Mark schemes

Q1.

    (a)   1.   Hydrogen (bonds);

            2.   Phosphodiester (bonds);
                    Accept ester/covalent bond

2

    (b)   Correct answer for 2 marks = 1489/1489.2;;

          Incorrect answer but for 1 mark accept:

          876

          OR

          1861 - 1862

2

Q2.

    (a)   4 rows correct = 2 marks;;
          2 or 3 rows correct = 1 mark;
          0 or 1 row correct = 0 marks

Biological molecules	Element			
	Carbon	**Nitrogen**	**Oxygen**	**Phosphorous**
Galactose	✓		✓	
Phospholipid	✓		✓	✓
RNA	✓	✓	✓	✓
Sucrose	✓		✓	

2

    (b)   Correct answer for 2 marks, 0.8376308/0.84/0.8 (hours);;

          Accept for 1 mark,

          Evidence of 4×10^6 **and** 3×10^9 (written in any format, for correct readings from graph)

          OR

          Evidence of 9.550746785 (correct number of generations)

          OR

          Evidence of 1.1938443348 (correct generations/ hour)

          OR

          Evidence of 50.26 (correct generation time in minutes)

Incorrect reading of graph, 3×10^6 **and** 2×10^9

Accept for 1 mark, calculation carried out correctly

Evidence of 9.380821784 (correct calculation of number of generations)

OR

Evidence of 1.172602723 (correct calculation of generations/ hour)

OR

Evidence of 51.16822503 (correct calculation of generation time in minutes)

OR

Evidence of 0.8528037505 (correct calculation of generation time in hours)

Incorrect reading of graph, $10^{6.4}$ **and** $10^{9.3}$ **OR** $10^{6.3}$ **and** $10^{9.2}$

Accept for 1 mark, calculation carried out correctly

Evidence of 9.633591475 (correct calculation of number of generations)

OR

Evidence of 1.204198934 (correct calculation of generations/ hour)

OR

Evidence of 49.82565445 (correct calculation of generation time in minutes)

OR

Evidence of 0.8304275742 (correct calculation of generation time in hours)

OR

Evidence of 0.83, with no other working
Accept correct rounding to any number of decimal places

2

(c) 1. (Model) Q **and**

(Name) Semi-conservative (replication);

Explanation

2. (Model) **P** (is unsupported because)

There should be two peaks in generation 1

OR

(Only) one peak is shown in generation 1

OR

There should be 3:1 (ratio) of peaks in generation 2

OR

There should **not** be an intermediate/^{15}N ^{14}N peak in generation 1/2/3

OR

The original/generation 0/^{15}N peak should be in generation 1/2/3;

3.   (Model) **R** (is unsupported because)

There should be >2 peaks in generation 2/3

OR

There should be one wide/overlapping peak in generation 3;
      Accept answers 2. and 3. in either order
      Accept for 'peak', density OR distribution
      Accept for '>2', many OR several

3

[7]

Q3.

(a)   1.   Polymer of nucleotides;
             Accept 'Polynucleotide'
             Accept for 'phosphate'. phosphoric acid

2.   Each nucleotide formed from deoxyribose, a phosphate (group) and an organic/nitrogenous base;

3.   Phosphodiester bonds (between nucleotides);

4.   Double helix/2 strands held by hydrogen bonds;

5.   (Hydrogen bonds/pairing) between adenine, thymine **and** cytosine, guanine;

5

Q4.

(a)   1.   Condensation (reaction)/loss of water;

2.   (Between) phosphate **and** deoxyribose;

3.   (Catalysed by) DNA polymerase;
             Reject if DNA polymerase joins AT/GC OR
             complementary nucleotides/bases OR forms
             hydrogen bonds

2 max

(b)   Correct answer for 2 marks = 70;;

Accept for 1 mark,

A = 42 **and** T = 42

OR

420 (total bases in gene)

OR

210 (bases in template strand)

2

(c)   Histone;

1

(d)   1.   DNA helicase;

2.   Breaks hydrogen bonds between base pairs/ AT and
GC/complementary bases

OR

Breaks hydrogen bonds between <u>polynucleotide</u> strands;
        Reject <u>hydrolysis</u> of hydrogen bonds

2

[7]

Q5.
(a)   1.   Joins (adjacent DNA) nucleotides;
        Reject suggestions that it forms hydrogen bonds or
        joins complementary bases.
        Reject 'nucleotide bases'.

2.   (Catalyses) condensation (reactions);

3.   (Catalyses formation of) phosphodiester bonds (between adjacent
nucleotides);

2 max

Q6.
(a)   Watson **and** Crick
OR
Crick **and** Watson;
        Correct spelling
        Ignore first/given/fore names

1

(b)   DNA polymerase;

Correct spelling

1

(c)   **Role of single-stranded DNA fragments**

1.   Template;
2.   Determines order of nucleotides/bases;

Role of DNA nucleotides

3.   Forms complementary pairs / A – T, G - C
       OR
       Forms complementary (DNA) strand;
              Ignore forms complementary bases
   *Accept sequence/ chain for strand*

3

[5]

Q7.

(a)   1.   Phosphate, deoxyribose and base correctly labelled;
              Accept P in a circle / P_i / PO_4^{3-} for phosphate.
              Do not accept phosphorus for phosphate.
              *Do not accept **only** pentose for deoxyribose.*
              Ignore references to sugar.
              Accept a named base, (eg adenine, thymine, guanine, cytosine).
              *Do not accept uracil or **only** letters (eg A, T, G or C).*
              Ignore labelled bonds

2.   Correct shapes **and** bonds in the correct positions (as shown below);
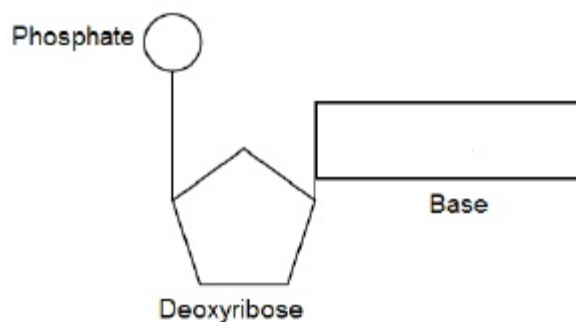
              Accept correct shapes with incorrect labels
              Accept any orientation of diagram, eg inverted / mirror image
              Accept any pentagon for deoxyribose

2

(b)   1.   Weak / easily broken hydrogen bonds between bases allow two strands to separate / unzip;
              may appear in the same feature

      2.   Two strands, so both can act as templates;

              may appear in the same feature

      3.   Complementary base pairing allows accurate replication;

              Allow description of complementary base pairing
              and accurate replication.

              2 max

(c)   C. 550 seconds;

              1

              [5]

Q8.

(a)   1.   (DNA) helicase causes breaking of hydrogen/H bonds (between DNA strands);

              Reject 'helicase hydrolyses hydrogen bonds'.

      2.   DNA polymerase joins the (DNA) nucleotides;

              Reject if suggestion that DNA polymerase joins the
              complementary <u>nucleotides</u> or forms H bonds.
              Reject if joining RNA nucleotides or forming RNA.

      3.   Forming <u>phosphodiester</u> bonds;

              3

(b)   1.   (Treatment **D** Antibody binds to cyclin A so) it cannot bind to DNA/enzyme/initiate DNA replication;

              For 'bind to enzyme' accept 'activate'.
              Idea of 'initiate DNA replication' must be linked to
              start not just less replication.
              For 'enzyme' accept named enzyme.

      2.   (Treatment **E**) RNA interferes with mRNA/tRNA/ribosome/polypeptide formation (so cyclin A not made);

      3.   In Treatment **F** added cyclin A can bind to DNA/enzyme (to initiate DNA replication)
             OR
             Treatment **F** shows that it is the cyclin A that is being affected in the other treatments
             OR
             Treatment **F** shows that cyclin A allows the enzyme to bind (to DNA)
             OR
             (Some cells in **D** or **E**) can continue with DNA replication because they have a different cyclin A <u>allele</u>
             OR
             (Some cells in **D** or **E**) can continue with DNA replication because the antibody/RNA has not bound to all the cyclin A protein/mRNA
             OR
             (Some cells in **E**) can continue with DNA replication because they contain previously translated cyclin A;

              Context needed for Treatment F but it does not

need to be named.
For 'enzyme' accept named enzyme.

3

[6]

Q9.

(a)   8;

Accept eight

1

(b)   Phosphodiester (bond);

Accept phonetic spellings

1

(c)   1.   DNA helicase – (unwinding DNA and)
            breaking hydrogen bonds / bonds between
            chains / bases / strands;
      2.   DNA polymerase – joins (adjacent)
            nucleotides **OR** forms phosphodiester bond /
            sugar-phosphate backbone;

            1.   *Accept H bonds.*
            1.   *Accept hydrolyses for breaks*
            2.   *Reject forms hydrogen bonds (between*
                 nucleotides / bases)

2

(d)   1.   ATP has ribose **and** DNA nucleotide has
            deoxyribose;
      2.   ATP has 3 phosphate (groups) **and** DNA
            nucleotide has 1 phosphate (group);
      3.   ATP – base always <u>adenine</u> **and** in DNA
            nucleotide base can be different / varies;

            Both parts of each MP needed
            3.   *Reject Uracil / U*
            3.   *Accept C, T or G for different bases*
            Accept annotated diagram for any of the three
            marks

2 max

[6]

Q10.

(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]

Q11.

(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]