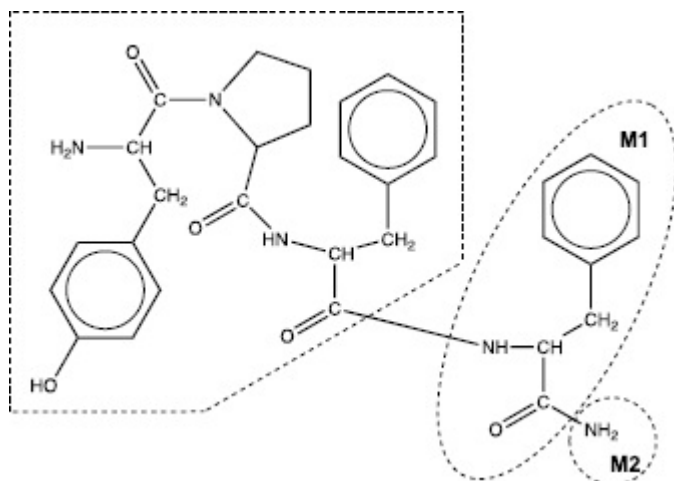


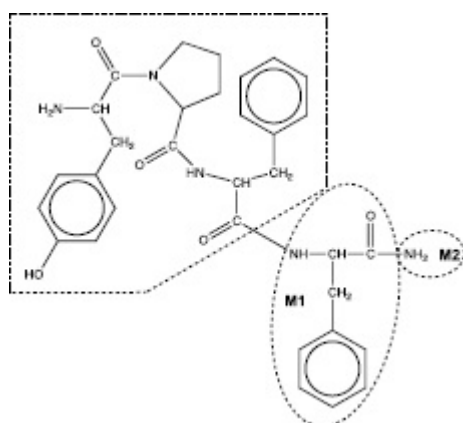
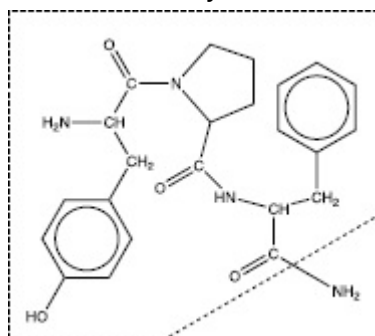
Mark schemes

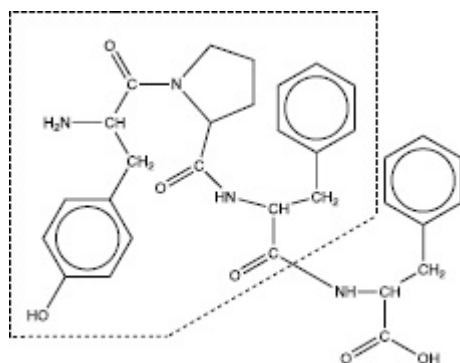
Q1.

(a)



Alternative form

**M1** Phe structure drawn with correct peptide link**M2** amide group shown on end**M1** if Phe drawn with COOH or CONH_2 **M2 ALLOW** if no Phe drawn i.e. if NH_2 only attached directly to C=O on diagramScores **M2** for ending in amide group

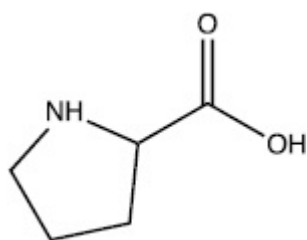


Scores **M1** for Phe group

M1 H needed on N of peptide link drawn unless C-CH-CH₂ drawn skeletal

2

(b)



ALLOW zwitterion

ALLOW -NH₂⁺ and/or COO⁻

ALLOW with C shown in COOH group

ALLOW without H on N

ALLOW N-H

NOT N-

1

(c) **M1** (aqueous) HCl/hydrochloric acid

Name or formula of any strong acid or alkali

M2 reflux/heat

ALLOW warm / hot / high temperature for heat

NOT T>200°C

IGNORE conc as condition with acid/alkali

IGNORE pressure

Alternative

M1 protease/(poly)peptidase/peptase/named protease

IGNORE enzyme

M2 warm

NOT hot / high temperature / T>50°C

2

(d) **M1** lid/cover (on beaker)

Then any 2 from these 3

- prevents escape of vapour (from beaker) / evaporation of solvent (from beaker)
- so atmosphere in beaker is saturated with solvent vapour
- to reduce evaporation from the plate

ALLOW (for bullet point 3) so solvent can rise up plate

ALLOW (for bullet point 3) to avoid plate drying out

3

(e) Difference in the balance between solubility in solvent/mobile phase and attraction to/retention on stationary phase

ALLOW difference between (relative) affinity/attraction for solvent and stationary phase

ALLOW absorption/adsorption for retention on stationary phase

1

(f) **M1** ninhydrin

M2 amino acids are colourless / to make the amino acids visible

ALLOW iodine

IGNORE UV

IGNORE stated final colour e.g. "turns the amino acids purple" is not enough on its own

IGNORE clear

2

(g) 0.54

ALLOW 0.53 - 0.55 (to min two sig figs)

1

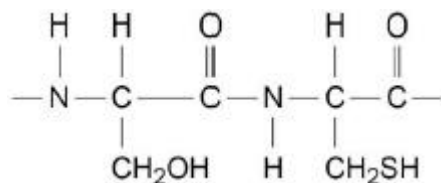
[12]

Q2.

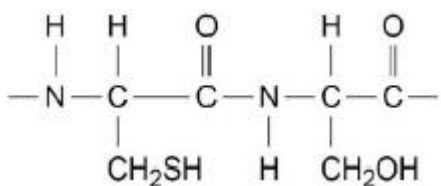
(a) Primary

1

(b)



OR



M1 for correct peptide link (Allow -CONH- as a minimum)

M1

M2 for the correct amino acid R groups

Dipeptide can only score M1

M2

Trailing bonds **not** needed

(c) Water

Allow H₂O

1

(d) Two Cys R groups form a disulfide bridge/link stated or described
 Could score via a correct diagram showing min
 -SS-

M1

Ser and Asp R groups form Hydrogen bonds

Allow H bonds

M2

Disulfide bridges are stronger than H bonds

Interactions between cys R groups are stronger

M3

Because disulfide bridges are covalent bonds (while H bonds aren't)

Because covalent bonds are stronger (than H bonds)

M4

(e) Ionic bond

1