D.1.2 · Protein synthesis

International Baccalaureate · IB Diploma · Biology · HL

Scope and prerequisites

This handout covers selected HL/SL topics for the course first assessed in 2025; it is not the whole syllabus.

Prerequisites: DNA structure and base pairing from A.1.2, and enzymes from B.1.

The examples are original and fictional: they are not real measurements or real student investigations.

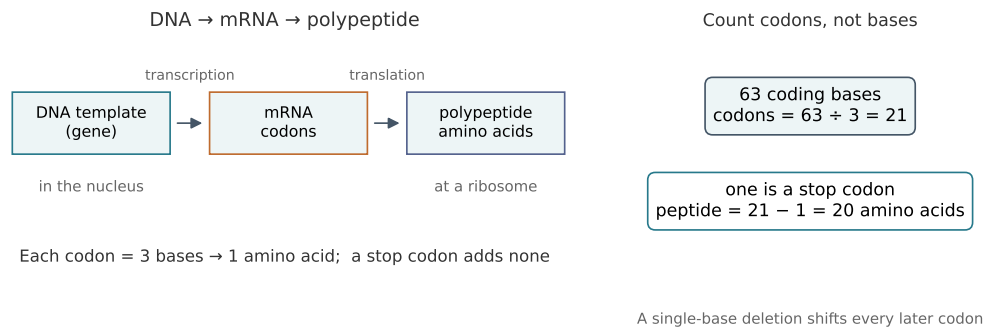
Protein synthesis

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?

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.



Protein synthesis: original worked-case diagram

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

- 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.

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.