OCR

RECOGNISING ACHIEVEMENT

Subject: BIOCHEMISTRY..... ..... Code: ...2815/02.....

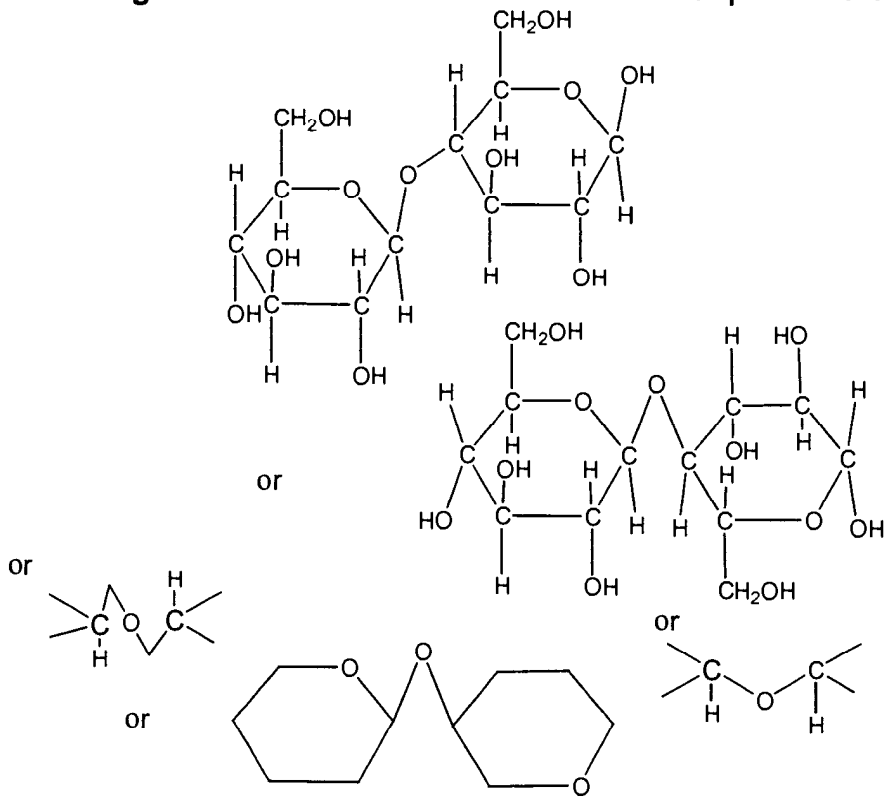
Session: ...June..... Year: ...2004.....

Mark Scheme
Post Qpec 16/1/03 Postcoord 5/7/04

MAXIMUM MARK	45

1 (a)(i)

Their diagram should show an ether link ✓ and β- orientation ✓ as in



(anything extra must be in right place)

Allow chain to continue **2**

(ii) **Hydrogen bonding ✓ with O —H --- OH_2 or HOH--- O shown ✓**
No need for dipoles or whole molecules.
Not G— H
In cellulose OH groups are hydrogen bonded <u>within the fibres</u> ✓
And few are available for hydrogen bonding to water ✓/ two OH used per glucose in making glycosidic links✓. AW **4**

(iii) **Structural/cell walls/support AW ✓** **1**

(iv) **Wrong shape ✓ to fit <u>active</u> site ✓ AW**
Accept detail of 1,4-a <u>and</u> β for the shape mark. **2**

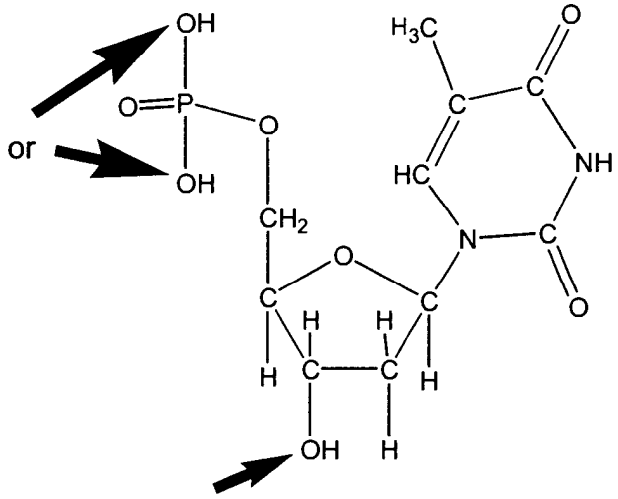
(b)(i) **Ester link ✓/ ether link ✓/covalent link✓/glycosidic link✓**
Hydrogen bond ✓ **2**

(ii) **Inhibitor does not compete for active site but elsewhere✓ changing shape of catalytic/binding site ✓**
Mercury ions could combine with SH in amino acid/cysteine/breaks S-S link✓. AW **3**

(c) **Any two of allows easy separation of product and enzyme ✓**
Reuse of enzyme ✓
Avoids inhibition of enzyme by excess product ✓
Allows higher temperatures/range of pH to be used ✓
Continuous rather than batch ✓ AW **2**

Question Total **16**

2 (a)(i) **Each point on diagram ✓ (accept P but not whole phosphate for top one)** **2**



(ii) **DNA because thymine is only found in DNA not RNA ✓** **2**

The sugar is deoxyribose ✓

(iii) **Hydrogen bonding between complementary base pairs A/T and C/G ✓ allows two complementary DNA strands to form a double helix✓ with the bases inside✓/or base pairing facilitates repair✓. AW** **3**

(b)(i) **Unchanged ✓** **1**

(ii) **Thr His Ser Leu ✓** **1**

(iii) **(ii) changes amino acids after the deletion ✓ which is very likely to change tertiary structure/shape of active site/ shape of enzyme ✓ and make it inactive.** **2**

Question total **11**

3 (a) The amino acid sequence ✓ 1

(b) Secondary structure , in α–helices/ β-pleated sheets ✓

by hydrogen bonding ✓

Between NH on one amide/peptide group ✓ and C=O on another ✓

Tertiary structure – caused by sidechain/ R-group interactions ✓

For each of the four following attractions they must have the detail or an example to earn the mark. If they list all four without any detail award one mark only.

Disulphide/covalent bridges between SH groups/cysteine residues/-S-S-✓ ✓

Ionic attraction between ionised carboxylic acid and amino sidechains ✓

Hydrogen bonding between , for example, OH groups (must see both electronegative atoms in a diagram)✓

Van der Waals/hydrophobic interaction between non-polar groups ✓

Somewhere a remark about folding, coiling, forming globular protein to show appreciation of role of attractions in shortening. (Diagram of a helix alone will not do).✓

Diagrams should help candidates to earn the marks throughout.

9 points from the above. AW 9

QWC Look for three complete sentences with not more than three spelling mistakes 1

Question total 11

4 (a)(i) o represents the (polar) phosphate head ✓
== represents the (non polar) fatty acid / hydrocarbon tails ✓ AW 2

(ii) van der Waals forces/hydrophobic interaction ✓(not hydrophobic bonding)
(iii) triglyceride has a fatty acid residue instead of phosphate ✓ 1

(b)(i) CONH or C-N bond ✓ 1

(ii) The $+NH_3$ group would be ionically attracted to the (negative) phosphate ✓
Accept 'negative' phosphate if ionically is missing.

While van der Waals/hydrophobic interactions could be set up between nonpolar tails and the benzene rings/alkyl groups ✓ AW 2

Question Total 7

PAPER TOTAL 45