IB · DP · Biology

2 hours 15 questions

Structured Questions: Paper 2

7.1 DNA Structure & Replication

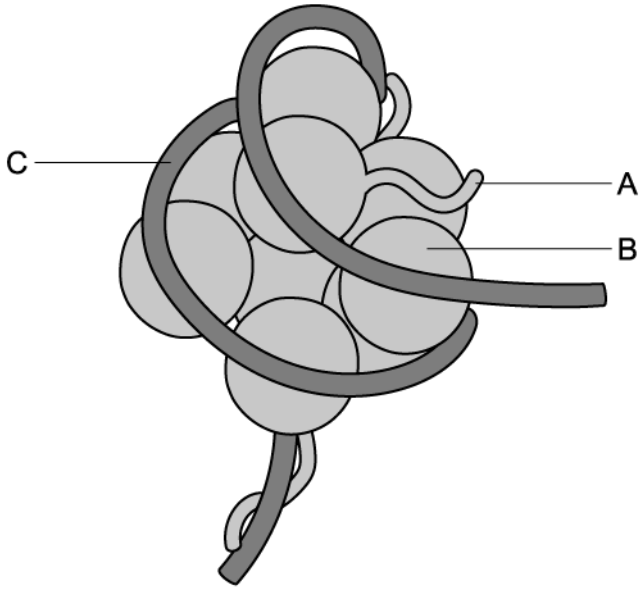
7.1.1 DNA Structure / 7.1.2 Mechanism of DNA Replication / 7.1.3 Non-coding DNA / 7.1.4 DNA Sequencing / 7.1.5 Skills: The Hershey & Chase Experiment / 7.1.6 Skills: Nucleosomes & Molecular Visualisation Software

Easy (5 questions)	/41
Medium (5 questions)	/50
Hard (5 questions)	/39
Total Marks	**/130**

Scan here to return to the course
or visit savemyexams.com

Easy Questions

1 (a) The diagram below represents a nucleosome.



Label parts **A** to **C** on the diagram.

.....

.....

.....

(3 marks)

(b) Prokaryotic DNA does not form nucleosomes.

State the reason for this.

.....

(1 mark)

(c) In eukaryotes, a great length of DNA is packed into a very small nucleus.

Describe how a nucleosome would contribute to make this possible.

.....

.....

(2 marks)

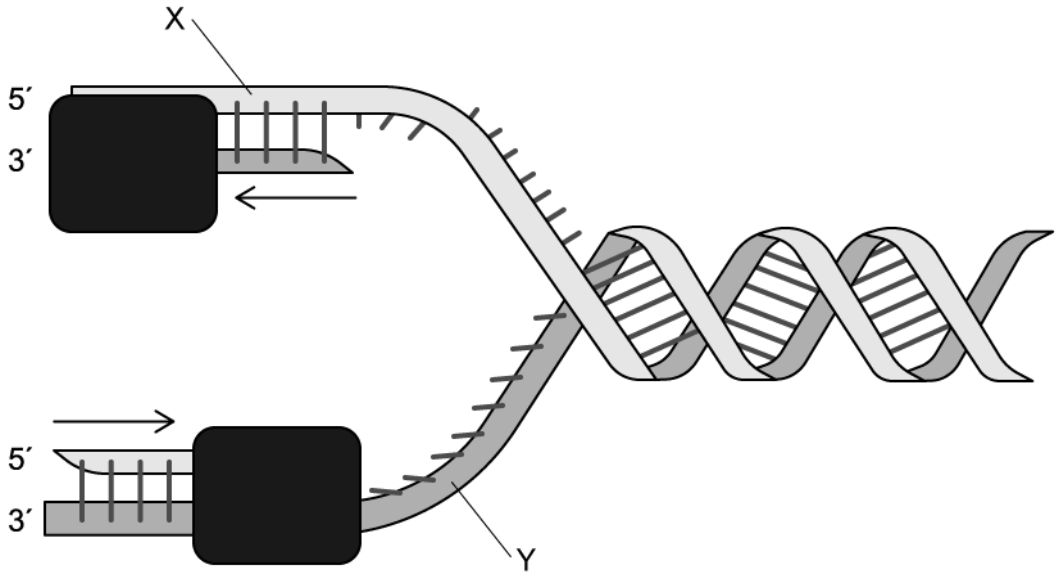
(d) Rosalind Franklin and Maurice Wilkins used a specific technique to study the structure of DNA.

State the name of this technique.

.....

(1 mark)

2 (a) The diagram below shows the process of DNA replication.



Identify which strand of **X** and **Y** is the leading and lagging strand of the original DNA molecule.

.....

.....

(2 marks)

(b) DNA replicates in a semi-conservative way.

Define the term 'semi-conservative' with regards to DNA replication.

.....

(1 mark)

(c) One of the enzymes involved with DNA replication is DNA primase.

Describe the role of DNA primase during DNA replication.

.....

.....

(2 marks)

(d) DNA replication can only occur in the 5' to 3' direction in the new strand.

State the reason for this.

.....

(1 mark)

3 (a) A crime was committed and the DNA profiles of the victim and a drop of blood found at the crime scene were constructed. These were compared to the DNA profiles of three possible suspects, as seen in the diagram below.

Identify the suspect that most likely committed the crime.

.....

(1 mark)

(b) Variable number tandem repeats (VNTRs) are short, non-coding regions of DNA that can be used in DNA profiling.

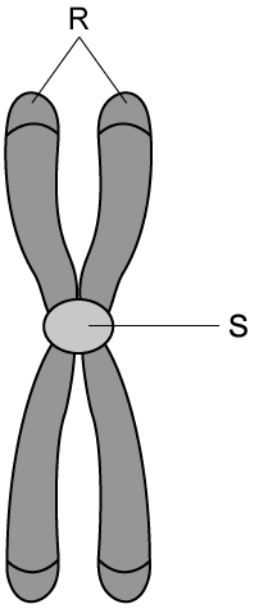
Explain the use of VNTRs in DNA profiling.

.....

.....

(2 marks)

(c) The diagram below represents the structure of a chromosome.



Label parts **R** and **S** of the chromosome.

.....

.....

(2 marks)

(d) **R** and **S** from the chromosome at part c) represents non-coding regions of DNA.

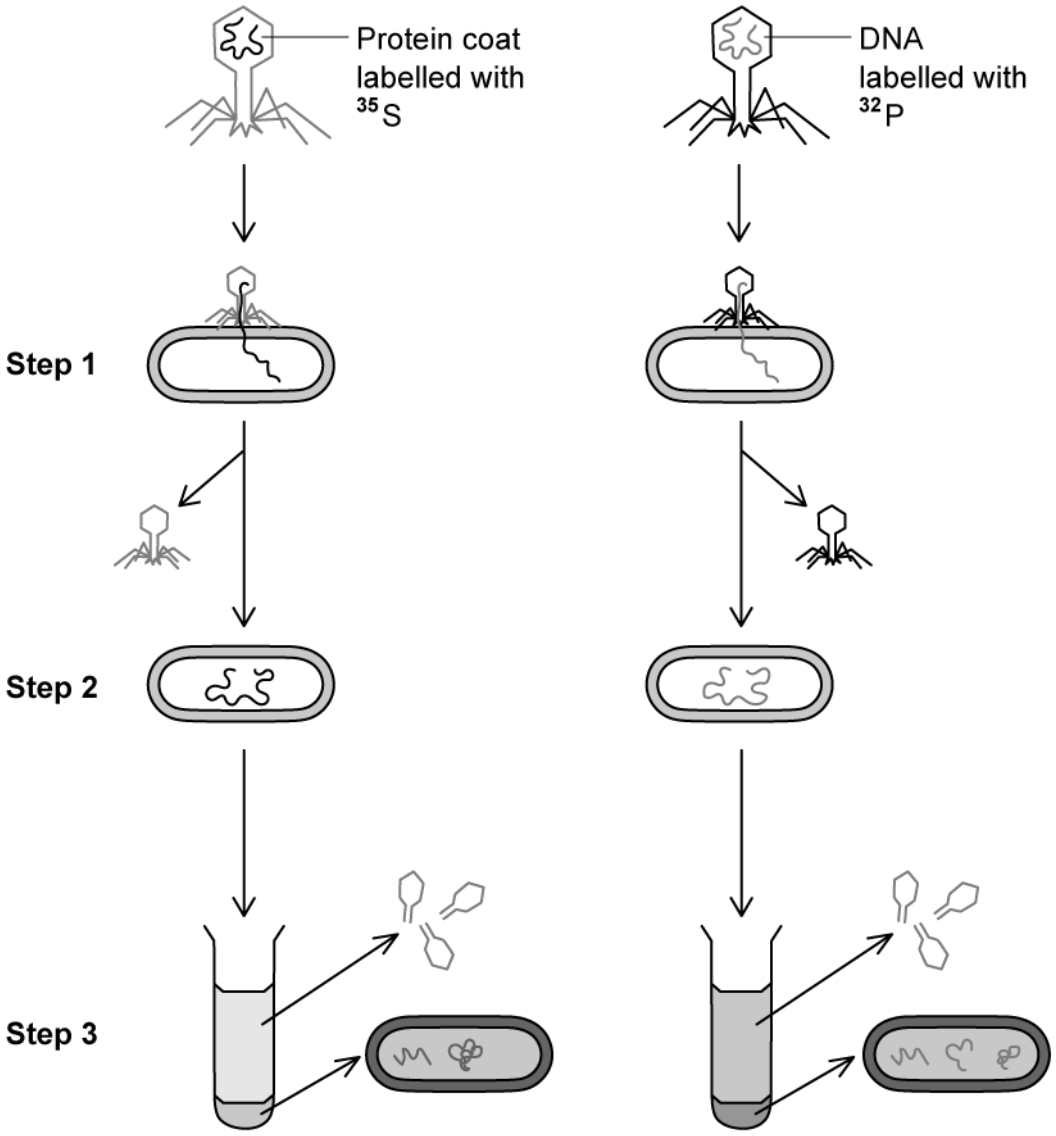
State the function of **R** and **S** in a chromosome.

.....

.....

(2 marks)

4 (a) The diagram below shows the experimental procedure followed by Alfred Hershey and Martha Chase.



State the aim of this experiment.

.....

(1 mark)

(b) Based on the information in the diagram at part a), state **one** reason why viruses were used in this experiment.

.....

(1 mark)

(c) Describe the events taking place between step **1** and **2** of the experiment.

.....

.....

(2 marks)

(d) State the results obtained at the end of step **3**.

.....

.....

(2 marks)

5 (a) *One mark is available for clarity of communication throughout this question.*

Describe the roles of non-coding regions of DNA molecules.

(4 marks)

(b) The chain-termination method is one way in which DNA can be sequenced.

Outline the steps of the chain termination method of DNA sequencing.

(6 marks)

(c) Molecular visualisation software is a useful tool with which to study the structure of molecules.

State **five** applications of molecular visualisation software in the fields of medicine and science.

(5 marks)

Medium Questions

1 (a) Some DNA is associated with a protein called histone, which packages the DNA into structures called nucleosomes.

Describe the structure of a nucleosome.

(2 marks)

(b) State the functions of nucleosomes.

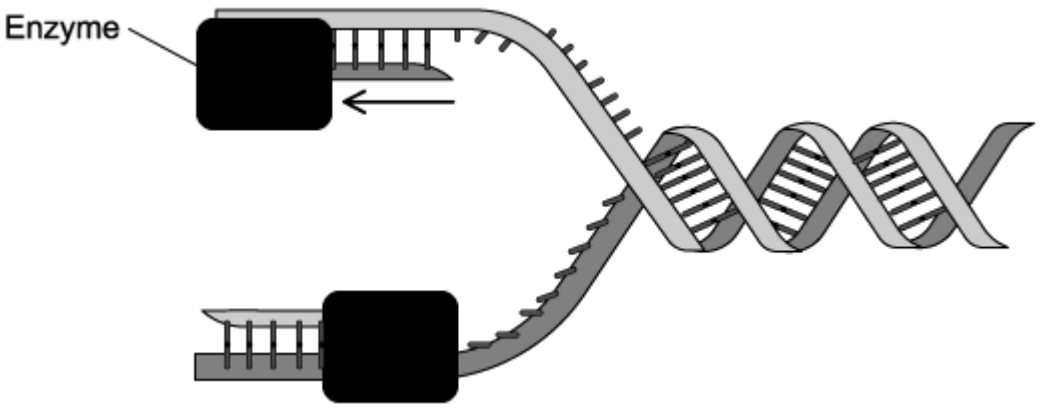
(2 marks)

(c) Within the nucleus, DNA is replicated semi-conservatively in order to produce new cells.

State **two** features of DNA and explain how these features are important in the process of semi-conservative replication of a cell's DNA.

(2 marks)

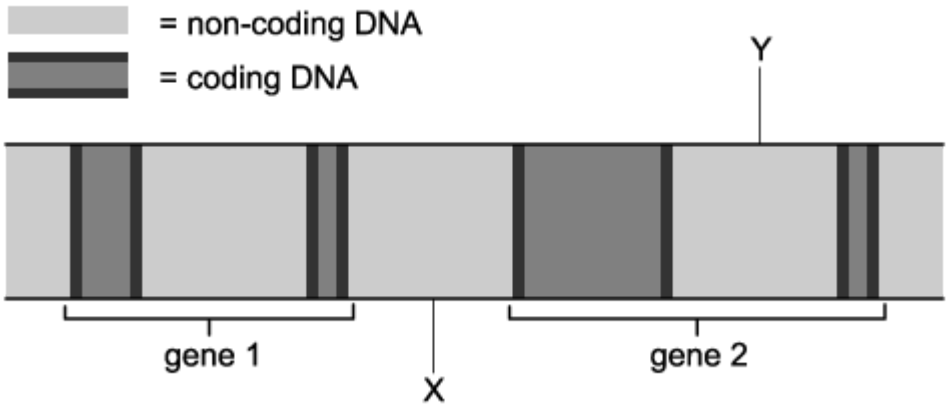
(d) The diagram below shows DNA replication.



Name the enzyme shown in the diagram and describe its function.

(3 marks)

2 (a) The diagram below illustrates a small section of a DNA molecule from the nucleus of a eukaryotic cell.



State the structures labelled **X** and **Y**.

.....

.....

(2 marks)

(b) A repetitive sequence of DNA occurs at the ends of eukaryotic chromosomes, called a telomere.

Explain the role of a telomere.

.....

.....

(2 marks)

(c) Most of the DNA in an organism is contained within the nucleus. Some of this DNA is unique, whilst some is made up of highly repetitive sequences.

Contrast unique and highly repetitive sequences of DNA

.....

.....

(3 marks)

(d) DNA was originally thought of as a protein. In the 1950s, Alfred Hershey and Martha Chase showed that DNA is a factor of heredity responsible for carrying genetic information from one generation to another.

Describe their experiment.

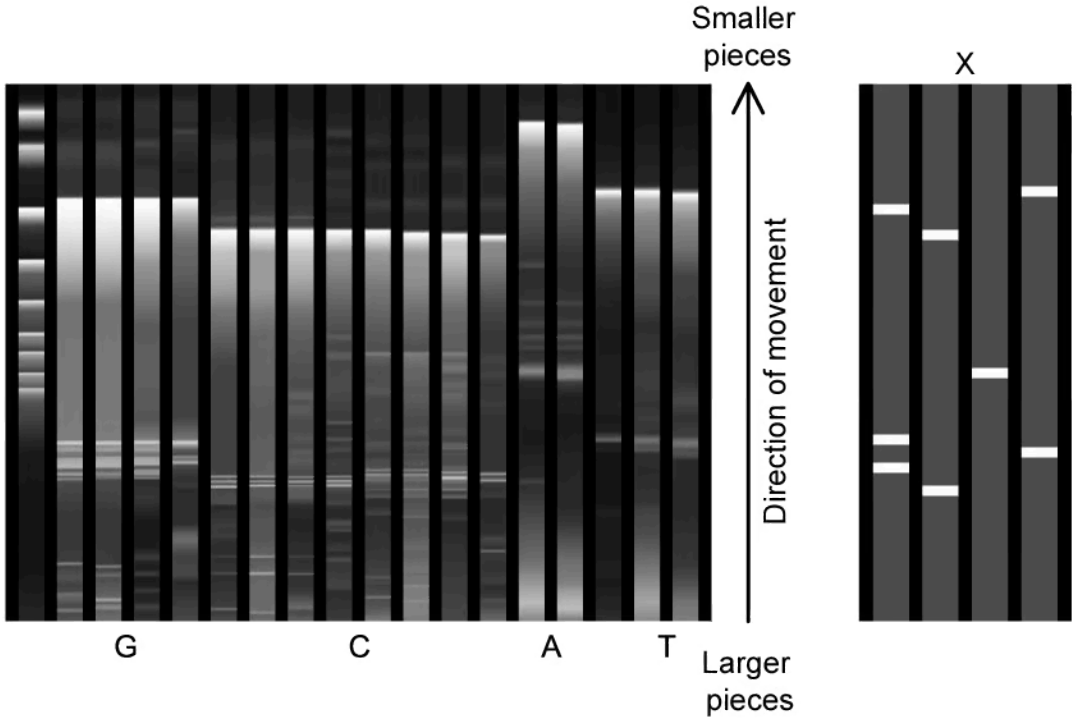
(3 marks)

3 (a) The sequence of DNA can be determined by a machine and technique developed by Frederick Sanger, called the dideoxyribonucleotide chain termination method.

Describe how nucleotides containing dideoxyribonucleic acid stop DNA replication.

(3 marks)

(b) The chain termination process can be used to identify the sequence of base pairs.

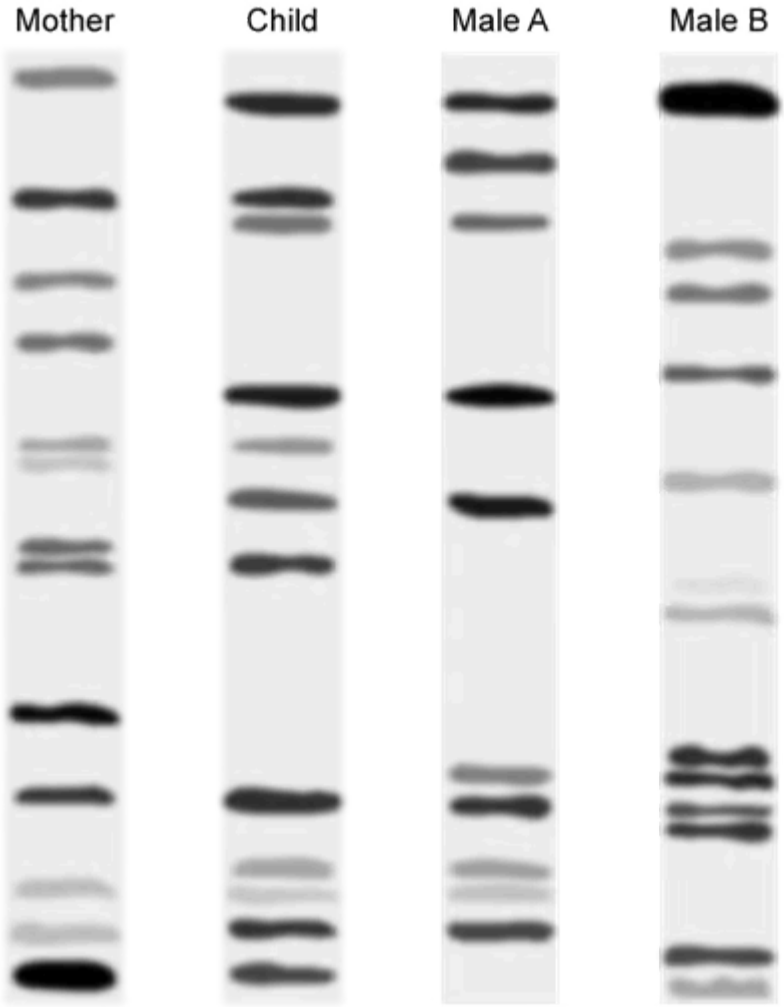


Use the image above to identify the order of bases, starting with the smallest, in the block of DNA labelled X, on the right.

(1 mark)

(c) Results from a paternity test using gel electrophoresis are shown in the image below. DNA was isolated from a mother, her child and two potential fathers. Primers designed

to amplify different satellite DNA regions were used and amplified alleles are shown in the results below.

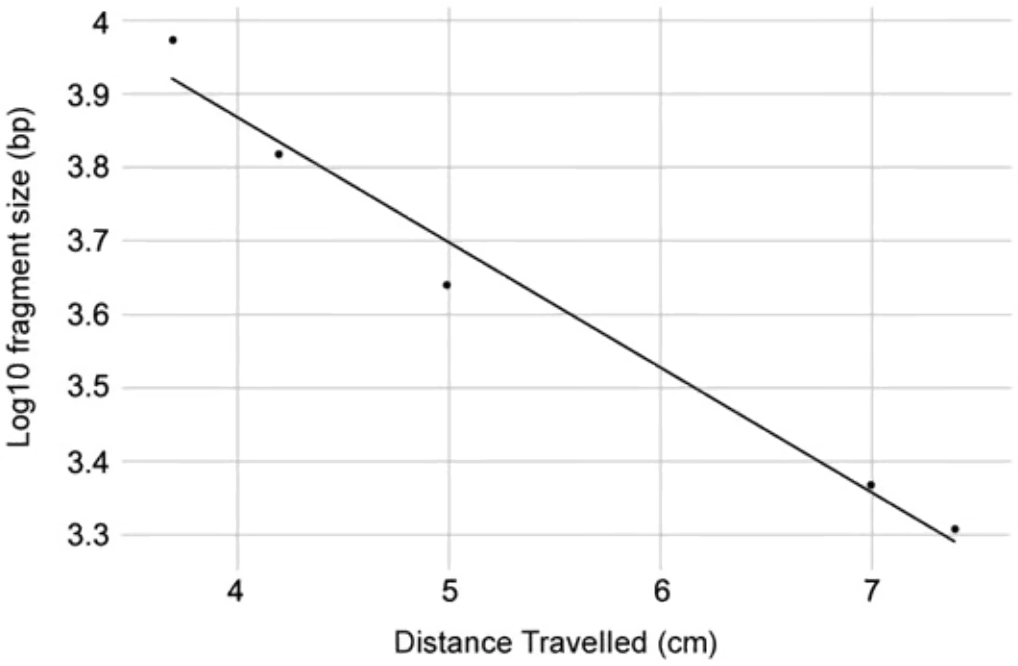


Use the gel electrophoresis DNA profiles in the image above to determine which male is the child's father.

.....

(1 mark)

(d) The DNA fragments separated in the gel electrophoresis in part (c) vary in size from 100 bp (base pairs) up to 5 000 bp. DNA fragments of known size were used to create the plot shown in the graph below.



Use the line of best fit on the graph to determine the base pair length for DNA fragments that travelled 5 cm on the gel electrophoresis plate. Give answers to the nearest whole number.

.....

.....

(2 marks)

4 (a) DNA was studied by X-ray diffraction by Rosalin Franklin and Maurice Wilkins in the 1950's.

Explain how X-ray diffraction allowed Franklin and Wilkins to view the molecular structure of DNA.

(3 marks)

(b) Today, visualisation software can be utilised to analyse DNA in very high detail. The association between protein and DNA within the nucleosome can be seen.

Describe what may be visualised when analysing a nucleosome.

(3 marks)

(c) Many visualisation techniques have been used to understand and study the structure of DNA. Watson and Crick used visualisation techniques, such as Franklin's X-ray diffraction, to build a physical model of DNA. Their models were also influenced by the findings of other researchers, such as Erwin Chargaff.

Describe how the research findings of Franklin and Chargaff facilitated Watson and Crick to determine the structure of DNA.

(3 marks)

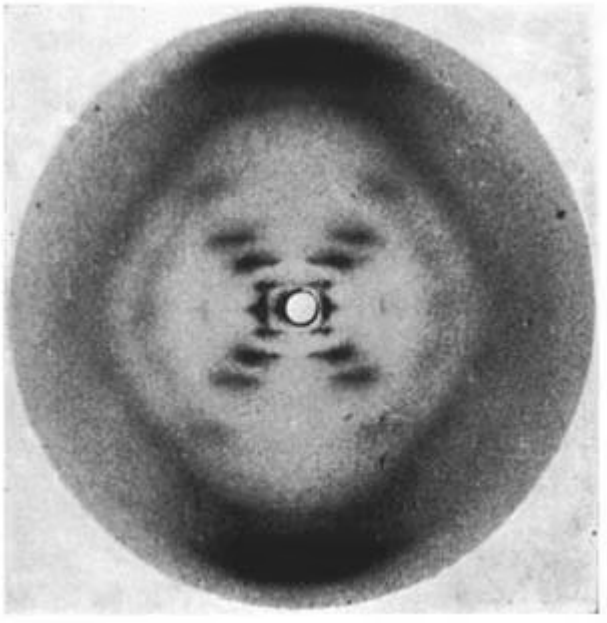
5 (a) *One mark is available for clarity of communication throughout this question.*

Outline the steps of DNA replication at a replication fork, describing the role of each of the enzymes involved.

(6 marks)

(b) Rosalind Franklin's X-ray diffraction helped to determine the double-helix structure of DNA.

Describe the deductions Franklin made from the images she produced by X-ray diffraction.



(4 marks)

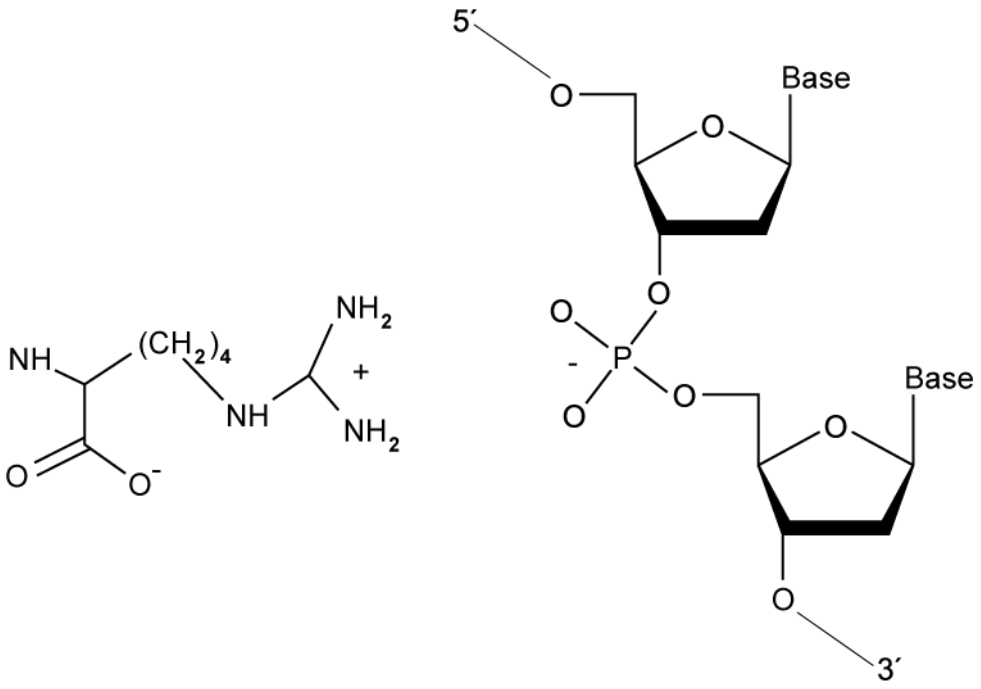
(c) Draw a labelled diagram to show four DNA nucleotides, each with a different base, linked together in two strands.

(5 marks)

Hard Questions

1 (a) Arginine is an amino acid found in histone proteins and plays an important role in the interaction between histones and DNA within nucleosomes.

The diagram below shows the structure of arginine and a section of DNA within a nucleosome.



Suggest how arginine facilitates the interaction between histones and DNA, by using the information in the diagram.

.....

.....

(2 marks)

(b) Explain the role of nucleosomes in chromosome structure.

.....

.....

(2 marks)

(c) Packing ratio is determined by dividing the length of DNA packed into a structure by the length of the structure.

Chromosome 11 consists of about 1.35×10^8 base pairs and the distance between adjacent base pairs is 3.4 nm. The chromosome is about 5 μm in length during metaphase.

Calculate the packing ratio of chromosome 11. Show your working.

.....

.....

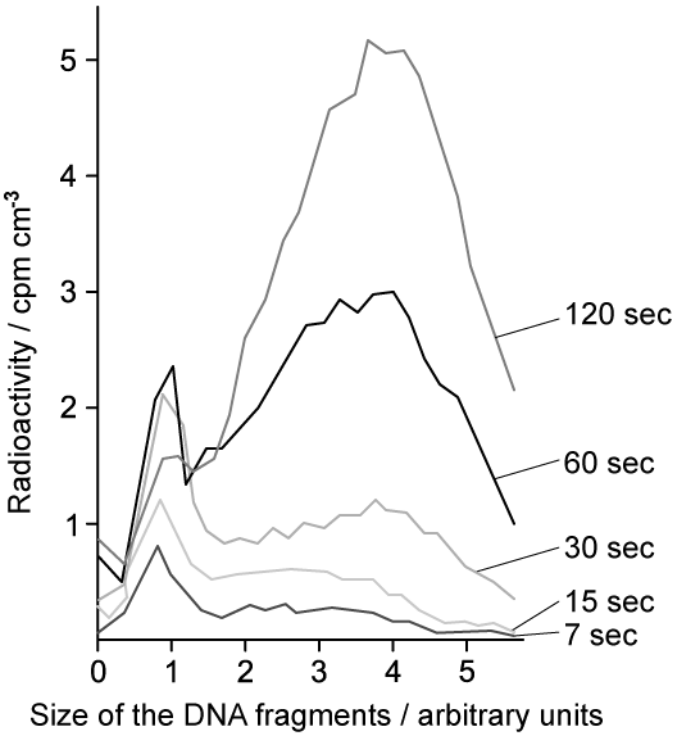
(2 marks)

2 (a) A group of scientists studied the replication of DNA in *Escherichia coli* bacteria.

During their investigation, radioactive nucleotides were added to DNA that was actively replicating in a short pulse of about 5 seconds. This allowed the radioactive nucleotides to be incorporated into the new DNA strands.

This was followed by a "chase" period, during which an abundance of unlabelled nucleotides was added to the DNA for different amounts of time, between 7 and 120 seconds. After the isolation and centrifugation of the DNA molecules, the results were obtained.

The graph below shows the results of their investigation.



Contrast the results obtained at a "chase" period of 7 seconds with those obtained at 120 seconds.

.....

.....

(2 marks)

(b) Explain the results obtained at a "chase" period of 60 seconds.

(2 marks)

(c) Suggest a possible explanation for the low number of small fragments present at 120 seconds.

(1 mark)

(d) Sketch a line on the graph of the predicted results that could be obtained at a "chase" period of 150 seconds.

(2 marks)

3 (a) The following table shows the DNA base composition of different organisms. Note that for *E. coli*, the %C and %T has deliberately been left out.

Organism	%A	%C	%T	%G
Maize	26.7	23.3	27.0	23.0
Chicken	28.0	21.9	27.8	22.3
Octopus	33.0	17.2	32.1	17.7
Grasshopper	29.8	20.2	29.2	20.8
Sea urchin	32.6	16.9	33.1	17.4
Yeast	31.5	18.1	32.1	18.3
E. coli	24.7	-	-	**X**

State **two** deductions that can be made from the data.

.....

.....

(2 marks)

(b) Calculate the possible value of **X** in the table in part a).

Show your working.

.....

.....

(2 marks)

(c) The results from part a) are similar to those first obtained by Erwin Chargaff in the 1950s.

Suggest how Chargaff's research may have impacted the work of Crick and Watson.

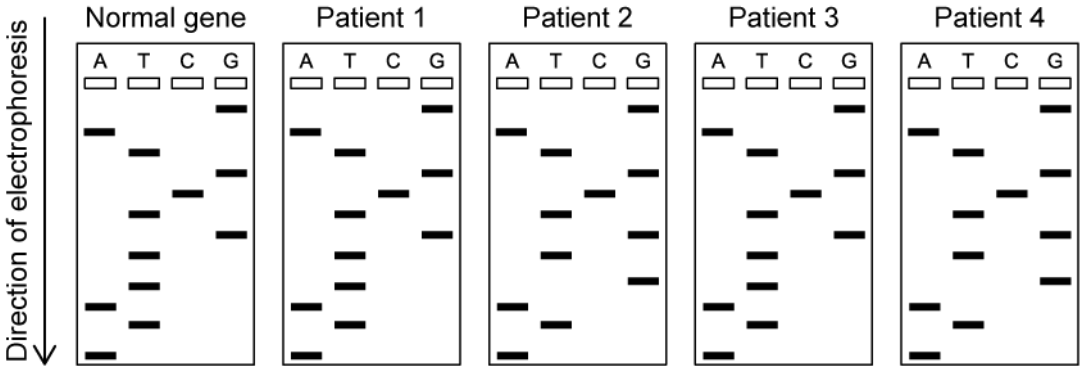
.....

.....

(2 marks)

4 (a) A mutation of the HTT gene may increase the risk of a person developing Huntington disease later in their lives. Blood samples from four different individuals were taken and the base sequences of a part of their HTT gene were sequenced using the chain termination method. These were compared to the normal base sequence of the HTT gene by reading from the smallest to the largest fragments.

The results from the gel electrophoresis are shown in the diagram below.



Identify the base sequence of the normal gene.

.....

(1 mark)

(b) Using the information in part a), deduce which patient(s) would have a higher risk of developing Huntington disease.

.....

(1 mark)

(c) During the chain termination method, modified nucleotides called dideoxynucleotides are used.

Contrast the structure and function of a dideoxynucleotide with a regular nucleotide.

.....

.....

(2 marks)

(d) Suggest what would happen to DNA polymerase once a dideoxynucleotide is incorporated into the growing DNA strand.

.....

(1 mark)

5 (a) *One mark is available for clarity of communication throughout this question.*

Compare and contrast DNA profiling with the chain termination method of DNA sequencing.

(6 marks)

(b) The structure of DNA was discovered due to the research and input from several different scientists.

Outline how the discovery of the structure of DNA led to the development of the theory of semi-conservative DNA replication.

(4 marks)

(c) Discuss the formation of Okazaki fragments during the process of replication on the lagging strand of a DNA molecule.

(5 marks)