

- M1.(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 pair fragments;
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 pair fragments.
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 than non-resistant flies.

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

4 max

[15]

M2.(a) Reverse transcriptase;

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 (each cycle) / 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]

- M3.(a)**
1. Carriers are heterozygous / have one normal copy and one mutant copy of gene / have one recessive allele / don't have the condition;
2. Both have DNA that binds (about) half / 50% amount of probe (that non-carrier does);
3. Probe binds to dominant / healthy allele so only one copy of exon in their DNA / have one copy of gene without exon / base sequence for probe to bind to;
- 3. Accept normal and gene*
3. Accept have a deletion mutation

3

- (b)
1. Introns not translated / not in mRNA / (exons) code for amino acids / introns do not code for amino acids;
- 1. Accept not expressed*
1. Accept polypeptide / protein for amino acids
2. Mutations of these (exons) affect amino acid sequences (that produce) faulty protein / change tertiary structure of protein;
- 2. Accept deletion leads to frameshift*
2. In this context, accept affects protein made
3. So important to know if parents' exons affected, rather than any other part of DNA / introns;
- Accept converse arguments involving - eg introns do not code for amino acids / proteins*
Reject references to making amino acids, once

3

- (c)
1. Restriction mapping / described;
2. DNA / base sequencing (of fragments) / description / name of method;

2

- M4.** (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]

- M5.(a)** 1. Closer the (amino acid) sequence the closer the relationship;
2. (Protein structure) related to (DNA) base / triplet sequence;
Amino acid sequence is related to (DNA) base / triplet sequence = two marks;

2

- (b) 1. Reference to base triplets / triplet code / more bases than amino acids / longer base sequence than amino acid sequence;
Different (base) triplets code for same amino acids = 2 marks;
Degeneracy of triplet code = 2 marks
2. Introns / non-coding DNA / degeneracy of code / more than one code for each amino acid;
Ignore reference to codon.

2

[4]