

Mark schemes

1

- (a) 1. Degenerate: more than one (base) triplet for each amino acid;
2. Non-overlapping: each base is part of only one triplet. *Accept codon (as would be applicable to mRNA code)*

2

- (b) A = adenine
C = cytosine
G = guanine
U = uracil

All four correct = 2

One error = 1

Two or more errors = 0

2 max

- (c) AGT;

1

- [5]** (a) 1. DNA of eukaryotic cell has non-coding regions / introns within gene

2

Allow converse: (But) a prokaryotic cell does not have non-coding regions / introns in DNA;

OR

pre-mRNA contains non-coding regions / introns;

2. (After transcription / during modification) these regions are removed from (pre-)mRNA;

Ignore references to 'cells need / bacteria do not need'

2 (b) 1. mRNA longer

OR

Has more nucleotides than tRNA;

2. mRNA is a straight molecule but tRNA is a folded molecule / clover-leaf shaped molecule;
3. mRNA contains no paired bases / hydrogen bonds but tRNA has some paired bases / hydrogen bonds.

2 max[4]

- (a) Translation.

3

1

- (b) Transfer RNA / tRNA. 1
- (c) TAC;
UAC. 2
- (d) Have different R group.
Accept in diagram 1
- (e) 1. Substitution would result in CCA / CCC / CCU;
2. (All) code for same amino acid / proline;
3. Deletion would cause frame shift / change in all following codons / change nextcodon from UAC to ACC. 3

[8] (a) 1. Reduction in ATP production by aerobic respiration;

4

2. Less force generated because fewer actin and myosin interactions in muscle;
3. Fatigue caused by lactate from anaerobic respiration. 3

- (b) Couple **A**,
1. Mutation in mitochondrial DNA / DNA of mitochondrion affected;
2. All children got affected mitochondria from mother;
3. (Probably mutation) during formation of mother's ovary / eggs;

- Couple **B**,
4. Mutation in nuclear gene / DNA in nucleus affected;
5. Parents heterozygous;
6. Expect 1 in 4 homozygous affected.

4

max

- (c) 1. Change to tRNA leads to wrong amino acid being incorporated into protein;
2. Tertiary structure (of protein) changed;
3. Protein required for oxidative phosphorylation / the Krebs cycle, so less / noATP made. 3
- (d) 1. Mitochondria / aerobic respiration not producing much / any ATP;
2. (With MD) increased use of ATP supplied by increase in anaerobic respiration;3. More lactate produced and leaves muscle by (facilitated) diffusion. 3
- (e) 1. Enough DNA using PCR;
2. Compare DNA sequence with 'normal' DNA. 2

- (a) 1. Helicase;

[15]

5

2. Breaks hydrogen bonds;
3. Only one DNA strand acts as template;
4. RNA nucleotides attracted to exposed bases;
5. (Attraction) according to base pairing rule;
6. RNA polymerase joins (RNA) nucleotides together;
7. Pre-mRNA spliced to remove introns.

6 max

- (b)
1. Polymer of amino acids;
 2. Joined by peptide bonds;
 3. Formed by condensation;
 4. Primary structure is order of amino acids;
 5. Secondary structure is folding of polypeptide chain due to hydrogen bonding; *Accept alpha helix / pleated sheet*
 6. Tertiary structure is 3-D folding due to hydrogen bonding and ionic / disulfide bonds;
 7. Quaternary structure is two or more polypeptide chains.

5 max

- (c)
1. Hydrolysis of peptide bonds;
 2. Endopeptidases break polypeptides into smaller peptide chains;
 3. Exopeptidases remove terminal amino acids;
 4. Dipeptidases hydrolyse / break down dipeptides into amino acids.

4

[15] (a)

6

Feature	Bacterium	Human immunodeficiency virus (HIV) particle
RNA	✓	✓
Cell wall	✓	
Enzyme molecules	✓	✓
Capsid		✓

1 mark for each

correct vertical column

2

- (b)
1. (Complementary) nucleotides/bases pair
OR
A to T and C to G;
Ignore '(DNA polymerase) forms base pairs/nucleotide pairs'
 2. DNA polymerase;
 3. Nucleotides join together (to form new strand)/phosphodiester bonds form;
Ignore '(DNA polymerase) forms base pairs/nucleotide pairs'
*If clearly writing rote answer about DNA replication **2 max** e.g. helicase or separating strands*

- (c) 1. DNA double stranded/double helix **and** mRNA single-stranded;
Contrast requires both parts of the statement
2. DNA (very) long **and** RNA short;
Accept 'RNA shorter' or 'DNA bigger/longer'
3. Thymine/T in DNA **and** uracil/U in RNA;
4. Deoxyribose in DNA **and** ribose in RNA; **R** Deoxyribonucleic/ ribonucleic acid
Ignore ref. to histones
Ignore ref. to helix and straight chain alone
5. DNA has base pairing **and** mRNA doesn't/ DNA has hydrogen bonding and mRNA doesn't;
6. DNA has introns/non-coding sequences **and** mRNA doesn't; **Ignore ref to splicing**

3 max

[8] (a) Quaternary (structure);

7

*Accept phonetic spelling eg quaternary/quarternery /4°**Award no mark for quaternary as part of a list*

1

- (b) 423;

1

- (c) 1. Oxyhaemoglobin formed/ haemoglobin is loaded/uptakes/associates/binds with oxygen in area of higher
- ppO_2
- / in gas exchange surface/lungs/gills;

*Reference to "react with" = max 1**Accept: reversible interaction with oxygen**Ignore: haemoglobin is carried / contained in red blood cells*

2. (oxygen) unloaded/dissociates from/released (in area of lower
- ppO_2
- / in capillaries/to cells/tissues);

2

- (d) (i) 56(%)

Accept responses in the range 54-58(%)

1

- (ii) 1. (Anaemia curve shifted to right) haemoglobin has lower affinity for oxygen / binds less tightly;
Assume reference is to haemoglobin of anaemia unless stated
2. releases more oxygen / oxygen is released quicker / oxygen dissociates/ unloads more readily to muscles/tissues/cells;
3. (For) respiration;
Accept: even with a lower haemoglobin concentration / meet demand for ATP/energy;

3

[8]

- (a) 1. (Reaction with ATP) breaks/allows binding of myosin to actin/ actinomyosin bridge;

8

2. Provides energy to move myosin head;
1. Credit 'breaks' or 'allows' binding to actin (because cyclical)
 2. Allow in context of 'power stroke' or 're-cocking' (because cyclical)
 2. Ignore contraction on its own
- 2

- (b) (i) Any value between 68.5 and 69.49 (%);;
- If get difference of 0.9 but calculation of percentage incorrect, then award 1 mark;
- 2

- (ii) (Mutant mice)
1. Unable to make phosphocreatine/ less phosphate available to make/recycle ATP;
 2. So less energy/so less ATP available for contraction/fast muscle fibres;
 - 1 and 2. Reject production/creation of energy once
 - 2 Accept less energy for grip
 2. Accept no energy/no ATP for contraction/fast muscle fibres
- 2

- (c) 1. (Heterozygous) have one dominant/normal allele (for creatine production);
2. (This) leads to production of enough/normal amount of creatine;
1. Accept has one allele/one copy of the gene for/that is making creatine
- 2

[8]

9

- (a) (i) 1. (Tumour suppressor) gene inactivated / not able to control / slow down cell division;

Ignore: references to growth

2. Rate of cell division too fast / out of control.
- 1 and 2 Accept: mitosis
 - 1 and 2 Reject: meiosis

2

- (ii) 1. (Genetic) code degenerate;
- Accept: codon for triplet*
- Accept description of degenerate code, e.g. another triplet codes for the same amino acid*
2. Mutation in intron.
- Accept: mutation in non-coding DNA*

- (b) 1. Antibody has specific tertiary structure / binding site / variable region; *Do not accept explanations involving undefined antigen*
2. Complementary (shape / fit) to receptor protein / GF / binds to receptor protein /to GF;
Ignore: same shape as receptor protein / GF
3. Prevents GF binding (to receptor).

3

[6] (a) (i) (In all organisms / DNA,) the same triplet codes for the same amino acid;

10

Accept codon / same three bases / nucleotides
Accept plurals if both triplets and amino acids
Reject triplets code for an amino acid
Reject reference to producing amino acid

1

(ii) 64;

1

(b) Splicing;

Ignore deletion references
Accept RNA splicing

1

- (c) (i) 1. (Mutation) changes triplets / codons after that point / causes frame shift;
Accept changes splicing site
Ignore changes in sequence of nucleotides / bases
2. Changes amino acid sequence (after this) / codes for different aminoacids (after this);
Accept changes primary structure
Reject changes amino acid formed / one amino acid changed
3. Affects hydrogen / ionic / sulfur bond (not peptide bond);
4. Changes tertiary structure of protein (so non-functional); *Neutral 3-D structure*

3 max

(ii) 1. Intron non-coding (DNA) / only exons coding;

Context is the intron

Do not mix and match from alternatives

Neutral references to introns removed during splicing

1. and 2. Ignore ref. to code degenerate and get same / different amino acid in sequence

2. (So) not translated / no change in mRNA produced / no effect (on protein) / no effect on amino acid sequence;
Accept does not code for amino acids

OR

3. Prevents / changes splicing;
4. (So) faulty mRNA formed;
Accept exons not joined together / introns not removed
5. Get different amino acid sequence;

2 max

[8]

11

- (a) 1. Sugar-phosphate (backbone) / double stranded / helix **so** provides strength / stability

/ protects bases / protects hydrogen bonds;
Must be a direct link / obvious to get the mark
Neutral: reference to histones

2. Long / large molecule **so** can store lots of information;
3. Helix / coiled **so** compact;
Accept: can store in a small amount of space for 'compact'
4. Base sequence allows information to be stored / base sequence codes for amino acids / protein;
Accept: base sequence allows transcription
5. Double stranded **so** replication can occur semi-conservatively / strands can act as templates / complementary base pairing / A-T and G-C so accurate replication / identical copies can be made;
6. (Weak) hydrogen bonds **for** replication / unzipping / strand separation / many hydrogen bonds **so** stable / strong;
Accept: 'H-bonds' for 'hydrogen bonds'

6

- (b) 1. (Mutation) in **E** produces highest risk / 1.78;
2. (Mutation) in **D** produces next highest risk / 1.45;
3. (Mutation) in **C** produces least risk / 1.30; *Must be stated directly and not implied*

E > D > C = 3 marks

Accept: values of 0.78, 0.45 and 0.30 for MP1, MP2 and MP3 respectively

If no mark is awarded, a principle mark can be given for the idea that all mutant alleles increase the risk

(c) 180;

1

(d) **(Similarities):**

1. Same / similar pattern / both decrease, stay the same then increase;
2. Number of cells stays the same for same length of time; *Ignore: wrong days stated*

(Differences):

(Per unit volume of blood)

3. Greater / faster decrease in number of healthy cells / more healthy cells killed / healthy cells killed faster;
Accept: converse for cancer cells
Accept: greater percentage decrease in number of cancer cells / greater proportion of cancer cells killed
4. Greater / faster increase in number of healthy cells / more healthy cells replaced / divide / healthy cells replaced / divide faster;
Accept: converse for cancer cells
*For **differences**, statements made must be comparative*

3 max

- (e)
1. More / too many healthy cells killed;
 2. (So) will take time to replace / increase in number; *Neutral: will take time to 'repair'*
 3. Person may die / have side effects;

2 max

[15] (a) 250 000;

12

1

- (b) (i) Loss of 3 bases / triplet = 2 marks;;
'Stop codon / code formed' = 1 mark max unless related to the last amino acid

Loss of base(s) = 1 mark; *eg triplet for last amino acid is changed to a stop codon / code = 2 marks*

3 bases / triplet forms an intron = 2 marks

Accept: descriptions for 'intron' eg non-coding DNA

'Loss of codon' = 2 marks

2

- (ii) 1. Change in tertiary structure / active site;
Neutral: change in 3D shape / structure

2. (So) faulty / non-functional protein / enzyme;
Accept: reference to examples of loss of function eg fewer E-S complexes formed

2

- [5] (a) 1. (Protein / molecule) that moves from cytoplasm to DNA;

13

*Accept 'it' as TF.
Accept moves into nucleus*

2. (TF) binds to specific gene / genes / to specific part of / site on DNA / binds to promoter / RNA polymerase;
Accept regulator / enhancer region
3. Leads to / blocks (pre)mRNA production / allows / blocks binding of RNA polymerase (to DNA) / allows RNA polymerase to work;
*Ignore translation unless context wrong
Max 1 if refer to oestrogen as a transcription factor*

2 max

- (b) 1. (Binding to CREB) prevents transcription / mRNA formation; *Accept that lack of protein leaves NAD reduced*
2. (Binding of huntingtin) prevents production / translation of protein (that removes electrons / protons from NAD);
3. Fewer electrons to electron transport chain / electron transport chain slows / stops / stops / slower oxidative phosphorylation;
4. Fewer protons for proton gradient;
5. Not enough ATP produced / energy supplied to keep cells alive / anaerobic respiration not enough to keep cell alive;
*Accept neurones require ATP for active transport of ions
Ignore references to resting potential*

3 max

- (c) 1. Mitochondrion has two membranes / inner and outer membranes; *Accept cristae for inner membrane*
2. For each (different) membrane a (different) carrier required;
Ignore reference to channel proteins

2

- [7] (a) One / an amino acid (can be) coded for by more than one triplet;

14

*Accept codon for triplet
Accept description of triplet – three bases / nucleotides*

1

- (b) 1. Triplet / three bases on mRNA;
 1. *Accept nucleotide for base*
 1. *Accept DNA for mRNA*
 1. *Ignore references to RNA unqualified*
 2. That code for an amino acid;
 2. *Accept code for stop / start* 2

- (c) (i) To join nucleotides together to form mRNA / premRNA / RNA;
 Reject forming base pairs
 Accept checking and correcting mismatched base pairs 1

- (ii) Reverse transcriptase;
 If they give two enzymes, no mark 1

- (d) GGATCC same as CCTAGG in opposite direction;
 Accept reads same both ways / same forward and back
 Neutral bases are the opposite of each other / reference to base pairs 1

[6] (a) (i) UGC;

15 1

- (ii) TGCTAC; 1

- (b) (DNA) contains introns / non-coding bases / mRNA only contains exons / codingbases;
 Assume that 'it' refers to DNA
 Neutral: DNA contains introns and exons
 Neutral: 'splicing'
 Neutral: pre-mRNA contains introns
 Ignore refs. to start and stop codons 1

- (c) Different primary structure / amino acid sequence / amino acid coded for;
 Reject: different amino acids produced / formed
 Neutral: refs. to bonds 1

- (d) 1. Acetylcholine not broken down / stays bound to receptor;
 2. Na⁺ ions (continue to) enter / (continued) depolarisation / Na⁺ channels (kept) open / action potentials / impulses fired (continuously);
 3. (Intercostal) muscles stay contracted / cannot relax;

'Muscles contract' is not enough
Accept: diaphragm stays contracted / cannot relax

3

[7] (a) (i) Repeating units / nucleotides / monomer / molecules;

16

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] (a) (i) Phosphate and ribose;

17

Accept in either order. Both correct for one mark.

For phosphate accept PO_4 / Pi / \textcircled{P} but not P.

*Do not accept phosphorus.
Ignore references to pentose / sugar.*

1

(ii) TAGGCA;

1

- (b) (i) Does not contain hydrogen bonds / base pairs / contains codons / does not contain anticodon / straight / not folded / no amino acid binding site / longer; Assume that "it" refers to mRNA.

Do not accept double stranded.

1

- (ii) (pre-mRNA) contains introns / mRNA contains only exons; Assume that "it" refers to pre-mRNA.

Accept non-coding as equivalent to intron.

1

(c) (i)

Part of chromosome	U
Middle	18
End	21

One mark for both figures correct

1

- (ii) 1. Have different (base) sequences / combinations of (bases);
2. (Pre-mRNA) transcribed from different DNA / codes for different proteins;

2

[7] (a) (i) 9;

18

Accept: nine

1

- (ii) Introns / non-coding DNA / junk DNA;

Start / stop code / triplet;

Neutral: Repeats.

Accept: 'Introns and exons present'.

Reject: 'Due to exons'.

1 max

- (b) Change in amino acid / s / primary structure;

Change in hydrogen / ionic / disulfide bonds;

Alters tertiary structure;

Reject: 'Different amino acid is formed' – negates first marking point.

Neutral: Reference to active site.

3

(c) Number of bases

	Number of bases			
	C	G	A	T
Strand A	26	19	20	9
Strand B	19	26	9	20

Second column correct;

Columns three and four correct;

2

[7]

19

(a) 1. Hydrolysis breaks proteins / hydrolyses proteins / produces amino acids (from proteins);

2. Protein synthesis involves condensation;

2

(b) Amino acids (from calliphorin) can be joined in different sequences /rearranged;

1

(c) 1. Fall, rise and fall;

2. Rise after 40 and fall after 80;

Ignore concentration values.

2

(d) (i) Fall / increase then fall;

Lysosomes associated with tissue breakdown;

2

(ii) 1. Tissues / cells are being broken down;

2. RNA is digested / hydrolysed / broken down;

3. By enzymes from lysosomes;

4. New proteins not made / no new RNA made;

2 max

(e) 1. (RNA) associated with making protein;

2. New / adult tissues are forming;

2

- (f) 1. In the first 6 days no / little oxygen supplied / with breakdown of tracheae, no / little oxygen supplied;
2. (Without tracheae) respire anaerobically;
3. Anaerobic respiration involves reactions catalysed by enzyme **B** / conversion of pyruvate to lactate / involves lactate production;
4. Enzyme **A** / Krebs cycle is part of aerobic respiration; *Or, with emphasis on aerobic respiration:*
1. Tracheae supply oxygen / after 6 days oxygen supplied;
 2. (With tracheae) tissues can respire aerobically.

4

[15]

(a) Banding pattern changes as cheetah gets older / difficult to judge as tail is short / fluffy;

20

- (b) (i) Mean not (always) a whole number;
Standard deviation not (always) zero;
- (ii) Movement of tail / angle of sight / confused it with another band / subjective estimation;

1

2

*Accept reference to **Figure 1***

E.g. Bands 2 and 3 have same thickness but look different

1

(c) Band width not the same on both sides of tail;

1

(d) Offspring of the same family will be more similar genetically;
As have same mother (and father) / parent;
Expect to see more differences in randomly chosen cheetahs;

3

[8] (a) Introns;

21

(b) Ile Gly Val Ser;

1

(c) (i) Has no effect / same amino acid (sequence) / same primary structure;
Q *Reject same amino acid formed or produced.*

1

Glycine named as same amino acid;

1 *It still codes for glycine = two marks.*

- (ii) Leu replaces Val / change in amino acid (sequence) / primary structure;
 Change in hydrogen / ionic bonds which alters tertiary structure / active site;
Q Different amino acid formed or produced negates first marking point.

Substrate cannot bind / no longer complementary /
 no enzyme-substrate complexes form;
Active site changed must be clear for third marking point but does not need reference to shape.

3

- (d) (i) Interphase / S / synthesis (phase);

1

- (ii) DNA / gene replication / synthesis occurs / longest stage; *Allow 'genetic information' = DNA.*

Allow 'copied' or 'formed' = replication / synthesis

1

[9]

- (a)

22

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

23

DNA polymerase is incorrect
Ignore references to RNA dependent or DNA dependent
Allow phonetic spelling

1

- (b) (i) (Receptor / transcription factor) binds to promoter which stimulates RNAPolymerase / enzyme X;

Transcribes gene / increase transcription;

2

- (ii) Other cells do not have the / oestrogen / ER α receptors;

But do not accept receptors in general.

1

- (c) Similar shape to oestrogen;

Binds receptor / prevents oestrogen binding;

Receptor not activated / will not attach to promoter / no transcription;

Accept alternative

Complementary to oestrogen;

Binds to oestrogen;

Will not fit receptor;

2 max

- [6] (a) Will replace themselves / keep dividing / replicate;

24

Undifferentiated / can differentiate / develop into other cells / totipotent / multipotent / pluripotent;

Accept tissues

2

- (b) Reverse transcriptase;

Allow phonetic spelling

1

- (c) (i) Alters base / nucleotide sequence / causes frame shift;

Different sequence of amino acids in polypeptide / protein / primary structure alters the tertiary structure;

Accept any reference, such as adding bases, to changing the base sequence of the gene. Reject deletion / substitution.

Idea of sequence essential so not makes different amino acids.

Accept answers involving stop / start codons and effect on protein.

2

- (ii) Affects tumour suppressor gene;

Inactivates (tumour suppressor) gene;

Rate of cell division increased / tumour cells continue to divide;

Ignore answers relating to oncogenes. May gain third point.

2 max

(d) Yes

SCID patients unlikely to survive / quality of life poor unless treated;

Cancer that develops is treatable / only affects 25% / five children;

No

Risk of developing cancer is high / 25%;

Cancer may recur / may not be treated successfully in future / only short time scale so more may develop cancer;

No mark for yes or no. Marks are for supporting argument based on biological reasoning.

Accept any points

2 max

[9]