Genetic Fingerprinting

These practice questions can be used by students and teachers and is

Suitable for AQA A Level 7402 Biology Topic Question

Level: AQA A LEVEL 7402

Subject: Biology

Exam Board: AQA A Level 7402

Topic: Genetic Fingerprinting

1

Scientists developed a method for finding out whether a fly was carrying a recessive allele, **r**, that gives resistance to an insecticide. The dominant allele, **R**, of this gene does not give resistance.

The scientists:

- crossed flies with genotype **RR** with flies with genotype **rr**
- obtained DNA samples from the parents and offspring
- used the same restriction endonuclease enzymes on each sample, to obtain DNAfragments.

(a) Explain why the scientists used the same restriction endonuclease enzymes on each DNA sample.

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(2)

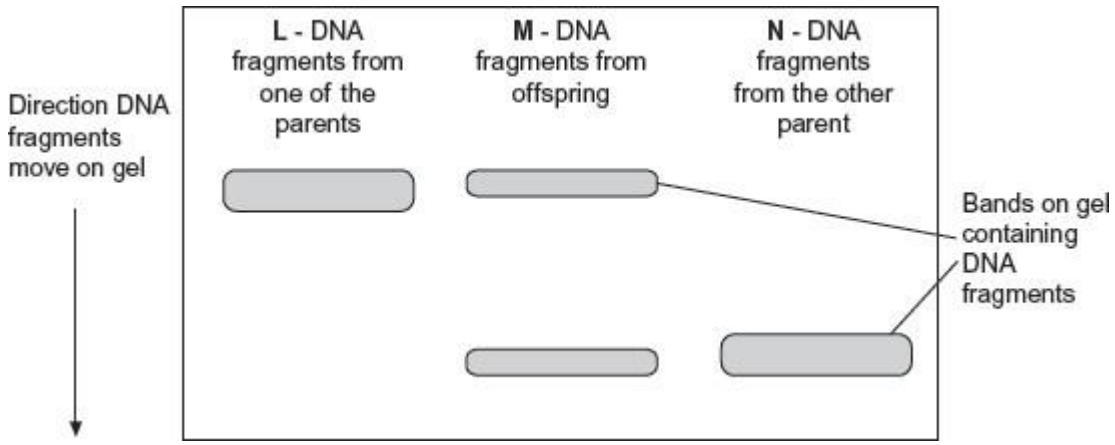
The scientists added two different primers to each sample of DNA fragments for the polymerase chain reaction (PCR).

- Primer A3 only binds to a 195 base-pair fragment from allele **r**.
- Primer A4 only binds to a 135 base-pair fragment from allele **R**.

The scientists separated the DNA fragments produced by the PCR on a gel where shorter fragments move further in a given time.

Their results are shown in **Figure 1**.

Figure 1



(b) Explain why primer A3 and primer A4 only bind to specific DNA fragments.

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(2)

(c) Use all the information given to explain the results in **Figure 1**.

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_____

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[Extra space]

(3)

(d) The scientists wanted to know on which chromosome the gene with alleles **R** and **r** was located. From the flies with genotype **RR**, they obtained cells that were in mitosis and added a labelled DNA probe specific for allele **R**. They then looked at the cells under an optical microscope.

Explain why they used cells that were in mitosis.

(2)

(e) Another group of scientists thought that pesticide resistance in some flies was related toincreased activity of an enzyme called P450 monooxygenase (PM). This enzyme breaks down insecticides.

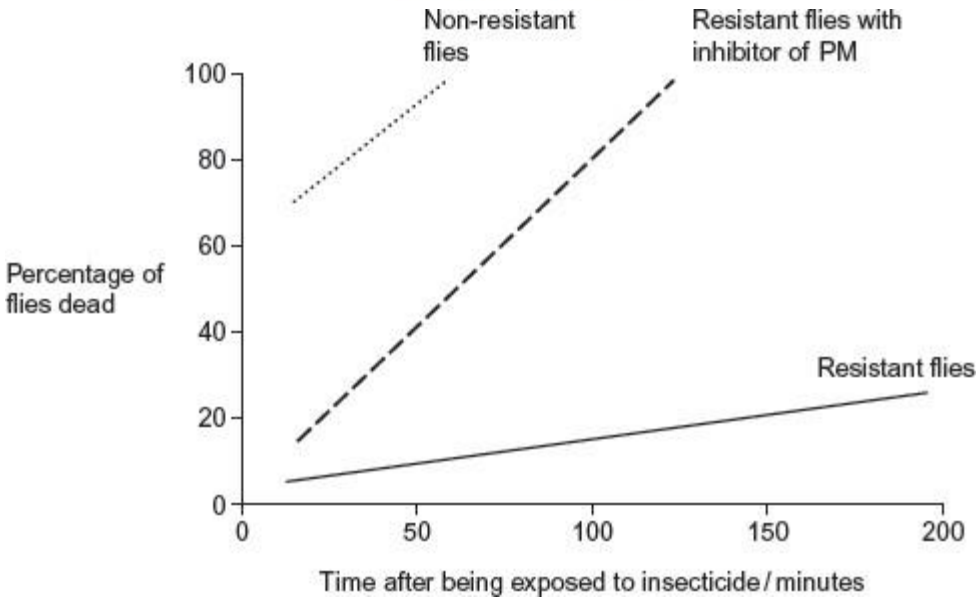
The scientists obtained large numbers of resistant and non-resistant flies. They then set up the following experiments.

- Non-resistant flies exposed to insecticide.
- Resistant flies exposed to insecticide.
- Resistant flies treated with an inhibitor of PM and then exposed to insecticide.

They then determined the percentage of flies that were dead at different times after being exposed to insecticide.

Figure 2 shows their results.

Figure 2



(i) Explain why the scientists carried out the control experiment with the non-resistantflies.

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(2)

(ii) The scientists concluded that the resistance of the flies to the insecticide is partly dueto increased activity of PM but other factors are also involved.

Explain how these data support this conclusion.

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[Extra space] _____

_____

_____

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(4)

(Total 15 marks)

2 Scientists wanted to measure how much mRNA was transcribed from allele **A** of a gene in a sample of cells. This gene exists in two forms, **A** and **a**.

The scientists isolated mRNA from the cells. They added an enzyme to mRNA to produce cDNA.

(a) Name the type of enzyme used to produce the cDNA.

_____

(1)

The scientists used the polymerase chain reaction (PCR) to produce copies of the cDNA. They added a DNA probe for allele **A** to the cDNA copies. This DNA probe had a dye attached to it. This dye glows with a green light **only** when the DNA probe is attached to its target cDNA. (b) Explain why this DNA probe will only detect allele **A**.

_____

_____

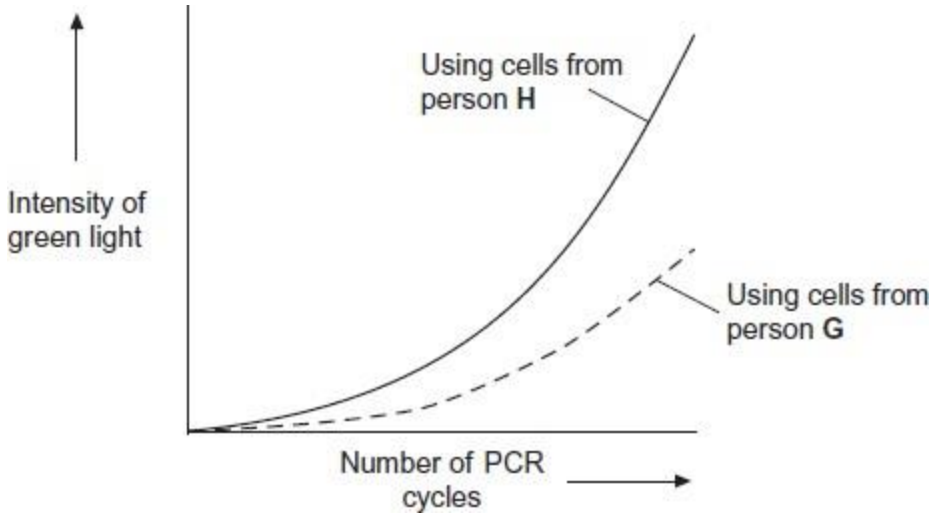
_____

_____

(2)

(c) The scientists used this method with cells from two people, **H** and **G**.
One person was homozygous, **AA**, and the other was heterozygous, **Aa**.
The scientists used the PCR and the DNA probe specific for allele **A** on the cDNA from both people.

The figure shows the scientists' results.



(i) Explain the curve for person **H**.

(Extra space)

(3)

(ii) Which person, **H** or **G**, was heterozygous, **Aa**? Explain your answer.

(2)
(Total 8 marks)

Essay

3

You should write your essay in continuous prose.

Your essay will be marked for its scientific accuracy.

It will also be marked for your selection of relevant material from different parts of the specification and for the quality of your written communication.

The maximum number of marks that can be awarded is

Scientific	16
Breadth of knowledge	3
Relevance	3
Quality of written communication	3

Write an essay on the following topic:

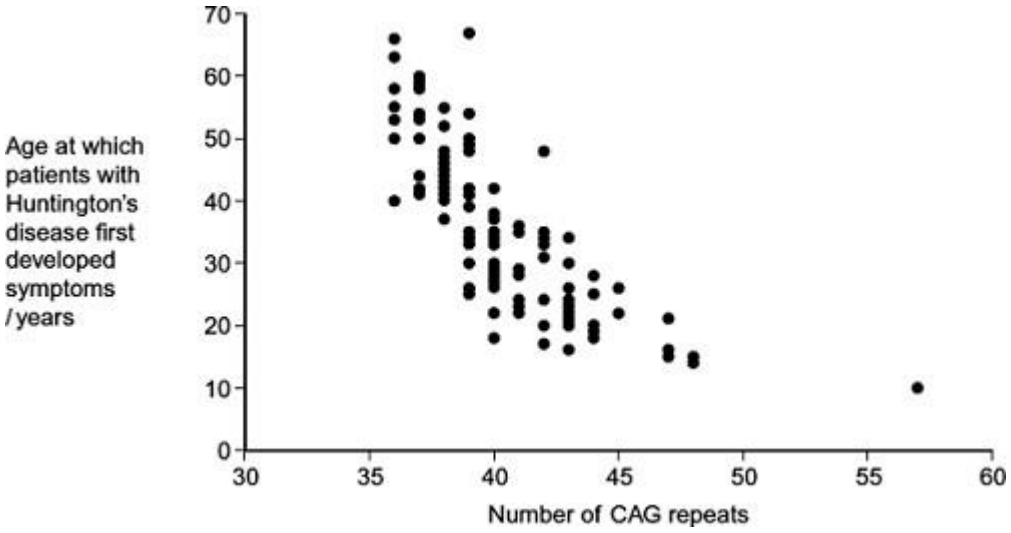
Using DNA in science and technology

(Total 25 marks)

4 Huntington's disease is a genetic condition that leads to a loss in brain function. The gene involved contains a section of DNA with many repeats of the base sequence CAG. The number of these repeats determines whether or not an allele of this gene will cause Huntington's disease.

- An allele with 40 or more CAG repeats will cause Huntington's disease.
- An allele with 36 – 39 CAG repeats may cause Huntington's disease.
- An allele with fewer than 36 CAG repeats will not cause Huntington's disease.

The graph shows the age at which a sample of patients with Huntington's disease first developed symptoms and the number of CAG repeats in the allele causing Huntington's disease in each patient.



(a) (i) People can be tested to see whether they have an allele for this gene with more than 36 CAG repeats. Some doctors suggest that the results can be used to predict the age at which someone will develop Huntington's disease.

Use information in the graph to evaluate this suggestion.

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*(Extra space)*_____

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_____

(3)

(ii) Huntington's disease is always fatal. Despite this, the allele is passed on in human populations. Use information in the graph to suggest why.

_____

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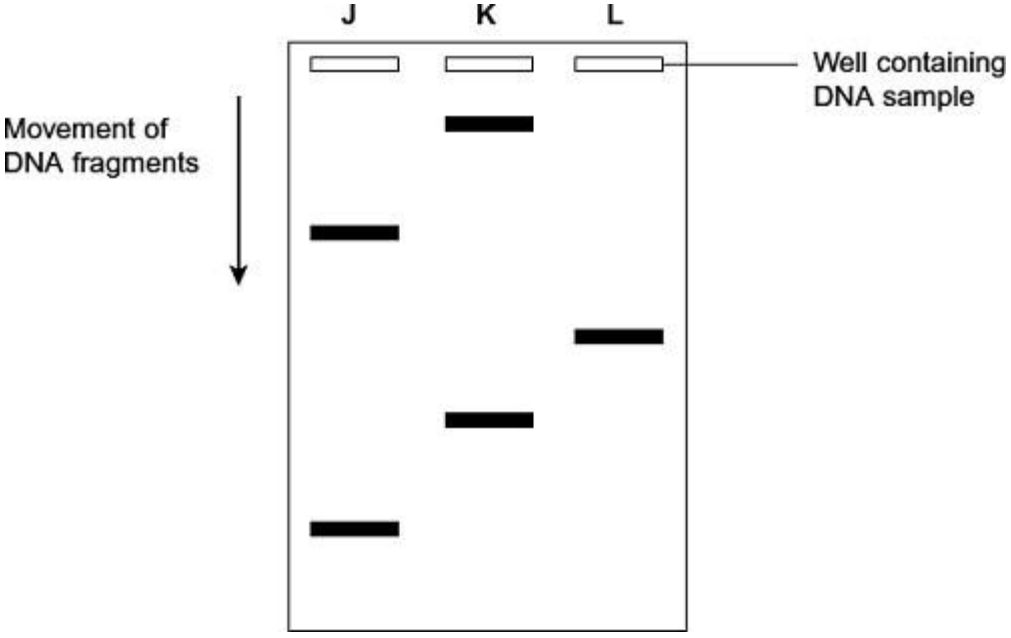
(2)

(b) Scientists took DNA samples from three people, **J**, **K** and **L**. They used the polymerase chain reaction (PCR) to produce many copies of the piece of DNA containing the CAG repeats obtained from each person. They separated the DNA fragments by gel electrophoresis. A radioactively labelled probe was then used to detect the fragments. The diagram shows the appearance of part of the gel after an X-ray was taken. The bands show the DNA fragments that contain the CAG repeats.



(i) Only one of these people tested positive for Huntington's disease. Which person wasthis? Explain your answer.

Person _____

Explanation _____

_____

_____

_____

(2)

(ii) The diagram only shows part of the gel. Suggest how the scientists found the numberof CAG repeats in the bands shown on the gel.

_____

_____

_____

(1)

(iii) Two bands are usually seen for each person tested. Suggest why only one band wasseen for Person **L**.

_____

EXAM PAPERS PRACTICE

(1)

(Total 9 marks)

5 There are wolves in many European countries. Scientists investigated the genetic diversity of these wolves. They collected samples of DNA from the mitochondria of wolves from different countries. For each sample they identified which haplotypes were present in the DNA. A haplotype is a particular sequence of bases on DNA. Mutations can produce new haplotypes.

Country	Number of wolves sampled	Number of different haplotypes in mitochondrial DNA
Spain	84	3
Portugal	19	2
Italy	101	1
France	7	1
Bulgaria	29	6
Sweden	93	1

The scientists wanted to find out whether one of the haplotypes in the Portuguese wolves was the same as one of those in the Spanish wolves. They used a restriction endonuclease, electrophoresis and a labelled DNA probe.

(a) For what purpose did they use

(i) the restriction endonuclease

_____

_____

(1)

(ii) electrophoresis?

_____

_____

(1)

(b) Explain why the labelled DNA probe could be used to find out whether the haplotypes werethe same.

(2)

(c) The scientists analysed the DNA on the Y chromosome and the DNA in the mitochondria ofthe Swedish wolves. They concluded that the Swedish wolf population descended from one male wolf from Finland and one female wolf from Russia.

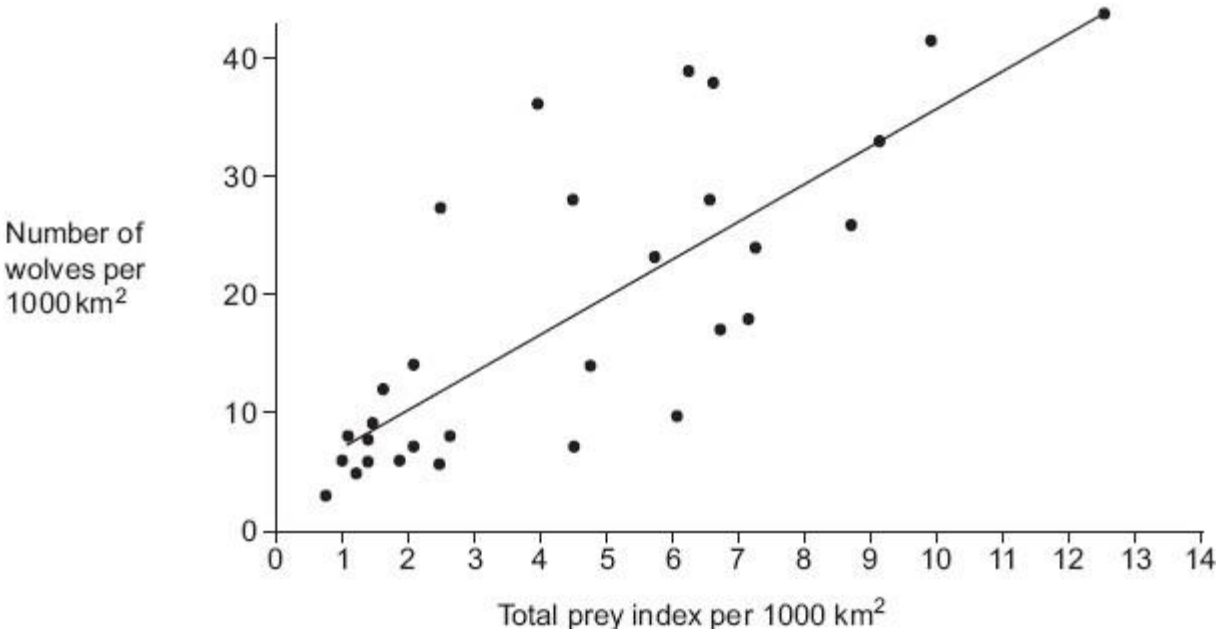
(i) Explain why DNA on the Y chromosome helped them to reach this conclusion.

(1)

(ii) Suggest why DNA in the mitochondria helped them to reach this conclusion.

(1)

Wolves eat different mammals. An ecologist investigated factors that affect wolf numbers in North America. He collected data from different field studies carried out in different places. The graph shows his results.



(d) (i) The wolf numbers are given per unit area. Explain why.

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(2)

(ii) The ecologist calculated the total prey index for each of the places that had been studied. In order to do this, he gave each prey species a value based on how much food was available to wolves from the prey animal concerned. He called this value the prey index.

The ecologist considered that the prey index gave a better idea of the food available than the prey biomass in kg. Suggest why the prey index gives a better idea of food available.

_____

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_____

(2)

(e) The ecologist calculated the total prey index by combining the prey indices and the totalnumber of animals of each species present in 1000 km^2. He plotted this information on the graph. What does the graph suggest about the factors that determine wolf numbers in North America? Explain your answer.

_____

_____

_____

_____

(2)

(Total 12 marks)

6

(a) What is meant by a gene?

_____

_____

(2)

The polymerase chain reaction (PCR) can be used to obtain many copies of a particular gene.

(b) Explain how the strands of DNA are separated during the PCR.

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_____

_____

_____

(2)

(c) In a particular PCR, two different primers are added to the DNA.

(i) Why are primers required?

_____

_____

(1)

(ii) Suggest why two different primers are required.

_____

_____

(1)

(d) Starting with a single molecule of DNA, the polymerase chain reaction was allowed to go through three complete cycles. How many molecules of DNA would be produced?

Answer _____

(1)

(Total 7 marks)

7 Read the following passage.

The giant panda is one of the rarest animals in the world and is considered to be on the brink of extinction in the wild. Giant pandas have been kept and bred in zoos with the hope that they could be released into the wild. One worry is that small populations, like those in zoos, reduce the genetic variation needed to allow the species to adapt to changing conditions. Unfortunately, pandas find it difficult to reproduce in captivity. Fertilisation of the females is guaranteed only by insemination with semen from several males. With so many potential fathers, the true paternity of the cubs is not clear. It is important to identify the fathers to maintain genetic variation. 5

Panda faeces can be collected in the wild. The faeces contain DNA from the panda, from the bamboo on which they feed and from bacteria. The DNA is subjected to the polymerase chain reaction (PCR). The primers used attach only to the panda DNA. The resulting DNA is subjected to genetic fingerprinting. This can help us to count the number of individuals in the wild because it allows us to identify individual pandas. 10

Use information in the passage and your own biological knowledge to answer the questions.

(a) Describe how genetic fingerprinting may be carried out on a sample of panda DNA.

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(6)

(b) (i) Explain how genetic fingerprinting allows scientists to identify the father of a particular panda cub.

(2)

(ii) When pandas are bred in zoos, it is important to ensure only unrelated pandas breed. Suggest how genetic fingerprints might be used to do this.

(1)

(c) (i) Suggest why panda DNA is found in faeces. (line 10)

(1)

(ii) Explain why the PCR is carried out on the DNA from the faeces. (line 12)

_____

_____

(1)

(iii) Explain why the primers used in the PCR will bind to panda DNA, but not to DNA from bacteria or bamboo. (line 12)

_____

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(2)

(d) DNA from wild pandas could also be obtained from blood samples. Suggest **two** advantages of using faeces, rather than blood samples, to obtain DNA from pandas.

1. _____

_____

2. _____

_____

(2)

(Total 15 marks)

8 Read the following passage.

DNA tests were used to confirm the identity of deposed Iraqi leader Saddam Hussein, after his capture in December 2003. DNA tests were carried out to prove the suspect was not one of the many alleged "look alikes" of the former leader.

Firstly, the DNA was extracted from the mouth of the captured man using a swab. Great care was taken to check that the swab did not become contaminated with any other DNA. DNA extracted from the swab was then subjected to a standard technique called the polymerase chain reaction (PCR), which takes a couple of hours. Lastly, the sample was "typed" to give the genetic fingerprint. This was produced within 24 hours of Saddam Hussein's capture. Tests for use in criminal cases often take much longer because samples are very small or contaminated.

It appears that Hussein's genetic fingerprint was already stored away for comparison. This was

obtained from personal items such as his toothbrush. DNA from the toothbrush would have been subjected to PCR before a DNA fingerprint could have been obtained.

Source: adapted from SHAONI BHATTACHARYA, *New Scientist* 15 December, 2003

Use information from the passage and your own knowledge to answer the questions.

(a) Describe how the technique of genetic fingerprinting is carried out and explain how it can be used to identify a person, such as Saddam Hussein.

(6)

(b) Explain how DNA could be present on a toothbrush (line 12).

(2)

(c) (i) Explain why the polymerase chain reaction was used on the sample of DNA from thetoothbrush (lines 12-13).

_____

_____

_____

_____

(2)

(ii) Explain **one** way in which the polymerase chain reaction differs from DNA replication in a cell.

_____

_____

_____

_____

(2)

(d) Tests for use in criminal cases often take much longer because samples are very small or contaminated (lines 8-10). Explain why it takes longer to obtain a genetic fingerprint if the sample is

(i) very small;

_____

_____

(1)

(ii) contaminated.

_____

_____

_____

_____

(2)

(Total 15 marks)

9 β-thalassaemia is a genetic condition in which abnormal haemoglobin is produced. In one form, the recessive allele for β-thalassaemia, **t**, differs from the normal allele, **T**, by a single base-pair. A radioactive DNA probe was used to investigate the genotypes of four members of one family. The flowchart summarises the technique involved.

DNA samples extracted and cut into fragments using a restriction enzyme

↓

Fragments separated from each other by electrophoresis

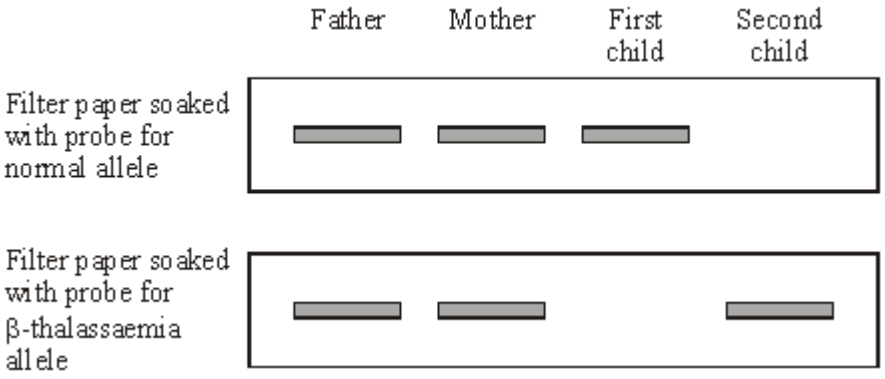
↓

One region of the resulting gel was blotted with two pieces of filter paper. The first was soaked in a solution containing a radioactive DNA probe for the normal allele. The second was soaked in a solution containing a radioactive DNA probe for the β-thalassaemia allele.

↓

Surplus probe washed off

The diagram below shows the appearance of the two pieces of filter paper which resulted from the investigation.



(a) What is the probability that the next child that this couple have is a girl who hasβ-thalassaemia? Explain your answer.

(3)

(b) (i) The fragment of DNA containing the normal allele and the fragment with theβ-thalassaemia allele moved the same distance on the gel. Explain why.

(2)

(ii) The allele for β-thalassaemia differs from the normal allele by only one base-pair. Explain why the probe used to identify these alleles consists of a piece of DNA twenty bases in length and not just one base.

(2)

(Total 7 marks)

Read the following passage.

10

Shark-fin soup is an expensive delicacy. To provide the basic ingredient, fishermen catch the sharks, hack the fins off and throw the dead bodies back into the ocean. But sharks are slow to mature and produce only a few offspring at a time, so they are vulnerable to overfishing. Monitoring the shark-fin trade is difficult, as once a fin has been cut off, it can be extremely difficult to work out precisely from which species it was taken.

The DNA from different species of sharks shows some differences in base sequence. This has enabled a new genetic fingerprinting technique to be developed. This technique would allow conservationists and fisheries managers to assess which of the 400 shark species are most threatened by the trade in shark fins.

An identification process has been developed using a range of "primers". These are short pieces of single-stranded DNA that are complementary to a particular sequence of DNA. Each primer is specific to the DNA of one shark species.

The primers are added to DNA taken from a shark's fin and the polymerase chain reaction is carried out. Only two primers, one at each end of a certain piece of DNA, will bind. The piece of DNA between the primers is replicated by the polymerase chain reaction. The primers that bind are specific to a particular species of shark and the length of the DNA fragment replicated differs for each species. When this DNA is run in an electrophoresis gel it produces a single band, enabling the researchers to identify which species of shark is involved.

Use information from the passage and your own knowledge to answer the questions.

(a) (i) Explain why the DNA for each species of shark shows differences in base sequence (line 6).

_____

_____

_____

_____

(2)

(ii) Each primer is specific to the DNA of one shark species (line 12).

Explain why a particular primer will only bind to the DNA of one species.

_____

_____

_____

(2)

(iii) The length of the replicated DNA fragment is different for each species.

Explain why this is important in identifying the shark species involved.

(3)

(b) In conventional DNA fingerprinting, a series of bands is produced on the electrophoresisgel, resembling the rungs of a ladder. When the DNA in this new genetic fingerprinting technique is run in an electrophoresis gel it produces just one of these 'rungs'.

Explain the reason for the difference in the number of 'rungs' produced.

(2)

(c) Describe the polymerase chain reaction.

(6)

(Total 15 marks)

11 A gene was broken into fragments using enzyme **Z**. The mixture of fragments produced was then separated by electrophoresis.

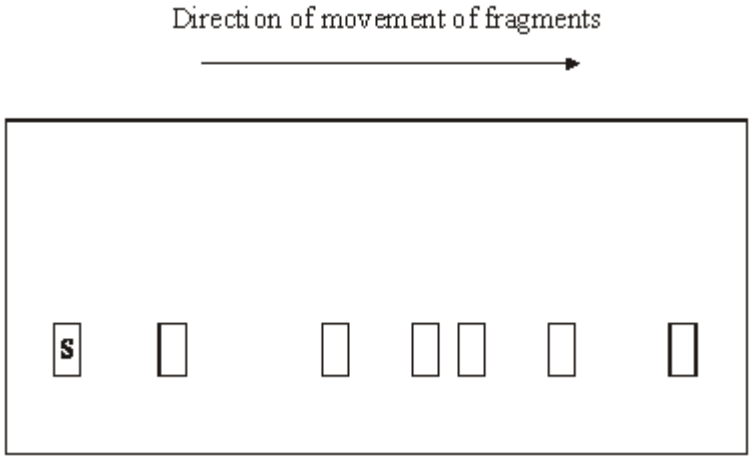
(a) What type of enzyme is enzyme **Z**?

(1)

The table shows the number of base pairs present in the fragments.

Fragment	Number of base pairs ($\times 10^3$)
1	4.65
2	5.72
3	10.71
4	2.39
5	5.35
6	7.53

The diagram shows the electrophoresis gel used. The mixture of fragments was placed at the start point marked **S** and the process started. The boxes indicate the positions reached by the different fragments.



(b) Explain why base pairs are a suitable way of measuring the length of a piece of DNA.

_____

_____

_____

_____

(2)

(c) (i) Write **6** above the appropriate box on the diagram to show the position you would expect fragment **6** to have reached.

(1)

(ii) Explain how you arrived at your answer.

_____

_____

(1)

(d) Enzyme **Z** recognises a particular sequence of bases in the gene. How many times does this sequence appear in the DNA of this gene?

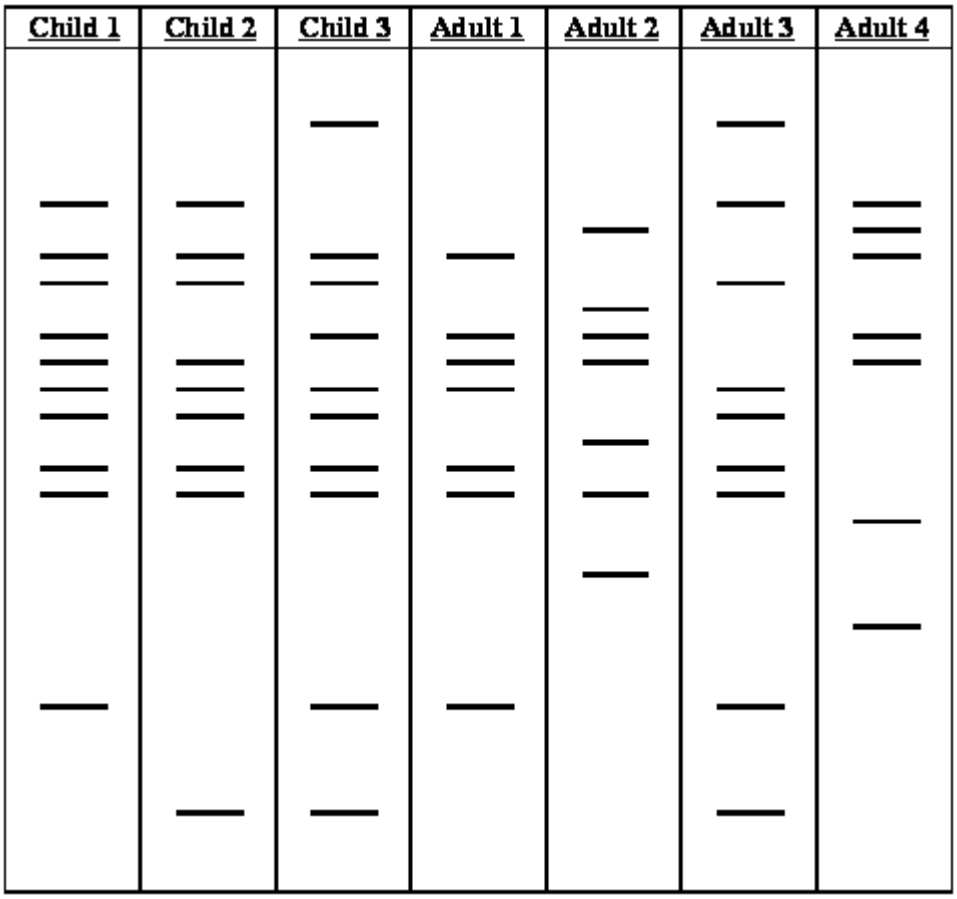
_____

(1)
(Total 6 marks)

12 Read the following passage.

In 1991, nine skeletons were found in Russia. They were believed to be those of Tsar Nicholas II, his family and staff who were killed in 1917 during the Russian revolution. Very small amounts of DNA were isolated from these skeletons. This DNA was used in the polymerase chain reaction (PCR). Genetic fingerprinting was then carried out on this DNA to identify the skeletons.

The chart shows some of the results obtained from the genetic fingerprinting of seven of the skeletons, three children and four adults.



Use information from the passage and your own knowledge to answer the following questions.

(a) Explain why the polymerase chain reaction was used in this investigation.

(2)

(b) In the polymerase chain reaction, DNA is heated to 95 °C and nucleotides, enzymes andDNA primers are added to the mixture.

(i) Explain why the DNA is heated to 95 °C.

(1)

(ii) What are DNA *primers*?

(1)

(iii) Why are DNA primers added during the polymerase chain reaction?

(1)

(iv) What is the advantage of the enzyme used in the polymerase chain reaction beingthermostable?

(2)

(c) Describe how genetic fingerprinting is carried out.

(6)

(d) All three children on the chart had the same parents. One of the parents was **Adult 1**.

Which of the other three adults on the chart was the other parent? Give the reason for your answer.

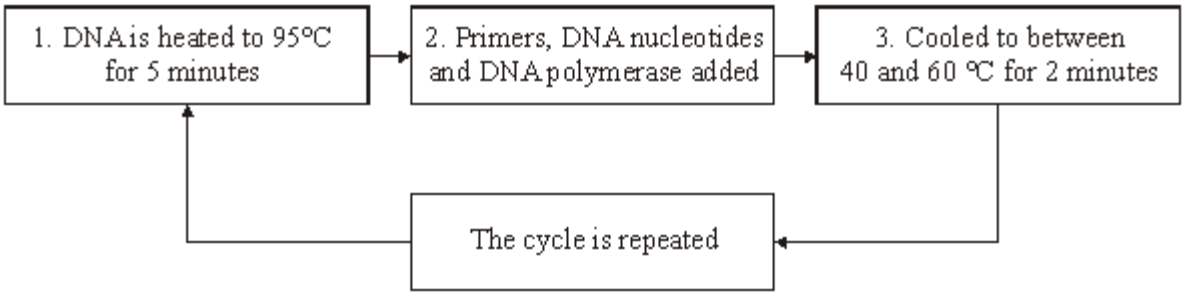
(2)
(Total 15 marks)

13 The polymerase chain reaction (PCR) can be used to produce large quantities of DNA.

Describe how the PCR is carried out.

(Total 6 marks)

14 The polymerase chain reaction is a process which can be carried out in a laboratory to replicate DNA. The diagram shows the main stages involved in the polymerase chain reaction.



(a) Explain why DNA is heated to 95 °C.

(1)

(b) What is the role of

(i) a primer in this process;

(1)

(ii) DNA polymerase?

_____

_____

(1)

(c) (i) How many DNA molecules will have been produced from one molecule of DNA after 6 complete cycles?

_____

(1)

(ii) Suggest **one** use of the polymerase chain reaction.

_____

_____

(1)

(d) Give **two** ways in which the polymerase chain reaction differs from the process of transcription.

1. _____

_____

2. _____

_____

(2)

(Total 7 marks)

15 (a) Explain the reason for each of the following in the polymerase chain reaction (PCR).

(i) DNA is heated to 95 °C.

_____

_____

(1)

(ii) DNA polymerase used is heat-stable.

_____

_____

(1)

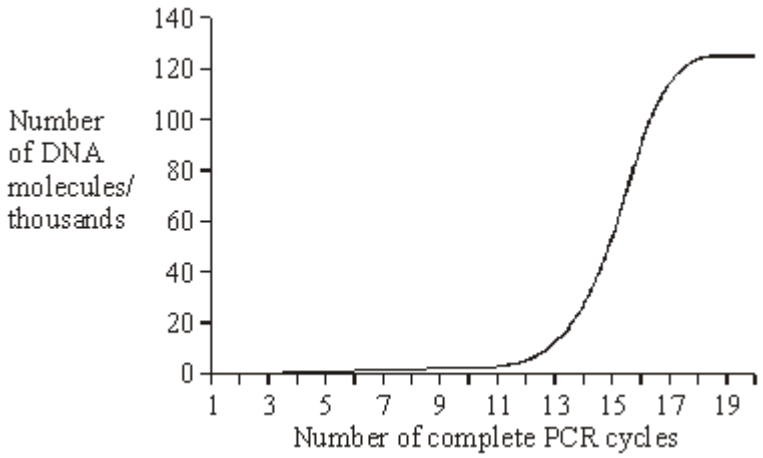
(iii) The reaction mixture is cooled to 40 °C.

_____

_____

(1)

(b) The graph shows the number of DNA molecules made using PCR, starting with one molecule.



(i) Explain the shape of the curve from cycles 1 to 16.

_____

_____

_____

_____

(2)

(ii) Suggest **one** explanation for the levelling out of the curve from cycles 17 to 20.

_____

_____

_____

_____

(2)
(Total 7 marks)

Mark schemes

1

(a) 1. Cut (DNA) at same (base) sequence / (recognition) sequence;

Accept: cut DNA at same place

2. (So) get (fragments with gene) **R** / required gene.

Accept: 'allele' for 'gene' / same gene

2

(b) 1. Each has / they have a specific base sequence;
2. That is complementary (to allele r or R). *Accept description of 'complementary'*

2

(c) 1. Fragments L from parent rr, because all longer fragments / 195 base pair fragments;

Ignore: references to fragments that move further / less, require identification of longer / shorter or 195 / 135 Accept: (homozygous) recessive

2. Fragments N from parent RR, because all shorter fragments / 135 base pairfragments;

1 and 2 Accept: A3 for 195 and A4 for 135

2. Accept: (homozygous) dominant

3. (M from) offspring heterozygous / Rr / have both 195 and 135 base pairfragments.

Accept: have both bands / strips

Reject: primer longer / shorter

3

(d) 1. (Cells in mitosis) chromosomes visible;
2. (So) can see which chromosome DNA probe attached to.

2

(e) (i) 1. For comparison with resistant flies / other (two) experiments / groups;

Ignore: compare results / data / no other factors

2. To see death rate (in non-resistant) / to see effect of insecticide in non-resistant / normal flies. *Accept: 'pesticide' as 'insecticide'*

Accept to see that insecticide worked / to see effect of enzyme

2

(ii) (PM must be involved because)

1. Few resistant flies die (without inhibitor);
2. More inhibited flies die than resistant flies;
3. (PM) inhibited flies die faster (than resistant flies);

(Other factors must be involved because)

4. Some resistant flies die;
5. But (with inhibitor) still have greater resistance / die slower thannon-resistant flies.

Accept: (with inhibitor) die slower than non-resistant flies

4 max

[15] (a) Reverse transcriptase;

2 **1**

(b) 1. Probe (base sequence) complementary (to DNA of allele A / where A is (and) binds by forming base pairs / hydrogen bonds; *Accept gene A*

2. So (only) this DNA labelled / has green dye / gives out (green) light;

Accept glows for green light

2

(c) (i) 1. More probe binding / more cDNA / mRNA / more allele / gene A means more light;

2. DNA (with **A**) doubles each (PCR) cycle;

3. So light (approximately) doubles / curve steepens more and more (eachcycle) / curve goes up exponentially / increases even faster;

3

(ii) (**G** because)

1. (Heterozygous) only has half the amount of probe for **A** attaching / only half the amount of DNA / allele A (to bind to); *Accept only one A to bind to*

2. (So,) only produced (about) half the light / glow / intensity (of **H**) (per cycle of PCR);

If reference to 'half' for point 1, allow 'less light' in 2.

2

[8]

Essay Using DNA in science and technology

3

DNA and classification

2.2 Structure of DNA

2.3 Differences in DNA lead to genetic diversity

2.9 Comparison of DNA base sequences

Genetic engineering and making useful substances

2.5 Plasmids

5.8 The use of recombinant DNA to produce transformed organisms that benefit humans

Other uses of DNA

2.5 Cell cycle and treatment of cancer

5.8 Gene therapy;

Medical diagnosis and the treatment of human disease;

The use of DNA probes to screen patients for clinically important genes.

4

(a) (i) 1. Negative correlation;

Accept: description for 'negative correlation'
Neutral: 'correlation'
Reject: positive correlation

2. Wide range;

3. Overlap;

4. (Graph suggests that) other factors may be involved (in age of onset);

2 / 3 Accept the use of figures from the graph

2 / 3 Can refer to age of onset or number of CAG repeats

Ignore references to methodology

3 **max**

(ii) 1. Age of onset can be high / symptoms appear later in life;

Accept: 'gene' for 'allele'

2. (So) individuals have already had children / allele has been passed on;

OR

3. Individuals have passed on the allele / already had children;

4. Before symptoms occur;

2 max

(b) (i) 1. Person **K**;

2. (As has) high(est) band / band that travelled a short(est) distance / (er) so has large(st) fragment / number of CAG repeats; *Must correctly link distance moved and fragment size*

2

(ii) Run fragments of known length / CAG repeats (at the same time);

Accept: references to a DNA ladder / DNA markers

Do not accept DNA sequencing

1

(iii) Homozygous / (CAG) fragments are the same length / size / mass;

Accept: small fragment has run off gel / travelled further

1

[9] (a) (i) To cut the DNA;

5

Reject breakdown, cutting out

1

(ii) To separate the (pieces of) DNA;

1

(c) Complimentary base sequence / complementary DNA; binds to both (haplotypes);

Label would show up in both;

Idea of complimentarity required

2

(d) (i) Y chromosome inherited / comes from male parents / only found in males;

1

(ii) Mitochondria in egg / female gamete / no mitochondria come from sperm / malegamete;

1

(e) (i) Allows comparison;

Different (sized) areas covered;

2

(ii) Wolves do not eat all of prey animal / do not eat (large) bones / skin;

Inedible parts make up different proportions / wolf eats different proportions;

2

(f) Limited by food / prey; as prey increases so do wolf numbers / positive correlation;

Large range so other factors involved;

2

[12] (a) a length of DNA;

6 that codes for a single protein / polypeptide;

2

(b) by heating;to break the H-bonds (between complementary bases);

2

(c) (i) to allow the DNA polymerase to attach / start addition ofnucleotides / mark start and end of sequence to be copied / prevents strands re-joining;

1

(ii) because the sequences at the ends of the target sequenceare different / one is at the beginning and one at the end;

1

(d) 8;

accept 7

1

[7] (a) 1 DNA is cut;

7

2 Using restriction enzyme;

3 Use electrophoresis;

4 Separates according to length / mass;

5 Southern blotting / transfer to (nylon) membrane;

6 Make single-stranded;

7 Apply probe;

8 Radioactive / fluorescent;

9 Reference to tandem repeats / VNTRs / minisatellites;

10 Autoradiography / eq;8 and 10 should be consistent

max 6

(c) (i) All bands in cub which don't come from mother;

Must be in father's DNA fingerprint;

Principle that all bands in cub must come from mother and father = 1

2

(ii) Select pairs with dissimilar DNA fingerprints;

1

(d) (i) Cells (from panda) in faeces / gut cells / blood cells;

1

(ii) To increase amount of DNA / only small amount present;

1

(iii) DNA / primer has specific base-sequence;
Reference to specific / complementary base-pairing;

2

(e) Taking samples from animals causes stress / injury to animal;

Difficult to find animals;

Pandas are dangerous / threat to human;

max 2

[15] (a) 1. DNA is cut;

8

2. using restriction enzyme;
3. electrophoresis;
4. separates according to length / mass / size;
5. DNA made single-stranded;
6. transfer to membrane / Southern blotting;
7. apply probe;
8. radioactive / single stranded / detected on film / fluorescent;

9. reference to tandem repeats / VNTRs / minisatellites;
10. pattern unique to every individual;

6 max

(b) cells on toothbrush;
DNA present in cell;

2

(c) (i) toothbrush gives small sample of DNA / need more DNAfor analysis;
PCR gives many copies;

2

(ii) uses heat;to separate strands;
OR
PCR replicates pieces of DNA;
because DNA has been cut;
OR
primer added in PCR;
to initiate replication

2 max

(d) (i) PCR / amplification needed;

1

(ii) other DNA present; need to identify 'required' DNA from rest;

2

[15] (a) Mother and father both heterozygotes / Tt / carriers;

9

Probability of thalassaemia 1/4 and female 1/2;
Probability of both 1/8;

3

(b) (i) Cut at same base sequence as same enzyme used;
Fragments are same length / size / have same charge;

2

(ii) Single base occurs many times;
Sequence of 20 unlikely to occur elsewhere;
Allow one mark for establishing the principle where neither marking point clearly made.

2

[7] (a) (i) Different genes / characteristics / features;

10

Reference to mutations;
Or
Base sequence determines protein;
Different species have different protein sequences;

max 2

(ii) Primer has different DNA sequence;
DNA specific / complementary base-pairing;

2

(iii) Electrophoresis separates DNA;
(So they can be) identified by position on gel;
Smaller / shortest fragments travel furthest / quicker / or reverse argument;

3

(b) (*conventional*) Many lengths / all DNA / (*new*) one length;
Each rung is DNA of one / specific length;

2

(c) 1 Heat DNA;
2 Breaks hydrogen bonds / separates strands;
3 Add primers;
4 Add nucleotides;
5 Cool;
6 (to allow) binding of nucleotides / primers;
7 DNA polymerase;
8 Role of (DNA) polymerase;9 Repeat cycle many times;

max 6

[15]

11 (a) Endonuclease / restriction enzyme;

1

(b) DNA made of base pairs;
Each base pair is same length / occupies same distance along backbone;

2

(c) (i) Second blank box from left labelled 6;

1

(ii) Distance moved depends on length / number of base pairs /second longest fragment / second shortest distance identified;

1

(d) 5;

[6] (a) only small amounts obtained / PCR increases the amount / mass of DNA;

12

so enough DNA available for genetic fingerprint

i
n
g
;

2

(b) (i) to separate the two strands of the DNA /to break the hydrogen bonds;

(Reject "unzip")

1

(ii) short lengths / fragments of DNA / nucleotides /single stranded DNA;

1

(iii) to mark beginning and / or ends of the part of DNA needed /for attachment of enzymes or nucleotides / initiator / keeps strands apart;

1

(iv) would not be denatured;must be heated to 95 °C / must withstand high temps;

2

(c) 1 DNA extracted from sample;
2 DNA cut / hydrolysed into segments using restriction endonucleases;
3 must leave minisatellites / required core sequences intact;
4 DNA fragments separated using electrophoresis;
5 detail of process e.g. mixture put into wells on gel and electric current passed through;
6 immerse gel in alkaline solution / two strands of DNA separated;
7 Southern blotting / cover with nylon / absorbent paper (to absorb DNA);
8 DNA fixed to nylon / membrane using uv light
9 radioactive marker / probe added (which is picked up by required fragments) / complementary to minisatellites;
10 (areas with probe) identified using X-ray film / autoradiography;

max 6

(d) adult 3;this is only one which, (with number 1), can provide (all) the DNA fragments which children have / all bars match;

(Reject 'genes')

2

[15]

13

1 DNA heated to 90 to 95°C;

2 strands separate;

3 cooled / to temperature below 70°C
4 primers bind;
5 nucleotides attach;
6 by complementary base pairing;
7 temperature 70 - 75°C;
8 DNA polymerase joins nucleotides together;
9 cycle repeated;

6 max

[6] (a) to separate the two strands / break hydrogen bonds;

14 **1**

(b) (i) enables replication / sequencing to start (*allow keeps strands separate*);

1

(ii) joins DNA nucleotides (*not complementary bases*);

1

(c) (i) 64;

1

(ii) replication of DNA from crime scene / tissue sample /for DNA sequencing / gene cloning;

1

(d) (transcription uses) RNA polymerase;RNA nucleotides / uracil; one (template) strand / PCR both strands; start / stop codons;
(*accept enzyme separates strands*)

2 max

[7] (a) (i) to separate polynucleotide strands / form single strands;

15 **1**

(ii) not denatured (at 95°C);

1

(iii) for binding of primers / nucleotides (to DNA strands);

1

(b) (i) doubling (of DNA) each cycle; but very low numbers to start with, so appears flat then exponential growth;

2

(ii) suggestion; with explanation e.g.:

nucleotides being used up; so less / nothing to make complementary chains;

primers used up; so cannot start complementary chains;

enzymes losing activity / denatured; so no polymerisation of complementary strands;

2 max

[7]