

**M1.(a)** (i) Joins nucleotides (to form new strand).

*Accept: joins sugar and phosphate / forms sugar-phosphate backbone*

*Reject: (DNA polymerase) forms base pairs / hydrogen bonds*

1

(ii) (Prokaryotic DNA)

1. Circular / non-linear (DNA);

*Accept converse for eukaryotic DNA*

*Ignore: references to nucleus, binary fission, strands and plasmids*

2. Not (associated) with proteins / histones;

*Accept does not form chromosomes / chromatin*

3. No introns / no non-coding DNA.

*Accept only exons*

**Q Neutral: no 'junk' DNA**

2 max

(b) (i) 1. Have different genes;

*Reject: different alleles*

2. (Sobases / triplets) are in a different sequence / order;

*Accept: base sequence that matters, not percentage*

3. (So) different amino acid (sequence / coded for) / different protein / different polypeptide / different enzyme.

*Unqualified 'different amino acids' does not gain a mark*

*Reject: references to different amino acids formed*

*Ignore: references to mutations / exons / non-coding / introns*

2 max

(ii) (Virus DNA)

1. A does not equal T / G does not equal C;

*Accept: similar for equal*

*Accept: virus has more C than G / has more A than T*

2. (So) no base pairing;

3. (So) DNA is not double stranded / is single stranded.

2 max

[7]

- M2.(a)**
1. DNA replicated;  
*Reject: DNA replication in the wrong stage*
  2. (Involving) specific / accurate / complementary base-pairing;  
*Accept: semi conservative replication*
  3. (Ref to) two identical / sister chromatids;
  4. Each chromatid / moves / is separated to (opposite) poles / ends of cell.  
*Reject: meiosis / homologous chromosomes / crossing over*  
*Note: sister chromatids move to opposite poles / ends = 2 marks for mp 3 and mp 4*  
*Reject: events in wrong phase / stage*

4

- (b) (i)
1. To allow (more) light through;  
*Accept: transparent*
  2. A single / few layer(s) of cells to be viewed.  
*Accept: (thin) for better / easier stain penetration*

2

- (ii)
1. More / faster mitosis / division near tip / at 0.2 mm;  
*Neutral: references to largest mitotic index*
  2. (Almost) no mitosis / division at / after 1.6 mm from tip;  
*Accept: cell division for mitosis*  
*Penalise once for references to meiosis*
  3. (So) roots grow by mitosis / adding new cells to the tip.  
*Accept: growth occurs at / near / just behind the tip (of the root)*  
*Accept: converse arguments*

2 max

[8]

- M3.(a)** Deoxyribose. 1
- (b) 1. Thymine 18 (%);  
2. Guanine 32 (%). 2
- (c) DNA polymerase. 1
- (d) 1. **(Figure 1 shows)** DNA has antiparallel strands / described;  
2. **(Figure 1 shows)** shape of the nucleotides is different / nucleotides aligned differently;  
3. Enzymes have active sites with specific shape;  
4. Only substrates with complementary shape / only the 3' end can bind with active site of enzyme / active site of DNA polymerase. 4
- [8]**
- M4.(a)** 1. Outside of virus has antigens / proteins;  
2. With complementary shape to receptor / protein in membrane of cells;  
3. (Receptor / protein) found only on membrane of nerve cells.  
*Accept converse argument* 3
- (b) 1. No more (nerve) cells infected / no more cold sores form;  
2. (Because) virus is not replicating. 2
- (c) Prevents replication of virus. 1
- (d) MicroRNA binds to cell's mRNA (no mark)  
1. (Binds) by specific base pairing;

2. (So) prevents mRNA being read by ribosomes;
3. (So) prevents translation / production of proteins;
4. (Proteins) that cause cell death.

4  
[10]

**M5.(a)** Box around single nucleotide.

1

(b)

DNA strand	Percentage of each base			
	A	C	G	T
Strand 1	(16)	34	21	29
Strand 2	29	(21)	(34)	16

2 rows correct = 2 marks;  
1 row correct = 1 mark.

2

- (c)
1. Reference to DNA polymerase;
  2. (Which is) specific;
  3. Only complementary with / binds to 5' end (of strand);  
*Reject hydrogen bonds / base pairing*
  4. Shapes of 5' end and 3' end are different / description of how different.

4  
[7]

**M6.(a)** (i) Repeating units / nucleotides / monomer / molecules;  
*Allow more than one, but reject two*

1

- (ii) 1. C = hydrogen bonds;

2. D = deoxyribose;  
*Ignore sugar*
3. E = phosphate;  
*Ignore phosphorus, Ignore molecule*

3

(iii)

Name of base	Percentage
Thymine	34
Cytosine / Guanine	16
Adenine	34
Cytosine / Guanine	16

*Spelling must be correct to gain MP1*

*First mark = names correct*

*Second mark = % correct, with adenine as 34%*

2

(b) (i) 153;

1

- (ii) Some regions of the gene are non-coding / introns / start / stop code / triplet / there are two DNA strands;

*Allow addition mutation*

*Ignore unqualified reference to mutation*

*Accept reference to introns and exons if given together*

*Ignore 'junk' DNA / multiple repeats*

1

**[8]**