Mark schemes

1

(a) Heating <u>speeds up</u> (hydrolysis / breaking of peptide bonds)

OR forms non-sweet (amino acids)

1

(b) (2-)aminobutan**<u>e</u>**dioic acid OR

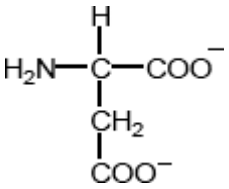
2 not necessary but penalise other numbers at start

(2-)aminobutan**<u>e</u>**(-1,4-)dioic acid

1,4 not necessary but penalise other numbers and 1,4 must be in correct place (QoL)

1

(c)

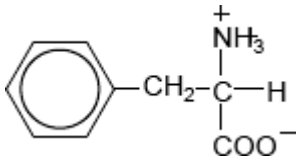


allow $-CO_2^-$

allow NH_2-

1

(d)



allow $-CO_2^-$

allow $+NH_3-$

don't penalize position of + on NH_3

1

(e) (i) **M1** Compounds/molecules with same <u>structural formula</u>

Not just structure

1

M2 But with <u>bonds/atoms/groups</u> arranged differently <u>in space</u> or <u>in 3D</u>

Allow –with different <u>spatial</u> arrangement of <u>atom/bond/group</u>

1

Independent marks

(ii) (Plane) polarised light

1

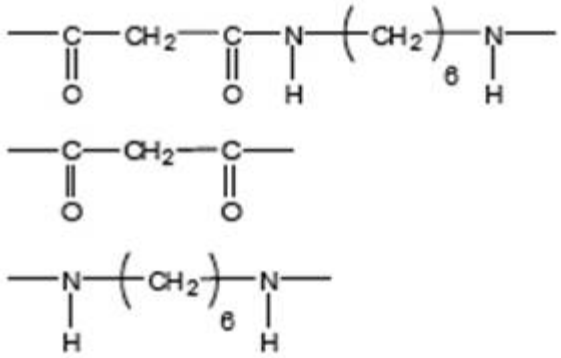
Rotated in opposite directions

Not bent or turned or twisted; not different directions (QoL)

1

[8]

2 (a) (i)



Allow –CONH- or - COHN -

Mark two halves separately

lose 1 each for missing trailing bonds at one or both ends or error in peptide link or either or both of H or OH on ends

1

Not allow –(C_6H_{12})–

Ignore n

1

(ii) **M1** in polyamides - H bonding

1

M2 in polyalkenes - van der Waals forces

Penalise forces between atoms or van der Waals bonds

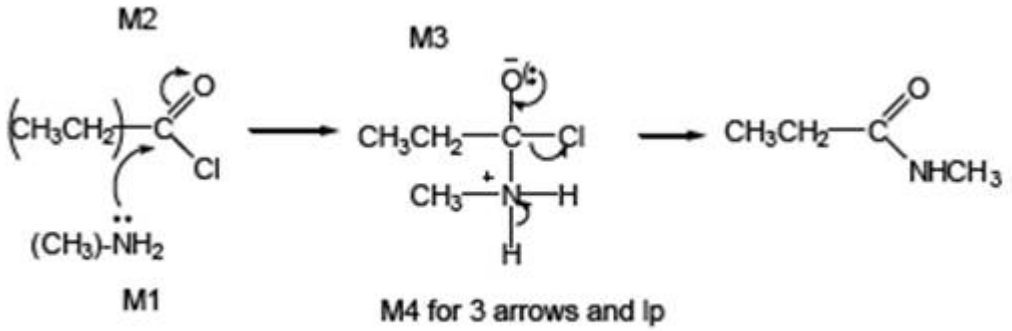
1

M3 Stronger forces (of attraction) in polyamides
Or H bonding is stronger
(must be a comparison of correct forces to score M3)

Do not award if refer to stronger bonds

1

(b) (i) (nucleophilic) addition elimination



Not allow N–H_2

*Minus sign on NH_2 loses **M1***

1

*M2 not allowed independent of **M1**, but allow **M1** for correct attack on C+*

*+ rather than δ+ on C=O loses **M2***

*If Cl lost with C=O breaking, max 1 for **M1***

***M3** for correct structure <u>with charges</u> but*

*lp on O is part of **M4***

*only allow **M4** after correct/ very close M3*

For M4, ignore NH_3 removing H^+ but lose

***M4** for Cl removing H^+ in mechanism,*

but ignore HCl as a product

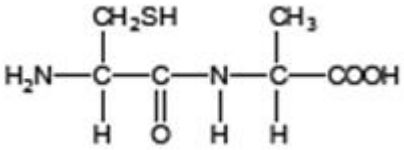
4

(ii) <u>N-methylpropanamide</u>

Not N-methylpropaneamide

1

(c)



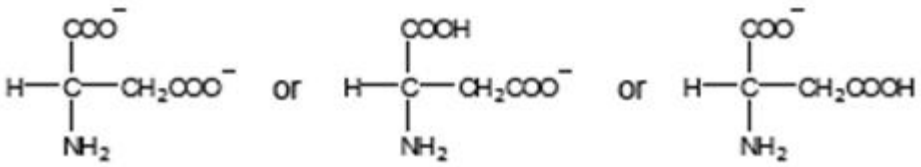
Allow –CONH– or –COHN–

1

(d) (i) <u>2-amino-3-hydroxypropanoic acid</u>

1

(ii)



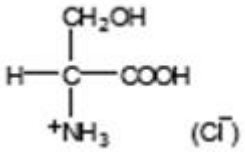
Must be salts of aspartic acid

allow $–CO_2^-$

allow NH_2–

1

(iii) Penalise use of aspartic acid once in d(iii) and d(iv)



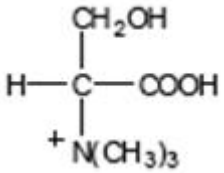
allow $–CO_2H$

allow $^+NH_3$–

don't penalize position of + on NH_3

1

(iv) Penalise use of aspartic acid once in d(iii) and d(iv)



(Br^-)

allow $–CO_2^-$

must show C-N bond

don't penalize position of + on $N(CH_3)_3$

1

[16]

3

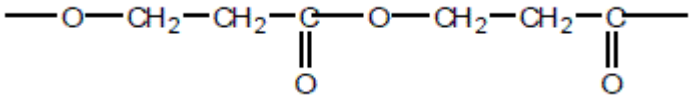
(a) 3-hydroxypropanoic acid

allow 3-hydroxypropionic acid

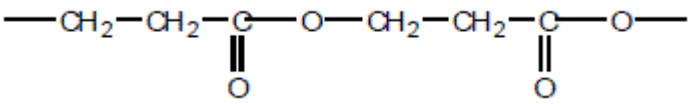
must be correct spelling

1

(b) (i) must show trailing bonds



or can start at any point in the sequence, e.g.



not allow dimer

allow –O–$CH_2CH_2COOCH_2CH_2CO$–

or –$CH_2CH_2COOCH_2CH_2COO$–

ignore ( ) or n

NB answer has a total of 6 carbons and 4 oxygens

1

(ii) condensation (polymerisation)

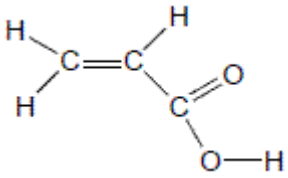
Allow close spelling

1

(c) (i) C=C or carbon-carbon <u>double</u> bond

1

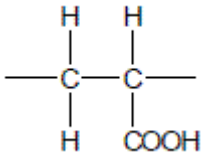
(ii)



*must show **ALL** bonds including O–H*

1

(iii) must show trailing bonds

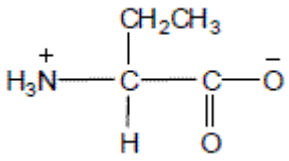


allow polyalkene conseq on their c(ii)

ignore n

1

(d)

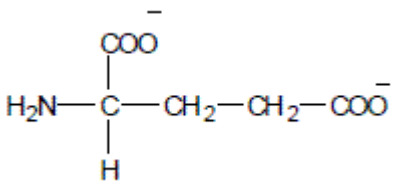


allow NH_3^+ —

allow COO^-

1

(e) (i)



In (e), do not penalise a slip in the number of carbons in the $-CH_2CH_2-$ chain, but all must be bonded correctly

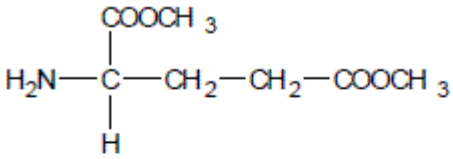
NB two carboxylate groups

Allow COONa or COO^- Na^+ but not covalent bond to Na

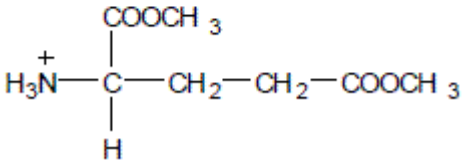
allow NH_2–

1

(ii)



OR



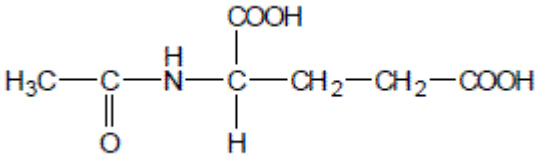
In (e), do not penalise a slip in the number of carbons in the $-CH_2CH_2-$ chain, but all must be bonded correctly

NB two ester groups

allow NH_2– or $^+NH_3$–

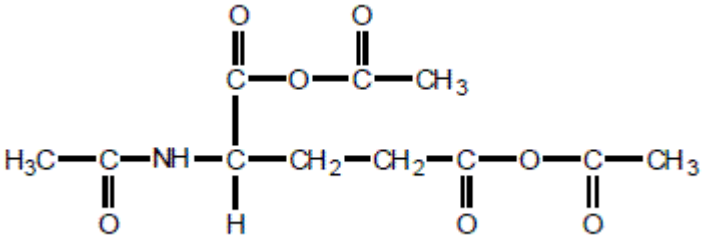
1

(iii)



In 4(e), do not penalise a slip in the number of carbons in the -CH_2CH_2- chain, but all must be bonded correctly

allow anhydride formation on either or both COOH groups (see below) with or without amide group formation



1

(f) **M1** phase or eluent or solvent (or named solvent) is moving or mobile

1

M2 stationary phase or solid or alumina/silica/resin

1

M3 separation depends on balance between solubility or affinity (of compounds) in each phase
OR
different adsorption or retention
OR
(amino acids have) different R_f values
OR
(amino acids) travel at different speeds or take different times

1

[13]

4

(a) (i) hydrolysis

not hydration

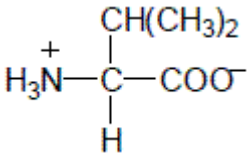
1

(ii) 2-aminopropanoic acid

ignore alanine
QoL

1

(iii)



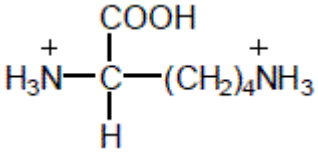
allow $-CO_2^-$

allow $^+NH_3-$

don't penalize position of + on NH_3

1

(iv)



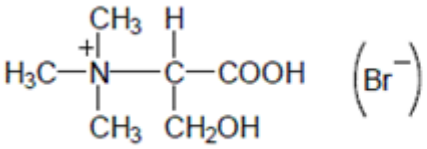
allow $-CO_2^-$

allow $^+NH_3-$

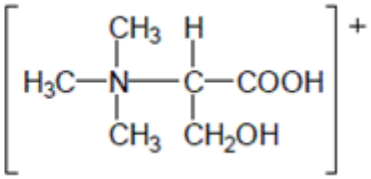
don't penalize position of + on NH_3

1

(b) (i)

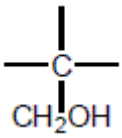


or



allow $-CO_2H$

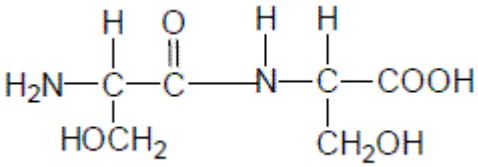
allow limit as



+ on N or outside [ ]

1

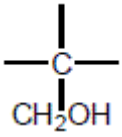
(ii)



allow $-CO_2H$ allow –CONH– or –COHN–

allow NH_2-

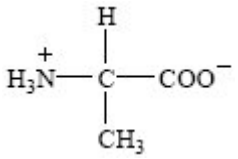
allow limit as



1

[6]

5 (a) (i)



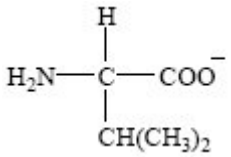
allow $-CO_2^-$

allow $^+NH_3-$

don't penalize position of + on NH_3

1

(ii)



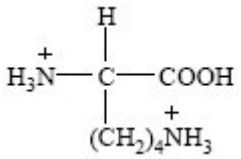
allow $-CO_2^-$

allow NH_2-

allow C_3H_7

1

(iii)



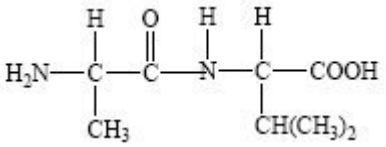
allow $-CO_2H$

allow $^+NH_3-$

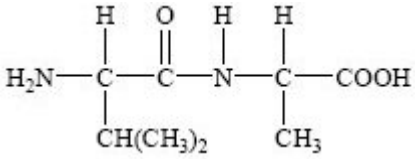
don't penalize position of + on NH_3

1

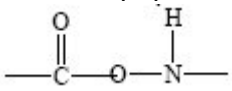
(b)



1



allow $-CO_2H$
allow NH_2-
allow C_3H_7
allow as zwitterions
if error in peptide link e.g.



if twice, penalise both times
not polymers
if wrong amino acid in both can score Max 1

1

(c) chromatography or electrophoresis

ignore qualification to chromatography

1

[6]

6 (a) $Pt(NH_3)_2Cl_2 + H_2O \rightarrow [Pt(NH_3)_2Cl(H_2O)]^+ + Cl^-$

Correct product

1

Balanced equation

1

(b) (i) Hydrogen bond

1

Oxygen (or nitrogen)

Only score this mark if type of bond is correct

1

(ii) Co-ordinate

1

Nitrogen (or oxygen)

Bond type must be correct to score this mark but allow M2 if bond is covalent

1

(c) Killing them or causing damage (medical side effects)

Allow any correct side effect (e.g. hair loss)
Allow kills healthy (or normal) cells

1

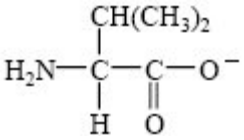
May attach to DNA in normal cells

1

[8]

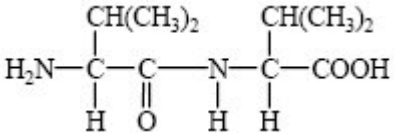
7

(a) (i)



1

(ii)



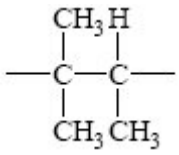
1

(iii) hydrogen bonding (do not allow H-bonding) QWC

do not penalise any error twice.

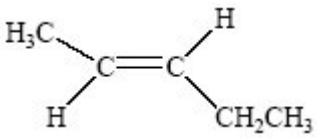
1

(b) (i)



1

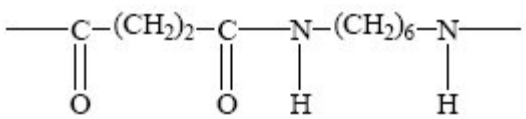
(ii)



1

(iii) Isomer must be saturated or must not contain a double bond

1

(c) 

2

(d) (i) heat/reflux with aqu NaOH

1

poly(alkene) is inert/ no reaction

1

polyamide is hydrolysed (or undergoes hydrolysis) to form acid salt and alcohol QWC

1

(ii) e.g combustion

1

heat energy produced

1

toxic gases produced

1

[14]