

A Level Biology A
H420/02 Biological Diversity

Question Set 12

1 Fred Sanger developed an effective DNA sequencing technique in 1977.

(a) Define the term *DNA sequencing*.
It's working out the sequence of nucleotides [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.

$$\frac{50 \times 10^6 \times 10^3}{500} = 1 \times 10^8$$

Answer 1×10^8 times faster [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.

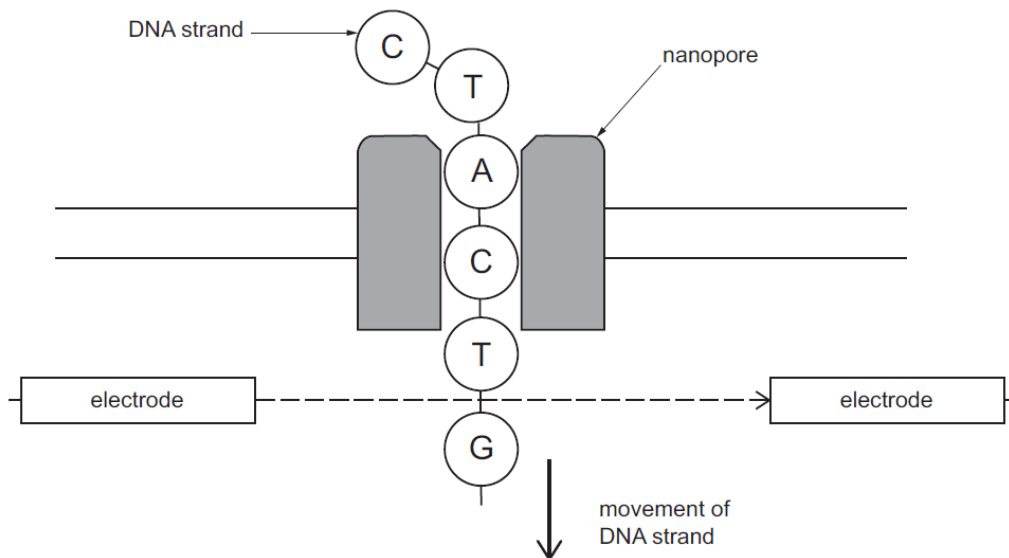


Fig. 21

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

massive parallel sequencing [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.

	G	Molecule of ATP
Difference 1	contains guanine	contains adenine
Difference 2	1 phosphate	3 phosphates

[2]

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

The sequence of bases codes for the sequence of amino acids. Each triplet codes for one amino acid.

[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 11 000 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.

sequencing ... high mutation rate means many strains of virus exists & sequencing can be used to predict the viral antigen so the vaccine contains the correct antigen

bioinformatics ... facilitates access to large amount of data on DNA and proteins thus can identify source of outbreak.

[4]

Total Marks for Question Set 12: 12

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