Rings, Polymers & Analysis
Chromatography MARK SCHEME

1. (i) adsorption ✓

__ALLOW__ partition __OR__ adsorbtion
__IGNORE__ solubility __OR__ desorption
__DO NOT ALLOW__ absorption

1

(ii) measure how far each spot travels relative to the solvent front or calculate the R_f value ✓

compare R_f values to those for known amino acids ✓

__ALLOW__ compare R_f values to database
__ALLOW__ compare to known amino acids
__DO NOT ALLOW__ retention times for first mark, but the 2nd mark would be available as ✓ ECF
__ALLOW__ alternative approach: on the same plate compare position of spots ✓ with known amino acids ✓

2

(iii) (amino acids won't separate because) similar compounds have similar R_f (values) ✓

__ALLOW__ spots often overlap __OR__ don't (fully) separate
__ALLOW__ they have similar R_f (values) or similar adsoptions or similar retention times ECF to __(ii)__

1

[4]

2. (i) one amide link shown correctly **(1)**
glycine and phenylalanine parts shown correctly **(1)**
proline linked correctly **(1)** 3

(ii) 6 **(1)** 1

(iii) gas/liquid chromatograph separates the tripeptides **(1)**
mass spectrometer produces a distinctive fragmentation pattern **(1)**
identification by computer using a spectral database **(1)** 3

[7]

3. (a) R_f value is distance moved by a component/spot/solute divided by distance moved by solvent. **(1)**

Retention time is the time between injection and emergence (or detection) of a component. **(1)** 2

(b) (i) Partition / adsorption **(1)** 1

(ii) Role of gas: carrier gas / mobile phase / to carry to sample through the chromatography column **(1)**

Role of liquid: stationary phase **(1)** 2

(iii) Trace with two peaks drawn **(1)** 1

(iv) Measure **area** under each peak **(1)**

Find total area **(1)**

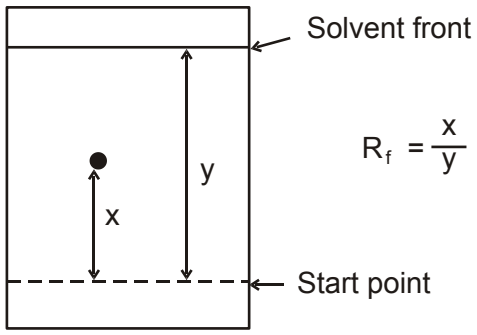
% = (area of one peak/total area) × 100% **(1)** 3

[9]

4. (i) Accept paper, column or thin-layer chromatography 1

(ii) The R_f value 1

(iii)

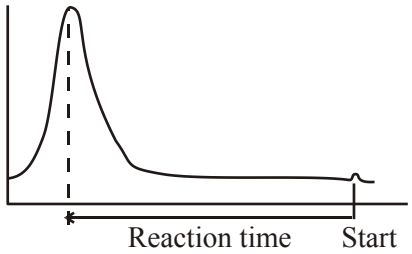


1

[3]

5. (a) (i) Retention time 1

(ii)



(or mirror image) 1

(b) Partition 1

[3]