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]