

10.1 Biomolecule structure: bonds, polarity and function

Name: _____ Class: _____ Date: _____

Total: 10 marks

KEY WORDS peptide bond • hydrolysis

Objective

Biomolecule structure: bonds, polarity and function. Supported HL concept preparation; original classroom practice, not an official IB paper or assessed learner work.

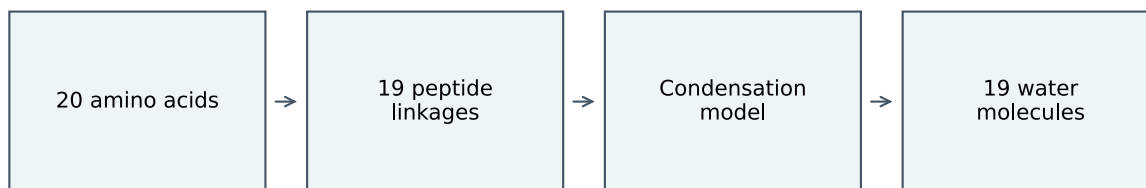
1 Key knowledge and worked examples

■ 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.
 - Start with a prediction. State the quantities or features you would compare, then decide what evidence could distinguish two explanations.
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■ 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.
- 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

- State the known values and their units. Choose the relation because its assumptions fit this case, then rearrange before substitution.
- 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.

Example:

A single unbranched peptide contains 35 amino-acid residues. How many peptide bonds join them? Use the same sequence: known quantities → model → relation → substitution → unit and interpretation.

■ 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.
- Return to the original observation. Explain what the result supports, which conditions it assumes, and one way to test a competing explanation.

Warn:

Every protein is an enzyme and every lipid is a repeating-monomer polymer. This claim is false: 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.

Key:

Biomolecule structure: bonds, polarity and function: 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.

2 Practice

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

- **A** Glycerol with three fatty acids joined by ester bonds
- **B** A chain consisting only of peptide 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: Every protein is an enzyme and every lipid is a repeating-monomer polymer.

[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]

Solutions

2.1 A 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.

2.2 An unbranched chain of n residues has $n-1$ links: $35-1=34$ peptide bonds.

2.3 False. 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.

2.4 peptide bond. peptide bond means A covalent linkage between amino-acid residues.

3.1 Initially $2 \times 9 = 18$; the 20-residue chain has 19. One new bond forms. This is linkage accounting, not a complete biosynthetic pathway.