

## 4.2 GENETIC INFORMATION, VARIATION AND RELATIONSHIP – DNA AND PROTEIN SYNTHESIS (1) – MARK SCHEME

### Q1.

- (a) 1. Low starch, fewer copies;  
2. Ranges overlap almost completely;  
**OR**  
Ranges overlap from 2 – 13 copies;  
3. (surprisingly) very few / 2 or 3% have only 2 copies / are diploid;  
4. the mode / highest percentage for low starch is 4 copies and for high starch is 6;  
5. the range / spread is greater with high starch;  
4. *“most people” is not equivalent to mode*

3 max

- (b) 1. More mRNA / more transcription;  
2. More translation / enzyme;  
3. So reaction faster;  
*The idea of “more” must be stated at least once.*  
2. *Accept ‘amylase’ for enzyme*  
3. *“More starch digested” is insufficient*

3

- (c) 1. Mutation(s) produce extra copies of (*AMY1*) gene;  
2. Those with more copies / this adaptation/mutation reproduce / survive better on high starch diet;  
2. And pass on multiple copies / this adaptation/mutation (to offspring);  
*Ignore ref. to single allele/gene*

3

[9]

### Q2.

- (a) 1. Hydrogen bonds between the base pairs holds two strands together  
2. Many hydrogen bonds provides strength  
*Reject strong hydrogen bonds*

2

- (b) (Because) ribosomes assemble polypeptides using mRNA code  
**OR**  
DNA has two strands each with a different (complementary) base sequence;

1

- (c) Codon;

1

- (d) 1. (Because) some amino acids have more than one codon / mRNA code;  
2. Correct example from table.

2

- (e) 1. Stop translation;  
2. Result in detachment of polypeptide chain from ribosome.

2

- (f)

CAC	ATG	ACC
Val	Tyr	Trp

Mark each row

2

[10]

**Q3.**

- (a) 1. Water lost from leaf because of transpiration / evaporation of water (molecules) / diffusion from mesophyll / leaf cells;  
**OR**  
 Transpiration / evaporation / diffusion of water (molecules) through stomata / from leaves;
2. Lowers water potential of mesophyll / leaf cells;
3. Water pulled up xylem (creating tension);
4. Water molecules cohere / 'stick' together by hydrogen bonds;
5. (forming continuous) water column;
6. Adhesion of water (molecules) to walls of xylem;
2. *Accept  $\Psi$  or WP*

5 max

- (b) 1. The DNA strands separate by breaking the H bonds;  
**OR**  
 H bonds broken between (complementary) (DNA) bases;
2. (Only) one of the strands/template strand is used (to make mRNA/is transcribed);
3. (Complementary) base pairing so A → U, T → A, C → G, G → C;
4. (RNA) nucleotides joined by RNA polymerase;
5. pre-mRNA formed;
6. Splicing / introns removed to form mRNA;
1. *Ignore 'hydrolysis' of bonds*
1. *Accept DNA "unzips" by breaking the H bonds*
6. *Accept 'non-coding' sections for introns*

5 max

[10]

**Q4.**

(a) Translation.

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 next codon from UAC to ACC.

3

**Q5.**

- (a) (Molecule contains) more than one polypeptide (chain).

*Accept: has four polypeptides*

1

- (b)  $\frac{\text{oxygenated haemoglobin}}{\text{maximum saturation}} \times 100$

1

- (c) 1. At low partial pressure of oxygen, little increase in saturation as oxygen increases;

2. (then) rapid rise as it gets easier for oxygen to bind.

*Accept use of appropriate numbers from graph*

2

- (d) Ensures rapid / more intake of oxygen in lungs / release of oxygen in tissues.

1

- (e) Volume of blood leaving heart =  $(0.6 \times 0.6) \text{ dm}^3 \text{ minute}^{-1} = 3.6 \text{ dm}^3 \text{ minute}^{-1}$

Mass of haemoglobin in this volume of blood =  $(3.6 \times 150) \text{ g} = 540 \text{ g}$

Volume of oxygen at 100% saturation of this haemoglobin =  $(540 \times 1.35) = 729 \text{ cm}^3$

The graph shows 60% of this volume of oxygen has been released to the tissues, so final answer is  $(729 \times 0.6) = 437.4 \text{ cm}^3 \text{ minute}^{-1}$

3

**Q6.**

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

*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

## Q7.

- (a) 1. **One of** RNA / ribonucleic acid(s) / nucleotide(s)/nucleic acid(s) / rRNA / ribosomal RNA / ribosomal ribonucleic acid  
**and**  
**one of** protein(s) / polypeptide(s) / amino acid(s) / peptide(s) / ribosomal protein;

*Reject DNA, deoxyribonucleic acid, tRNA, transfer RNA, transfer ribonucleic acid, mRNA, messenger RNA, messenger ribonucleic acid.  
Ignore enzyme(s), base(s).*

1

- (b) 1. mRNA binds to ribosome;  
2. Idea of two codons / binding sites;  
3. (Allows) tRNA with anticodons to bind / associate;  
4. (Catalyses) formation of peptide bond between **amino acids** (held by tRNA molecules);  
5. Moves along (mRNA to the next codon) / translocation described;  
*Assume 'it' refers to ribosome.*

3 max

- (c) TGC GTAATA;  
Any errors = 0 marks

1

- (d) 1. Introns (in pre-mRNA);  
2. Removal of sections of (pre-mRNA) / splicing;  
*Introns removed' scores 2 marks.  
Reference to 'introns present in mRNA' disqualifies mp1 but allow ECF for mp2.  
Accept for 1 mark mRNA contains only exons.*

2

[7]

## Q8.

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

### Q9.

- (a) Quaternary (structure);  
*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]

### Q10.

- (a) 1. Reduction in ATP production by aerobic respiration;

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 / no ATP 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

[15]

**Q11.**

- (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*

3

(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]

**Q12.**

- (a) (i) (In all organisms / DNA,) the same triplet codes for the same amino acid;  
*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; 1  
*Ignore deletion references*  
*Accept RNA splicing*
- (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 amino acids (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]

**Q13.**

- (a) 1. Helicase;  
 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]

#### Q14.

- (a) 250 000;

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]

#### Q15.

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

**Q16.**

- (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* 1 max
- (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]**

**Q17.**

- (a) (i) UGC; 1
- (ii) TGCTAC; 1

- (b) (DNA) contains introns / non-coding bases / mRNA only contains exons / coding bases;

*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<sup>+</sup> ions (continue to) enter / (continued) depolarisation / Na<sup>+</sup> 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]

### Q18.

- (a) (i) Phosphate and ribose;

*Accept in either order. Both correct for one mark.*

*For phosphate accept PO<sub>4</sub> / Pi /  $\textcircled{\text{P}}$  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]

**Q19.**

- (a) (i) Repeating units / nucleotides / monomer / molecules;  
*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]

**Q20.**

- (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]

**Q21.**

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

**Q22.**

- (a) (i) 9;  
*Accept: nine*
- (ii) Introns / non-coding DNA / junk DNA;  
Start / stop code / triplet;  
*Neutral: Repeats.*  
*Accept: 'Introns and exons present'.*  
*Reject: 'Due to exons'.*

1

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]

**Q23.**

(a) Introns;

1

(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]

**Q24.**

(a)

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*

3

- (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]

### Q25.

- (a) Banding pattern changes as cheetah gets older / difficult to judge as tail is short / fluffy;  
1
- (b) (i) Mean not (always) a whole number;  
Standard deviation not (always) zero;  
2
- (ii) Movement of tail / angle of sight / confused it with another band / subjective estimation;  
*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]

**Q26.**

- (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]

