

Nucleic acids · supported focus

Supported focus · HL

Supported scope

- 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.
- State model conditions and distinguish fictional data from measurements.

Dna · 1.1

Reasoning

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.

Dna · 2.1

Reasoning

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.

Dna · 3.1

Reasoning

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.

Dna · 4.1

Reasoning

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.

Dna · 4.2

Reasoning

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.

Dna · 5.1

Reasoning

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.

Dna · 5.2

Reasoning

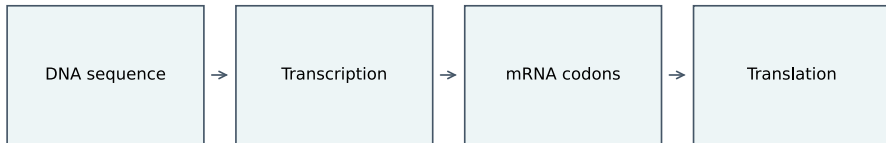
Each DNA base encodes one complete amino acid. This claim is false: The number of bases is not automatically the number of amino acids. Real genes include regulatory regions and, in eukaryotes, often introns; a whole gene length is not a peptide-length calculation.

Dna · 5.3

Reasoning

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.

Dna · diagram



- Original teaching diagram: DNA, protein synthesis and evidence
- Use the labels and the stated model together.

Dna · original transfer

Your turn

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.

Dna · transfer reasoning

Method and interpretation

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.

Check yourself

- Explain transcription using the stated model.
- Explain translation using the stated model.
- Change one value in the original transfer; explain which assumption still matters.