IB / A-Level Biology

B1.2 PROTEINS

Exam-focused preparation notes

Guiding questions

- What is the relationship between amino acid sequence and the diversity in form and function of proteins?
- How are protein molecules affected by their chemical and physical environments?

Revision focus	What you must be able to do
Draw	Generalized amino acid; condensation reaction; dipeptide; labelled section of a polypeptide.
Explain	How primary structure determines shape and function; why pH and temperature can denature proteins.
Compare	Fibrous vs globular proteins; non-conjugated vs conjugated proteins; essential vs non-essential amino acids.
HL	How R-groups control folding, secondary/tertiary/quaternary structure, and solubility.

Core storyline of the topic

- DNA determines the amino acid sequence of a polypeptide.
- The sequence of amino acids determines which bonds and interactions form.
- Those interactions determine the final 3D shape.
- The final shape determines function.
- Change the environment too much and the shape, and therefore function, may change.

1. Amino acids: the monomers of proteins

B1.2.1 and B1.2.2

Proteins are polymers built from 20 naturally occurring amino acids. Every amino acid has the same core structure but a different R-group. The side chain is what gives each amino acid its chemical identity.

Exam definitions

- Amino acid: monomer of proteins containing an amine group, a carboxyl group, a hydrogen atom and a variable R-group attached to a central alpha carbon.
- Variable group / side chain: the part that differs between amino acids and influences solubility, charge and folding.
- Amino acids are amphoteric: in aqueous solution they can act as both acids and bases.

How to draw the generalized amino acid from memory

1. Draw the central alpha carbon with four bonds.

2. Add an amine group (-NH2) and a carboxyl group (-COOH).

3. Add a hydrogen atom.

4. Put R on the remaining bond.

High-yield recall: every amino acid has the same backbone; only the R-group changes.

2. Condensation reactions and peptide bonds

B1.2.2

Amino acids join by condensation reactions. A hydroxyl group from the carboxyl end of one amino acid and a hydrogen from the amine end of another combine to form water. The remaining atoms form a peptide bond.

Must know

- Word equation: amino acid + amino acid -> dipeptide + water
- A polypeptide containing n amino acids has n - 1 peptide bonds.
- A polypeptide has one free amino end and one free carboxyl end.

Fast calculation rule

- 2 amino acids -> 1 peptide bond
- 42 amino acids -> 41 peptide bonds
- 166 amino acids -> 165 peptide bonds

3. Dietary amino acids and essential amino acids

B1.2.3

Humans can synthesize 11 amino acids, but 9 essential amino acids must be obtained from food. A balanced diet supplies the full amino acid set needed for protein synthesis.

Term	Meaning
Essential amino acids	Cannot be synthesized by the body and must be obtained from the diet.
Non-essential amino acids	Can be synthesized from other amino acids or metabolic intermediates.
Diet point	Vegan or restricted diets require planning so that all essential amino acids are included.

- You do not need to memorize the names of essential amino acids for this topic.
- Exam link: a varied diet is important because protein synthesis depends on amino acid availability.

4. Why proteins are so diverse

B1.2.4

Protein diversity comes from three main sources: there are 20 amino acids, chains can be any practical length from a few residues to thousands, and amino acids can occur in any order. DNA determines both the number and sequence of amino acids in a protein.

Examples you should recognize

Protein	Typical function
Haemoglobin	Oxygen transport in red blood cells.
Keratin	Structural support in hair, nails, claws and hooves.
Lipase	Digestive enzyme that hydrolyses lipids.
Collagen	Strength and elasticity in connective tissues.
Histones	DNA packaging in chromatin and chromosomes.
Insulin	Hormone involved in blood glucose regulation.

Exam explanation frame

- Different amino acid sequences produce different bonding patterns.
- Different bonding patterns produce different shapes.
- Different shapes allow different biological functions.

5. Effect of temperature and pH on protein structure

B1.2.5

Protein function depends on precise 3D structure. Heat and non-optimal pH can disrupt the bonds that maintain that structure, especially hydrogen bonds. The result is denaturation: loss of normal shape and therefore loss of function.

Key term

- Denaturation: change in protein shape caused by disruption of the interactions that maintain structure, leading to loss of function.

What examiners want in explanations

- Higher temperature increases molecular motion, placing stress on weak bonds such as hydrogen bonds.
- Extreme pH changes charge distribution, so normal hydrogen and ionic bonding cannot be maintained.

- If only weak interactions are disrupted, renaturation may occur when conditions return to normal.
- If peptide bonds or other covalent bonds are broken, the protein usually cannot regain its original shape.

Typical exam wording

- At slightly above optimum temperature the active site changes shape, so substrate binding decreases and enzyme activity falls.
- At very high temperature or extreme pH, denaturation may become irreversible.

HL Extension - how protein chemistry creates structure

B1.2.6 to B1.2.12

HL big picture

- R-groups determine whether amino acids are hydrophobic, hydrophilic, acidic or basic.
- Those properties control how a polypeptide folds in water.
- Folding produces secondary, tertiary and sometimes quaternary structure.

6. R-groups provide chemical diversity

B1.2.6

The R-group is the part of an amino acid that varies. It determines whether the side chain is non-polar, polar, acidic or basic. This chemical diversity is the basis of protein diversity.

Category	What it means for the protein
Non-polar	Hydrophobic side chains tend to cluster away from water, often in the interior of globular proteins.
Polar	Hydrophilic side chains interact readily with water and are often found on the outside of soluble proteins.
Acidic	Can carry negative charge and take part in ionic bonding.
Basic	Can carry positive charge and take part in ionic bonding.

HL recall: amino acids are grouped as non-polar, polar, negatively charged, or positively charged because of their R-groups.

7. Primary structure

B1.2.7

Primary structure is the sequence of amino acids in a polypeptide. DNA determines this sequence. Because each gene has a precise nucleotide sequence, it produces a predictable amino acid order every time the protein is synthesized.

- Primary structure = the order of amino acids only.
- A change in sequence can change bonding patterns, folding and function.
- This is why a mutation in DNA can alter a protein and produce a phenotypic effect.

8-11. Secondary, tertiary and quaternary structure

B1.2.8 to B1.2.11

Level	Features to mention in answers
Secondary	Regular local folding into alpha helices and beta-pleated sheets, stabilized by hydrogen bonds between non-adjacent residues in the backbone.
Tertiary	Overall 3D folding of one polypeptide caused by hydrogen bonds, ionic bonds, disulfide bonds and hydrophobic interactions.
Quaternary	Association of two or more polypeptide chains into one functional protein; may be conjugated if non-protein groups are present.

For tertiary structure, know these four forces

- Hydrogen bonds between polar groups.
- Ionic bonds between oppositely charged R-groups.
- Disulfide bonds between two cysteine residues. These are covalent and especially strong.
- Hydrophobic interactions that push non-polar side chains into the protein core.

Named protein examples

- Insulin: non-conjugated protein; active hormone is based on two polypeptide chains linked by disulfide bonds.
- Collagen: non-conjugated fibrous protein made of three polypeptide chains wound together.
- Haemoglobin: conjugated quaternary protein with four polypeptides and four haem groups containing Fe^{2+}.

12. Solubility, fibrous proteins and globular proteins

B1.2.10 and B1.2.12

Protein shape is tied to biological role. Fibrous proteins are elongated and usually structural. Globular proteins are compact and often carry out specific dynamic functions such as catalysis, signalling or transport.

Feature	Fibrous protein	Globular protein
Shape	Long, narrow, repetitive	Compact, folded, roughly spherical
Solubility	Often insoluble	Often soluble in water

Function	Structural / support / movement	Enzymes, hormones, transport, antibodies, receptors
Example	Collagen	Insulin

Link between polarity and location

- Soluble globular proteins usually have hydrophobic amino acids in the core and hydrophilic amino acids on the outside.
- Integral membrane proteins require hydrophobic regions so that part of the protein can embed in the phospholipid bilayer.
- Lipase illustrates both needs: a hydrophobic interior region can interact with lipids, while a hydrophilic exterior keeps the enzyme soluble in the aqueous intestine.

13. Worked comparison: insulin, collagen and haemoglobin

High-yield named examples

Protein	What to say in an exam answer
Insulin	Globular, non-conjugated protein hormone. Two polypeptide chains joined by disulfide bonds. Specific shape allows binding to insulin receptors.
Collagen	Fibrous, non-conjugated quaternary protein. Three chains form a strong triple helix suited to tensile strength in connective tissue.
Haemoglobin	Globular, conjugated quaternary protein. Four polypeptides plus haem groups. Reversibly binds oxygen using Fe2+ in each haem group.

14. Exam toolkit and memory sheet

Use this page for last-minute revision

Definitions you should be able to state exactly

- Peptide bond: covalent bond formed between amino acids during a condensation reaction.
- Primary structure: the sequence of amino acids in a polypeptide.
- Secondary structure: alpha helix or beta-pleated sheet formed by hydrogen bonding in regular positions.
- Tertiary structure: overall 3D folding of one polypeptide caused by interactions between side chains.
- Quaternary structure: association of two or more polypeptide chains in one protein.

- Denaturation: loss of normal protein shape and function due to heat or unsuitable pH.

Common exam traps

- Do not say denaturation breaks peptide bonds unless conditions are extreme enough to damage covalent bonds.
- Do not confuse peptide bonds (between amino acids) with hydrogen bonds (important in folding).
- Primary structure is not shape; it is sequence.
- Haemoglobin is conjugated because it includes haem, which is not made of amino acids.
- Collagen and insulin are non-conjugated because they are made only of amino acids.

Command-word starters

- State: give the key fact only.
- Outline: give a brief account, usually 2-4 linked points.
- Explain: link cause to effect, for example heat -> bond disruption -> altered shape -> lost function.
- Distinguish: give both sides of the comparison.

10-second memory chain

DNA -> amino acid sequence -> bonding pattern -> 3D shape -> function

Quick-check questions

1. How many peptide bonds are in a polypeptide of 166 amino acids?
2. Why can high temperature reduce enzyme activity?
3. What is the difference between essential and non-essential amino acids?
4. Why are hydrophobic side chains often buried inside a globular protein?
5. What feature makes haemoglobin a conjugated protein?

One-paragraph summary

- Proteins are built from amino acids joined by peptide bonds. DNA determines the amino acid sequence. Side-chain interactions produce 3D shape, and shape determines function. Heat and pH can disrupt bonding and denature the protein.