M1.(a) 1. Sugar-phosphate (backbone) / double stranded / helix **so** provides strength / stability / protects bases / protects hydrogen bonds;

Must be a direct link / obvious to get the mark

Neutral: reference to histones

2. Long / large molecule **so** can store lots of information;

3. Helix / coiled **so** compact;

Accept: can store in a small amount of space for 'compact'

4. Base sequence allows information to be stored / base sequence codes for amino acids / protein;

Accept: base sequence allows transcription

5. Double stranded **so** replication can occur semi-conservatively / strands can act as templates / complementary base pairing / A-T and G-C so accurate replication / identical copies can be made;

6. (Weak) hydrogen bonds **for** replication / unzipping / strand separation / many hydrogen bonds **so** stable / strong;

Accept: 'H-bonds' for 'hydrogen bonds'

6

(b) 1. (Mutation) in **E** produces highest risk / 1.78;

2. (Mutation) in **D** produces next highest risk / 1.45;

3. (Mutation) in **C** produces least risk / 1.30;

Must be stated directly and not implied

E *>* ***D*** *>* ***C*** *= 3 marks*

Accept: values of 0.78, 0.45 and 0.30 for MP1, MP2 and MP3 respectively

If no mark is awarded, a principle mark can be given for the idea that all mutant alleles increase the risk

3

(c) **180**;

1

(d) **(Similarities):**

1. Same / similar pattern / both decrease, stay the same then increase;

2. Number of cells stays the same for same length of time;
Ignore: wrong days stated

(Differences):

(Per unit volume of blood)

3. Greater / faster decrease in number of healthy cells / more healthy cells killed / healthy cells killed faster;
Accept: converse for cancer cells
Accept: greater <u>percentage</u> decrease in number of cancer cells / greater <u>proportion</u> of cancer cells killed

4. Greater / faster increase in number of healthy cells / more healthy cells replaced / divide / healthy cells replaced / divide faster;
Accept: converse for cancer cells
*For **differences**, statements made must be comparative*

3 max

(e) 1. More / too many healthy cells killed;

2. (So) will take time to replace / increase in number;
Neutral: will take time to 'repair'

3. Person may die / have side effects;

2 max

[15]

M2.(a) 250 000;

1

(b) (i) Loss of 3 bases / triplet = 2 marks;;
'Stop codon / code formed' = 1 mark max unless related to the last amino acid

Loss of base(s) = 1 mark;
eg triplet for last amino acid is changed to a stop codon / code = 2 marks
3 bases / triplet forms an intron = 2 marks
Accept: descriptions for 'intron' eg non-coding DNA
'Loss of codon' = 2 marks

2

(ii) 1. Change in tertiary structure / active site;
Neutral: change in 3D shape / structure

2. (So) faulty / non-functional protein / enzyme;
Accept: reference to examples of loss of function eg fewer E-S complexes formed

2

[5]

M3.(a) 1. Cell wall not formed / production inhibited;
*1. **Q** Accept: weakened cell wall, but do not accept 'cell wall is broken down'*

2. Lower water potential in bacterium;
2. Accept: converse
2. Must be clear that the lower water potential is in the bacterium

3. Water enters and causes lysis / expansion / pressure;

2 max

(b) Human cells lack enzyme (**B**) / have a different enzyme / produce different fatty acids / use different substrates;
Neutral: 'human cells do not have cell walls' as out of context

1

(c) 1. Change in base sequence (of DNA / gene) leading to change in amino acid sequence / primary structure (of enzyme);
1. Accept: different amino acids coded for
1. Reject: different amino acids produced

2. Change in hydrogen / ionic / disulphide bonds leading to change in the tertiary structure / active site (of enzyme);
2. Neutral: alters 3D structure / 3D shape

3. Substrate not complementary / cannot bind (to enzyme / active site) / no enzyme-substrate complexes form;

3

[6]

M4.(a) (i) 4;

1

(ii) 1. Change in amino acid / (sequence of) amino acids / primary structure;

1. Reject = different amino acids are 'formed'

2. Change in hydrogen / ionic / disulphide bonds alters tertiary structure / active site (of enzyme);

2. Alters 3D structure on its own is not enough for this marking point.

3. Substrate not complementary / cannot bind (to enzyme / active site) / no enzyme- substrate complexes form;

3

(b) 1. Lack of skin pigment / pale / light skin / albino;

2. Lack of coordination / muscles action affected;

2 max

(c) Founder effect / colonies split off / migration / interbreeding;

Allow description of interbreeding e.g. reproduction between individuals from different populations

1

[7]

M5. (a) Introns;

1

(b) Ile Gly Val Ser;

1

(c) (i) Has no effect / same amino acid (sequence) / same primary structure;

Q *Reject same amino acid formed or produced.*

1

Glycine named as same amino acid;

1

It still codes for glycine = two marks.

(ii) Leu replaces Val / change in amino acid (sequence) / primary structure;

Change in hydrogen / ionic bonds which alters tertiary structure / active site;

Q *Different amino acid formed or produced negates first marking point.*

Substrate cannot bind / no longer complementary / no enzyme-substrate complexes form;

Active site changed must be clear for third marking point but does not need reference to shape.

3

(d) (i) Interphase / S / synthesis (phase);

1

(ii) DNA / gene replication / synthesis occurs / longest stage;

Allow 'genetic information' = DNA.

Allow 'copied' or 'formed' = replication / synthesis

1

[9]