Mark schemes

1

(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 shapedmolecule;

3. mRNA contains no paired bases / hydrogen bonds but tRNA has some paired bases /hydrogen bonds.

2 max [4]

2

(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 nextcodon from UAC to ACC.

3

[8]

3

(b) 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

(c) 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

(d) 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) 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

(e) 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

(f) 1. Enough DNA using PCR;
2. Compare DNA sequence with 'normal' DNA.

2

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

5

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]

6

(a) Locus;

Accept: loci

1

(b) Differences in DNA / differences in base sequence of DNA;

Accept: number of different alleles / size/variation in gene pool

Reject: genes

1

(c)
1. Jack Russell (genetic) diversity is (significantly) greatest;
2. Bull terrier (genetic) diversity is (significantly) smallest / is mostinbred;
3. Miniature terrier and Airedale terriers are similar;

1-3: do not credit just a list of values

4. Standard deviations do not overlap / do overlap with correct ref tosignificance;

Reference to significance must be relevant to examples given

Max 3

(d)
1. (Bull terrier) breeding has included a genetic bottleneck/ smallpopulation/more inbreeding/ greater selection (pressure);

Accept: founder effect

2. Reduced number of different alleles/size of gene pool;

Reject: decrease in number of genes

Ignore ref to mutations

OR

3. Miniature (terrier) breeding has included more outbreeding/lessselection (pressure);
4. Increased number of different alleles/larger gene pool/more varietyof alleles;

Reject if genes used instead of alleles

Reject: lower frequency of alleles

Ignore ref to mutations

2

[7]

7

(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]

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

Accept codon for triplet

Accept description of triplet − <u>three</u> 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 <u>nucleotides</u> 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]

9 (a) (i) 4;

1

(ii) 1. Change in amino acid / (sequence of) amino acids / primary structure;

1. Reject = different amino acids are 'formed'

2. Change in hydrogen / ionic / disulphide bonds alters tertiary structure /active site (of enzyme);

2. *Alters 3D structure on its own is not enough for this markingpoint.*

3. Substrate not complementary / cannot bind (to enzyme / active site) / noenzyme- substrate complexes form;

3

(b) 1. Lack of skin pigment / pale / light skin / albino;

2. Lack of coordination / muscles action affected;

2 max

(c) Founder effect / colonies split off / migration / interbreeding;

Allow description of interbreeding e.g. reproduction between individuals from different populations

1

[7]

10 (a) (i) 9;

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] (a) (i) Phosphate and ribose;

11

Accept in either order. Both correct for one mark.

For phosphate accept PO_4/ Pi / Ⓟ *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 / containscodons / 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) More that one polypeptide / chain;

12

Ignore references to haem / other groups

1

(b) (i) 141;

1

(ii) 1. Stop / start sequences;

2. Non coding DNA (in the gene) / introns / multiple repeats / junk DNA;*Do not credit "some bases repeated"*

3. Two chains / a non-coding strand / complementary base pairs;

4. Addition of base by mutation;

2 max

(c) Different primary structure / amino acids / different number of polypeptide chains;

Question is about haemoglobin so do not credit differences in DNA

1

(d) 1. Low partial pressure of oxygen in lungs;

2. (Llama) haemoglobin able to load more oxygen / (llama) haemoglobin saturated (at low / particular partial pressure of oxygen);

3. Higher affinity for oxygen;

The terms used in the graph (or near approximations) should be used in this answer.

Ignore references to unloading

The answer must relate to llamas

3

[8

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

13

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] (a) Introns;

14

(b) Ile Gly Val Ser;

1

(c) (i) Has no effect / same amino acid (sequence) / sameprimary 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]

15 (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] (a) (i) Deoxyribose;

16 *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 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] (a) Phosphate;

17

Deoxyribose;

Q *Candidates must specify deoxyribose. This term is a specification requirement.*
Ignore anything that is not incorrect.

2

(b) 4;

1

(c) (i) 14;

1

(ii) 36;

If (c)(i) incorrect accept [50 – (c)(i)]

1

(d) Different genes;

Different (DNA) base sequences;

2

[7]

18 (a) a length of DNA;

that codes for a single protein / polypeptide;

2

(b) by heating;to break the H-bonds (between complementary bases);

2

(c) (i) to allow the DNA polymerase to attach / start addition ofnucleotides / mark start and end of sequence to be copied / prevents strands re-joining;

1

(ii) because the sequences at the ends of the target sequence are different / one is at the beginning and one at the end;

1

(d) 8;

accept 7

1

[7]

19 (a) (i) actin (*Accept* tropomyosin);

1

(ii) myosin head;

1

(b) (i) Ca^{2+} binds to [part of] the actin / troponin;
this causes tropomyosin to be displaced;
uncovers [myosin] binding sites [on actin] / allows actin to bind;

max 2

(ii) myosin heads bind to actin / cross bridge formation /actomyosin formed; myosin heads / crossbridges swivel / ratchet mechanism; causing actin to slide relative to myosin; energy provided by hydrolysis of ATP;

max 3

(c) (i) (number lightly stained fibres / total number of fibres) × 100;
(actual numbers are 10 / 18 × 100)

1

(ii) sample not representative / large enough / individual muscle fibresdifferent sizes / contain different number of myofibrils;

1

(d) all some stain = 1 fast dark and slow lighter = 2

2

(e) change in base sequence in DNA / addition / deletion / substitution of a base in DNAof the gene which codes for myosin; change in amino acid sequence / primary structure; causes a different tertiary structure; which alters the binding properties of myosin;

4

[15]

20

(a) (i) join / attach nucleotides, to form a strand / along backbone / phosphodiester bonds;

(reject reference to H bonds, complementary base pairing)

1

(ii) ribosome / RER;

1

(b) (i) CGTTACCAA;

1

(ii) CGU UAC CAA;

1

(c) <u>substitution</u>;

1

(d) (i) alanine;

1

(ii) (mutation 1) no change(to sequence of amino acids);
codon for alanine / degenerate codon / same amino acid coded for;

2

(mutation 2)
(change in sequence) <u>valine</u> replaced by <u>alanine /</u> codon for <u>alanine</u>;
folding / shape / tertiary structure / position of bonds may change;
(reject peptide bonds)

2

[10]

21

(a) high energy radiation / ionising particles;

named particles / α, β, γ;
colchicine; x rays /
cosmic rays; uv (light);
carcinogen / named carcinogen;
mustard gas / phenols / tar (qualified);

1 max

(b) (i) removal of one or more bases / nucleotide;
frameshift / (from point of mutation) base sequence change;

2

(ii) sequence of bases in mRNA would change;
(sequence of) amino acids different / different primary structure;
(active site / enzyme 1) changed tertiary shape / changed active sites; white pigment does not bind; lilac pigment not produced / white pigment remains unchanged / enzyme 1 does not function;

4 max

(iii) blue and lilac; white;

colour of petal
(white)
blue
lilac;
white;

2

[9]

change in base / nucleotide (in DNA);

22

change in base sequence of mRNA / change in codons / idea of frameshift following deletion or addition / incorrect tRNA / anticodon; incorrect amino acids / different primary structure / fomation of new stop codon; different tertiary structure / different 3D structure / different polypeptide / shortened polypeptide; different shape of active site / no active site present;

[5] (i) mRNA attaches to ribosome;

23

codon on mRNA; binds to an anti-codon on tRNA; each tRNA brings a specific amino acid; sequence of codons / bases on mRNA determines order of amino acids; formation of peptide bonds / amino acids joined by condensation reactions;

4 max

(iii) inserted gene / mRNA complementary to normal gene / mRNA; binds to it to prevent protein synthesis / form double strand / prevents mRNA binding to ribosomes; will not stop all translation, some mRNA reaches ribosomes / because not all mRNA is bound by inserted gene mRNA;

2 max

[6]

24 (a) mutation changes the amino acid sequence / primary structure of Factor VIII protein;
changes the tertiary structure / 3D shape;

2

(b) (mutant) Factor VIII protein is non-functional / does not work with Factor IX;so no conversion of Factor X to active form and pathway blocked;

2

(c) boy's blood contains (active) Factor VIII;
Factor VIII haemophiliac's blood contains (active) Factor IX;
the mixture has both Factors and so the pathway can complete / blood clots;

2 max

[6]