



A-Level Biology

DNA Structure and Replication

Mark Scheme

Time available: 70 minutes

Marks available: 55 marks

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Mark schemes

1.

(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

(c) 1. tRNA is 'clover leaf shape', mRNA is linear;

Must be a comparison

Reject tRNA is double stranded

Accept tRNA is folded for tRNA is 'clover leaf shaped'

2. tRNA has hydrogen bonds, mRNA does not;

3. tRNA has an amino acid binding site, mRNA does not;

Accept 'CCA end' for amino acid binding site

4. tRNA has anticodon, mRNA has codon;

2

(d) 1. mRNA fewer nucleotides

OR

Pre-mRNA more nucleotides

OR

mRNA has no introns/has (only) exons

OR

Pre-mRNA has (exons and) introns;

Accept mRNA is shorter OR pre-mRNA is longer

2. (Because of) splicing;

2

[8]

- 2.** (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/¹⁵N ¹⁴N peak in generation 1/2/3

OR

The original/generation 0/¹⁵N 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]

3.

- (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 polynucleotide strands;

Reject hydrolysis of hydrogen bonds

2

[7]

4.

(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]

5.	(a) 8; <i>Accept eight</i>	1
	(b) Phosphodiester (bond); <i>Accept phonetic spellings</i>	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. <i>Accept H bonds.</i> 1. <i>Accept hydrolyses for breaks</i> 2. <i>Reject forms hydrogen bonds (between nucleotides / bases)</i>	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; <i>Both parts of each MP needed</i> 3. <i>Reject Uracil / U</i> 3. <i>Accept C, T or G for different bases</i> <i>Accept annotated diagram for any of the three marks</i>	2 max
		[6]
6.	(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]
7.	(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)
- Reference to DNA polymerase;
 - (Which is) specific;
 - Only complementary with / binds to 5' end (of strand);
Reject hydrogen bonds / base pairing
 - Shapes of 5' end and 3' end are different / description of how different.

4

[7]

8.

- (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)
- Circular / non-linear (DNA);
Accept converse for eukaryotic DNA
Ignore: references to nucleus, binary fission, strands and plasmids
 - Not (associated) with proteins / histones;
Accept does not form chromosomes / chromatin
 - 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. (So) bases / 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]