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Detailed mark scheme

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2002

XVIII

1583

Time allowed

52 Minutes

Score

/43

Percentage

%

Biology

**AQA
AS & A LEVEL**

Mark Scheme

3.4 Genetic information, variation and relationships between organisms

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1

(a) 250 000;

(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]



- 2 (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]



3

- (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]

- 4 (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
- [8]**