

2.1 DNA, protein synthesis and evidence

Name: _____ Class: _____ Date: _____

Total: 10 marks

KEY WORDS transcription • translation

Objective

DNA, protein synthesis and evidence. Supported HL concept preparation; original classroom practice, not an official IB paper or assessed learner work.

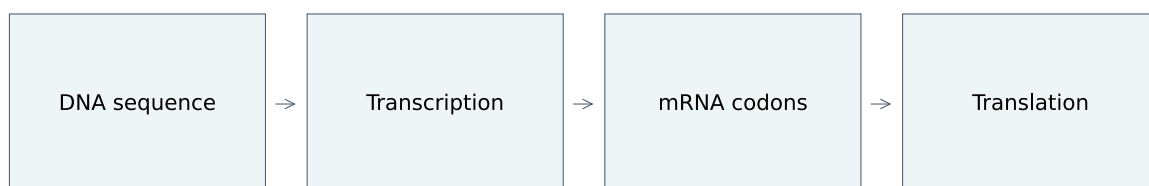
1 Key knowledge and worked examples

■ What would explain this observation?

- 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.

■ 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. 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.

2 Practice

2.1 Which change can leave the amino-acid sequence unchanged? Choose one answer.

- **A** A substitution producing a synonymous codon
- **B** Every deletion of one base
- **C** Every insertion of one base

[1]

2.2 A coding mRNA segment has 63 bases including a stop codon. Find peptide length. Show the relation, substitution and units.

[2]

2.3 Decide whether this claim is true and justify: Each DNA base encodes one complete amino acid.

[2]

2.4 Formation of RNA using a DNA template: write the technical term.

[1]

3 Exam-style questions

3.1 An mRNA coding region has 126 bases including one stop. A substitution turns codon 11 into a stop. Compare peptide lengths, assuming translation starts at the same codon. [4]

Solutions

2.1 A 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.

2.2 $63/3=21$ codons including one stop. Peptide length= $21-1=20$ amino acids.

2.3 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.

2.4 transcription. transcription means Formation of RNA using a DNA template.

3.1 Original $126/3-1=41$ amino acids. New codon 11 is not translated into an amino acid: 10 residues. The model excludes altered initiation, splicing and readthrough.