

6.2 Protein synthesis

Name: _____ Class: _____ Date: _____

Total: 17 marks

KEY WORDS gene • triplet • mutation • intron • translation

Objective

Build the skills to answer exam questions on **protein synthesis** – the **genetic code**, **transcription** and **translation**, splicing, and **gene mutations**.

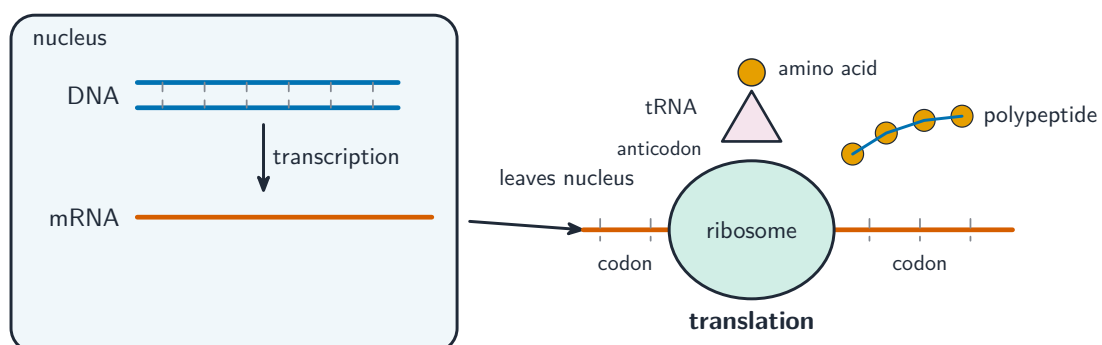
You must be able to:

- describe the universal triplet code and the roles of RNA polymerase, mRNA, codons, tRNA, anticodons and ribosomes
- work out an mRNA sequence and amino acids from a DNA template
- explain splicing (introns/exons) and the effects of substitution, deletion and insertion mutations

1 Key knowledge and worked examples

■ The genetic code and protein synthesis

A **gene** is a DNA sequence coding for one **polypeptide**. The code is read in **triplets** (three bases): each codes one amino acid or a start/stop signal. It is **universal**.



Transcription (nucleus) → mRNA → translation (ribosome) → polypeptide

- **transcription** – RNA polymerase copies the DNA **template strand** into mRNA (uracil pairs with adenine).

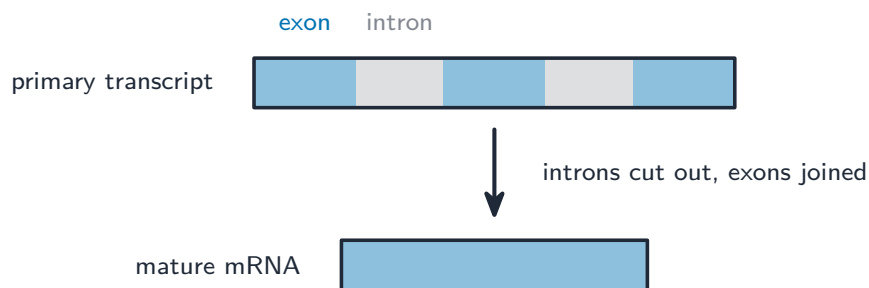
- **translation** – at the **ribosome**, mRNA is read in **codons**; **tRNA** brings amino acids whose **anticodon** pairs with the codon; amino acids join by peptide bonds.

■ Reading the code from a DNA template

To find the amino acids, copy the template into mRNA (A→U, T→A, C→G, G→C), then read the mRNA codons. Example: DNA template TAC → mRNA codon AUG (the start codon, methionine); the tRNA anticodon is UAC.

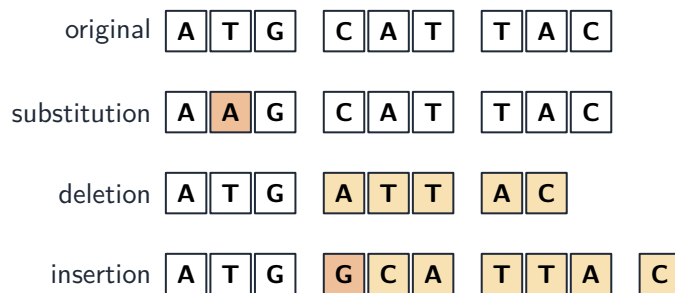
■ Splicing

In eukaryotes the **primary transcript** has coding **exons** and non-coding **introns**. The introns are removed and exons joined to make the finished mRNA.



Splicing removes introns and joins exons

■ Mutations



red = changed base; shaded = shifted by a frameshift (deletion or insertion)

A substitution changes one triplet; a deletion or insertion shifts every later triplet (a frameshift)

- **substitution** – one base swapped; changes at most one amino acid (sometimes none).
- **deletion** / **insertion** – shifts how every later triplet is read (a **frameshift**), usually changing many amino acids.

2 Practice

2.1 Name the molecule that (a) carries the code from the nucleus to the ribosome, and (b) brings amino acids to the ribosome. [2]

2.2 Complete the table for this DNA template strand. [3]

DNA template	mRNA codon	tRNA anticodon
T A C		
C G A		

3 Exam-style questions

3.1 What is a codon? [1]

- ☐ **A** a triplet of DNA bases on the template strand
B a triplet of mRNA bases coding for one amino acid
C a tRNA molecule
D an enzyme that builds mRNA

3.2 Which type of mutation is most likely to change **every** amino acid after the point of mutation? [1]

- ☐ **A** a substitution
B a deletion of one base
C no mutation changes later amino acids
D a substitution at the start codon

3.3 (a) Describe what happens during transcription. [3]

(b) Explain the roles of tRNA and the ribosome during translation. [3]

3.4 (a) Explain why a substitution mutation sometimes has no effect on the polypeptide. [2]

(b) Explain why removing introns is necessary before translation. [2]

Solutions

Each answer shows the steps, then the **result**.

2.1

(a)

- messenger RNA (mRNA)

(b)

- transfer RNA (tRNA)

2.2

- TAC
- mRNA AUG
- anticodon UAC; CGA
- mRNA GCU
- anticodon CGA

3.1 B

- A codon is a triplet of mRNA bases coding for one amino acid (or stop)

3.2 B

- A deletion causes a frameshift, changing every later triplet

3.3

(a)

- RNA polymerase binds and the DNA unwinds at the gene; free RNA nucleotides pair with the template strand (A with U); they are joined into mRNA, which leaves the nucleus

(b)

- each tRNA brings a specific amino acid and its anticodon pairs with the matching mRNA codon; the ribosome moves along the mRNA and joins the amino acids by peptide bonds in order

3.4

(a)

- most amino acids are coded by more than one triplet, so the changed triplet may still code for the same amino acid

(b)

- introns are non-coding; if left in they would be translated into wrong/extra amino acids, giving a faulty polypeptide