Helicate

HELICATE · A-LEVEL BIOLOGY · TOPIC BANK

3.8.3 Using genome projects

Topic question bank

Version 2 · 17 October 2026

Name

Date

QUESTIONS	TOTAL MARKS	TIME	YOUR SCORE
5	37	No time limit	/ 37

Contents

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Total		**37**

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 A-level Biology (7402), specification section 3.8.3. Not affiliated with or endorsed by AQA.

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Genome sequencing projects 3.8.3

Table 1 shows information about the genomes of five organisms.

Table 1

Organism	Genome size / base pairs	Number of protein-coding genes	Percentage of genome that codes for proteins
Bacterium	2.8×10^6	2 600	87
Yeast	1.2×10^7	6 000	70
Nematode worm	1.0×10^8	20 000	26
Fruit fly	1.4×10^8	14 000	16
Human	3.1×10^9	20 000	1.5

0 1 . 1 Which statement about genome sequencing projects is correct?
Tick (✓) one box.

[1 mark]

Only the genomes of prokaryotes have been fully sequenced. ☐

Genome sequencing is used only for organisms that cause disease. ☐

The genomes of a wide range of organisms, including humans, have been sequenced. ☐

Sequencing methods have stayed the same since the first genome was sequenced. ☐

Question 1 continues on the next page

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0 1 . 2 Which organism in Table 1 has a mean of about 100 protein-coding genes for every million base pairs of its genome?
Tick (✓) one box.

[1 mark]

Bacterium ☐

Yeast ☐

Nematode worm ☐

Fruit fly ☐

0 1 . 3 Calculate the number of base pairs in the human genome that code for proteins.
Give your answer in standard form.

[2 marks]

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.....

Answer ..... **base pairs**

Question 1 continues on the next page

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0 1 . 4 A student made this claim:

'The human genome is more than 1000 times larger than the genome of the bacterium. So the human proteome must contain more than 1000 times as many different proteins as the proteome of the bacterium.'

Use Table 1 to evaluate the student's claim.

[3 marks]

In the 1990s, sequencing the genome of one bacterium took a team of scientists more than a year. Today, a single laboratory can sequence a bacterial genome of the same size in a few hours.

0 1 . 5 Explain how changes in sequencing methods have allowed bacterial genomes to be sequenced so much faster.

[2 marks]

9

Turn over for the next question

Do not write outside the box

Genomes of simpler organisms and vaccines 3.8.3

Bacterium M causes meningitis, a serious infection. Scientists sequenced the genome of one strain of bacterium M. The genome contained 2 160 protein-coding genes. A computer program predicted that 580 of the proteins coded for by these genes would be found on the surface of the bacterium.

0 2 . 1 Antibodies made after vaccination can bind only to proteins exposed on the outside of an intact bacterium.
Explain how sequencing the genome of bacterium M allowed the scientists to identify proteins that might be used in a vaccine, and why the computer prediction of surface proteins was useful.

[3 marks]

Question 2 continues on the next page

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The scientists made large amounts of five of the surface proteins, P, Q, R, S and T. They used mice to test each protein as a possible vaccine.

- Each of five groups of 20 mice was injected with one protein dissolved in salt solution.
- Another group of 20 mice was injected with salt solution only.
- Four weeks later, every mouse was injected with live bacterium M of the strain that had been sequenced.
- The scientists recorded the number of mice in each group that were still alive after 10 days.

The scientists also looked for the gene for each protein in the genomes of 50 other strains of bacterium M that cause meningitis.

Table 2 shows their results.

Table 2

Protein injected	Number of mice alive after 10 days (out of 20)	Percentage of the 50 strains that have the gene for this protein
None (salt solution only)	2	–
P	4	100
Q	15	46
R	18	72
S	6	88
T	13	100

0 2 . 2 Explain why the scientists injected one group of mice with salt solution only.

[2 marks]

Question 2 continues on the next page

Do not write outside the box

0 2 . 3 Calculate the percentage increase in the number of mice alive after 10 days in the group injected with protein R, compared with the group injected with salt solution only.

[1 mark]

Answer _____ **%**

0 2 . 4 A scientist suggested that a vaccine containing protein R alone would protect people against meningitis caused by bacterium M.
Use Table 2 to evaluate this suggestion.

[4 marks]

10

Turn over for the next question

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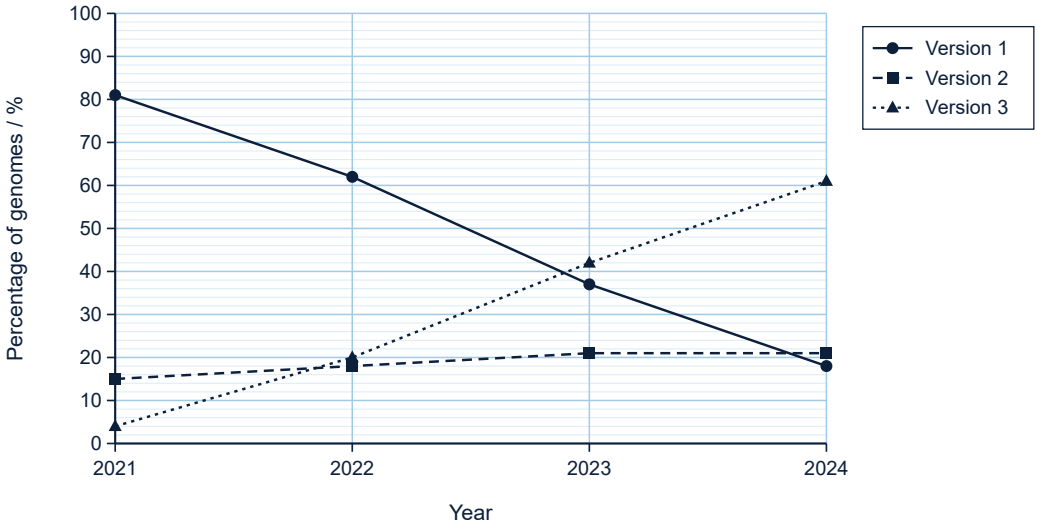
Virus V causes infections of the respiratory system in humans. The genome of virus V contains 11 genes. One of these genes codes for an attachment protein on the surface of the virus. A vaccine against virus V contains the attachment protein.

Three versions of the attachment protein have been found. Each version has a different amino acid sequence. Each year, scientists sequence the genomes of virus V from samples taken from between 420 and 1 530 infected people. Figure 1 shows the percentage of these genomes that coded for each version of the attachment protein.

Figure 1



0 3 . 1 Explain how sequencing the genome of each virus sample allowed the scientists to find out which version of the attachment protein the virus had.

[2 marks]

Question 3 continues on the next page

Do not write outside the box

0 3 . 2 The scientists must choose one version of the attachment protein for the vaccine to be used in 2025.
Use Figure 1 to suggest which version they should choose. Explain your answer.

[3 marks]

5

Turn over for the next question

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Genomes and proteomes of more complex organisms 3.8.3

Table 3 compares the genome of a bacterium with the human genome.

Table 3

Feature	Bacterium	Human
Number of protein-coding genes	2 600	20 000
Percentage of genome that codes for proteins	87	1.5
Percentage of protein-coding genes that contain introns	Less than 1	95
Number of regulatory genes	140	1 600

0 4 . 1 Scientists know the base sequence of a human gene.
What is the main reason why they cannot simply read the amino acid sequence of the protein it codes for from this base sequence?
Tick (✓) one box.

[1 mark]

The genetic code is degenerate. ☐

The gene contains non-coding sequences within it. ☐

The DNA of the gene is wound around histones. ☐

The genetic code is different in each type of human cell. ☐

Question 4 continues on the next page

Do not write outside the box

0 4 . 2 Use Table 3 to explain why scientists can predict the proteome of the bacterium from its genome more easily than they can predict the human proteome from the human genome.

[5 marks]

6

Turn over for the next question

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The parasite *Plasmodium* causes malaria in humans. Each *Plasmodium* cell is eukaryotic. Its genome contains about 5 300 protein-coding genes.

When an infected mosquito bites a human, *Plasmodium* cells pass from the mosquito's salivary glands into the blood. Within a few hours, they enter liver cells. Later, new *Plasmodium* cells leave the liver and infect red blood cells.

Scientists identified the different proteins present in *Plasmodium* cells at three stages of its life cycle. Table 4 shows their results.

Table 4

Stage of *Plasmodium* life cycle	**Number of different proteins detected**	**Number of proteins detected only at this stage**
In the salivary glands of a mosquito	1 120	410
In human liver cells	980	290
In human red blood cells	1 440	520

Of these proteins, 330 were detected at both the salivary gland stage and the liver stage. 180 of these were detected at all three stages.

0 5 . 1 Assume that each protein detected is coded for by a different gene. Calculate the percentage of *Plasmodium* protein-coding genes whose proteins were detected at the red blood cell stage.

[1 mark]

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.....

.....

Answer ..... **%**

Question 5 continues on the next page

Do not write outside the box

0 5 . 2 Scientists want to develop a vaccine that stops *Plasmodium* infecting liver cells after a mosquito bite. They have sequenced the whole *Plasmodium* genome. Use the information given and your knowledge of genome projects to explain why the genome sequence alone does not tell the scientists which proteins to test in the vaccine. Suggest which proteins they should test first. Give reasons for your suggestion.

[6 marks]

7

END OF QUESTIONS

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