

Nucleic acids 2

Level: CIE A Level 9700

Subject: Biology

Exam Board: Suitable for all boards

Topic: Nucleic acids 2

Type: Mark Scheme

To be used by all students preparing for CIE Biology A Level 9700 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}N makes up $\frac{1}{2}$ after 1 division;

Makes up $\frac{1}{4}$ after 2nd 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}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)

	DNA	RNA
	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]

9

(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}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}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]

14

- (a) appropriately placed box;

1

- (b) (i) B;

- (ii) A;

2

- (c) (i) determines (sequence of) amino acids / specific protein
produced / mRNA formation;

1

- (ii) hydrogen bonds;

1

- (iii) stability / protects bases / replication;

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

[8]

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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

[8]

18

(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

[6]

19

(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

[9]