

- M1.(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]**
- M2.(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]

- M3.(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]

M4.(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]