

## Nucleic Acids & Protein Synthesis

A-Level Biology ■ Topic 6

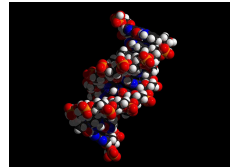
A-Level Biology



Nucleic Acids & Protein Synthesis

### What we will cover

- 1 Nucleotides & bases
- 2 DNA structure
- 3 DNA replication
- 4 The genetic code
- 5 Transcription & translation
- 6 Mutations



the DNA double helix

# 1 Nucleotides and DNA

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└ Nucleotides and DNA

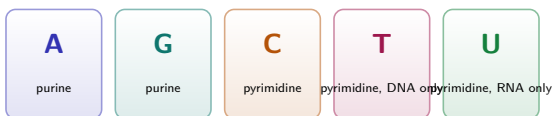
### Nucleotides

A **nucleotide** 核苷酸 has three parts: a pentose sugar, a phosphate, and a nitrogenous base. DNA uses deoxyribose; RNA uses ribose. Nucleotides join by **phosphodiester** 磷酸二酯 bonds between the 5' phosphate of one and the 3' OH of the next.

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└ Nucleotides and DNA

### The five bases



A pairs with T (or U in RNA); G pairs with C. Two H-bonds vs three.

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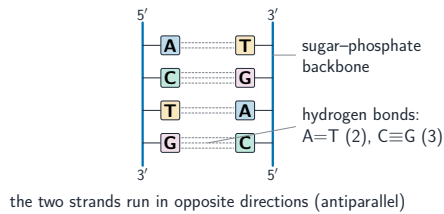
└ Nucleotides and DNA

### DNA structure

Two **antiparallel** 反平行 strands twist into a **double helix** 双螺旋.

**Complementary base pairing** 碱基互补配对: A-T by 2 hydrogen bonds, C-G by 3 – joined along a **phosphodiester** 磷酸二酯键 backbone.

## DNA structure, in detail



Two **antiparallel** 反平行 strands twist into a **double helix** 双螺旋.

## The double helix, and the strands of replication

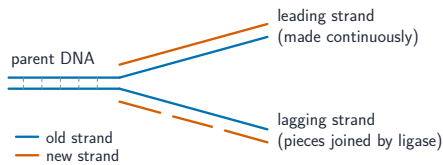
|                            |                                                                                                       |
|----------------------------|-------------------------------------------------------------------------------------------------------|
| the shape                  | the flat ladder is twisted into a <b>double helix</b> 双螺旋 – a space-filling model shows the real form |
| the bases                  | adenine 腺嘌呤, thymine 胸腺嘧啶, cytosine 胞嘧啶, guanine 鸟嘌呤 – A pairs with T, C with G                       |
| purines 嘌呤 and pyrimidines | a large base always pairs with a small one, which keeps the helix a constant width                    |
| the leading strand         | built <b>continuously</b> toward the unwinding point                                                  |
| the lagging strand 后随链     | built in <b>short pieces</b> working away from it; <b>DNA ligase</b> 连接酶 joins them                   |
| why two ways               | DNA polymerase can only build in one direction, and the two strands are antiparallel                  |

The lagging strand exists because of the enzyme's one-way constraint, not because the two strands differ chemically. That is the explanation the mark scheme wants.

## DNA replication

Replication is **semi-conservative** 半保留复制 – each new molecule keeps one old strand.

- **DNA polymerase** 聚合酶 adds nucleotides 5' → 3'
- **leading strand** 前导链 continuous; **lagging strand** 后随链 in pieces, joined by **ligase** 连接酶



# 2 The genetic code

## The genetic code

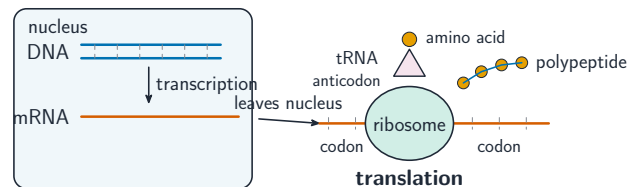
**gene** 基因 → polypeptide    **triplet** 三联体 = 3 bases    **universal** 通用

64 triplets, 20 amino acids ⇒ most amino acids have more than one triplet

**RNA** 核糖核酸 is a single strand with the sugar **ribose** 核糖, and uses **uracil** 尿嘧啶 in place of thymine.

## Transcription and translation

- **transcription** 转录 – DNA → **mRNA** 信使 RNA in the nucleus
- **translation** 翻译 – the ribosome reads **codons** 密码子; **tRNA** 转运 RNA **anticodons** 反密码子 bring amino acids

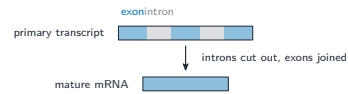


## Which strand is copied, and what happens next

|                                 |                                                                                        |
|---------------------------------|----------------------------------------------------------------------------------------|
| the template strand 模板链         | the strand of DNA that is copied                                                       |
| the non-transcribed strand 非转录链 | its partner – and its base sequence matches the mRNA, with U for T                     |
| the primary transcript 初级转录本    | the first RNA made, still containing introns                                           |
| splicing                        | introns are cut out and exons joined, giving mature mRNA                               |
| translation                     | ribosomes read codons; tRNA brings the matching amino acid; peptide bonds 肽键 join them |
| the energy 能量                   | ATP is needed at several steps – transcription, tRNA loading, and each peptide bond    |

Name which strand is the template. Reading the wrong one gives a sequence that is complementary to the right answer, and scores nothing.

## Splicing



In eukaryotes the first transcript has coding **exons** 外显子 and non-coding **introns** 内含子.

**Splicing** 剪接 cuts out the introns and joins the exons to make the finished mRNA.

# 3 Mutations

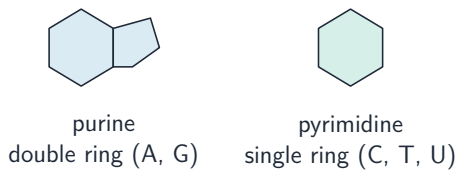
## Gene mutations

original **ATG CAT TAC**  
substitution **AAG CAT TAC**  
deletion **ATG ATT ACG**  
insertion **ATG GCA TTA C**  
red = changed base; shaded = shifted by a frameshift (deletion or insertion)

A **mutation** 突变 changes the base sequence:

- **substitution** 替换 – swaps one base (small effect)
- **deletion** 缺失 / **insertion** 插入 – shift every later triplet (a frameshift 移码)

## Nucleotides – the building blocks



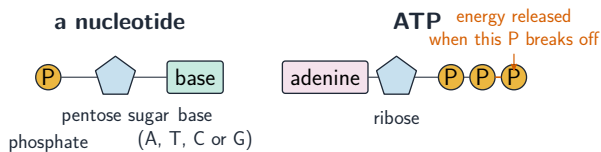
The two groups differ in shape: a purine is a double ring, a pyrimidine a single ring – which is why a purine always pairs with a pyrimidine

## Nucleotides – the building blocks, continued



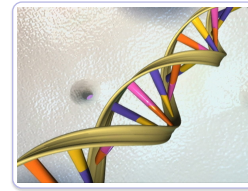
DNA extracted from cells appears as pale, stringy strands of these nucleotide polymers

## Nucleotides – the building blocks, continued (2)



A nucleotide is a phosphate, a sugar and a base; ATP is a nucleotide with three phosphates

## RNA



DNA double helix: RNA is a related nucleic acid that carries genetic information into protein synthesis

## Exam tips

- DNA is **antiparallel**, held by hydrogen bonds (A=T two, C G three); replication is **semi-conservative** (each product keeps one old strand).
- State **where** and **what**: transcription (nucleus → mRNA), translation (ribosome, mRNA + tRNA → polypeptide).
- Describe the code with all four terms: **triplet, non-overlapping, degenerate, universal**.
- For a **gene mutation** (substitution, insertion, deletion) explain the effect on the protein – and why a substitution can be silent (degeneracy).

# 4

## Recap

## Worked example – transcribe and translate

A DNA template strand reads TAC GGA TTT. Give the mRNA and say how many amino acids result.

- mRNA is built **complementary** to the template, with **U** in place of **T**.
- TAC → AUG; GGA → CCU; TTT → AAA.
- mRNA: AUG CCU AAA – and **AUG** is always the **start codon**.
- 3 codons ⇒ 3 amino acids; each tRNA anticodon pairs with one codon.

A → U (never T) when transcribing. **Codon** is on the mRNA, **anticodon** on the tRNA, and the **triplet** on the DNA – do not mix the three names.

## Topic 6 – key takeaways

1

### Base pairing

A–T (2 bonds), C–G (3); antiparallel

2

### Replication

semi-conservative; leading & lagging strands

3

### Code

triplets; transcription then translation

4

### Mutations

substitution vs frameshift (indel)

## Check yourself

- 1 How many hydrogen bonds join C and G?
- 2 What does "semi-conservative" mean?
- 3 Where does translation take place?
- 4 Which mutation causes a frameshift?



**Answers** 1. three 2. each new molecule keeps one old strand 3. at the ribosome  
4. deletion or insertion