

Mark schemes

Q1.

- (c) Locus/loci; 1
- (d) 1. (Because) base/nucleotide sequence;
2. (In) triplet(s);
3. (Determines) order/sequence of amino acid sequence/primary structure (in polypeptide); 3

Q2.

- (b) Base/nucleotide/triplet sequence coding for polypeptide/sequence of amino acids/primary structure; 1
- (c) Serine Alanine Glycine Proline;
- Must be in this order Accept Ser Ala Gly Pro / S A
G P*
- 1

Q3.

- (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

Q4.

(a) Plant v prokaryote

1. (Associated with) histones/proteins v no histones/proteins;

2. Linear v circular;

3. No plasmids v plasmids;

Do not credit if suggestion that prokaryotic DNA only exists as plasmids.

4. Introns v no introns;

5. Long(er) v short(er);

Alternatives must be written directly opposite one another.

Do not award if only half of a mark point is written.

Reference to prokaryotic DNA being single stranded = max 2.

Reference to prokaryotic DNA not being helical = max 2.

3 max

(b) 1. DNA that does not code for protein/polypeptides

OR

DNA that does not code for (sequences of) amino acids

OR

DNA that does not code for tRNA/rRNA;

Accept the idea of not transcribed for 'does not code for'.

*Do not credit 'DNA that does not code for **an** amino acid'.*

Ignore reference to introns.

2. (Positioned) between genes;

Reject (positioned) 'in introns' or 'between exons'.

Accept '(Positioned) at the end of chromosomes' or

'(Positioned) in the telomeres'.

2

Q5.

(a) **In chloroplasts**

Must be comparative statements.

Accept alternatives in context of nuclear DNA

1. DNA shorter;
Accept smaller
 2. Fewer 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 = amino acid 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]

Q6.**(a) Comparisons**

1. Nucleotide structure is identical;
Accept labelled diagram or description of nucleotide as phosphate, deoxyribose and base
2. Nucleotides joined by phosphodiester bond;

OR

Deoxyribose joined to phosphate (in sugar, phosphate backbone);

3. DNA in mitochondria / chloroplasts same / similar (structure) to DNA in prokaryotes;
Accept shorter than nuclear DNA/is circular not linear/is not associated with protein/histones unlike nuclear DNA;

Contrasts

4. Eukaryotic DNA is longer;
5. Eukaryotic DNA contain introns, prokaryotic DNA does not;
6. Eukaryotic DNA is linear, prokaryotic DNA is circular;
7. Eukaryotic DNA is associated with / bound to protein / histones, prokaryotic DNA is not;

5 max

Q7.

- (d) Differences in base sequences

OR

Differences in histones/interaction with histones

OR

Differences in condensation/(super)coiling;

Answer must be in context of differences in arrangement of chromosomes not just related to the properties of the stain.

Accept spec section 8 ideas e.g. different methylation/acetylation

Accept different genes

Reject different alleles

1

- (e) (Two chromosomes that) carry the same genes;

Reject 'same alleles'

Accept 'same loci' (plural) or 'genes for the same characteristics'

1