6.1 Structure of nucleic acids and replication of DNA

Name: _____ Class: _____ Date: _____ **Total: 27 marks**

KEY WORDS base • strand • nucleotide • adenine • replication

Objective

Build the skills to answer exam questions on the **structure of nucleic acids and replication of DNA** – **nucleotides**, **complementary base pairing**, and **semi-conservative replication**.

You must be able to:

- describe a nucleotide (including ATP) and classify bases as **purines** or **pyrimidines**
- describe the DNA double helix (base pairing, hydrogen bonds, antiparallel strands, phosphodiester bonds)
- use base-pairing ratios in calculations and describe semi-conservative replication

1 Key knowledge and worked examples

Nucleotides and bases

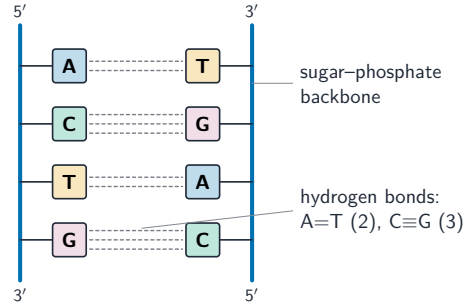
A **nucleotide** is a **phosphate** + a 5-carbon sugar + a nitrogen **base**. **ATP** is a nucleotide with adenine, ribose and **three** phosphates.

A nucleotide; ATP has three phosphates

Bases come in two groups: **purines** (double ring) = adenine, guanine; **pyrimidines** (single ring) = cytosine, thymine, uracil.

DNA structure and base pairing

Two **antiparallel** strands (one 5′→3′, one 3′→5′) twist into a **double helix**. Backbones are sugar–phosphate joined by **phosphodiester bonds**. The strands are held by base pairs: **A=T** (2 hydrogen bonds), **C≡G** (3 hydrogen bonds).



the two strands run in opposite directions (antiparallel)

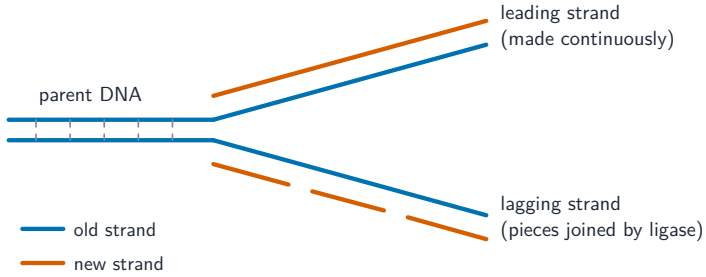
A pairs with T (2 H-bonds), C with G (3); the strands are antiparallel

Base-ratio calculations

Because A pairs with T and C pairs with G, **%A = %T** and **%C = %G**, and all four add to 100%. So if 28% of bases are adenine: %T = 28, so %A + %T = 56, leaving %C + %G = 44, so %G = 22%.

Semi-conservative replication

In the S phase the helix unwinds; each old strand is a template; **DNA polymerase** adds nucleotides only 5′→3′. So the **leading strand** is made continuously and the **lagging strand** in pieces joined by **DNA ligase**. Each new molecule keeps one old and one new strand.



each new molecule = one old strand + one new strand (semi-conservative)

Semi-conservative: each new molecule keeps one old strand and one new strand

2 Practice

2.1 State the three parts of a nucleotide. [3]

2.2 State the number of hydrogen bonds between (a) A and T, and (b) C and G. [2]

3 Exam-style questions

3.1 Which statement about the two strands of a DNA molecule is correct? [1]

- ☐ **A** they are identical in base sequence
- **B** they run in the same direction
- **C** they are antiparallel and complementary
- **D** they are joined by phosphodiester bonds between bases

3.2 In a sample of DNA, 20% of the bases are cytosine. What percentage are adenine? [1]

- ☐ **A** 20%
- **B** 30%
- **C** 40%
- **D** 60%

3.3 DNA replication is described as semi-conservative.

(a) Explain what "semi-conservative" means. [2]

(b) Explain why one new strand (the lagging strand) is made in short pieces. [2]

3.4 A DNA molecule contains 1200 bases, of which 360 are guanine. Calculate the number of adenine bases. Show your working. [3]

3.5 A short length of one DNA strand has the base sequence **T A C G G A T C A A T**.

(a) Write the sequence of the complementary strand, and state the rule you used. [2]

(b) Describe the structure of a DNA nucleotide, and explain how nucleotides are joined into a strand. [4]

(c) Explain what is meant by *semi-conservative* replication, and describe the roles of DNA helicase and DNA polymerase. [4]

(d) In one organism 22% of the bases in its DNA are adenine. Calculate the percentage that is guanine, and explain your reasoning. [3]

Solutions

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

2.1

- a phosphate group; a (5-carbon/pentose) sugar; a nitrogen-containing base

2.2

(a)

- 2

(b)

- 3

3.1 C

- The strands are antiparallel and complementary; bases pair by hydrogen bonds, and phosphodiester bonds are within each backbone

3.2 B

- %C = %G = 20, so C+G = 40; A+T = 60, so %A = 30

3.3

(a)

- each new DNA molecule contains one original (old) strand and one newly made strand

(b)

- DNA polymerase can only add nucleotides in the 5′
- 3′ direction, so on the strand running the "wrong" way it must work in short pieces away from the fork, later joined by ligase

3.4

- guanine = 360, so cytosine = 360; C+G = 720, so A+T = $1200 - 720 = 480$; adenine = $480/2 = 240$

3.5

(a)

- **A T G C C T A G T T A**; complementary base pairing – adenine always pairs with thymine and cytosine with guanine

(b)

- A nucleotide is a deoxyribose sugar, a phosphate group and one of four nitrogenous bases. Nucleotides join by **condensation** between the phosphate on carbon 5 of one sugar and the hydroxyl on carbon 3 of the next, giving a sugar–phosphate backbone linked by phosphodiester bonds

(c)

- Each new double helix contains **one** original strand and one newly made strand. DNA helicase unwinds the helix and breaks the hydrogen bonds between the base pairs, separating the two strands; free nucleotides then pair with the exposed bases; DNA polymerase joins those nucleotides together by forming the phosphodiester bonds of the new backbone

(d)

- Adenine pairs only with thymine, so thymine is also 22%; A + T = 44%, leaving 56% for C + G; C and G are equal, so guanine is 28%