



EXAM PAPERS PRACTICE

## Nucleic acids 2

Level: OCR AS H020

Subject: Biology

Exam Board: Suitable for all boards

Topic: Nucleic acids 2

Type: Mark Scheme

To be used by all students preparing for OCR AS Biology H020 foundation or higher tier but also suitable for students of other boards.

## Mark schemes

- 1** (a) (Pentose) sugar/deoxyribose and phosphate;  
*Reject ribose and phosphorus*
- 1**
- (b) Semi-conservative replication;  
Complementary pairing;  
Hydrogen bonding (of bases/nucleotides);  
Condensation/described of nucleotides;  
DNA polymerase involved;  
*Accept example (A, T and C, G)*
- 3 max**
- 2** (a) Two suitable differences between DNA and RNA;  
*1 mark per correct row to 2 max*
- e.g.
- DNA is double stranded, RNA is single stranded;  
DNA has thymine present, RNA has Uracil present;  
*Accept T and U*
- DNA is larger/heavier/longer, RNA is smaller/lighter/shorter;  
DNA has a deoxyribose sugar, RNA has a ribose sugar;  
DNA stays in the nucleus, RNA leaves the nucleus;
- 2 max**
- (b) Three suitable examples;
- e.g.
- Carries coded information about the sequence of amino acids;  
Copied from DNA/gene;  
Code is in sequence of bases / triplet / three bases / a codon codes for one amino acid;  
Moves out of nucleus/goes into cytoplasm;  
To ribosomes;
- Accept codons allow anticodons / tRNA to bind*  
*Accept carries 'start' and 'stop' codes*  
*Accept moves through ribosomes*
- 3 max**
- [4]**
- [5]**



3

(a) Any two of:

DNA	RNA
Large molecule	Smaller
Double stranded	Single stranded
Contains Thymine (T)	Contains Uracil (U)
Contains deoxyribose	Contains ribose

2 max

(b) Base sequence (on DNA/in gene);  
Determines sequence of amino acids;  
By determining base sequence on (messenger) RNA;  
Code is a triplet code/three base code for an amino acid;

2 max

(c) Pairs of chromosomes/two chromosomes;  
With genes for same features / with same genes;  
At same loci / in same sequence;  
*Accept same alleles*

2 max

[6]

4

(a) Decreases by 50%;  
Per generation / per division;  
*Only accessible if linked to first marking point*

**OR**

$^{15}\text{N}$  makes up  $\frac{1}{2}$  after 1 division;

Makes up  $\frac{1}{4}$  after 2<sup>nd</sup> division;

2

(b) In DNA replication strands separate;  
Each acts as template (for formation of new strand);  
One strand in each new molecule / semi-conservative replication;  
New strands made using  $^{14}\text{N}$ .

2 max

[4]



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- (a) **D** phosphate;  
**E** pentose sugar/deoxyribose;  
**F** (nitrogenous) base/ organic base/ thymine/adenine/ cytosine/guanine;

*In D reject phosphorous*

*In E*

*Accept 5-carbon sugar*

*Reject sugar alone*

3

(b)

	<b>DNA</b>	<b>RNA</b>
	double-stranded	single-stranded
	deoxyribose	ribose
	Thymine/T	Uracil/U
	very large/long	very small/short

*Accept double helix for DNA*

*Accept longer and shorter*

*Need comparison but could be in one box*

*List rule applies.*

2 max

[5]



6

(a)

✓	✓	✓	
			✓
		✓	✓

*One mark for each correct column*

*Mark ticks only and ignore crosses*

4

- (b) 1. Two marks for box round two hydrogens and one of the oxygens from OH groups on carbons 1 and 4;;
2. One mark from incorrect answer involving any two hydrogens and an oxygen from carbons 1 and 4;

*Do not award marks if all atoms concerned are on same carbon atom or are on carbon atoms other than 1 and 4 or where the answer does not have two hydrogen and one oxygen*

2

- (c) (i) 1. Holds chains / cellulose molecules together / forms cross links between chains / cellulose molecules / forms microfibrils, providing strength / rigidity (to cellulose / cell wall);
2. Hydrogen bonds strong in large numbers;x  
*Principles here are first mark for where hydrogen bonds are formed and second for a consequence of this.*  
*Accept microfibrils*

2

- (ii) Compact / occupies small space / tightly packed;  
*Answer indicates depth required. Answers such as "good for storage", "easily stored" or "small" are insufficient.*

1

[9]

7

- (a) (i) Deoxyribose;

*pentose / 5C sugar = neutral*

1

- (ii) Phosphate / Phosphoric acid;

*phosphorus / P = neutral*

1

- (b) Hydrogen (bonds);

1

- (c) 381 / 384 / 387;

1

- (d) (Gln) Met Met Arg Arg Asn;

1



(e) Change in (sequence of) amino acids / primary structure;

Change in hydrogen / ionic / disulfide bonds leads to change in tertiary structure / active site (of enzyme);

Substrate cannot bind / no enzyme-substrate complexes form;

*Q Reject = different amino acids are formed*

3

[8]

8

(a)

DNA	✓	2
mRNA	✗	1
tRNA	✓	1

*One mark for each correct column*

*Regard blank as incorrect in the context of this question*

*Accept numbers written out: two, one, one*

2

(b) (i) Marking principles

1 mark for complete piece transcribed;

*Correct answer*

*UGU CAU GAA UGC UAG*

1 mark for complementary bases from sequence transcribed;

*but allow 1 mark for complementary bases from section transcribed, providing all four bases are involved*

2

(ii) Marking principle

1 mark for bases corresponding to exons taken from (b)(i)

*Correct answer*

*UGU UGC UAG*

*If sequence is incorrect in (b)(i), award mark if section is from exons. Ignore gaps.*

1

[5]

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(i) sugar or phosphate / S-P / nucleotide chain / backbone / original / parent DNA;

1

(ii) X thymine; Y guanine; Z adenine;

*(Allow T, G and A) Reject: thiamine*

3

[4]



- 10** (a) each strand copied / acts as a template;  
(daughter) DNA one new strand and one original / parent strand; 2
- (b) (i)  $^{15}\text{N}$  / tube **B** (DNA), more / greater density;  
(reject heavier) 1
- (ii) DNA with one heavy and one light strand;  
new / synthesised strand, made with  $^{14}\text{N}$  / light strand; 2
- (c) 32; 28 32 26; 2
- [7]**
- 11** (a) (i) ATA; 1
- (ii) AUA; 1
- (b) tRNA 'clover leaf' shape; (allow reference to loop / folded structure)  
tRNA standard length;  
tRNA has an amino acid binding site;  
tRNA has anticodon available / three exposed bases;  
tRNA has hydrogen bonds (between base pairs); 2 max
- [4]**
- 12** (a) different form of a gene; 1
- (b) hydrogen bonds broken;  
semi-conservative replication / both strands used (as templates);  
nucleotides line up complementary / specific base pairing / A and T / C and G;  
DNA polymerase; 4
- (c) deletion causes frame shift / alters base sequence (from point of mutation);  
changes many amino acids / sequence of amino acids (from this point);  
substitution alters one codon / triplet / one amino acid altered / code  
degenerate / same amino acid coded for; 3
- [8]**
- 13** (a) X, phosphate;  
Y, deoxyribose / pentose / 5-carbon sugar;  
Z, (nitrogenous) base;  
(accept named base) 3
- (b) (specific) hydrogen (bonds); 1



- (c) thymine 28% so adenine 28%  
therefore 44% cytosine and guanine;  
therefore 22% cytosine;  
*(idea of equal amounts T and A, C and G – 1 mark, correct answer  
2 marks)*

2

[6]

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- (a) appropriately placed box;
- (b) (i) B;  
(ii) A;
- (c) (i) determines (sequence of) amino acids / specific protein  
produced / mRNA formation;  
(ii) hydrogen bonds;  
(iii) stability / protects bases / replication;

1

2

1

1

1

[6]





15

- (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. (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]



16

- (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

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- (a) (i) Repeating units / nucleotides / monomer / molecules;  
*Allow more than one, but reject two*
- (ii) 1. C = hydrogen bonds;
2. D = deoxyribose;  
*Ignore sugar*
3. E = phosphate;  
*Ignore phosphorus, Ignore molecule*

1

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

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(a) (i) Anaphase

1

(ii) 1. Sister / identical chromatids / identical chromosomes;

*Reject: Homologous chromosomes separate.*

*Allow any reference to chromatids / chromosomes being identical e.g. same DNA*

2. To (opposite) poles / ends / sides;

2

(b) (i) 1. 8.4 / cells with twice DNA content = replicated DNA / late interphase / prophase / metaphase / anaphase;

*Any reference to interphase must suggest towards end of interphase.*

*'Chromosomes replicate' is not enough for DNA replicates.*

2. 4.2 = DNA not replicated / (early) interphase / telophase / cell just divided / finished mitosis;

2



(ii) 2.1;

1

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(a) (i) Spindle formed / chromosome / centromere / chromatids attaches to spindle;

Chromosomes / chromatids line up / move to middle / equator (of cell);

*Do not award second mark for answers referring to chromosomes 'pairing up'.*

*Ignore reference to homologous chromosomes unless context suggests pairing which negates second mark.*

*Neutral: Details on nuclear membrane.*

*Accept: Diagram for second marking point.*

2

(ii) Chromosome / centromere splits / chromatids / 'chromosomes' separate / pulled apart;

To (opposite) sides / poles / centrioles (of cell);

*Reject: Homologous chromosomes separate for first marking point.*

*Accept: Diagram for second marking point.*

*Chromatids / 'chromosomes' move to poles / sides / centrioles = 2 marks.*

2

(b) (i) Form / replace cells quickly / rapidly / divide / multiply / replicate rapidly;

*Neutral: Repair cells.*

*Answers must convey idea of 'speed'.*

1

(li) Correct answer = 774 minutes / 12 hours 54mins = 2 marks;;

Incorrect answer but indicates 3 cell cycles involved = one mark;

2

(c) Prevents / slows DNA replication / doubling / prevents / slows mitosis;

New strand not formed / nucleotides (of new strand) not joined together / sugar-phosphate bonds not formed;

*First marking point must be in context of DNA replication not cell replication.*

*Do not negate first marking point if role of DNA polymerase is described incorrectly e.g. Reject: 'joins bases / strands together'.*

*Role of DNA polymerase must be correct for last marking point.*

2

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