

- 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 percentage decrease in number of cancer cells / greater proportion 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*

- (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]**