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.

(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

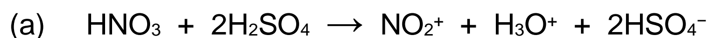
Some amino acids have the same Rf value or have the same affinity with the first/either solvent

Not amino acids have different Rf values in different solvents

1

[4]

Q3.

(a) 
$HNO_3 + 2H_2SO_4 \longrightarrow NO_2^+ + H_3O^+ + 2HSO_4^-$

Allow $H_2SO_4 + HNO_3 \longrightarrow NO_2^+ + HSO_4^- + H_2O$

Allow a combination of equations which produce NO_2^+

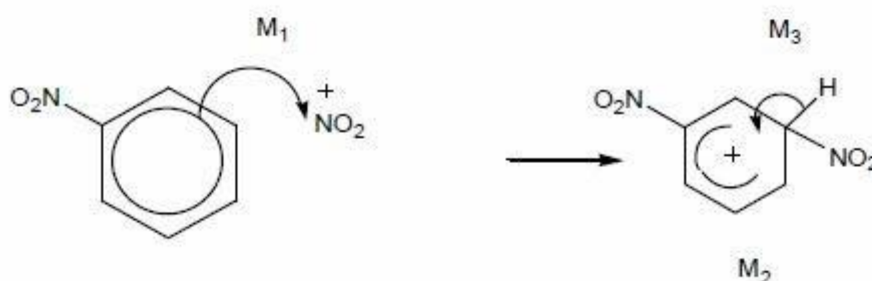
Penalise equations which produce SO_4^{2-}

1

(b) Electrophilic substitution.

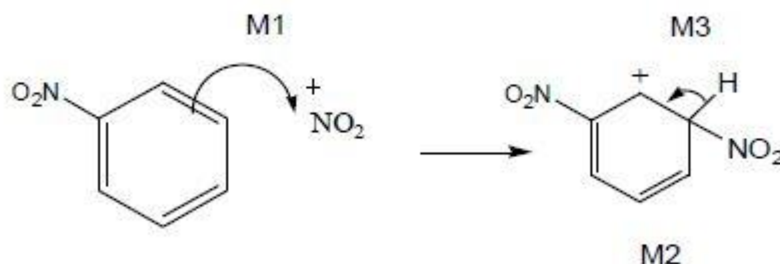
Ignore nitration

1



3

OR Kekule



M1 Arrow from inside hexagon to N or + on N (Allow NO_2^+)

M2 Structure of intermediate

- *horseshoe centred on C1 and must not extend beyond C2 and C6, but can be smaller*
- *+ in intermediate not too close to C1 (allow on or "below" a line from C2 to C6)*

M3 Arrow from bond into hexagon (Unless Kekule)

- *Allow M3 arrow independent of M2 structure*
- *+ on H in intermediate loses M2 not M3*

(c) D

1

(d) (Balance between) solubility in moving phase and retention by stationary phase

OR (relative) affinity for stationary / solid and mobile / liquid / solvent (phase)

(e) Solvent depth must be below start line

Ignore safety

1

(f) 1,2- is more polar **OR** 1,4- is less polar
OR 1,2 is polar, 1,4- is non-polar

1

1,4- (or Less/non polar is) less attracted to (polar) plate / stationary phase / solid
OR (Less/non polar is) more attracted to / more soluble in (non-polar) solvent / mobile phase / hexane

1

M2 dependent on correct M1

If M1 is blank then read explanation for possible M1 and M2

Allow converse argument for 1,2

(g) No CE = 0

Yes - mark on but there is **NO MARK FOR YES**

Mark independently following yes

Solvent (more) polar or ethyl ethanoate is polar

1

Polar isomer more attracted to / more soluble in / stronger affinity to the solvent (than before)

Penalise bonded to mobile phase in M2

1

[12]

Q4.

(a) **Gas chromatography explanation**

Different retention times / dipeptides appear at different times.

1

Different balance between solubility in the moving phase / gas carrier **and** retention by the stationary phase / column **OR** different relative affinity for mobile and stationary phases.

1

Mass spectrometry explanation

Same *m/z* values.

1

(Both) dipeptides / **J** and **K** have same molecular formula / M_r.

1

(b) ser-ala

1

ala-lys

1

ser-ala-lys

This order only.

1

[7]

Q5.

(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]