Helicate

HELICATE · AS AND A-LEVEL BIOLOGY · TOPIC BANK

3.4.1 DNA, genes and chromosomes

Topic question bank

Version 1 · 9 October 2026

Name

Date

QUESTIONS	TOTAL MARKS	TIME	YOUR SCORE
8	48	No time limit	/ 48

Contents

Subtopic	Questions	Marks
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Total		**48**

Instructions

- Answer the questions in the spaces provided. Show all your working.
- The marks for each question are shown in brackets. Use them to judge how much detail to give.
- Work through a subtopic at a time, then mark your answers with the matching mark scheme.

Original questions by Helicate for AQA AS and A-level Biology (7401/7402), specification section 3.4.1. Not affiliated with or endorsed by AQA.

Do not write outside the box

DNA in prokaryotic and eukaryotic cells 3.4.1

0 1 . 1 Which row describes the DNA found in a mitochondrion?
Tick (✓) one box.

[1 mark]

Shape of DNA molecule	Associated with histones	Length compared with nuclear DNA	
Linear	Yes	Longer	☐
Circular	Yes	Shorter	☐
Circular	No	Shorter	☐
Linear	No	Shorter	☐

A student wrote this description of the DNA in a bacterial cell.

"The DNA of a bacterium is single-stranded. All of the bacterium's DNA is found in plasmids. Like the DNA in the nucleus of a human cell, it is wound around histones."

0 1 . 2 The description contains **three** errors.
For each error, give the correct information.

[3 marks]

1 .....

.....

2 .....

.....

3 .....

.....

4

Turn over for the next question

Do not write outside the box

Scientists investigated the DNA in the leaf cells of a plant.

- They broke open leaf cells and used cell fractionation to obtain three separate fractions: nuclei, chloroplasts and mitochondria.
- They added enzyme **D** to the chloroplast fraction and to the mitochondrial fraction. Enzyme **D** hydrolyses any DNA molecule. After 30 minutes, they washed enzyme **D** out of each fraction.
- They then broke open the organelles in each fraction and extracted the DNA.

0 2 . 1 Suggest why the scientists added enzyme **D** to the chloroplast and mitochondrial fractions before breaking open these organelles.

[2 marks]

Question 2 continues on the next page

Do not write outside the box

The scientists tested a sample of the material extracted from each fraction for histones. They then removed all of the proteins from the DNA and added enzyme **E**. Enzyme **E** hydrolyses DNA by removing nucleotides one at a time, but it can only start at a free end of a DNA strand.

In sample 4, the chloroplast DNA was first treated with enzyme **R**, which cuts each chloroplast DNA molecule at only one position. Enzyme **E** was then added.

Table 1 shows the results.

Table 1

Sample	Source of DNA	Histones present	Percentage of DNA hydrolysed by enzyme **E** after 60 minutes
1	Nuclear DNA	Yes	97
2	Chloroplast DNA	No	4
3	Mitochondrial DNA	No	3
4	Chloroplast DNA cut once by enzyme **R**	No	96

0 2 . 2 Explain the results for samples 1, 2 and 3 in Table 1.

[3 marks]

Question 2 continues on the next page

Do not write outside the box

0 2 . 3 Explain why the scientists included sample 4.

[2 marks]

0 2 . 4 In the nucleus, a DNA molecule and its associated histones together form a structure.
Name this structure.

[1 mark]

The chloroplast DNA molecule contains 1.5×10^5 base pairs. In a DNA double helix, each base pair adds 0.34 nm to the length of the molecule.

0 2 . 5 Calculate the total length of the chloroplast DNA molecule.
Give your answer in μm.

[2 marks]

Answer ..... **μm**

10

Turn over for the next question

Genes and the genetic code 3.4.1

In humans, the gene that codes for the enzyme lactase is always found at the same position on the DNA molecule of chromosome 2.

0 3 . 1 Give the term for the position of the lactase gene described above.

[1 mark]

.....

0 3 . 2 Which statement about genes is correct?
Tick (✓) one box.

[1 mark]

- A gene is a sequence of amino acids that codes for a polypeptide. ☐
- Every base sequence in nuclear DNA is part of a gene. ☐
- Some genes code for a functional RNA, such as tRNA, instead of a polypeptide. ☐
- Each gene codes for a single amino acid. ☐

0 3 . 3 The genetic code is universal.
What is meant by this?
Tick (✓) one box.

[1 mark]

- All organisms have the same base sequence in their genes. ☐
- In all organisms, the same triplet codes for the same amino acid. ☐
- In all organisms, each amino acid is coded for by more than one triplet. ☐
- All organisms use the genetic code to make the same proteins. ☐

3

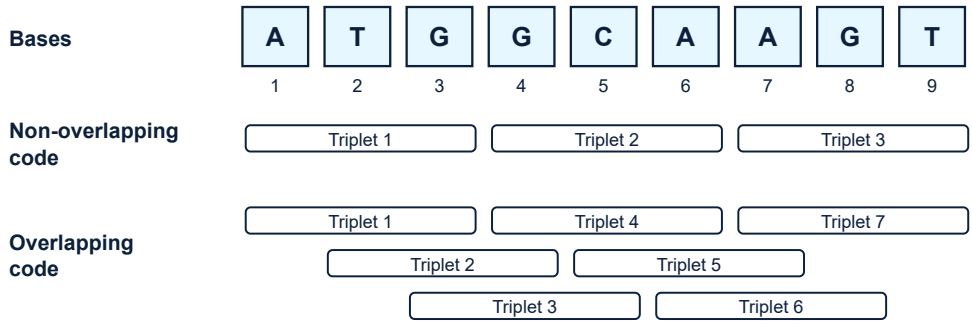
Turn over for the next question

Do not write outside the box

Before the genetic code was worked out, some scientists suggested that it might be overlapping.

Figure 1 shows how a sequence of nine DNA bases would be read as triplets in a non-overlapping code and in an overlapping code.

Figure 1



Numbers under the bases show the position of each base.

0 4 . 1 Use Figure 1 to explain why, in an overlapping code, the substitution of one base could change up to three amino acids in a polypeptide, but in a non-overlapping code it could change no more than one.

[2 marks]

Question 4 continues on the next page

Do not write outside the box

Scientists exposed a bacterium to a chemical that causes the substitution of single bases in DNA. They isolated 80 strains of the bacterium that still produced a complete enzyme **G**. In each strain, exactly one base had been substituted within the triplets of the gene that codes for enzyme **G**.

The scientists then compared the amino acid sequence of enzyme **G** from each strain with the original enzyme. Table 2 shows their results.

Table 2

Number of amino acids in enzyme **G** that differed from the original enzyme	Number of strains
0	19
1	61
2 or more	0

0 4 . 2 Explain how the results in Table 2 support the hypothesis that the genetic code is non-overlapping **and** degenerate.

[4 marks]

Question 4 continues on the next page

Do not write outside the box

Table 3 shows the DNA triplets that code for four amino acids.

Table 3

Amino acid	DNA triplets that code for the amino acid
Glycine	GGA, GGC, GGG, GGT
Lysine	AAA, AAG
Methionine	ATG
Tryptophan	TGG

0 4 . 3 A short polypeptide has the amino acid sequence:

tryptophan – glycine – lysine – glycine

Use Table 3 to find how many different DNA base sequences could code for this polypeptide.
Tick (✓) one box.

[1 mark]

8 ☐

11 ☐

16 ☐

32 ☐

7

Turn over for the next question

Do not write outside the box

Exons, introns and non-coding DNA 3.4.1

The human nuclear genome contains about 3.1×10^9 base pairs. It contains about 2.0×10^4 genes that code for polypeptides. In these genes, the exons have a mean total length of 1.5×10^3 base pairs per gene.

0 5 . 1 Calculate the percentage of the human nuclear genome that consists of the exons of these genes.
Give your answer to **two** significant figures.

[2 marks]

Answer ..... **%**

0 5 . 2 In the bacterium *Escherichia coli*, about 88% of the DNA codes for polypeptides. Suggest **two** reasons why this percentage is much higher than in the human nuclear genome.

[2 marks]

1 .....

.....

2 .....

.....

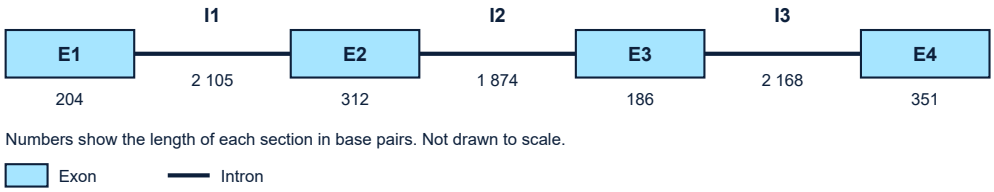
4

Turn over for the next question

Do not write outside the box

Enzyme **P** is found in both humans and bacteria. Figure 2 shows the human gene that codes for enzyme **P**. The sections labelled E1 to E4 are exons. The sections labelled I1 to I3 are introns.

Figure 2



0 6 . 1 Describe how the base sequences of exons differ from the base sequences of introns.

[1 mark]

0 6 . 2 The human gene is 7 200 base pairs long, from the start of E1 to the end of E4. Calculate the percentage of the human gene that consists of introns.
Give your answer to **three** significant figures.

[2 marks]

Answer ..... **%**

Question 6 continues on the next page

Do not write outside the box

The bacterial gene that codes for enzyme **P** is 1 062 base pairs long.

A student said: *"The human gene for enzyme **P** is almost seven times as long as the bacterial gene, so human enzyme **P** must contain almost seven times as many amino acids as bacterial enzyme **P**."*

0 6 . 3 Use Figure 2 and your knowledge of genes to evaluate the student's statement.

[5 marks]

8

Turn over for the next question

Do not write outside the box

Yeast is a single-celled eukaryote. The yeast cells used in this investigation contain one copy of each chromosome.

On one chromosome, the DNA between two genes, **K** and **L**, contains a sequence of 6 base pairs that is repeated many times.

Scientists made many copies of this region of DNA from four strains of yeast, **W**, **X**, **Y** and **Z**. They separated the DNA fragments by length using gel electrophoresis and found the length of the fragment from each strain. Table 4 shows their results.

Table 4

Strain	Length of DNA fragment / base pairs
W	222
X	258
Y	300
Z	342

The length of each fragment is given by:

length of fragment = 150 + (6 × number of repeats)

0 7 . 1 Calculate the number of repeats in strain **Z**.

[2 marks]

Answer .....

Question 7 continues on the next page

Do not write outside the box

0 7 . 2 Strains **W** and **Z** produce identical polypeptides from genes **K** and **L**. Explain why, even though they have different numbers of repeats.

[2 marks]

In gel electrophoresis, DNA fragments move through a gel when an electric current is applied. Shorter fragments move further than longer fragments. The scientists also ran DNA fragments of known length on the same gel as the yeast DNA.

0 7 . 3 Explain why the scientists ran DNA fragments of known length on the same gel as the yeast DNA.

[2 marks]

6

Turn over for the next question

Do not write outside the box

Extended response: DNA in organelles 3.4.1

Scientists think that mitochondria and chloroplasts evolved from prokaryotic cells that once lived inside larger cells.

0 8 Compare the DNA in mitochondria and chloroplasts with the DNA of prokaryotes **and** with the DNA in the nucleus of the same eukaryotic cell.
Explain how your comparisons support this idea.

[6 marks]

6

END OF QUESTIONS

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