 20°C</u>.
 - Consist of relatively short unsaturated fatty acid chains.
 - Presence of double bonds results in kinks in the fatty acid chain, thus packed less tightly and less compact.
 - Less hydrophobic interactions between fatty acid chains, resulting in lower melting points.
 - Solubility: They are <u>insoluble in water</u> but <u>soluble in organic solvents</u> such as ether, chloroform and benzene.
 - C-H bonds in the hydrocarbon chains of fatty acids are non-polar and thus do not form hydrogen bonds with water molecules.
 - Soluble in organic solvents because hydrophobic interactions can be formed.
 - Density: Triglycerides have lower density than water and thus floats on water.

• Test for Fats

- > Add 2cm³ of ethanol to 2 drops of sample solution in a test tube.
- Shake vigorously to dissolve the lipids.
- > Add an equal volume of cold water to test tube and mix well.
- If lipids are present, a <u>white emulsion</u> forms.

Are lipids monomers or polymer? Explain.

They are not considered polymer. Polymers are macromolecules made of repeated units of monomers. Lipids are large molecules assembled from smaller molecules (fatty acid, glycerol) by condensation reaction.

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(iv) Function

- Energy storage
 - Triglycerides are a <u>respiratory substrate</u>, having long hydrocarbon chains that can be hydrolysed and oxidised during respiration to <u>produce energy</u> in the form of ATP.
 - Lipids have a <u>higher calorific value</u> than other respiratory substrates (i.e. carbohydrates), releasing a <u>higher amount of metabolic energy per unit</u> <u>mass</u> as are there are <u>more C-H bonds to release more ATP upon</u> <u>hydrolysis</u>.
 - Lipids (38.9KJ/g) yield double the amount of metabolic energy on oxidation than carbohydrates (17.2kJ/g).
 - Triglycerides release <u>twice as much metabolic water</u> (1.07g/g lipid) as <u>compared to carbohydrates</u> (0.56g/g lipid) when oxidised in respiration.
 - $\circ\,$ Desert animals such as kangaroo rats and camels store fat for this purpose.
 - Lipids can be stored in large amounts <u>without exerting any osmotic</u> <u>effect</u> on cells.
 - They are large molecules and non-polar due to the presence of hydrocarbon tails thus insoluble in water. Therefore, they are unable to diffuse out of cells.
 - They are less dense (lighter) than carbohydrates as they are more compact and are unhydrated.
 - Main energy source for highly active animals due to the demands of locomotion.
 - Main energy storage for seeds dispersed by wind, resulting in a light seed which can be carried over longer distances.
 - Plants, on the other hand, are generally immobile thus can function with bulky energy storage in the form of starch.

• Heat insulation

- Fat stored in adipose tissues below the dermis of the skin of vertebrates serves as a <u>heat insulator</u> as it is a <u>poor conductor of heat</u>.
- Found extensively in mammals living in cold climates e.g. blubber in whales to prevent excessive heat loss.
- Protection
 - Adipose tissues around vital internal organs protect from shock and physical impact.
 - Cushioning of internal organs also prevents abrasion with adjacent organs.

• Buoyancy

Lipids are less dense than water and thus large aquatic animals living in cold environments e.g. seals and whales make use of their thick layer of blubber for buoyancy.

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(b) Phospholipids

(i) Structure

- Phospholipids are lipids containing a phosphate group.
- Made up of <u>1 glycerol molecule, 2 fatty acid molecules and 1 phosphate</u> <u>group</u> (derived from phosphoric acid).
- Formed when one of the three hydroxyl (–OH) groups in glycerol reacts with phosphoric acid and the other two –OH groups react with fatty acids as in the formation of triglycerides.
- Formed by a <u>condensation</u> reaction resulting in the formation of <u>two ester</u> <u>bonds</u> and <u>one phosphoester bond</u> with the <u>removal of 3 water molecules</u>.
- Amphipathic molecule due to the <u>hydrophilic phosphate head</u> and <u>two</u> <u>hydrophobic hydrocarbon / fatty acid chains</u>.
- The phosphate head is hydrophilic as it is <u>charged</u> (carries a negative electrical charge). Thus the head of the molecule is soluble in water but the tails are insoluble in water.
- When placed in water, phospholipids self-assemble and congregate to form micelles and membrane bilayers.

(a) Structure of a phospholipid (b) Simplified representation

A phospholipid is formed by a condensation reaction between 1 glycerol, 2 fatty acids and 1 phosphoric acid with the removal of 3 molecules of water.

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Structure of phosphatidylcholine (a type of phospholipid)

(ii) Function

- Form the basic structure of cell surface membrane and internal membranes of cells called the <u>phospholipid bilayer</u> (Fluid Mosaic Model).
- Can associate with hydrophilic oligosaccharides, which are short polysaccharides, to form <u>glycolipids</u> which help in <u>cell-cell recognition</u> and <u>cell-cell adhesion</u>.
- Phospholipids are necessary for the formation of acetylcholine (a neurotransmitter).
- Phospholipids that form micelles help in the transport of fats from the gut to the liver.

Lipids form a micelle when placed in water.

(c) Steroids and Sterols

- (i) Structure
 - Are not typical lipids as they have little in common.
 - Possess a much more complex molecular structure comprising of a carbon skeleton of four fused carbon rings.
 - Sterols of plants are called phytosterols and sterols of animals are called zoosterols. An example of animal sterol is <u>cholesterol</u>.
- (ii) Property
 - Insoluble in water, as they are non-polar.
 - Soluble in organic solvents.

(iii) Function

- Sterols are precursors from which other steroids are synthesized. For example, cholesterol is used to synthesize sex hormones such as testosterone and oestrogen, and bile acids.
- Cholesterol is an important component of biological membranes where it regulates membrane fluidity.
- Cholesterol is insoluble in water. Therefore, cholesterol combines with proteins to form lipoproteins which transport cholesterol and triglycerides in the blood. There are various types of lipoproteins.
 - Low density lipoproteins (LDL) deposit cholesterol into tissues such as blood vessels causing obstruction. This may increase the risk of coronary heart disease.
 - High density lipoproteins (HDL) help remove excess cholesterol from tissues and arteries. This helps reduce the risk of heart disease. Some of this cholesterol is also converted to bile salts in the liver.

4. Proteins

Proteins contain the elements <u>carbon, hydrogen, oxygen and nitrogen, and</u> in some cases <u>sulphur</u>. Each protein has a <u>unique 3-dimensional conformation</u>.

(a) Amino acids

Amino acids are the monomers of proteins. There are 20 common amino acids found in plants and animals proteins, divided into essential and non-essential amino acids.

Essential amino acids must be obtained from the diet because organisms lack the long and complex reaction pathways required for their synthesis. This is to ensure proper nitrogen balance and adequate growth. Non-essential amino acids are synthesized from readily available metabolites.

(i) Structure

- The central carbon atom, known as the α-carbon is bonded to 4 different groups of atoms:
 - hydrogen atom
 - basic <u>amino group</u> (-NH₂) which accepts protons
 - > acidic carboxyl group (-COOH) which donates protons
 - R group / side chain which is unique to each amino acid

General structure of an amino acid

Amino acid has a central α -carbon bonded to H atom, amino group, carboxyl group and side chain.

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The different chemical properties of amino acids are determined by their unique R groups.

The 20 amino acids of proteins

The amino acids are grouped here according to the properties of their side chains (R groups) and shown in their prevailing ionic forms at pH 7.2, the pH within a cell.

The three-letter and one-letter abbreviations for the amino acids are in parentheses.

• Amino acids are classified into uncharged and charged R groups. Uncharged amino acids can be non-polar (glycine) or polar (cysteine). Charged R groups can be **basic** or **acidic**.

Classification of amino acids

An amino acid can be grouped according to the nature of their side chain or R group.

(ii) Properties of amino acids

- Insoluble in organic solvents but can dissolve in water to form <u>zwitterions</u>.
- Dipolar as they carry a positive charge on the basic group and a negative charge on the acidic group.

Zwitterion formation in amino acids

• <u>Amphoteric</u>, as they contain both acidic and basic groups. They are able to resist slight changes in pH, thus are able to act as pH buffers.

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(iii) Peptide Bond

- A peptide bond is the covalent bond between two amino acids.
- <u>Peptide bonds</u> are formed between the <u>carboxyl group</u> of one amino acid and the <u>amino group</u> of another in a <u>condensation reaction</u> with the <u>removal</u> <u>of one molecule of water</u>.
- A dipeptide is two amino acids held together by a peptide bond.
- The dipeptide possesses a free amino group at one end and a free carboxyl group at the other. This enables further condensation with other amino acids forming polypeptides.
- By convention, the N-terminal is taken to be the start of a polypeptide chain. The sequence of amino acids in a polypeptide chain is always written with the N-terminal residue first.
- Peptide bonds can be broken by <u>hydrolysis</u> reactions using enzymes or acid hydrolysis.
- The <u>peptide bond</u> is broken between two amino acids (in a dipeptide) in a <u>hydrolysis</u> reaction with the <u>addition of one molecule of water</u>, to form the <u>amino group</u> and the <u>carboxyl group</u> on two different amino acids.

The formation of a peptide bond

Polypeptides and proteins are formed of chains of amino acids joined together by linkages called peptide bonds. With the formation of each such bond, a molecule of water is released.

(iv) Biuret Test for proteins

- Add 2 cm³ of sample solution in a test tube.
- Add equal volume of Biuret Solution to sample solution and mix.
- If proteins are present, a purple coloration is observed.
- The Cu²⁺ ions will form complexes with the peptide bonds under alkaline conditions. The greater the amount of protein, the more intense the purple coloration due to more complexes formed.
- Therefore, Biuret's Test is both a qualitative and quantitative test.

Biuret Test results for different protein concentrations

(b) Structure of Proteins

Each protein possesses a unique three-dimensional conformation. There are 4 levels of structural organisation in proteins: **primary**, **secondary**, **tertiary** and **guaternary**.

The structural hierarchy in proteins

(a) Primary structure, (b) secondary structure, (c) tertiary structure and (d) quaternary structure

(i) Primary Structure

The primary structure is the **specific number and sequence** of amino acids joined by **peptide bonds** in a polypeptide chain.

• Sequence

- Every protein molecule has a unique sequence of amino acids which is determined by base sequence of DNA.
- The unique sequence of amino acids with its side chains of different chemical and physical properties determines the three-dimensional conformation of the protein.

• Number

- Every polypeptide possesses a carboxyl terminus (C-terminus) and amino terminus (N-terminus).
- The possible amino acid residues in a polypeptide chain can be of any number and arrangements of the 20 common amino acids.
- (The total possible number of different combinations of polypeptide chains can be denoted as n^r, where n = number of different amino acids and r = number of residues in polypeptide chain.)

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(ii) Secondary Structure

The secondary structure is the <u>repeated coiling and folding</u> of a polypeptide chain, maintained by <u>hydrogen bonds</u> formed between <u>peptide bonds</u>. Hydrogen bonds are formed between <u>N-H group in a peptide bond</u> of an amino acid and <u>C=O group in a peptide bond</u> of another amino acid.

The secondary structure also refers to the local spatial conformation of a polypeptide backbone, excluding the side chains of its amino acids.

There are two main forms of secondary structures, namely $\underline{\alpha}$ -helix and $\underline{\beta}$ -pleated sheets.

- α-helix
 - Unbranched polypeptide chain <u>tightly coiled into a spiral</u>.
 - Each turn of the helix consists of **<u>3.6 amino acids</u>**.
 - Held by <u>intra-chain hydrogen bonding</u> between N-H group in a peptide bond of an amino acid and C=O group in a peptide bond of another amino acid <u>four amino acids away</u>.
 - The numerous hydrogen bonds make the α-helix structurally strong and inelastic (cannot be stretched) but flexible (can be bent) e.g. α-keratin (the structural protein found in hair and nails)

Structure of a α -helix

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β-pleated sheet

- Consist of extended <u>adjacent polypeptide chains</u> arranged in a parallel or antiparallel manner.
- Held together by <u>hydrogen bonding</u> which exists between the N-H group in a peptide bond of a chain and C=O group in a peptide bond of adjacent chain.
- > "Pleated" appearance of the β -pleated sheet arises from the tetrahedral chemical bonding at the α -carbon atom.
- > The numerous hydrogen bonds make the structure very stable and rigid. The β sheet also has high tensile strength thus it cannot be stretched. e.g. silk fibroin protein.

Adjacent polypeptide chains running in alternating directions.

Adjacent polypeptide chains running in the same direction.

Structure of β pleated sheets

(a) Antiparallel β -pleated sheet (b) Parallel β -pleated sheet (c) "pleated" appearance of β -pleated sheet

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(iii) Tertiary Structure

Tertiary structure is the compact <u>unique three-dimensional conformation</u> due to further coiling and folding of secondary structures.

The tertiary structure of a protein is held by <u>hydrogen bonds</u>, <u>ionic bonds</u>, <u>disulfide bonds</u>, and/or <u>hydrophobic interactions</u> between <u>R groups/side</u> <u>chains</u> of amino acids on a <u>single</u> polypeptide chain.

• Hydrogen bonds

- Hydrogen bonds are formed between an electronegative atom and a hydrogen atom bonded to another electronegative atom (such as nitrogen or oxygen).
- Each hydrogen bond is weak. However, a large number of weak hydrogen bonds are sufficiently strong to hold protein structure together.

• Ionic bonds

- Electrostatic attraction between positively and negatively charged R groups
- eg ionised carboxyl group (COO⁻) of acidic amino acids and amino group (NH₃⁺) of basic amino acids
- Relatively strong, although easily disrupted by changes in pH.

• Disulphide bonds

- Strong covalent bond (S-S)
- Formed from oxidation of sulphydryl (-SH) groups of two neighbouring cysteine R groups. Only cysteine contains a sulphydryl (–SH) group in its R group.
- Very strong and not easily broken except by reducing agents.

Hydrophobic interactions

- > Weak interactions between non-polar R groups.
- When a polypeptide chain with non-polar amino acids is placed in an aqueous medium, the chain will fold such that the non-polar R groups are in close contact and shielded from the aqueous medium.

The different bonds present in the tertiary structure of a protein

(iv) Quaternary Structure

Quaternary structure is when <u>more than one polypeptide chain</u> is held together by <u>hydrogen bonds</u>, <u>ionic bonds</u>, <u>disulfide bonds</u> and/or <u>hydrophobic</u> <u>interaction</u> between R-groups of <u>different polypeptide chains</u>. E.g. haemoglobin is a protein comprises four polypeptide chains.

Quaternary structure involves inter-chain interactions, in addition to the intra-chain interactions seen in the primary, secondary and tertiary structure.

(c) <u>Types of Proteins</u>

Proteins can be classified into globular proteins and fibrous proteins.

(i) Globular Protein – Haemoglobin

- A red pigment in red blood cells responsible for transporting oxygen in blood.
- A <u>quaternary globular protein</u> of 4 subunits, each consisting of a polypeptide chain and a prosthetic group called haem group.
- (Prosthetic group: Non-protein species that is tightly bound to a protein and helps it to perform its function)

Polypeptide chains

- > **<u>2 identical \alpha-chains</u> of 141 amino acids.**
- > **<u>2 identical \beta-chains</u> of 146 amino acids.**
- > Each polypeptide is coiled into α -helices and then folded into a spherical globular shape. (No β -pleated sheets)
- Hydrophobic amino acid residues are in the interior of the folded structure and hydrophilic amino acid residues are found at the exterior surface to maintain solubility of the protein.
- The four polypeptides are held by <u>hydrophobic interactions</u>, <u>ionic bonds</u> and <u>hydrogen bonds</u>. (No disulfide bonds are involved)

Haem group

- > A porphyrin ring with an iron ion (Fe^{2+}) in the centre.
- ➢ Fe²⁺ binds to an oxygen molecule reversibly.
- Each haem group resides in a <u>hydrophobic pocket</u> in the tertiary structure of a polypeptide chain.
- Hence, a haemoglobin molecule has four haem groups and can carry 4 oxygen molecules to form oxyhaemoglobin.

 $Hb + 4O_2 \leftrightarrow Hb(O_2)_4$

Oxygen is transported in this state to other tissues of the body. In the tissues, oxyhaemoglobin releases oxygen, which diffuses into the tissue fluid and from there into the cells.

- Structure in relation to Function
 - The <u>hydrophobic amino acids</u> in the <u>interior of the protein</u> and <u>hydrophilic amino acids</u> found at the <u>exterior surface of the protein</u>.
 - Allow the haemoglobin to be **<u>soluble</u>** to take part in chemical reactions.
 - The haem group, a porphyrin ring with an iron ion (Fe²⁺) centre, is held in the <u>hydrophobic pocket of the polypeptide chain</u>.
 - Allow haemoglobin to <u>bind reversibly to oxygen</u> and transport oxygen to the rest of the body.
 - The quaternary structure, of four subunits, are held by <u>weak bonds</u> such as <u>hydrophobic interactions</u>, <u>ionic bonds</u> and <u>hydrogen bonds</u>
 - o Allows cooperative binding of oxygen to haemoglobin.
 - Binding of one O_2 molecule to one subunit results in a <u>conformation</u> <u>change</u> of the adjacent subunits in the haemoglobin molecule, making it easier for another O_2 molecule to bind with the other haem groups in the molecule. This increases the rate of uptake of oxygen by haemoglobin.
 - > Haemoglobin is a **<u>globular</u>** protein and is folded into a **<u>spherical</u>** shape.
 - Allow the protein to be **<u>compact</u>** and many haemoglobin molecules to be dissolved in the cytoplasm of a red blood cell.

The quaternary structure of haemoglobin and the haem group Each haem group has a porphyrin ring with an iron ion (Fe²⁺) at the centre.

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(ii) Fibrous Protein – Collagen

- **Fibrous protein** performing a **structural and supportive function** in skin, bone, connective tissue and tendons.
- Basic structural unit of collagen is <u>tropocollagen</u>, which comprises <u>3</u> <u>polypeptide chains</u> wound around each other to form <u>a triple helix</u>.
- Each chain:
 - > 1050 amino acids residues in each chain.
 - Has a high proportion of <u>glycine</u>, <u>proline</u> and <u>hydroxyproline</u>
 - > A <u>repeated triplet sequence of Gly-X-Y</u>.
 - 1/3 of amino acid residues are glycine.
 - X is often proline, and Y is often hydroxyproline.
 - Proline and hydroxyproline are **bulky and relatively inflexible**.
 - > Each of the three polypeptide chains is in a helical conformation (not to be confused with α -helix).

The structure of one polypeptide chain of collagen and the constituent amino acids.

• Structure in relation to Function

- Every 3rd amino acid residue is a glycine and this allows each helical chain to makes a turn every 3 residues and intertwine around two other chains to form the triple helix, as <u>only glycine is small enough to fit into the</u> <u>centre</u>.
 - Allows the structure to be very **<u>compact.</u>**
- The 3 helical chains are held together by <u>hydrogen bonds</u> forming <u>tropocollagen</u>.
 - Allows the structure to be relatively **<u>rigid</u>**.
- > Hydrophobic amino acids are found at the exterior surface of collagen.
 - Allows it to be <u>insoluble in water</u> (distinct feature of fibrous proteins) and <u>metabolically inactive</u>, and thus, <u>resistant to chemical changes</u>.
- Many triple helices <u>lie parallel</u> in a <u>staggered pattern</u> to form <u>fibrils</u>, with <u>covalent bonds</u> between neighbouring triple helix chains. Fibrils unite to form <u>fibres</u>.
 - Allows collagen to have <u>high tensile strength</u>, and high resistance to stretching.

The formation of collagen fibres

Molecular structure of collagen (© 2000 Griffiths et al.)

Figure 4.3 Collagen fibrils at right have a characteristic banding pattern, reflecting the regularly staggered packing of the individual collagen molecules in the fibril.

(d) **Denaturation**

A protein's specific 3-dimensional conformation determines its biological function which may involve recognising and binding to other molecules.

Denaturation is the **loss of the specific 3-dimensional conformation of a protein molecule**. This involves the **breakage of bonds** maintaining protein structure, resulting in the protein **losing its biological function**. Depending on the degree of denaturation, the molecule may partially or completely lose it biological activity.

The change may be temporary or permanent. In the case of temporary denaturation (reversible denaturation), removal of the mildly denaturing conditions will result in spontaneous and correct refolding of the polypeptide chain to regain its normal tertiary structure and the protein is still functional.

What does this show? (Check out "The Anfinsen Experiment in Protein Folding")

The information for building specific shape is in the protein's primary structure. The sequence of amino acids contains all the information necessary to determine the protein's shape (tertiary structure) e.g. where an α -helix can form, where β -pleated sheets can exist, where disulphide bridges are located, where ionic bonds can form, and so on.

In all forms of denaturation, only protein conformation is lost and the amino acid sequence remains unaffected.

The factors causing denaturation are:

(i) Temperature

- High temperature <u>increases kinetic energy</u> and causes atoms in proteins to vibrate.
- Therefore, <u>disrupting weak hydrophobic interactions</u>, <u>hydrogen bonds and</u> <u>ionic bonds</u>.
- E.g. soluble and transparent egg albumin (egg white) becomes insoluble and coagulates upon heating.
- (ii) **pH** (strong acids or alkalis)
 - A drastic change in pH affects <u>charged R-groups</u> and <u>disrupts ionic bonds</u> <u>and hydrogen bonds of proteins</u>.
 - If the medium is too acidic (sudden increase of H⁺ ions), the acidic R-group COO⁻ will accept H⁺ ions to form COOH.
 - If the medium is too basic (sudden decrease of H⁺ ions), the basic R-group NH₃⁺ will donate H⁺ ions to form NH₂.
 - If either COOH or NH₂ are no longer charged, ionic bonds will be disrupted.
 - Presence of very high concentration of H⁺ may even cause peptide bonds to be broken (acid hydrolysis).

(iii) Heavy metals

- <u>Heavy metals</u> are <u>positively charged</u> and form strong bonds with negativelycharged carboxyl R-groups of proteins, disrupting <u>ionic bonds</u>.
- With less negative charges on the protein, the <u>solubility</u> of protein is <u>reduced</u>, as there is less interaction with polar water molecules.

(iv) Reducing / oxidising agents

• Reducing / oxidising agents disrupt disulfide bonds formed between cysteine, thus causing proteins to lose their 3-dimensional conformation.

(v) Organic solvents (e.g. alcohol) and detergents

- Organic solvents and detergents disrupt <u>hydrogen bonding</u> and <u>hydrophobic</u> <u>interactions</u> of proteins, respectively.
- For example, alcohol is used as a disinfectant to denature the proteins of any bacteria.

Denaturation is the loss of protein function from structural change or chemical reaction. At what level of protein structure and which chemical bonds does each of the following denaturation agents act on?

a. heat - hydrogen bonds (secondary and tertiary structure), , hydrophobic interactions, ionic bonds (tertiary structure)

b. strong acid - hydrogen bonds (secondary and tertiary structure) and ionic

bonds (tertiary structure)

- c. heavy metal ionic bonds (tertiary structure)
- d. organic solvent hydrophobic interactions (tertiary structure)

In general, what types of bonds are disrupted during denaturation of a protein? Is there any particular order?

Weak hydrogen bonds and hydrophobic interactions, followed by ionic bonds. Lastly disulfide bonds (covalent bonds).

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Anfinsen's Experiment

(Read more at: http://www.mhhe.com/biosci/genbio/raven6b/graphics/raven06b/howscientiststhink/01-lab.pdf)

The hypothesis that "protein amino acid sequence determines the final shape a protein assumes in a water solution" was proven to be correct when Christian B. Anfinsen showed that if the enzyme ribonuclease was opened out into a linear chain and then allowed to reform, it reassumed the correct catalytic shape. This experiment is a critical one in the understanding of the nature of gene expression, because it establishes the ultimate translation of the genetic information into functional difference. It is in determining the shape of proteins that genes express the information necessary to carry out and govern metabolism.

Guiding questions for article:

- Why did he choose to study Ribonuclease? How does it help in proving the hypothesis?
- What is the role of (a) b-mercaptoethanol (b) urea?
- What happens when both (a) and (b) were added? Why must both be added?
- What happens when both (a) and (b) were removed? What does this show?
- What happens when (a) was removed, but (b) added? Why? What does this show?
- Why is it that "only one combination corresponds to a ribonuclease protein that is active"?

(Follow up reading on how an error in protein conformation can lead to disease – http://www.nature.com/scitable/topicpage/protein-misfolding-and-degenerativediseases-14434929)

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How Do Proteins Arrive at Their Final Shapes? http://www.nature.com/scitable/topicpage/protein-structure-14122136

In theory, once their constituent amino acids are strung together, proteins attain their final shapes without any energy input. In reality, however, the cytoplasm is a crowded place, filled with many other macromolecules capable of interacting with a partially folded protein. Inappropriate associations with nearby proteins can interfere with proper folding and cause large aggregates of proteins to form in cells. Cells therefore rely on so-called **chaperone proteins** to prevent these inappropriate associations with unintended folding partners.

Chaperone proteins surround a protein during the folding process, sequestering the protein until folding is complete. For example, in bacteria, multiple molecules of the chaperone GroEL form a hollow chamber around proteins that are in the process of folding. Molecules of a second chaperone, GroES, then form a lid over the chamber. Eukaryotes use different families of chaperone proteins, although they function in similar ways.

Chaperone proteins are abundant in cells. These chaperones use energy from ATP to bind and release polypeptides as they go through the folding process. Chaperones also assist in the refolding of proteins in cells. Folded proteins are actually fragile structures, which can easily denature, or unfold. Although many thousands of bonds hold proteins together, most of the bonds are noncovalent and fairly weak. Even under normal circumstances, a portion of all cellular proteins are unfolded. Increasing body temperature by only a few degrees can significantly increase the rate of unfolding. When this happens, repairing existing proteins using chaperones is much more efficient than synthesizing new ones. Interestingly, cells synthesize additional chaperone proteins in response to "heat shock."

Structures, Properties and Functions of Biomolecules

1. Carbohydrates

Feature	Starch	Glycogen	Cellulose
Monomer	<u>α-glucose</u>	<u>α-glucose</u>	<u>β-glucose</u>
Bonds between monomers	amylose: <u>α-1,4-glycosidic bonds</u> amylopectin: <u>α-1,4-glycosidic bonds</u> and <u>α-1,6-glycosidic bond</u> at branch point	α -1,4-glycosidic bonds and α -1,6-glycosidic bond at branch point	<u>β-1,4-glycosidic bonds</u>
Orientation of monomer	Adjacent glucose monomers are in the same orientation (No rotation)	Adjacent glucose monomers are in the same orientation (No rotation)	Adjacent glucose monomers are rotated 180° with respect to each other
Overall structure	Amylose: <u>Unbranched chain</u> polymer which coils into a <u>helical</u> , compact structure Amylopectin: <u>Branched</u> chain polymer which coils into a <u>helical</u> , compact structure	Branched chain polymer which coils into a <u>helical</u> , compact structure (<u>More extensive branching</u> as compared to amylopectin)	$\frac{\text{Unbranched}}{\text{Straight chains of }\beta \text{ glucose run}}$ $\frac{\text{Straight chains of }\beta \text{ glucose run}}{\text{parallel to each other}}$ Cellulose chains associate in groups to bundle into <u>microfibrils</u> and then <u>macrofibrils</u> .
Bonds that hold overall structure	Hydrogen bonds between hydroxyl (-OH) group of adjacent glucose residue	Hydrogen bonds between hydroxyl (-OH) group of adjacent glucose residue	Intra-chain <u>hydrogen bonds</u> between adjacent molecules. Inter-chain <u>hydrogen bonds</u> between parallel chains.
Properties	Large Compact Insoluble (exert no osmotic effect on cells) Easily hydrolysed	Large Compact Insoluble (exert no osmotic effect on cells) Easily hydrolysed	Rigid High tensile strength Insoluble Large intermolecular spaces between macrofibrils cause the cell wall to be permeable
Function	Energy storage in plant cells in the form of starch grains in chloroplasts.	Energy storage in animal cells in the form of glycogen granules in liver and muscle cells.	Structural support and mechanical strength in plant cell wall.

2. Lipids

Feature	Triglyceride	Phospholipid	Cholesterol
Components	<u>3 fatty acids</u> <u>1 glycerol molecule</u>	2 fatty acids 1 glycerol molecule 1 phosphate group Nitrogen-containing base, choline	Carbon skeleton consisting of four fused carbon rings
Bonds between components	<u>3 Ester bonds</u> (Each –OH group in glycerol molecule reacts with –COOH in fatty acid molecule)	Two ester bonds(Two –OH groups in glycerol reacts with –COOH in fatty acid)One phosphoester bond(One –OH groups of glycerol reacts with phosphoric acid)	-
	Formed by condensation reaction	Formed by condensation reaction	
Properties	Large Non-polar Insoluble in water (exert no osmotic effect on cells) Soluble in organic solvents More compact (than carbohydrates) Low density as it is unhydrated (Less dense than carbohydrates)	Amphipathic <u>Hydrophilic phosphate</u> and <u>2 hydrophobic fatty acid chains</u>	Non-polar Insoluble in water Soluble in organic solvents
Function	Energy storage Heat insulation Protection Buoyancy	Basic structure of cell membrane by forming phospholipid bilayer Association with oligosaccharides to form glycolipids which help in <u>cell-cell</u> <u>recognition</u> and <u>cell-cell adhesion</u> .	Component of cell membrane <u>Regulates membrane fluidity</u> , <u>Maintains mechanical stability</u> , <u>Prevent leakage of small polar</u> <u>molecules</u> , Precursor for synthesis of steroid hormones.

3. Proteins

Feature	Haemoglobin	Collagen	
Function	Involved in metabolic reaction i.e. Transport oxygen in blood	Structural and supportive function in skin, bone	
Number of polypeptide chains	 <u>4</u> polypeptide chains: 2 identical α-chains and 2 identical β-chains 	<u>3</u> polypeptide chains	
	Primary structure		
Number & Sequence	2 identical α -chains of 141 amino acids. 2 identical β -chains of 146 amino acids. Each chain with a specific sequence of amino acids	Each polypeptide chain has 1050 amino acids. Each chain has a repeated triplet sequence of Gly-X-Y, where X is often proline, and Y is often hydroxyproline.	
Bonds between monomers	Peptide bonds between amino acids	Peptide bonds between amino acids	
Variety of amino acids	Large variety of amino acids present	Mainly 3 amino acids. Each polypeptide chain has a high proportion of glycine, proline and hydroxyproline.	
	Secondary structure		
Structure & Bonds	Coiling of polypeptide chain to form α -helices held by hydrogen bonds between peptide bonds	Left-handed <u>helix</u> (FYI) held by <u>hydrogen bonds</u>	
Tertiary structure			
Structure & Bonds	Further folding secondary structure (α -helices) to form compact spherical shape held by <u>hydrogen bonds, ionic bonds and</u> <u>hydrophobic interactions</u> between R-groups of a <u>single</u> polypeptide chain	No tertiary structure	
Quaternary structure			
Structure & Bonds	Four subunits held by hydrogen bonds, ionic bonds and hydrophobic interactions between R-groups	<u>Three</u> helical chains held by <u>hydrogen bonds</u> to form <u>triple</u> <u>helix</u> / <u>tropocollagen</u>	
Arrangement of amino acids	The hydrophobic amino acids in the interior of the protein and hydrophilic amino acids found at the exterior surface.	Hydrophobic amino acids are found at the exterior surface of collagen.	

Feature	Haemoglobin	Collagen
Overall structure	<u>Globular</u> protein Four subunits, each fold into a compact spherical shape.	Fibrousprotein3 unbranched polypeptide chains wound around each other to form a triple helix / tropocollagen.Many triple helicesIie parallelin a staggered patternto formfibrilswithcovalent bondsbetween neighbouring chains.Fibrils unite to form
Properties	Soluble Able to bind reversibly to oxygen Cooperative binding of oxygen to haemoglobin Compact	Insoluble High tensile strength Rigid Compact