

Nucleic acids · supported focus

International Baccalaureate · IB Diploma · Biology · HL

Scope and prerequisites

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

Prerequisites: read the stated quantities and units, use arithmetic and the model conditions below. 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.

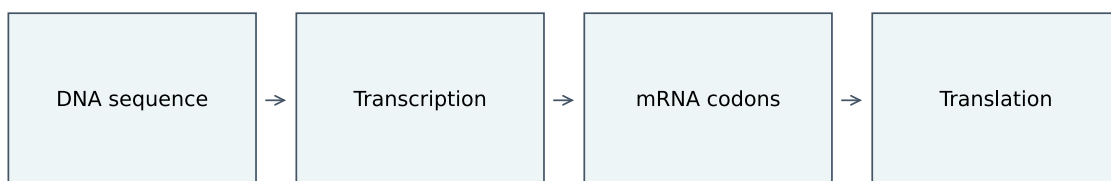
DNA, protein synthesis and evidence

■ What would explain this observation?

- A change in DNA can affect a protein, but not every DNA change changes the amino-acid sequence. The effect depends on the sequence and how it is used.
 - 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

- DNA stores information in a base sequence. Complementary base pairing supports copying. During gene expression, **transcription** makes RNA and **translation** uses codons to assemble an amino-acid sequence.
- transcription: Formation of RNA using a DNA template; translation: Formation of a polypeptide using an mRNA sequence.



■ Choose evidence that can test it

- A codon comprises three bases. The genetic code is degenerate: more than one codon can specify the same amino acid. A substitution can therefore be silent, while insertions or deletions can shift the reading frame.
 - Keep DNA template, coding DNA and mRNA distinct. State the strand used and write sequences in the required direction. Use a codon table for mRNA, not an unexplained DNA triplet.
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■ 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: an mRNA coding region contains 90 bases, including one stop codon. $\text{Codons} = \text{bases}/3 = 90/3 = 30$. A stop codon does not encode an amino acid, so the peptide contains 29 amino acids under this stated model.

Example:

A coding mRNA segment has 63 bases including a stop codon. Find peptide length. Use the same sequence: known quantities $\rightarrow$ model $\rightarrow$ relation $\rightarrow$ substitution $\rightarrow$ unit and interpretation.

■ Check the conclusion and its limits

- The number of bases is not automatically the number of amino acids. Real genes include regulatory regions and, in eukaryotes, often introns; a whole gene length is not a peptide-length calculation.
- Return to the original observation. Explain what the result supports, which conditions it assumes, and one way to test a competing explanation.

Warn:

Each DNA base encodes one complete amino acid. This claim is false: The number of bases is not automatically the number of amino acids. Real genes include regulatory regions and, in eukaryotes, often introns; a whole gene length is not a peptide-length calculation.

Key:

DNA, protein synthesis and evidence: A codon comprises three bases. The genetic code is degenerate: more than one codon can specify the same amino acid. A substitution can therefore be silent, while insertions or deletions can shift the reading frame.