



Viruses: practice questions

7 questions • 23 marks • mark scheme at the back

For IB Diploma Biology, Standard Level and Higher Level (first assessment 2025). **HL only** is additional higher level content, for HL students only.

Name

Total / 23

1 PAPER 1A STYLE

[1 mark]

HL only

Which feature is shared by all viruses?

- A. ☐ An envelope derived from host cell membrane
- B. ☐ A capsid made of protein
- C. ☐ Double-stranded DNA
- D. ☐ The enzyme reverse transcriptase

2 PAPER 1A STYLE

[1 mark]

HL only

During the lysogenic cycle of bacteriophage lambda, what happens to the viral DNA?

- A. ☐ It is packed into new capsids straight away.
- B. ☐ It is transcribed to make enzymes that lyse the cell.
- C. ☐ It is integrated into the host chromosome and replicated when the host divides.
- D. ☐ It is broken down by host enzymes.

HL only

The viral load (number of copies of HIV RNA per cm³ of blood) was monitored in two groups of patients. One group took a single antiviral drug and the other took a combination of three drugs with different targets. The data are for practice. (a) Calculate the percentage decrease in viral load in the single-drug group between week 0 and week 8. [1] (b) Describe the trend in viral load in the single-drug group after week 8. [1] (c) Explain the change in viral load in the single-drug group after week 8. [2] (d) Suggest why the viral load stayed low in the combination group. [2]

Viral load in patients with HIV (practice data)		
Time / weeks	Single drug / copies per cm ³	Three-drug combination / copies per cm ³
0	100 000	100 000
4	2 000	1 500
8	1 500	200
12	9 000	below 50
16	40 000	below 50
24	90 000	below 50

Answer =

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HL only

Compare and contrast the structure of bacteriophage lambda and HIV. [4]

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PAPER 2B STYLE

HL only

[illegible]

PAPER 2A STYLE

HL only

[illegible]

PAPER 2A STYLE

HL only

[illegible]

Mark scheme

One mark for each point unless a maximum is given. Words in brackets are not needed for the mark.

1. [1] **HL only**

B B [1]

2. [1] **HL only**

C C [1]

3. [6] **HL only**

- (a) $(100\,000 - 1\,500) \div 100\,000 \times 100 = 98.5\%$ [1]
- (b) increases from 1 500 to 90 000 copies per cm^3 / rises back almost to the starting level by week 24 [1]
- (c) HIV has a high mutation rate / reverse transcriptase makes errors / does not proofread [1]
- (c) some variants are resistant to the drug [1]
- (c) the drug selects for resistant variants, which multiply / natural selection [1]
- max 2 for (c)
- (d) a variant would need mutations giving resistance to all three drugs at the same time [1]
- (d) this is very unlikely / the probability is very low [1]
- (d) the drugs act on different targets, so replication is blocked at more than one stage [1]
- max 2 for (d)

4. [4] **HL only**

- both have a protein capsid [1]
- both have nucleic acid as genetic material / both lack cytoplasm [1]
- lambda has double-stranded DNA; HIV has single-stranded RNA [1]
- lambda is not enveloped; HIV is enveloped in host cell membrane [1]
- HIV has glycoproteins in its envelope that bind host receptors; lambda binds the host with its tail [1]
- lambda has an icosahedral head and a tail; HIV has a cone-shaped capsid [1]
- HIV carries reverse transcriptase / integrase / protease; lambda carries no enzymes [1]
- max 4, with at least one similarity for full marks

5. [5] **HL only**

- the phage tail attaches to specific receptors on E. coli [1]
- viral DNA is injected; the capsid stays outside [1]
- the viral DNA circularises [1]
- viral genes are transcribed by host RNA polymerase [1]
- and translated by host ribosomes to make capsid proteins / viral enzymes [1]
- the host supplies ATP / energy, nucleotides and amino acids [1]
- viral DNA is replicated many times [1]
- new phages are assembled / DNA is packed into heads [1]
- viral enzymes break down the cell wall [1]
- the cell lyses / bursts, releasing many (about 100) phages [1]
- released phages infect other cells [1]
- max 5

6. [3] HL only

- viruses are very diverse in structure / in genetic material (DNA or RNA, single- or double-stranded) [1]
- suggesting they did not all descend from one common ancestor [1]
- their shared features may be the result of convergent evolution [1]
- because all share the same extreme obligate parasitism / way of life [1]
- the genetic code is shared with living organisms, suggesting origins from cells [1]
- some may have escaped from cells (e.g. as plasmids), others reduced from parasitic cells [1]
- max 3

7. [3] HL only

- influenza has an RNA genome with a high mutation rate / its RNA polymerase does not proofread [1]
- mutations change the surface antigens haemagglutinin / neuraminidase [1]
- this is antigenic drift [1]
- antibodies / memory cells from earlier vaccines no longer bind / recognise the new strain [1]
- segments from two strains can mix in one host (antigenic shift), producing a new subtype [1]
- the vaccine is matched to the strains predicted to circulate [1]
- max 3