Section B

21 (a) (i) **A =** pyruvate **;**

                                            accept other names e.g. 2-oxopropanoic acid

        B = reduced NAD / NADH

                                ;

        C = NAD($^+$)

                                           ignore attempts to balance equation   **[2]**

    (ii) cytosol / cytoplasm **;**   **[1]**

   (iii) 1 allows glycolysis to continue (during oxygen deficit) **;**
          2 regenerates NAD (for use in glycolysis) **;**
          3 allows ATP production (to continue) **;**
          4 (ATP) for (muscle) contraction **;**
                              accept details of ATP involvement in contraction
          5, AVP **; ;**
          6 e.g. temporary storage of hydrogen / hydrogen transferred prevents
              accumulation of reduced NAD / AW
              e.g. lactate transported areas with (more) oxygen (for oxidation)
              e.g. lactate prevents damage to muscles by overexertion / AW   **[max 4]**

  (b) *allow points linked to named enzymes*
      1 tertiary structure / folded chain, held in place by, bonds / interactions between R groups **;**
      2 three correctly named bonds **;**
          from:
          hydrogen bond
                              accept H bond
          ionic / electrovalent, bond
          disulfide bond
          hydrophobic interactions
          van der Waal's (forces)
      3 ref. specificity **;**
          e.g. active site shape complementary to substrate shape
          e.g. substrate binding to active site by lock and key mechanism
          e.g. specific active site means enzyme catalyses only one specific, reaction /
          interconversion
                              accept active site in terms of tertiary and
                                         quaternary structure
      4 *idea* that conformational changes occur to improve fit / induced fit, described **;**
      5 (amino acids with) hydrophilic / polar, R-groups / side chains, on the outside / facing
          water / AW / ora hydrophobic, R-groups / central area **;**
      6 solubility / interact with water / reactions occur in aqueous environment **;**
      7, AVP **; ;**
      8 e.g. reference to primary and secondary protein structure
          e.g. further detail of R-groups involved in catalysis
          e.g. details of how structure lowers activation energy for catalysis   **[max 4]**

(c) 1 each (nucleated) cell has both genes **;**

                                        accept *idea* that all cells have the same genetic information

      2 ref. to differential expression / control of gene expression / tissue-specific expression **;**

                                          accept in context of transcription

      3 use of data from 21.1 to qualify **;**

         in terms of genes, *LDH-A* and *LDH-B* transcribed

      4 ref. transcription factors required to initiate transcription / ref. to binding of RNA polymerase to promoter / ref. to transcription complex **;**

      5 AVP **;**

         e.g. developmental control

         e.g. control of assembly of transcribed polypeptides   **[max 2]**

(d) (i) 1 ref. (events leading to heart attack take place in the) coronary arteries **;**

        2 ref. presence of, atheroma / atheromatous plaque, and, uneven / turbulent blood flow **;**

        3 (causes) clot / thrombus, formation (by platelets) **;**

        4 decreased blood flow caused by, stenosis / narrow(ed) lumen **;**

                                      accept no blood flow caused by blocked lumen

                                      accept embolism / described, linked to reduced blood flow

                                      accept thrombosis linked to reduced blood flow

        5 less (blood with), glucose / oxygen, reaches the, heart / cardiac, muscle / heart / cardiac, muscle, deprived / AW, of oxygen / glucose **;**

                                      accept myocardial infarction occurs

       4/5   **accept** ischaemia in context of heart if no mp 4 and 5

        6 heart attack caused by, damage to / death of, heart tissue **;**   **[max 3]**

    (ii) 1 different conditions (usually) affect different, tissues / body locations **;**

        2 *idea* that, damage / injury (because of condition), to, tissues / cells, causes release of LDH / LDH to enter blood **;**

                                      accept named examples, e.g. cardiac muscle

        3 (as) different tissues have different isoenzymes / each tissue has particular isoenzyme(s) / heart tissue will have particular isoenzymes **;**

                                      accept other named tissue

        4 *idea* of comparing test LDH isoenzyme concentrations (in blood) against normal concentrations **;**

         detail – use of Table 21.1 to max 2

        5 results indicate tissue from where damage originates **;**

        6 heart damage indicated by higher concentrations of, LDH-1 / LDH-2 **;**

                                      accept HHHH / HHHM

        7 presence of, LDH-3 / HHMM, indicates, brain / lung, damage / LDH-4 / HMMM, indicates, kidney / placenta, damage / LDH-5 / MMMM, indicates, liver / skeletal muscle, damage **;**

        8 AVP **;**

         e.g. ratio of isoenzymes may change with damage to different tissues

         e.g. useful in differentiating between conditions with tissue damage and those without (where symptoms exist)

         e.g. (suggestion of) use of electrophoresis to identify the different isoenzymes present   **[max 4]**

(e) 1 base sequences are from the non-template / non-transcribed / AW, strand / polynucleotide ;

2 (m)RNA is equivalent to DNA strand shown except U replaces T / is complementary copy of transcribed strand of DNA ;

3 further detail from Fig. 21.2 and Table 21.2 ;
e.g. met start amino acid = AUG mRNA codon, so transcribed DNA would be TAC, instead of ATG

4 *either*
stated similarity of nucleotide sequence ;
e.g. first 11, nucleotides / bases, identical
e.g. first three triplets identical
e.g. triplet, 5 / 9, the same

or

stated differences in nucleotide sequence ;
<div align="center">**accept** codon for triplet</div>
e.g. fourth, sixth, seventh, eighth and tenth triplets different
e.g. fourth triplet CTA in *LDH-A* but CTT in *LDH-B*
e.g. sixth triplet GAT in *LDH-A* but GAA in *LDH-B*
e.g. seventh triplet CAG in *LDH-A* but AAA in *LDH-B*
e.g. eighth triplet CTG in *LDH-A* but CTC in *LDH-B*
e.g. tenth triplet TAT in *LDH-A* but AAA in *LDH-B*

5 *either*
stated similarity of amino acid sequence ; *10 amino acids in sequence*
e.g. first five amino acids are, met-ala-thr-leu-lys / the same
e.g. eighth and ninth amino acids are, leu and ile / the same
e.g. 70% homology

or

stated differences in amino acid sequence ;
e.g. sixth, asp v glu / seventh, gln v lys / tenth, tyr v ala

6 ref. same amino acid but different, nucleotide sequence / triplet ;
e.g. first leu / fourth amino acid = CTA in *LDH-A* and CTT in *LDH-B*
e.g. second leu / eighth amino acid = CTG in *LDH-A* and CTC in *LDH-B*

7 explanation in terms of genetic code ;
e.g. same amino acid can be specified by different codons / degeneracy of code / wobble on third nucleotide of codon

8 both have retained met, start amino acid ;

9 AVP ;
e.g. different amino acid sequences may allow for different polypeptide folding
e.g. different amino acid sequences may lead to changes in, active site / other named or described site
<div align="center">**reject** if suggestion made that this would alter the type of reaction catalysed</div>
e.g. comment on evolutionary nature of the homology of the amino acid sequence
e.g. additional use of data from, Fig. 21.2 / Table 21.1, such as further examples of genetic wobble   **[max 6]**

[Total: 26]