Manipulating Genomes

Question Paper 1

Level	A Level
Subject	Biology
Exam Board	OCR
Module	Genetics, evolution and ecosystems
Topic	Manipulating genomes
Booklet	Question Paper 1

Time allowed: **63 minutes**

Score: **/47**

Percentage: **/100**

Grade Boundaries:

A*	A	B	C	D	E
>69%	56%	50%	42%	34%	26%

Question 1

Which of the following statements about gene therapy is **not** correct?

A. changes resulting from gene therapy cannot be passed on to offspring

B. germ-line gene therapy affects the whole organism

C. gene therapy is a form of genetic engineering

D. somatic cell gene therapy can only affect a limited number of cells

[Total: 1]

Which statement correctly describes a difference between somatic and germ line gene therapy?

A. Germ line therapy involves the use of liposomes; somatic therapy involves use of viral vectors.

B. Somatic therapy can target specific tissues in need of treatment, germ line therapy cannot.

C Somatic therapy is most successful when targeting single gene defects, but germ line therapy can target multiple defects.

D Long term success is theoretically more likely with somatic cell therapy than germ line therapy.

[Total: 1]

Fred Sanger developed an effective DNA sequencing technique in 1977.

(a) Define the term *DNA sequencing*. **[1]**

(b) The speed at which DNA can be sequenced has been increasing rapidly since the introduction of DNA sequencing.

The length of DNA that can be sequenced in a given time is measured in base pairs or kilobase pairs.

In 1980, the speed at which DNA could be sequenced by a single machine was approximately 500 **base pairs** per hour. In 2016 that speed had increased to approximately 50 million **kilobase pairs** per hour.

Calculate how many times faster the speed of DNA sequencing is in 2016 compared with 1980.

[2]

(c) One technique that has allowed the speed of DNA sequencing to increase has been the development of nanopores.

Fig. 21 shows how nanopores can be used to sequence DNA.

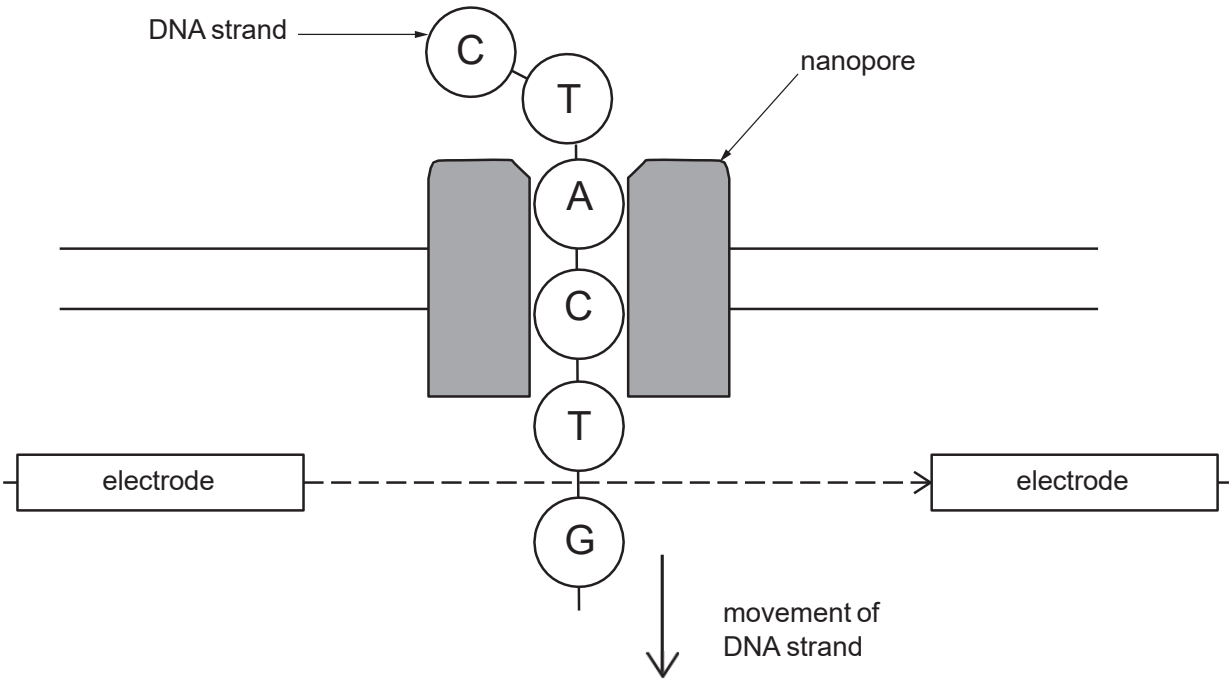

Fig. 21

(i) State one development, other than nanopore technology, that has led to an increase in the speed at which DNA can be sequenced.

[1]

(ii) Part of Fig. 21 is labelled **G**.

Use the table below to identify two differences between the part labelled **G** and the structure of a molecule of ATP.

[2]

	G	**Molecule of ATP**
Difference 1	....	....
Difference 2	....	....

(iii) Explain how DNA sequencing allows the sequence of amino acids in a polypeptide to be predicted.

[2]

(d) DNA sequencing can be used to determine the genome of an entire organism.

The first organism to have its entire genome sequenced was a virus.

Ebola is a virus that caused the death of over 11000 people in West Africa between 2014 and 2016. The DNA of ebola virus has a rapid rate of mutation.

Since the first outbreak in 2014 scientists have been working to develop an effective vaccination against ebola.

Other scientists have developed a portable nanopore sequencing technique that could be used to sequence rapidly the entire ebola genome.

Outline how DNA sequencing and bioinformatics could be used to increase the effectiveness of a vaccination programme against ebola.

[4]

sequencing

bioinformatics

[Total: 12]

Gene sequencing is an important technique in molecular biology.

Fig. 3.1, **of the Insert**, shows part of a computerised graph obtained from an automated gene sequencing machine.

- The section of the DNA molecule represented in Fig. 3.1 is from base position 117 (on the left of the graph) to base position 137 (on the right of the graph).
- The bases in the DNA sequence are labelled with four different coloured fluorescent dyes.
- The identities of some of the bases (117 to 119 inclusive and 129 to 137 inclusive) are indicated below the graph.

(a) Use Fig. 3.1 to identify the order of bases from positions 120 to 128. **[1]**

.....	.....	.....	.....	.....	.....	.....	.....	.....
120	121	122	123	124	125	126	127	128

(b) To produce the type of graph shown in Fig. 3.1, the automated gene sequencing machine needs to be loaded with the following:

- the DNA to be sequenced
- short primer sequences specific to the DNA to be sequenced
- many normal DNA nucleotides
- some chain-terminating DNA nucleotides labelled with coloured dyes
- the enzyme *Taq* polymerase.

A regular cycle of temperature changes allows many DNA fragments of different lengths to be built up by the polymerase chain reaction (PCR).

Fig. 3.2 (**on the next page**) shows the end parts of the sequences of seven of these different length fragments, labelled 1 to 7. The end parts of the sequences for fragments 1 to 4 are complete but those for fragments 5 to 7 are not.
These seven fragments correspond to the **last seven peaks** on the right hand side of the graph in Fig. 3.1.

The letters in boxes represent labelled chain-terminating DNA nucleotides.
The letters not in boxes represent normal DNA nucleotides.

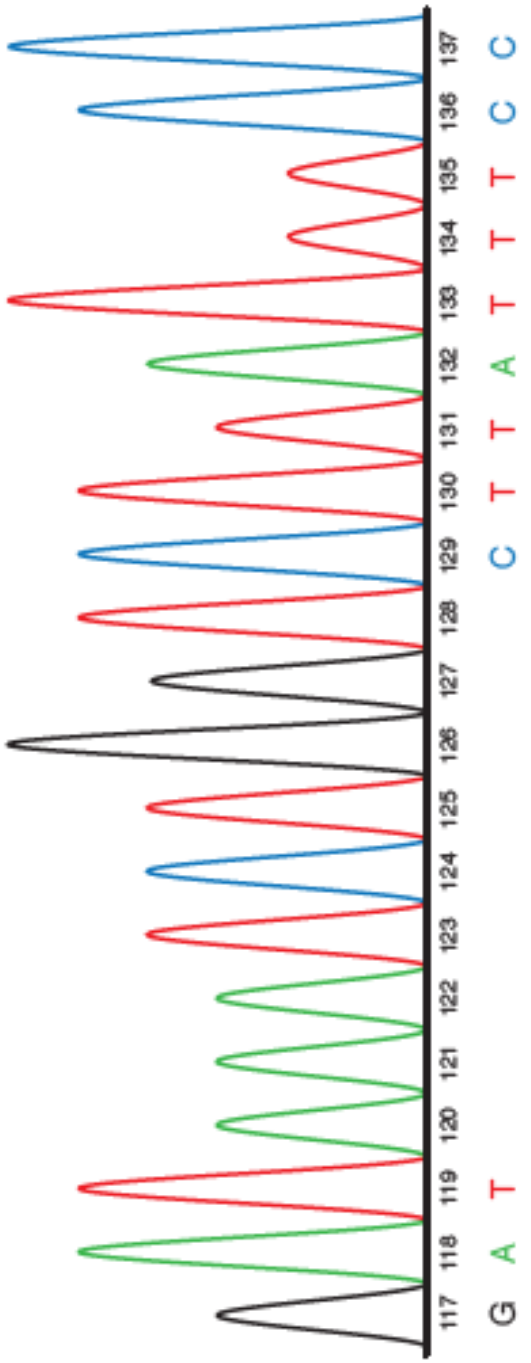
117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137
G A T C T T A T T C C

Fig. 3.1

(i) Use the information in Fig. 3.1 to fill in the missing nucleotide bases on fragments 5 to 7 on Fig. 3.2.

You should distinguish between the normal and labelled nucleotides in the sequence for each fragment.

[2]

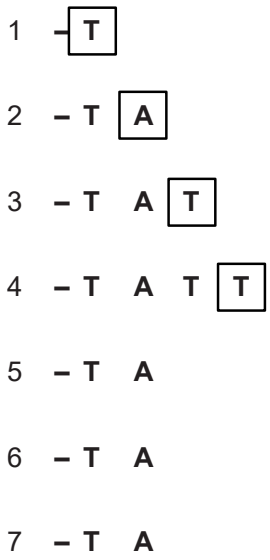

Fig. 3.2

(ii) Explain how the automated sequencing machine orders the DNA fragments from the PCR reaction into the size order shown in Fig. 3.2.

[3]

(c) Gene sequencing can help us to understand how an individual's genome affects their body's response to drugs.

One research study has looked at the effectiveness of drugs used to treat asthma in children. Asthma is a condition in which the bronchioles become reduced in diameter. This results in the child finding it difficult to breathe.

(i) Using your knowledge of the structure of bronchioles, suggest how their diameter might become reduced.

[2]

(ii) Explain why it is difficult to expel air from the lungs if the bronchioles become reduced in diameter.

[1]

(d) Asthma in children may be treated with drugs. One of the most commonly used drugs is salmeterol.

Salmeterol acts by binding to protein receptors in the lining of the bronchioles. However, in approximately 14% of children with asthma, salmeterol is not very effective. This is thought to be the result of a genetic mutation in these children.

Suggest why this mutation reduces the effectiveness of salmeterol. **[3]**

(e) In a recent medical trial, 62 children with this genetic mutation were studied.

- Their asthma was not controlled well by salmeterol.
- 31 children continued using salmeterol and the remaining 31 were given an alternative drug, montelukast.
- Montelukast is not routinely prescribed because salmeterol is far more effective for most children with asthma.

(i) After one year, the children taking montelukast had better control of their asthma and were able to reduce their use of montelukast.

Suggest why these children responded better to montelukast than to salmeterol. **[2]**

(ii) Comment on the reliability of the results of this medical trial. **[1]**

(iii) It is proposed that a simple saliva test could identify those children who have the mutation.

What would be the source of the genetic material used in this test? **[1]**

[Total: 16]

This question is about genetic engineering and the techniques used for making multiple copies of genes (gene cloning).

(a) Genetic engineering uses the following:

A. an enzyme that synthesises new DNA
B. an enzyme that cuts DNA at specific sequences
C. an enzyme that reseals cut ends of DNA
D. small circular pieces of DNA found in bacteria; these pieces of DNA have antibiotic resistance genes
E. an enzyme found in some viruses with an RNA genome; this enzyme converts RNA into DNA.

Name **A** to **E**. **[5]**

A .....

B .....

C .....

D .....

E .....

(b) Genes are cloned for a number of reasons. For example,

- one group of research scientists at a hospital wanted to sequence a disease-causing mutation to learn more about a human disease; these scientists started their research using white blood cells;

- another group of scientists at a biotechnology company wanted to clone the insulin gene in order to manufacture its protein product to treat diabetes; these scientists started their research using cells from the pancreas.

Suggest **and** explain the biological reasons why the two groups each started with a different cell.

[4]

(c) A gene can be cloned *in vitro* (in a test-tube) by the polymerase chain reaction (PCR). Alternatively, a gene can be cloned *in vivo* (in living cells) by introducing the gene into bacterial host cells.

Table 5.1 identifies some of the key steps in each process.

Table 5.1

in vitro gene cloning (PCR)	*in vivo* gene cloning
At 95 °C, DNA extracted from a cell separates into two strands.	A library of gene fragments is produced and introduced into host bacteria.
At 50 °C, specially-made primer sequences attach to the ends of the desired gene only.	Bacteria are screened for antibiotic resistance to identify those with recombinant DNA.
At 72°C complementary copies of both DNA strands are made.	A gene probe is used to select the bacterial colony containing the desired gene.
The cycle of temperature changes is repeated and more copies of the gene are made.	This colony is grown on in nutrient broth and the DNA is then purified.

Compare the two processes of gene cloning by explaining the advantages of each.

In your answer you should ensure that clear comparisons between the two processes are made and explained.

[8]

[Total: 17]