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

[8]

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]