

## 6.2 Protein synthesis

Name: \_\_\_\_\_ Class: \_\_\_\_\_ Date: \_\_\_\_\_

Total: 17 marks

**KEY WORDS** mutation 突变 • gene 基因 • triplet 三联体 • intron 内含子 • translation 翻译

### Objective

Build the skills to answer exam questions on **protein synthesis** — the **genetic code** 遗传密码, **transcription** 转录 and **translation** 翻译, splicing, and **gene mutations** 基因突变.

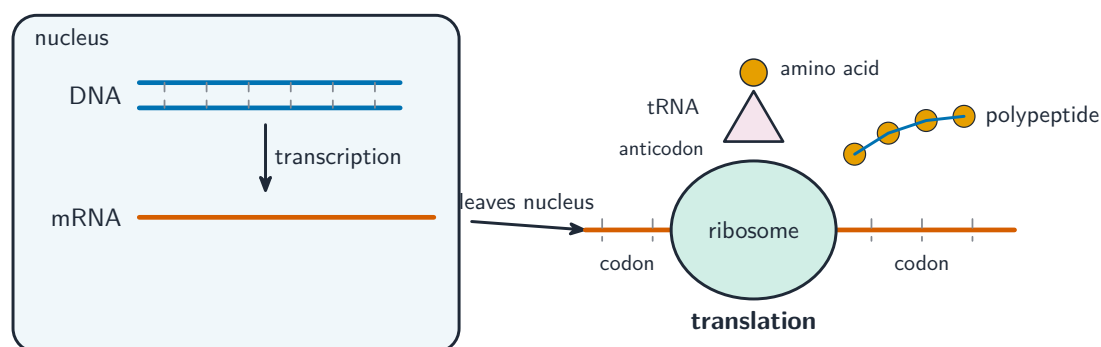
You must be able to:

- 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 Worked examples

#### ■ The genetic code and protein synthesis

A **gene** 基因 is a DNA sequence coding for one **polypeptide** 多肽. The code is read in **triplets** 三联体 (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** 模板链 into mRNA (uracil pairs with adenine).
- **translation** — at the **ribosome** 核糖体, mRNA is read in **codons** 密码子;

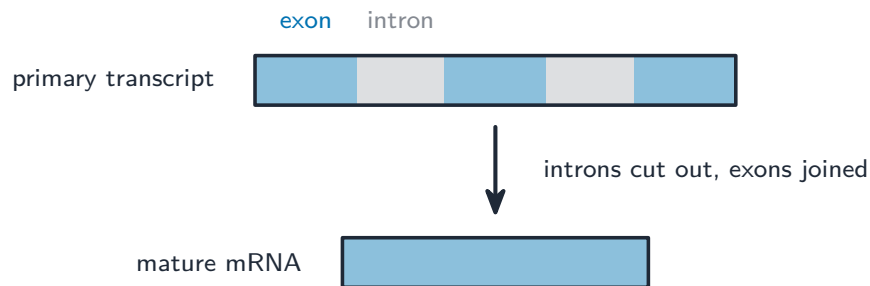
**tRNA** 转运 RNA brings amino acids whose **anticodon** 反密码子 pairs with the codon; amino acids join by peptide bonds.

### ■ 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.

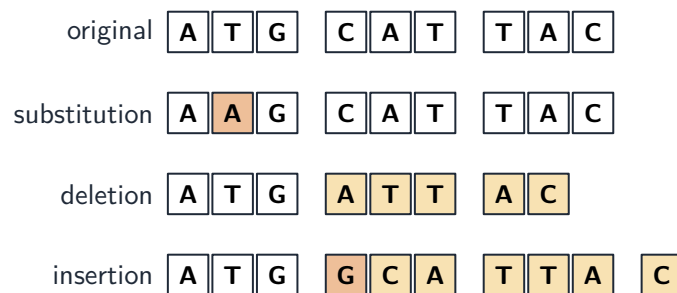
### ■ Splicing

In eukaryotes the **primary transcript** 初级转录本 has coding **exons** 外显子 and non-coding **introns** 内含子. 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** 替换 — one base swapped; changes at most one amino acid (sometimes none).
- **deletion** 缺失 / **insertion** 插入 — shifts how every later triplet is read (a frameshift), usually changing many amino acids.

## 2 Practice

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**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]

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**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

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**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

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**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

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

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

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

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

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## Solutions

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**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.