Mark schemes

Q1.

(a) **M1** $\frac{27}{80}$ = 0.34

1

M2 glycine

M1 *some relevant working is needed to arrive at 0.325 - 0.35*

no ECF based on ***M1***

1

(b) use uv lamp or ninhydrin

allow *developing / locating agent / iodine*

1

(c) each amino acid has different (relative) affinity/attraction to/solubility in stationary and mobile phases

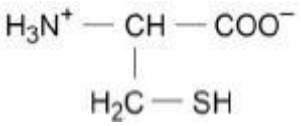
allow *reference to different solubility in solvent OR different affinity for stationary phase*

1

[4]

Q2.

D



[1]

Q3.

C

Base 1 *cytosine* ***Base 2*** *guanine*

[1]

Q4.

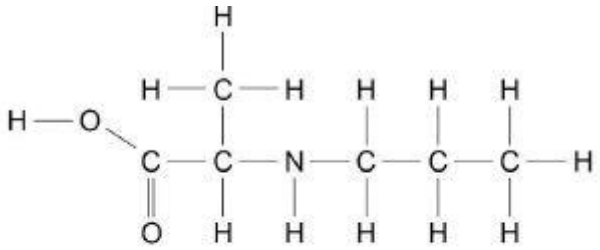
(a) One circled C atom only – The C attached to CH_3/C=O/ H and NH

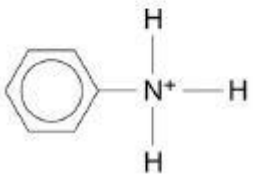
1

(b) Two ticks only for amine and amide

1

(c)

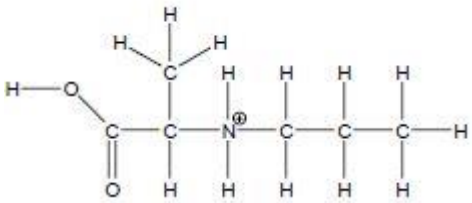




***M1** for choosing the correct bond to hydrolyse*

***M2** and **M3** for the correct structures of the products*

Allow protonated amino acid for M2



Allow $C_6H_5NH_3^+$ or + outside a square bracket

3

(d) **M1** Enzyme has an <u>active site</u>

1

M2
The G-Enantiomer / Enzyme has the correct stereo chemistry / stereospecific
Or
The G-Enantiomer / Enzyme has the complementary shape

For M2 allow opposite argument for F-Enantiomer

1

[7]

Q5.

D

[1]

Q6.

(a) <u>Conc</u> HCl

Allow concentrations of 5M or higher

Allow <u>conc</u> sulfuric or <u>conc</u> strong alkalis

1

(b) Using ninhydrin or ultraviolet light

Allow I_2 (vapour)

1

(c) 7 or seven

1

(d) Some of the amino acids did not separate/dissolve with the first/either solvent

OR

Some amino acids have the same Rf value or have the same affinity with the first/either solvent

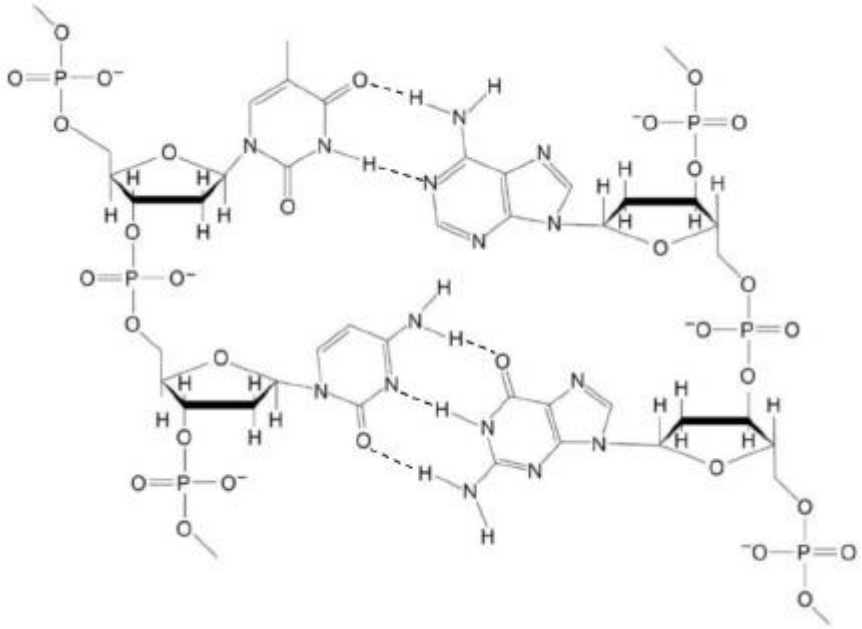
Not amino acids have different Rf values in different solvents

1

[4]

Q7.

(a)



***M1** scored for the 2 H 'bonds' between A and T*

1

***M2** scores for the 3 H 'bonds' between C and G*

1

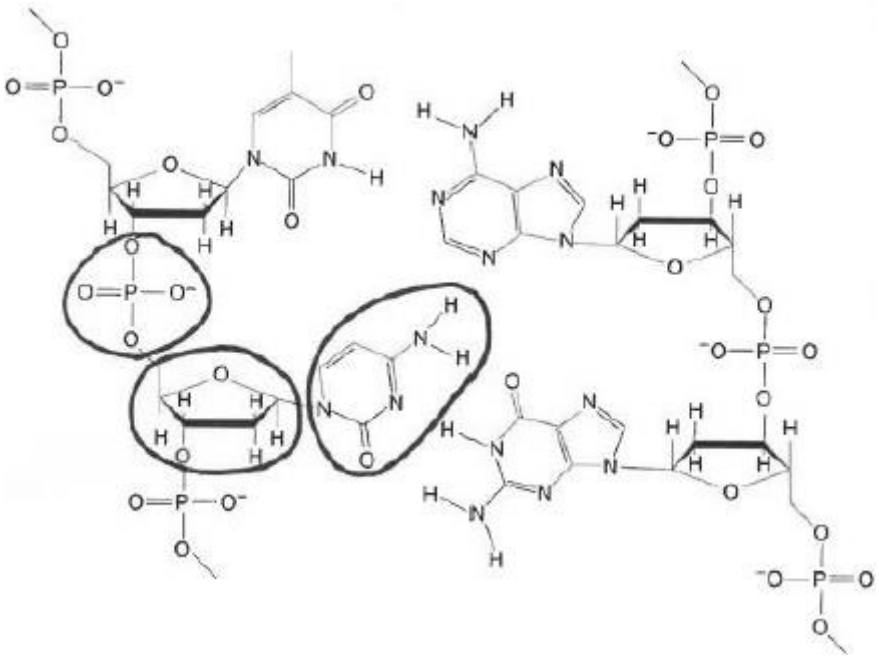
Lose 1 for each extra 'bond'

H bonds must be linear

Penalise the use of full bonds instead of dashed lines once only

Ignore lone pairs and partial charges even if wrong

(b)



***M1** scored for correct selection of cytosine and associated sugar*

1

***M2** scored for selection of <u>correct</u> (upper) phosphate*

1

***M1** & **M2** can be scored with one 'ring'*

Allow ring either side of the top O of either phosphate

*If wrong base circled, can score **M2** for correct phosphate conseq to their base, i.e. top left, Thymine it's the upper phosphate top right, Adenine it's the lower phosphate bottom right, Guanine it's the lower phosphate*

(c) (Complementary means the two strands must have base sequences) that match (all) <u>A to T and C to G</u>

Ignore reference to (hydrogen) bonding

1

[5]

Q8.

D

[1]

Q9.

C

[1]

Q11.

(a) 1 2 3 4 5

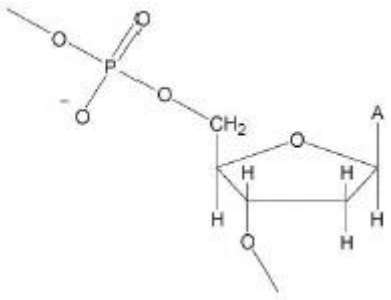
T G C A G

1

(b) 13

1

(c)



1 for completed 2-deoxyribose plus A

Allow either OH or trailing bonds

Don't penalise 'sticks' in 2-deoxyribose.

1

1 for correct phosphate joined to CH_2

If two phosphates shown CE=0

If CH_2 missing award 1 if no further errors

If phosphate attached to oxygen on C3 award 1 if no further errors

1

[4]

Q12.

D

[1]

Q13.

(a) X – base

1

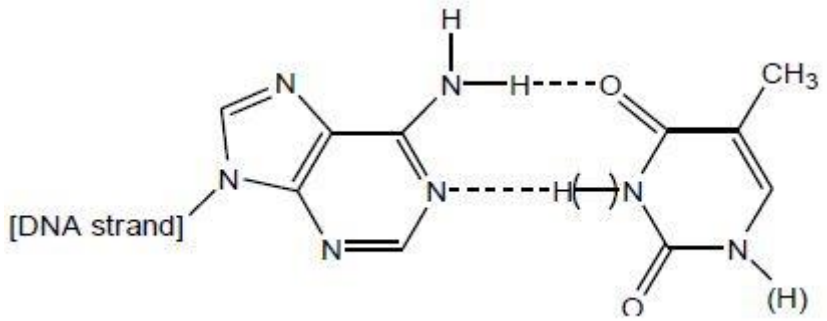
Y – phosphate (group)

1

Ignore organic

Any mention of sugar in either loses that mark

(b) If not Thymine CE=0



Correct structure scores 2, penalise by 1 each error in

- structure of thymine
- orientation of thymine
- hydrogen bonding

Ignore lp on N and O

Don't penalise non-linear H bonds

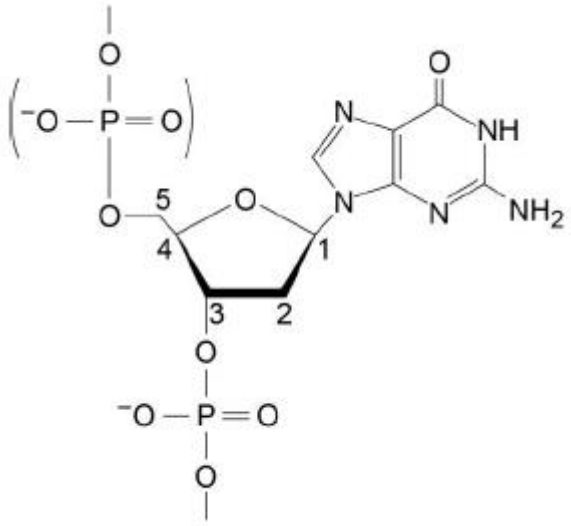
on RHS of thymine – allow with or without H or – [DNA strand]

2

[4]

Q14.

(a)



*CE=0 if **nucleotide** does not contain one base, one sugar and one phosphate.*

Max 2 for any slips in structures.

Correct phosphate-sugar link on C3.

Allow phosphate attached to C5.

1

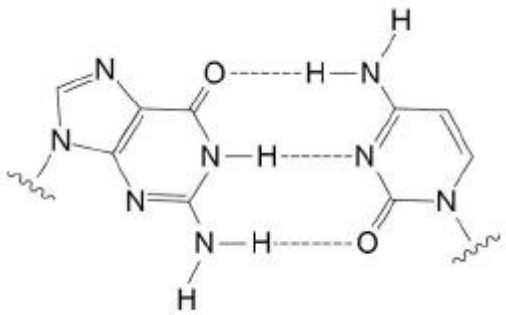
Correct sugar-guanine link on C1.

1

Remainder of molecule correct.

1

(b)



Correct diagram of cytosine (base pair with guanine).

CE=0 if wrong base shown.

1

Three hydrogen bonds drawn.

Allow M2 if slip in M1.

1

(c) There are only two H-bonds in the adenine-thymine base pair.

Allow there is one fewer H-bond in the AT base pair.

1

(d) The amino/-NH_2 groups in urea

1

are able to substitute for the H–bonds in the double helix.

Allow H bonds will form between the urea and the DNA strands.

1

[8]

Q15.

B

[1]

Q16.

(a) Secondary

1

(b) Nitrogen and oxygen are very electronegative

1

Therefore, C=O and N–H are polar

1

Which results in the formation of a hydrogen bond between O and H

1

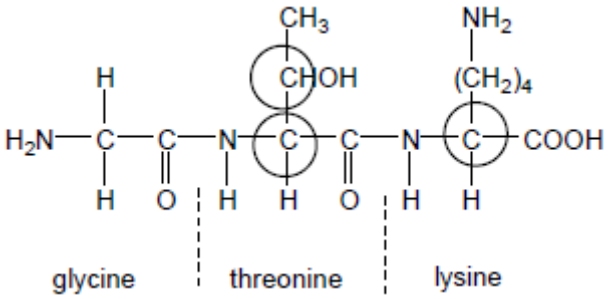
In which a lone pair of electrons on an oxygen atom is strongly attracted to the δ+H

1

[5]

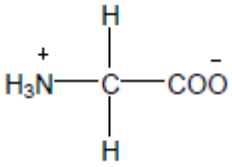
Q17.

(a)



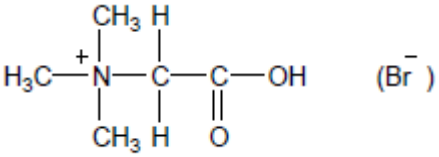
1

(b)

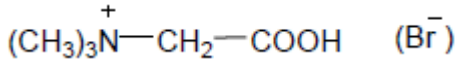


1

(c)



Allow

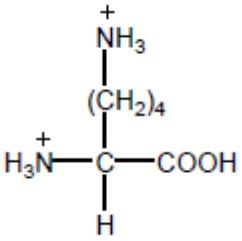


1

(d) 2-amino-3-hydroxybutanoic acid

1

(e)



1

[5]

Q18.

(a) 2-deoxyribose

1

(b) Base A

If Base B stated, allow 1 mark only for response including hydrogen bonding

1

Top N–H forms hydrogen bonds to lone pair on O of guanine

1

The lone pair of electrons on N bonds to H–N of guanine

1

A lone pair of electrons on O bonds to lower H–N of guanine

Allow all 4 marks for a correct diagram showing the hydrogen bonding

Students could also answer this question using labels on the diagram

1

(c) Allow either of the nitrogen atoms with a lone pair NOT involved in bonding to cytosine

1

(d) Use in very small amounts / target the application to the tumour

1

[7]

Q19.

(a) **Wear plastic gloves:**

Essential – to prevent contamination from the hands to the plate

1

Add developing solvent to a depth of not more than 1 cm^3:

Essential – if the solvent is too deep it will dissolve the mixture from the plate

1

Allow the solvent to rise up the plate to the top:

Not essential – the R_f value can be calculated if the solvent front does not reach the top of the plate

1

Allow the plate to dry in a fume cupboard:

Essential – the solvent is toxic

Allow hazardous

1

(b) Spray with developing agent or use UV

1

Measure distances from initial pencil line to the spots (*x*)

1

Measure distance from initial pencil line to solvent front line (*y*)

1

R_f value = *x* / *y*

1

(c) Amino acids have different polarities

1

Therefore, have different retention on the stationary phase or different solubility in the developing solvent

1

[10]

Q20.

C

[1]