B.1.2 · Proteins · supported focus

International Baccalaureate · IB Diploma · Biology · SL

Scope and prerequisites

Supported SL core focus. First assessment 2025; current subject brief acquired; full Biology guide not acquired. Remaining guide, assessment and practical requirements retain their recorded holds.

Prerequisites: amino-acid structure and condensation reactions from B.1.1 (carbohydrates and lipids), and microscopy units from B.1. Each lesson develops its own method before independent transfer.

These are original or explicitly fictional teaching examples, not actual measurements or completed assessed learner investigations.

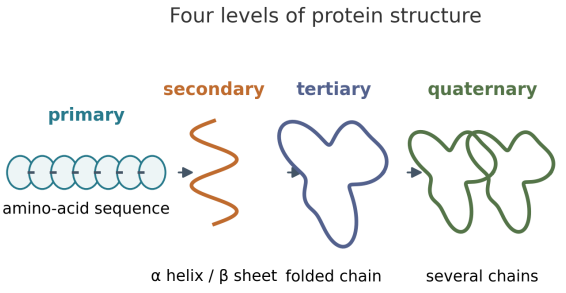
Proteins

■ What would explain this observation?

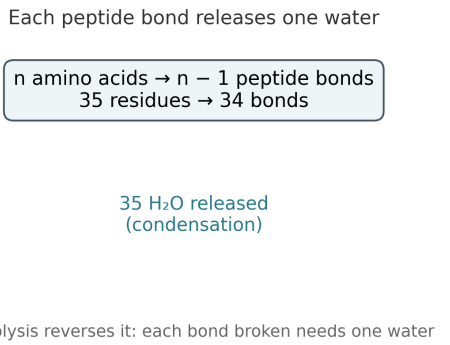
- An egg white turns from clear runny liquid to firm white solid when heated – and cooling never turns it back. What happened to its proteins?
- Start with a prediction. State the quantities or features you would compare, then decide what evidence could distinguish two explanations.

■ Build the model

- Proteins are chains of amino acids joined by **peptide bonds** in condensation reactions; each bond forms with the loss of one water molecule. The chain order is the **primary structure**, which folds into local helices and sheets (secondary), then into a working three-dimensional shape (tertiary), sometimes with several chains together (quaternary).
- The twenty R groups differ in charge and polarity, so the sequence decides the fold. Heating or extreme pH breaks the weak bonds holding the fold – **denaturation** – while the peptide bonds survive; the protein unravels and loses its function, which is why the egg does not run again on cooling.
- peptide bond: The covalent link between two amino acids, formed with the loss of water; primary structure: The sequence of amino acids in a protein chain; denaturation: The loss of a protein's working shape when its weak structure bonds break.



Each level follows from the one before; the sequence decides the fold



Hydrolysis reverses it: each bond broken needs one water

■ Choose evidence that can test it

- The Biuret test identifies peptide bonds: it turns from blue to purple with protein but not with free amino acids. Use it to check whether a sample contains peptide linkages.
- Compare an enzyme's activity before and after heating, keeping substrate and pH constant: a lasting loss of activity after cooling supports permanent denaturation, not just a reversible pause.

■ 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 peptide chain contains 35 amino-acid residues joined in one unbranched chain. Each link between two neighbours is one peptide bond, so bonds = residues $- 1 = 35 - 1 = 34$. Each bond formed by condensation releases one water molecule, so 34 water molecules were released when this chain formed.

Example:

A different chain contains 120 amino-acid residues. Find the number of peptide bonds and the number of water molecules released during its formation, using the same sequence: known quantities → model → relation → substitution → unit and interpretation. (Answer: bonds $= 120 - 1 = 119$; waters released $= 119$. Hydrolysis back to single amino acids would need 119 water molecules.)

■ Check the conclusion and its limits

- The bond count assumes a single unbranched chain; real proteins may be branched or cross-linked by disulfide bridges, which are not peptide bonds. Denaturation is usually irreversible in food but some small proteins can refold under careful laboratory conditions.

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

Warn:

Heating denatures a protein by breaking its peptide bonds. This claim is false: denaturation breaks the weaker hydrogen bonds and interactions that hold the fold; the peptide bonds of the primary structure survive, which is why the amino-acid sequence is unchanged in a cooked egg.

Key:

Proteins: amino acids join by peptide bonds through condensation, releasing one water per bond (n residues $\rightarrow$ n$-$1 bonds). The sequence folds through secondary and tertiary structure into the working shape; denaturation destroys the fold, not the chain.