D.1.2 · Protein synthesis · supported focus

International Baccalaureate · IB Diploma · Biology · HL

Scope and prerequisites

Supported HL/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: DNA structure and base pairing from A.1.2, and enzymes 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.

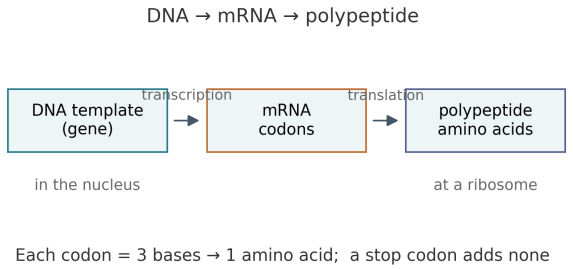
Protein synthesis

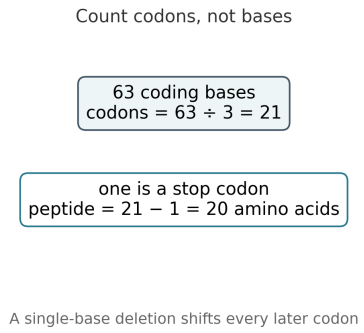
What would explain this observation?

- A gene hundreds of bases long produces a much shorter protein, and a one-base mutation can destroy the whole product. How does the cell read a base sequence into an amino-acid sequence?
- Start with a prediction. State the quantities or features you would compare, then decide what evidence could distinguish two explanations.

Build the model

- In **transcription**, the enzyme RNA polymerase builds an mRNA strand complementary to one DNA template strand. In **translation**, a ribosome reads the mRNA in groups of three bases – **codons** – and joins the matching amino acids into a polypeptide.
- Each codon specifies one amino acid through the genetic code, which is degenerate: several codons can give the same amino acid. A **stop codon** ends the chain and codes for nothing. Because the reading frame runs in threes, inserting or deleting one base shifts every later codon – a frameshift.
- transcription: Copying a gene's DNA sequence into a complementary mRNA; translation: Reading mRNA codons at a ribosome to build a polypeptide; codon: A group of three mRNA bases specifying one amino acid; stop codon: A codon that ends the chain without coding for an amino acid.





Choose evidence that can test it

- The base sequence of a gene predicts the amino-acid sequence of its protein through the code table; compare a known gene and its protein to check. Radioactive-labelling experiments placed amino acids in the order the mRNA specified – evidence for the codon reading, not a guess.
- Mutations that change a codon to a stop codon truncate the protein exactly at that point, which can be checked against the sequence.

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 coding mRNA segment has 63 bases, including one stop codon. Codons = bases / 3 = 63 / 3 = 21. The stop codon codes for no amino acid, so the peptide has 21 − 1 = 20 amino acids.

Example:

A coding segment of 90 bases includes one stop codon. Find the peptide length using the same sequence: known quantities → model → relation → substitution → unit and interpretation. (Answer: codons = 90/3 = 30; peptide = 30 − 1 = 29 amino acids. Bases are not amino acids – divide by three first.)

Check the conclusion and its limits

- This counting model covers the coding sequence only: real genes also carry promoters, untranslated regions and, in eukaryotes, introns that are removed before translation. A gene's total base count is therefore 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 base in the coding sequence codes for one amino acid. This claim is false: amino acids are coded by triplets – three bases per codon – and the stop codon adds none, so a 63-base segment gives 20 amino acids, not 63.

Key:

Protein synthesis: transcription copies the gene into mRNA; translation reads codons in threes at the ribosome. Codons = bases ÷ 3, and the stop codon codes for no amino acid; a one-base insertion or deletion shifts the whole reading frame.