A-Level Biology

DNA Structure

Mark Scheme

Time available: 65 minutes
Marks available: 55 marks

www.accesstuition.com

Mark schemes

1. (a) 1. Condensation (reaction)/loss of water;

    2. (Between) phosphate **and** deoxyribose;

    3. (Catalysed by) DNA polymerase;
> *Reject if DNA polymerase joins AT/GC OR complementary nucleotides/bases OR forms hydrogen bonds*

2 max

(b) Correct answer for 2 marks = 70;;

Accept for 1 mark,

A = 42 **and** T = 42

OR

420 (total bases in gene)

OR

210 (bases in template strand)

2

(c) Histone;

1

(d) 1. DNA helicase;

    2. Breaks hydrogen bonds between base pairs/ AT and GC/complementary bases

    OR

    Breaks hydrogen bonds between <u>polynucleotide</u> strands;
> *Reject <u>hydrolysis</u> of hydrogen bonds*

2

[7]

2.

(a) **In chloroplasts**

Must be comparative statements.
Accept alternatives in context of nuclear DNA

1. DNA shor<u>ter</u>;
   Accept smaller

2. Few<u>er</u> genes;

3. DNA circular not linear;
   Accept DNA in a loop not linear
   Accept no chromosomes (in chloroplast) unlike nucleus

4. Not associated with protein/histones, unlike nuclear DNA;

5. Introns absent but present in nuclear DNA;
   Ignore references to double and single stranded DNA

3 max

(b) Deoxyribose in DNA **and** ribose in RNA;

1

(c) W = <u>amino acid</u> binding site **and** X = anticodon;
   W *Idea of binding site needed*

1

(d) 1. Triplets code for same amino acid
   Accept: DNA/code/triplets are degenerate
   Reject: codons (as question states within genes)

2. Occurs in introns /non-coding sequence;
   Reject: codons (as question states within genes)
   Ignore junk DNA
   Reject: multiple repeats

2

[7]

3.

(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]

4. (a) 1. Hydrogen (bonds);

2. Phosphodiester (bonds);
   Accept ester/covalent bond

2

(b) Correct answer for 2 marks = 1489/1489.2;;

Incorrect answer but for 1 mark accept:

876

OR

1861 - 1862

2

(c) 1. tRNA is 'clover leaf shape', mRNA is linear;
   Must be a comparison
   Reject tRNA is double stranded
   Accept tRNA is folded for tRNA is 'clover leaf shaped'

2. tRNA has hydrogen bonds, mRNA does not;

3. tRNA has an amino acid binding site, mRNA does not;
   Accept 'CCA end' for amino acid binding site

4. tRNA has anticodon, mRNA has codon;

2

(d) 1.   mRNA fewer nucleotides

OR

Pre-mRNA more nucleotides

OR

mRNA has no introns/has (only) exons

OR

Pre-mRNA has (exons and) introns;
        Accept mRNA is shorter OR pre-mRNA is longer

2.   (Because of) splicing;

2

[8]

5. (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;
        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 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]

6. (a) (i) Repeating units / nucleotides / monomer / molecules;

Allow more than one, but reject two

1

(ii) 1. C = hydrogen bonds;

2. D = <u>deoxy</u>ribose;

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 <u>adenine as 34%</u>

2

(b) (i) 153;

1

(ii) Some regions of the gene are non-coding / <u>introns</u> / start / stop code / triplet / there are two DNA strands;

     Allow <u>addition</u> mutation

     Ignore unqualified reference to mutation

     Accept reference to introns and exons if given together

     Ignore 'junk' DNA / multiple repeats

1

[8]

7. (a) (i) Phosphate and ribose;

     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 / 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]