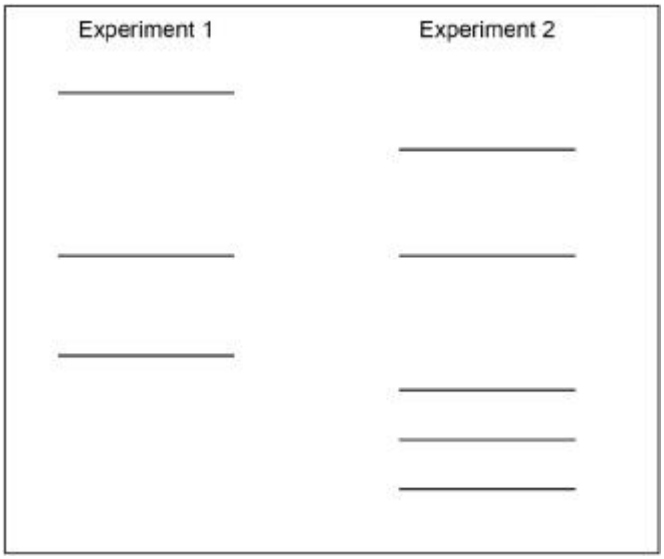
Mark schemes

Q1.

(a) Experiment 1 with 3 bands and experiment 2 with 5 bands in correct positions = **2 marks**;;

Experiment 1 with 3 bands and experiment 2 with 5 bands but not in correct positions = **1 mark**;



*For **two marks**, the position of the second band from the top must be in the same position for both experiments.*

The lengths of the bands do not need to be the same, but the relative positions should be similar to the diagram shown.

2

(b) 1. (Separate) DNA fragments/ladder of known sizes/lengths;

Ignore mass

2. Compare position/distance/bands with unknown fragment(s);

2

(c) 4 or four;

1

(d) 1. Restriction endonucleases/enzymes cuts <u>plasmid</u>

OR

Restriction endonucleases/enzymes produce 'sticky ends';

Accept 'cuts DNA of plasmid'.

Ignore restriction enzymes cuts out the gene.

2. Ligase joins gene/DNA and plasmid

OR

Ligase joins 'sticky ends'

OR

Ligase forms phosphodiester bonds;

Ignore reference to hydrogen bonds or joining complementary base pairs.

2

[7]

Q2.

(a) 1. Restriction endonucleases/enzymes;

2. (Cut DNA) at specific <u>base</u> sequences/pairs

OR

(Cut DNA) at recognition/restriction sites;
Accept 'at palindromic sequences'

2

(b) 1. (For) primers;

2. (To produce) a complementary base sequence
OR

(Primers provide starting sequence) for DNA/taq polymerase
OR

(Primers) stop (original) DNA strands re-joining;

2

(c) Correct answer of 1.35×10^{16} = **2 marks**
OR

Correct answer of 1.36×10^{16} (due to rounding at an earlier stage of the calculation) = **2 marks**

OR

Correct answer of 1.4×10^{16} = **2 marks**;;

Incorrect answer but shows 2^{50} = **1 mark**;
Ignore any numbers after 1.35.

2

(d) 1. Number of nucleotides/repeats/bases

OR

Length/mass;
Accept weight for mass.
Ignore 'short' on its own.
Accept number of base pairs.
Ignore density/size.

2. (Negative) charge;
Accept 'polarity'.
Reject positive (charge).

2

[8]

Q3.

(a) 1. Change in DNA base sequence/triplet;

2. Change in (sequence of) amino acids
OR
Change in primary/tertiary/3^0 structure;
Ignore reference to protein not being formed.
Reject (different) amino acids formed.
Ignore 3D structure.

3. (Results in) rapid/uncontrollable cell division;
Accept cell division cannot be regulated.
Ignore growth.
Accept cell replication but ignore cell reproduction.

3

(b) 1. Use of PCR to amplify (DNA sample);
Accept description of amplification.

2. Cut (DNA) using restriction endonuclease/enzymes;

3. Separate (DNA fragments) using electrophoresis;
Accept use of microarray for electrophoresis.

4. Addition of (labelled) DNA probes **and** binding (by DNA hybridisation);
Ignore primers.
Reference to probe being complementary is insufficient.

5. (Mutations) identified by fluorescence/radioactivity
OR
Compare positions/bands (to known) DNA sample with (all harmful) mutations;
Accept identification using X-ray/photographic/film/autoradiography or UV light.

***Note if only DNA sequencing** is used award **max 3 marks** for the following.*
1 Use of PCR to amplify (DNA/sample);
2. Sequence the DNA sample;
3. Compare DNA sequence with known DNA sequence of mutation;

4 max

(c) 1. (Drug) binds to (oestrogen/ER) receptor;
Accept (inactive) transcription factor for receptor.

2. Prevents binding of oestrogen/hormone;
Reject active site/enzyme-substrate complex once only.

3. No/fewer transcription factor(s) bind to promoter
OR
RNA polymerase not stimulated/activated;

3

(d) 1. High/increased (concentration of) PSA not always linked to (prostate) cancer
OR
High/increased (concentration of) PSA could be a false positive;

2. 2.(Could be) due to urinary infection
OR
(Could be) due to enlarged prostate;
Accept 'urine infection'.

2

(e) 1. (Drugs could) increase methylation of oncogene(s);

2. (Drugs could) decrease methylation of tumour suppressor gene(s);

3. (Increased) methylation of DNA/gene(s) inhibits transcription/expression (of genes)
OR
Decreased methylation of DNA/gene(s) stimulates transcription/expression (of genes);
Accept promoter (region) for DNA/gene

4. Decreased acetylation of histones inhibits transcription/expression (of genes)
OR
(Increased) acetylation of histones stimulates transcription/expression (of genes);
Ignore 'switching on' and 'switching off' genes once but accept as alternative(s) for 1 mark if used correctly in context of transcription/ expression for both points 3 and 4.

Ignore methylation of histones and acetylation of DNA/genes.
Ignore proto-oncogenes.

3 max

[15]

Q4.

(a) **Genome**

1. (The) complete set of genes in a cell/organism
OR
(All) the DNA in a cell/organism;

Accept (all) the genes/alleles/genetic material/genetic code in a cell/organism

Accept the total number of DNA bases in a cell/organism

Reject all the DNA/genes within a species/population

Proteome

2. Range of proteins that a cell/organism **can produce**
OR
Range of proteins the genome/DNA **can code for**;

Do not accept number of proteins unqualified

Ignore range of proteins that a species/population can produce

2

(b) 1. (The) genetic/DNA code is universal
OR
The same triplets/codons code for the same amino acids (in all species);

Do not accept 'DNA is universal' unqualified

Reject the genetic code is degenerate

Ignore anything after 'genetic/DNA code is universal' unless incorrect

2. (The mechanism of) transcription is universal;

3. (The mechanism of) translation is universal;

2 and 3 Accept descriptions of universal, eg transcription/translation are the same in humans and bacteria

2 and 3 If neither is stated, accept '(the mechanism of) protein synthesis is universal' for 1 mark

Accept bacteria have ribosomes, and so could translate (human mRNA)

2 max

(c) Cannot splice (pre-mRNA), **so** cannot remove introns

OR

Do not have Golgi (apparatus), **so** cannot process/modify (proteins);

OR

Do not have transcriptional factors (required), **so** cannot carry out transcription/produce mRNA;

Accept do not have spliceosomes/spliceozyme for cannot splice

Accept 'rough endoplasmic reticulum' for 'Golgi'

Accept (human protein) is too complex and bacteria do not have Golgi (apparatus)

1

(d) 1. (Region **M**) promoter;

2. (Region **N**) terminator;

Accept phonetic spellings

2

(e) Shows that the (antithrombin) gene has been taken up (by cells/embryos/goats)

OR

Shows transgenic/transformed goat cells/goat embryos/goats

OR

Allows detection of genetically modified cells/organisms/mammals/goats;

Accept 'GM' for 'genetically modified'

1

(f) 1. Milk/protein/antithrombin is easy to extract from a goat
OR
Extracting milk/protein/antithrombin from a goat does it no harm;

2. If (antithrombin was produced) in their blood, could prevent/affect clotting
OR
(Antithrombin) could damage other cells;

2

[10]