

SUPERVISOR TO ATTACH PROCESSING LABEL HERE

STUDENT NUMBER

Letter

Figures

Words



**Victorian Certificate of Education
1998**

BIOLOGY**Common Assessment Task 3: Written examination**

Monday 2 November 1998: 3.00 pm to 4.45 pm

Reading time: 3.00 pm to 3.15 pm

Writing time: 3.15 pm to 4.45 pm

Total writing time: 1 hour 30 minutes

QUESTION AND ANSWER BOOK**Structure of book**

<i>Number of articles</i>	<i>Number of questions in each article</i>	<i>Number of questions to be answered</i>
8	1	8

Directions to students**Materials**

Question and answer book of 19 pages.

The task

Please ensure that you write your **student number** in the space provided on the cover of this book. Answer **all** questions.

Write your answers in the spaces provided in this question and answer book.

The marks for each question give you an idea of how much time you should spend, and how much information you should provide. There is a total of 75 marks available.

All responses must be in ink or ball point pen.

All written responses should be in English.

Students should attempt all parts of all questions

Article 1

Repeated mutations

In humans the locus of many genes is now known. A gene, known as the SCA1 gene, is found on chromosome 6. A mutation in the SCA1 gene can result in spinocerebellar ataxia type 1, a condition which causes a loss of muscle coordination. Only one copy of this mutant SCA1 allele will result in spinocerebellar ataxia type 1.

The symbols for the alleles of the SCA1 gene are

SB : spinocerebellar ataxia type 1, loss of muscle coordination

sb : normal muscle coordination.

Question 1

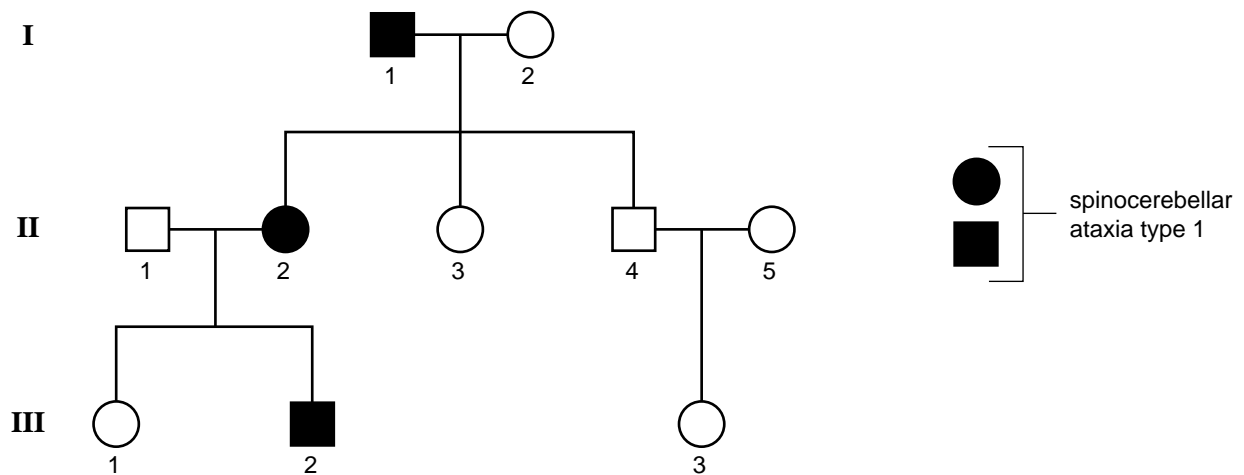
- a. From the information given, state the mode of inheritance of spinocerebellar ataxia type 1. Explain how you reached this decision.

Mode of inheritance _____

Explanation _____

3 marks

Figure 1 Pedigree of a family in which spinocerebellar ataxia type 1 is present



- b. Refer to the pedigree in Figure 1.

- i. Name any **two** individuals who must be heterozygous with respect to the SCA1 gene.

- ii. If individuals II-4 and II-5 have another child, what is the chance that this child will develop spinocerebellar ataxia type 1?

- iii. If individual III-2 and a female with normal muscle coordination have a child, what are the possible genotypes **and** phenotypes of this child?

2 + 1 + 2 = 5 marks

The mutation which leads to spinocerebellar ataxia type 1 results from an increase in the number of repeats of the DNA triplet GTC. In the template strand of DNA the normal allele has between 25 and 36 GTC repeats, but in the mutant allele there are between 43 and 81 repeats of GTC. The SCA1 gene on chromosome 6 normally codes for a protein called ataxin-1.

- c. Of what units would you expect the protein ataxin-1 to be made?

1 mark

- d. i. What is the **codon** which would be repeated in the messenger RNA produced by this gene?

- ii. What is the **anticodon** which would pair with the codon named in your answer to **d.i.**?

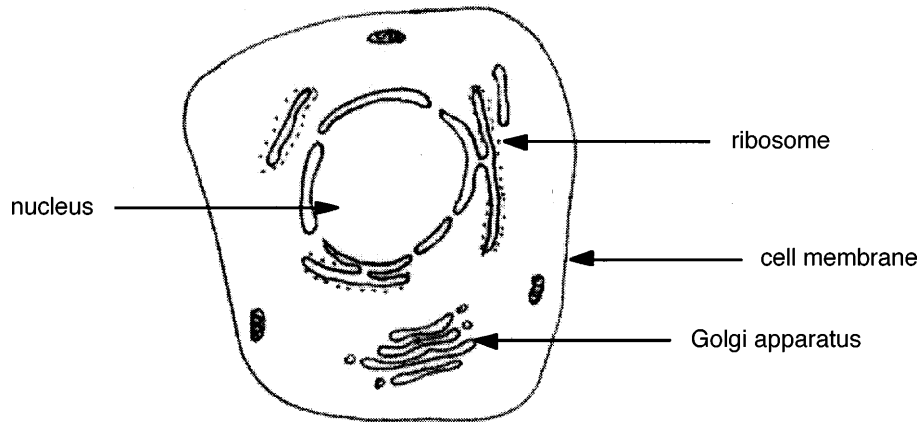
1 + 1 = 2 marks

- e. The SCA1 gene contains sequences of DNA which are transcribed but are not translated. These regions are cut out during RNA processing. What is the name for these regions of DNA?

1 mark

Four structures are labelled on the diagram of a eukaryotic cell shown in Figure 2.

Figure 2



f. For each of the following processes select the structure in or on which the process takes place.

Transcription occurs in or on structure _____

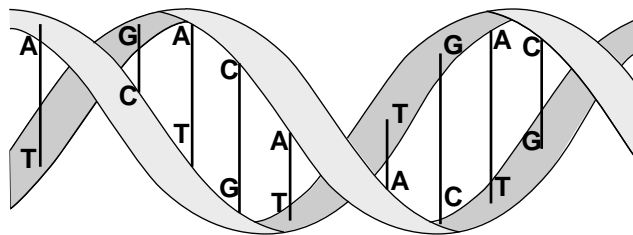
Translation occurs in or on structure _____

DNA replication occurs in or on structure _____

3 marks

g. Draw a labelled diagram to show what happens in DNA replication. Use the piece of DNA given in Figure 3 as a starting point.

Figure 3



2 marks

Total 17 marks

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Article 2

Grasshoppers

In certain species of grasshopper the female has 16 chromosomes in all somatic cells. The 16 chromosomes form 8 pairs of homologous chromosomes. The male has only 15 chromosomes in all somatic cells.

Question 2

- a. What are **homologous chromosomes**?

2 marks

- b. What is the diploid number of the female grasshopper?

1 mark

- c. How many chromosomes would you expect in sperm cells of the male grasshopper?

2 marks

You are to investigate two inherited characteristics in grasshoppers, each of which is under the control of a single gene. The two genes are found on different chromosomes. Each gene has two alleles. The symbols for the alleles that can be found at each locus are shown in Table 1.

Table 1

Locus	Allelic symbols
1	A or a
2	B or b

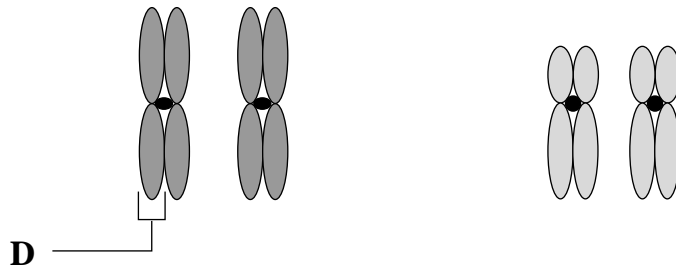
A female grasshopper has the genotype Aa; Bb.

- d. What term is used to describe the **genotype** of this grasshopper at locus 1?

1 mark

The chromosomes of a female grasshopper on which these two loci are found are drawn in Figure 4. They have been drawn as they appear in an early stage of meiosis.

Figure 4



e. Refer to Figure 4.

i. What is the name given to structure D?

ii. How many molecules of DNA are there in structure D?

iii. In Figure 4 at this stage of meiosis, how many copies of the **A** allele will there be in this cell of the female grasshopper mentioned in d.?

1 + 1 + 1 = 3 marks

f. Using the diagram in Figure 5 and the previous information provided, label possible positions of the alleles for these two gene loci if the female is genotype **Aa; Bb**.

Figure 5



2 marks

Total 11 marks

TURN OVER

Article 3

Multiple petals

A garden plant commonly called nasturtium, *Tropaeolum majus*, can have flowers which are either single, double or superdouble. The three flower types differ in their number of petals; single flowers have the least number of petals, and superdouble flowers have the largest number of petals.

Several plants, each expressing one of the three different phenotypes, were grown. All these plants were allowed to self-pollinate so the parents in a particular cross had the same genotype. The phenotypes and ratios of offspring produced from these self-pollination experiments were recorded.

In Table 2 the outcome of all self-pollination experiments are shown.

Table 2

Self-pollination experiments	Ratios and phenotypes of offspring
Cross 1 single-flowered plants	all single flower
Cross 2 double-flowered plants	all double flower
Cross 3 double-flowered plants	3 double flower: 1 single flower
Cross 4 superdouble-flowered plants	all superdouble flower
Cross 5 superdouble-flowered plants	3 superdouble flower: 1 double flower
Cross 6 superdouble-flowered plants	3 superdouble flower: 1 single flower

Question 3

- a. Consider only the information provided by **Cross 1**.

Explain whether there is sufficient evidence from Cross 1 to conclude that the single-flower phenotype is **recessive**.

1 mark

- b. i.** Which cross in the table indicates that the double-flower phenotype is **dominant** to the single-flower phenotype?

Cross _____

- ii.** Explain your answer to **b.i.**

1 + 1 = 2 marks

A single gene locus with multiple alleles determines the number of petals in this plant. The three alleles at this locus have been given the symbols F^S ; F^d and f .

- c.** What is an **allele**?

1 mark

- d.** Refer to **Cross 4**.

- i.** Using the allelic symbols given, what is the **genotype** of the parental plants?

- ii.** What other genotype/s could produce a superdouble-flower phenotype?

1 + 2 = 3 marks

- e.** Refer to the offspring of **Crosses 5 and 6**.

If the double-flower **offspring** of Cross 5 were crossed to the single-flower **offspring** of Cross 6, what genotype/s and phenotype/s would you expect in the offspring?

2 marks

Total 9 marks

TURN OVER

Article 4

Mouse mutations

In the mouse the location of many genes is known. Mutations in these genes have been identified. Three such mutations are tilted head, extra toes and deafness. Allele symbols and phenotypes for these three gene loci are listed in Table 3.

Table 3

Mutation name	Allele symbol	Phenotype
tilted head	<i>t</i> <i>T</i>	head tilted to one side head held straight
extra toes	<i>p</i> <i>P</i>	extra toes normal number of toes
deafness	<i>d</i> <i>D</i>	deafness normal hearing

The mutant phenotypes, tilted head, extra toes and deafness, are all recessive to the normal condition. The tilted head mutation is located on chromosome 1. To determine the location of the other mutations two different **test crosses** were carried out and the phenotypes of a large number of offspring were recorded. The results are shown in Tables 4 and 5.

Table 4

Cross 1 – *TtPp* X *tpp*

	Phenotypes of the offspring			
	head straight and normal number of toes	head straight and extra toes	tilted head and normal number of toes	tilted head and extra toes
number of offspring	14	36	34	16

Table 5

Cross 2 – *TtDd* X *tdd*

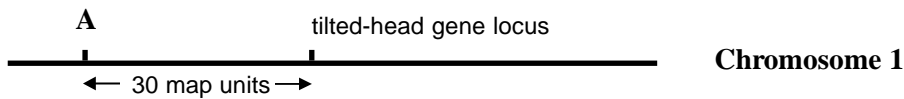
	Phenotypes of the offspring			
	head held straight and normal hearing	head held straight and deaf	head tilted to one side and normal hearing	head tilted to one side and deaf
number of offspring	24	27	24	25

Question 4

- a. In Cross 2, what is the **genotype** of the offspring with tilted heads and deafness?

1 mark

In Figure 6 the position of the tilted-head gene locus on chromosome 1 is shown. The letter A represents another gene locus close to the tilted-head gene locus on chromosome 1.

Figure 6

- b. What term is used to describe two gene loci located close together on the same chromosome?

1 mark

- c. i. Based on the outcomes of Crosses 1 and 2, which gene locus, deafness or extra toes, is most likely represented by the letter A?

- ii. Using the data from Crosses 1 **and** 2, explain your answer to c.i.

1 + 2 = 3 marks

Rough fur (r) is a recessive mutation occurring on chromosome 2. The hair of mice homozygous for this condition has a rough appearance. Mice pure breeding for tilted head and rough fur were crossed with mice pure breeding for straight head and normal fur. The offspring of this cross (the F_1 generation) all had straight head and normal fur. These offspring were then interbred with each other to produce an F_2 generation.

d. i. What are the expected **phenotypes** in the F_2 generation and in what **proportions** would they occur?

ii. What proportion of the F_2 generation would be expected to have the genotype $TTrr$?

2 + 1 = 3 marks

Total 8 marks

Article 5

Control of the diamondback moth

Cabbage is one of the most popular vegetables in Southeast Asia. It is grown throughout the year. A serious pest of the cabbage is the diamondback moth, *Plutella xylostella*. The diamondback moth has been controlled by spraying the cabbages with insecticides. One of these insecticides is obtained from soil bacterium, *Bacillus thuringiensis*. The bacteria produce a toxin (abbreviated name is Bt) which has been an effective insecticide against the diamondback moth and is also an environmentally friendly chemical. Since 1990, strains of the diamondback moth which are resistant to the Bt toxin have been increasing in the population.

Question 5

- a. What change has occurred in the frequency of the Bt-resistant allele in the diamondback moth population since 1990?

1 mark

- b. Explain the steps which have occurred to bring about this change in the frequency of the Bt-resistant allele in the population of diamondback moths.

4 marks

It has been suggested that the Bt-resistant phenotype is recessive and the Bt-sensitive phenotype is dominant. In Thailand a resistance-management strategy is currently being organised. This strategy recommends that a cabbage field **untreated** with the Bt insecticide should be grown alongside a cabbage field **treated** with the Bt insecticide.

- c. Explain how this strategy might help to control the increase in Bt resistance in the population of diamondback moths.

2 marks

Total 7 marks

TURN OVER

Article 6

On the trail of the lonesome pine

In 1994, three bushwalkers hiking through a wet gully in the Wollemi National Park, New South Wales, discovered 23 unusual looking pine trees, since named the Wollemi pine, *Wollemia nobilis*. Since this discovery, another stand of 17 trees, at an even more secluded spot about a kilometre upstream from the first stand, has been found. The group to which all these trees belong is thought to have disappeared long before humans were present on Earth.

To trace the history of the trees the fossil record was investigated. No fossils of either Wollemi pine trees or their pollen have been discovered. The closest match found so far is between Wollemi pollen and fossilised pollen that may have come from trees belonging to the ancient conifer family of Araucariaceae.

The fossil record shows that the Araucariaceae family was widely distributed across the planet between 200 and 65 million years ago. The family disappeared from the northern hemisphere at the end of this time but was still widespread in the southern hemisphere until 30 million years ago. At this point a decline in range and diversity is evident from the fossil record.

Question 6

- a. Identify **one** factor and explain how it may have caused the decline in range and diversity of pines in the family Araucariaceae over the past 30 million years.

Factor _____

Explanation _____

2 marks

- b. Pollen is abundant in the fossil record. Name **one** structural feature of pollen that assists in its fossilisation.

1 mark

- c. i. Fossilised plant parts have been found which have structural similarities to the Wollemi pines. What additional evidence would be required to indicate a close evolutionary relationship between the fossil plant and the Wollemi pines?

- ii. Explain how this evidence would indicate a close evolutionary relationship between the fossil plant and the Wollemi pines.

1 + 1 = 2 marks

Biologists studied the genetic variation of the Wollemi pines. They analysed genetic markers in eight trees from the first stand and four from the second stand. They found no genetic variation within the stands or between the stands. To explain this lack of variation, the suggestion has been made that the trees are clones of a single, remnant pine tree.

- d.** Explain how this clone of trees could have no genetic variation.

2 marks

- e.** State **one** disadvantage to the survival of the population in having no genetic variation.

1 mark

Total 8 marks

TURN OVER

Article 7

The dolphin, the cow, the hippopotamus, the pig and the camel

Not many people would think that a dolphin, a cow and a hippopotamus are closely related, but recent evidence suggests that they may be! The dolphin, cow, hippopotamus, pig and camel represent families that form a group which shares a common ancestor not shared by any other group. There are two possible views about the evolutionary relationships between these mammals: the traditional view and the revised view.

The traditional view, based on morphology (structure), groups the cow, the hippopotamus, the pig and the camel together as artiodactyls. The traditional view is represented in Figure 7. The revised view, based on recent molecular studies, is shown in Figure 8.

Figure 7 The traditional view

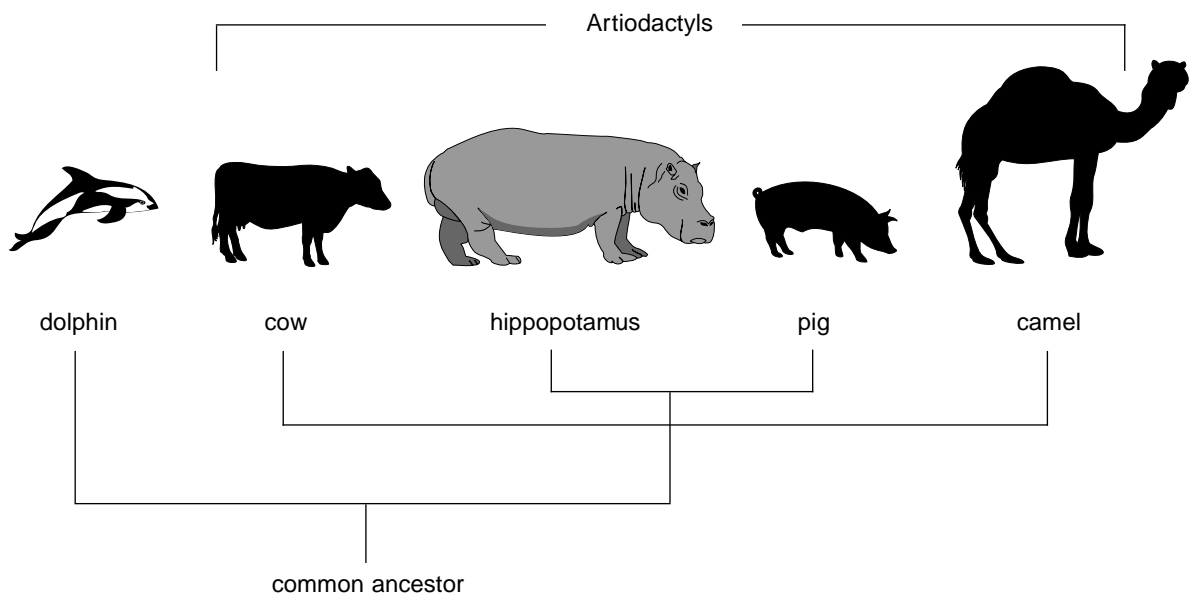
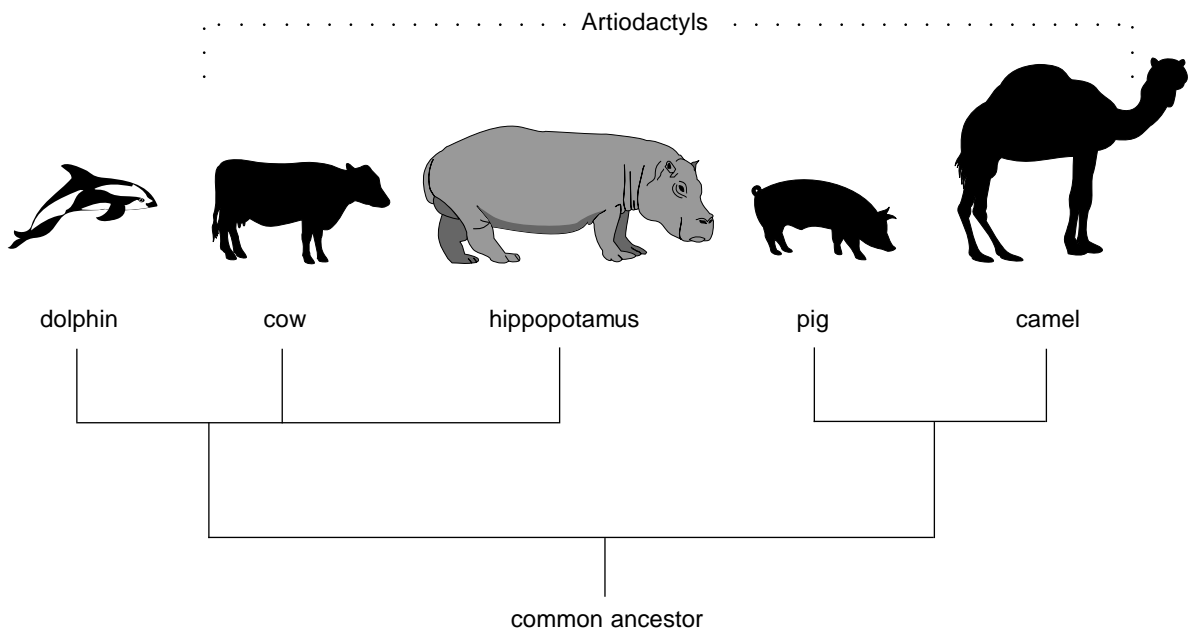


Figure 8 The revised view



Question 7

- a. Use the data in Figures 7 and 8 to complete Table 6.

Table 6

	Traditional view Figure 7	Revised view Figure 8
Which animal/s share most features in common with the pig?		
Which animal/s have fewest features in common with the pig?		

2 marks

Morphological evidence, used to support the traditional view, is the presence of a three-lobed lower premolar tooth in all artiodactyls which is not present in dolphins. This morphological feature may still support the revised view.

- b. Suggest a hypothesis which supports the **revised view** to explain the presence of the three-lobed lower premolar tooth in all artiodactyls and not dolphins.

2 marks

Dolphins share many characteristics in common with sharks, such as a streamlined body and 'fins', and at first glance may appear similar. Dolphins, however, are more closely related to cows.

- c. i. What term is used to describe the similarities in structure between the dolphin and the shark?

A student argued that dolphins are not closely related to sharks because they do not have a common ancestor.

- ii. Explain why you agree or disagree with this student.

1 + 1 = 2 marks

Total 6 marks

TURN OVER

Article 8

A lakeside supper

After rain, Cuddie Springs in New South Wales is a shallow transient lake surrounded by saltbush scrub. More than 30 000 years ago the lake was a more permanent feature of the landscape. Excavations have uncovered a series of layers of undisturbed sediments. The sediments contained fossil remains of the inhabitants of the area over the last 100 000 years including some of Australia’s unique Megafauna. Megafauna were the gigantic animals that developed during the later part of the Cainozoic era and included the giant marsupial kangaroos, wombats, flightless birds and reptiles. These giant animals appear to have become extinct about 28 000 years ago.

Table 7

Sediment layer	Age of sedimentary layer (age in years)	Fossil remains
I	100 000 to 35 000	Palorchestes (giant marsupial ‘kangaroo’) Genyornis (giant emu-like flightless bird) Huge reptiles (horned turtles, crocodiles, predatory goanna)
II	35 000 to 28 000	Genyornis Diprotodon (giant wombat) Stenutus (giant kangaroo) Stone tools and charcoal Stone tools associated with some animal bones Seed-grinding stones
III	28 000 to 19 000	Very hard, thin layer of rock formed during an extended dry period corresponding to the last Ice Age. The rock layer contains no fossils
IV	19 000 to recent	Animal remains (no Megafauna) Stone tools including seed-grinding stones

Question 8

- a. What inference can be made when different fossil remains are found in the one sedimentary layer?

1 mark

- b. Using the information given, suggest why there are no fossils in the sediment layer III.

1 mark

- c. i. From the evidence in Table 7, describe **two** features of the early human way of life at Cuddie Springs.

Feature one _____

Feature two _____

ii. Explain how you reached your conclusion for each feature in c.i.

Explanation for feature one _____

Explanation for feature two _____

2 + 2 = 4 marks

It was possible to extract DNA from animal and plant fossil material found at the excavation site. One section of DNA analysed has three regions which identify the type of organism from which the DNA has been extracted.

Figure 9 DNA with the three regions shown

Region A	Region B	Region C
Common to all animals	Characteristic of mammals	Variable within mammals

Three fossil DNA samples were collected. It was thought that one DNA sample was from a **wombat-like animal**, another from an **emu-like bird** and another from a **fern-like plant**.

Comparisons of the DNA from the three fossil samples were made to this section of DNA from a modern-day wombat. The results of the comparisons are summarised in Table 8.

Table 8

Fossil sample DNA	Comparison with modern-day wombat DNA		
	Region A	Region B	Region C
Sample I	matched	matched	no match
Sample II	matched	no match	no match
Sample III	no match	no match	no match

d. i. Which sample is most likely from an emu-like bird?

ii. Explain your choice in d.i.

1 + 2 = 3 marks

Total 9 marks