7.1 Biomolecule structure: bonds, polarity and function

Name: _____ Class: _____ Date: _____ **Total: 10 marks**

KEY WORDS peptide bond • hydrolysis

Objective

Biomolecule structure: bonds, polarity and function. Original classroom practice for IB SL; not an official IB paper.

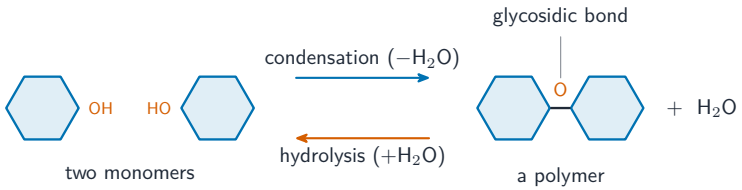
1 Key knowledge and worked examples

■ What would explain this observation?

- Starch, a triglyceride and a protein can all contain carbon, hydrogen and oxygen, yet their structures and functions differ. An element list alone does not identify a biomolecule.

■ Build the model

- Carbohydrates include monosaccharides and polymers joined by glycosidic bonds.
- A triglyceride has glycerol joined to three fatty acids by ester bonds.
- Proteins contain amino-acid residues joined by **peptide bonds** ; side chains and folding contribute to their properties.
- These structures support storage, membrane or functional roles depending on the molecule.
- peptide bond: A covalent linkage between amino-acid residues.
- **hydrolysis** : Breaking a linkage using water.



■ Choose evidence that can test it

- Condensation forms a linkage with a small molecule such as water released in the simplified model; hydrolysis uses water to break such a linkage.
- Polymer sequence, branching, polarity and three-dimensional shape matter.
- Saturated fatty acids have no carbon-carbon double bond, while unsaturated fatty acids have at least one; this difference can influence packing under stated conditions.

In the lab: Use labelled molecular models and identify the actual linkage rather than memorizing shapes alone. Compare an attributed structure with the proposed function, mark polar and non-polar regions where justified, and distinguish a monomer from a residue within a polymer. Food tests provide evidence of chemical groups under specific conditions, not complete molecular structures.

■ Work from known quantities

- Known: a single unbranched peptide formed from 20 amino acids contains 19 peptide linkages.
- In a simplified condensation accounting model, forming these links releases 19 water molecules.
- A triglyceride formed from one glycerol and three fatty acids has three ester linkages and releases three waters in the corresponding model.
- These are linkage counts, not complete pathways in living cells.

Your turn: A single unbranched peptide contains 35 amino-acid residues. How many peptide bonds join them?

■ Check the conclusion and its limits

- Not every protein is an enzyme, and not every catalyst is a protein.
- Lipids are not all polymers of repeating monomers.
- A protein can lose function when its folding changes without every peptide bond being broken.

Not true: Every protein is an enzyme and every lipid is a repeating-monomer polymer. Enzymes are one functional class of protein; structural and transport proteins are not enzymes. And lipids such as triglycerides are built from unlike parts, not repeating monomers, so they are not polymers.

Key:

- Carbohydrates include monosaccharides and polymers joined by glycosidic bonds.
- Condensation forms a linkage with a small molecule such as water released in the simplified model; hydrolysis uses water to break such a linkage.
- Watch for: not every protein is an enzyme, and not every catalyst is a protein.

Write from 21 peptide bonds

- A single unbranched peptide contains 22 amino-acid residues.
- Find the number of peptide bonds. Not every protein is an enzyme.

2 Practice

2.1 What distinguishes a triglyceride in this model? Choose one answer.

- **A** A chain consisting only of peptide bonds
- **B** Glycerol with three fatty acids joined by ester bonds
- **C** A DNA sequence with thymine [1]

2.2 A single unbranched peptide contains 35 amino-acid residues. How many peptide bonds join them? Show the relation, substitution and units. [2]

2.3 Decide whether this claim is true and justify: Enzymes are one functional class of protein; structural and transport proteins are not enzymes. [2]

2.4 A covalent linkage between amino-acid residues: write the technical term. [1]

3 Exam-style questions

3.1 Two separate linear peptides each contain 10 residues. How many peptide bonds exist before and after joining them end to end by one peptide linkage? State the model boundary. [4]