**Q1.** (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]**

**Q2.** (a)     (i)      Does not code for amino acid/tRNA/rRNA;

*Accept ‘does not code for production of protein/polypeptide’*

*Reject ‘that produces/makes amino acid'*

**1**

(ii)     Deletion mutation;

*Accept ‘deletion’*

*Ignore references to splicing*

**1**

(b)     (The) polymerase chain reaction;

*Accept PCR*

**1**

(c)     1.      Probes are single stranded / have a specific base sequence;

2.      Complementary base sequence on (specific) spacer

**OR**

3.      Complementary/specific to (particular) spacer;

4.      (In white squares probe) binds (to single-stranded spacer) and glows/produces light/fluoresce;

*2. Need idea of complementary to spacer*

*3. Accept converse for dark squares*

**3**

(d)     1.      To see if strain is resistant to any antibiotics;

2.      So can prescribe effective/right antibiotic;

**OR**

3.      To see whether (any) vaccine works against this strain/ see which vaccine to use/ to produce specific vaccine;

4.      (So) can vaccinate potential contacts/to stop spread;

**OR**

5.      Can test other people to see if they have the same strain/ to trace where people caught TB;

6.      Allowing control of spread of disease/vaccinate/treat contacts (of people with same strain) before they get TB;

*Do not allow mix and match of points from different alternative pairs*

**2 max**

**[8]**

**Q3.** (a)     restriction (enzyme) / endonuclease / named example;

**1**

(b)     unpaired bases / sticky ends / staggered;
complementary / explained;

**2**

(c)     *1 mark for each correct outcome*plasmid with foreign DNA joined in ring;
ring with plasmid only; ring of foreign DNA only;
*ignore linear structures*

**3**

**[6]**

**Q4.** (a)     1.      Human DNA / human gene / HGH gene contains introns

**OR**

Methods 2 and 3 produce DNA / *HGH* without introns;

2.      *E. coli* cannot remove introns / cannot splice mRNA / cannot splice pre-mRNA;

**2**

(b)     Faster to use gene machine than all the enzyme-catalysed reactions (involving reverse transcriptase);

*Accept extra step / more steps involved in isolating mRNA*

**1**

(c)     1.      Cut the plasmid with a restriction endonuclease;

*Allow ‘add base sequences to blunt ends of plasmid and HGH gene’*

2.      (So that) both have complementary / sticky ends;

3.      (Mix together) and add ligase to join the complementary / sticky ends;

**3**

(d)     Can quickly identify transformed bacteria using UV light;

**1**

(e)     1.      Arabinose alters structure of araC protein / reduces effect of araC protein;

2.      So stops / reduces inhibition of promoter gene and GFP gene is transcribed;

**OR**

So stops / reduces inhibition of promoter gene and GFP is produced;

**2**

**[9]**

**Q5.** (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;

**1**

**[6]**

**Q6.** (a)     1.      (Requires DNA fragment) DNA polymerase, (DNA) nucleotides and primers;

2.      Heat to 95 °C to break hydrogen bonds (and separate strands);

*Accept temperature in range 90 to 95 °C.*

3.      Reduce temperature so primers bind to DNA/strands;

*Accept temperature in range 40 to 65 °C.*

4.      Increase temperature, DNA polymerase joins nucleotides (and repeat method);

*Accept Taq polymerase for DNA polymerase.*

*Accept temperature in range 70 to 75 °C.*

**4**

(b)     1.      (Initially) number (of molecules) doubling is low

**OR**

Doubles each cycle to produce exponential increase;

*First alternative relates to idea of low numbers i.e., 2, 4, 8, 16, 32 etc.*

2.      Plateaus as no more nucleotides/primers;

*Accept ‘levels out’ or ‘flattens’ for plateaus.*

*Accept enzyme/polymerase (eventually) denatures.*

**2**

**[6]**

**Q7.** (a)     Produces (c)DNA using (m)RNA;

*Accept: ‘converts’ (m)RNA to (c)DNA.*

*Reject: tRNA*

**1**

(b)     Joins nucleotides to produce (complementary strand/s of) DNA;

*Accept: ‘joins DNA nucleotides’.*

**1**

(c)     1.      To remove any DNA present;

2.      As this DNA would be amplified / replicated;

*1.      Must be idea of removal / destruction.*

*2.      Accept: idea of DNA not being used as template.*

**2**

(d)     1.      Ratio in range of 1.4 :1 to 1.5 :1 = **2 marks**;

2.      One mark for answers which shows incorrect ratio but

Shows 0.24 as a number or line on the graph

**OR**

Ratio in correct range, but the wrong way round

**OR**

Ratio in correct range but not expressed to 1

**OR**

Ratio shown the other way round in range

1: 0.67 to 1:0.71;

*Note: ratio not expressed to 1 in correct range may be shown in different ways, for example as:*

*3:2 or simply as 1.5 for one mark.*

**2**

(e)     Limited number of primers / nucleotides;

*Accept: DNA polymerase (eventually) denatures*

*Accept: primers / nucleotides ‘used up’.*

**1**

(f)      1.      Base sequences differ;

2.      (Different) complementary primers required;

*1.      Accept: reference to either RNA or DNA base sequences but reject reference to DNA base sequence in viruses.*

**2**

**[9]**

**Q8.** (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]**

**Q9.** (a)     (i)      Restriction endonuclease;

**1**

(ii)     (DNA) ligase;

**1**

(b)     (For those plants that contained the desired gene in the nucleus/plant DNA)

1.      (DNA of desired gene) copied/replicated with host DNA/inside nucleus;

2.      Passed on by mitosis/plant grows by mitosis;

3.      Produces genetically identical cells/clones;

*Ignore references to protein synthesis or plasmids not taking up the gene*

*1. Accept DNA replication during mitosis*

*1. and 2. Accept converse for plants with the gene in the cytoplasm*

*3. Neutral ‘identical unqualified’*

*3. Accept description, e.g., DNA is the same*

**3**

(c)     1.      Genetic code is universal/triplets in DNA always code for same amino acid;

2.      It/insect DNA can be transcribed;

3.      Can be translated (process/mechanism same in all organisms/cells);

*2. Accept (basic) transcription (process/mechanism) same in all organisms/cells;*

*2. Accept descriptions of process*

*3. Accept descriptions of process*

**3**

**[8]**

**Q10.** (a)  1.   (Short) single strand of DNA;

2.   Bases complementary (with DNA/allele/gene);

**2**

(b)  1.   Restriction endonuclease/enzyme;

2.   (Cuts DNA at specific) base sequence

**OR**

(Breaks) phosphodiester bonds

**OR**

(Cuts DNA) at recognition/restriction site;

*Accept palindromic sequence.*

**2**

(c)   (So DNA) probe binds/attaches/anneals;

**1**

(d)  1.   (Lane 1 has DNA fragments) of known sizes/lengths;

2.   Compare (position of viral fragment/s);

**2**

(e)  3, 4, 5 with these numbers in any sequence;

*All three numbers required.*

*Reject if more than three numbers given.*

**1**

**[8]**