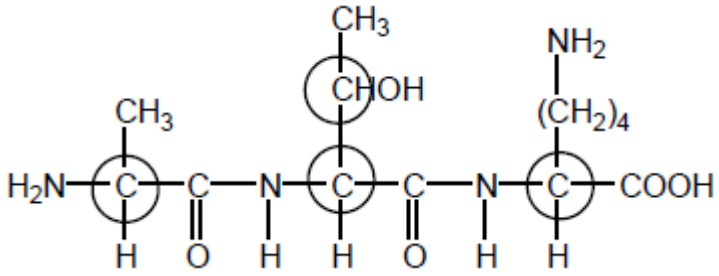
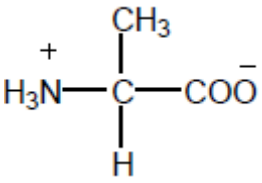
**M1.**(a) (i)



*These four only*

**1**

(ii)



*Allow − $NH_3^+$ and $^+NH_3^-$*

**1**

(iii) <u>2-amino-3-hydroxybutanoic acid</u>

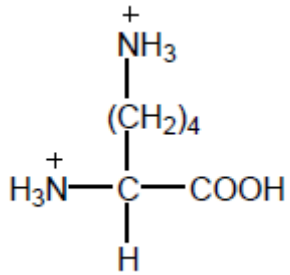
*Ignore 1 in butan-1-oic acid*

Do not penalise commas or missing hyphens

*Penalise other numbers*

**1**

(iv)



*Allow –$NH_3^+$ and $^+NH_3^-$*

**1**

(b) (i) Condensation

*Allow polyester*

**1**

(ii) propan**e**-1,3-diol

*Must have e*

*Allow 1,3-propan**e**diol*

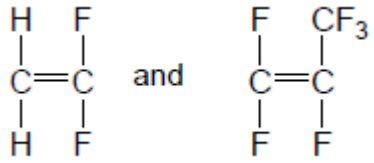
**1**

(c) (i) Addition

*Not additional*

**1**

(ii)

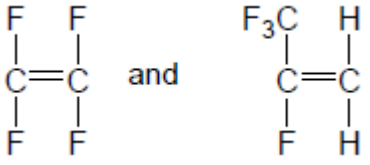


*Allow monomers drawn either way round*

*Allow bond to F in $CF_3$*

**1**

***OR***



*1 for each structure within each pair*

**1**

(d) c

*If wrong, CE = 0*

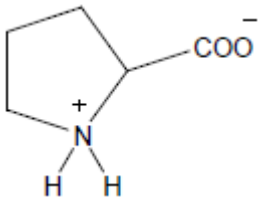
**1**

C-C or C-F bonds too strong

1

**[11]**

**M2.**(a) (i)




*Allow $CO_2^-$ and $NH_2^+$*

1

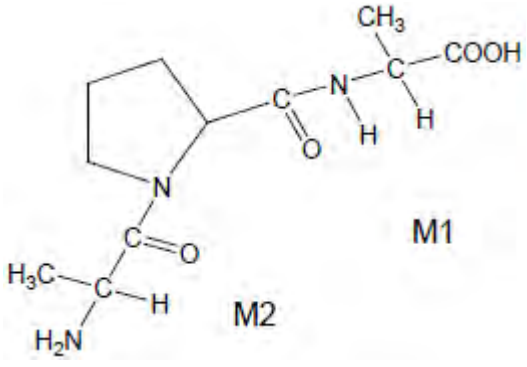
(ii) NOTE − **Two** marks for this clip

*M1 for alanine section bonded through N*

*M2 for alanine section bonded through C*

*But penalise error in proline ring*

1




*Allow MAX 1 for correct tripeptide in polymer structure*

1

(b) (i) 3-methylpent-2-ene

*Ignore E-Z, commas, spaces or missing hyphens*

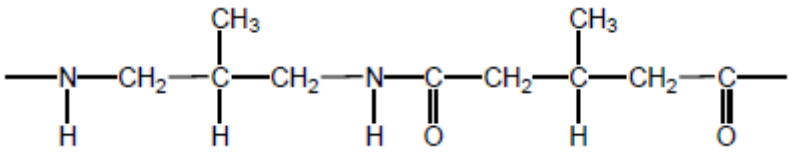
1

(ii) 4-amino-3-methylbutanoic acid

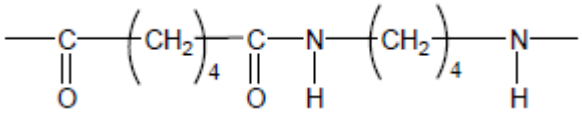
*Ignore commas, spaces or missing hyphens*

1

(iii)



*or any polyamide section containing*
*8 carbons plus two C=O plus two N-H, such as*



*Trailing bonds are required*

1

(iv) Non polar OR no polar groups / bonds (for attack by water / acids / alkalis / nucleophiles or for hydrolysis)

C-C bonds are strong

1

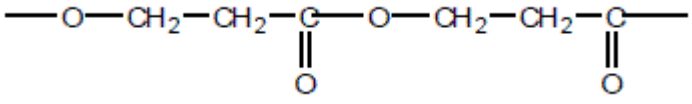
**[7]**

**M3.** (a) 3-hydroxypropanoic acid

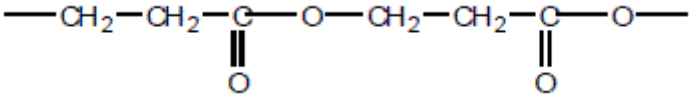
*allow 3-hydroxypropionic acid*
*must be correct spelling*

1

(b) (i) must show trailing bonds



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



*not allow dimer*
*allow –O–CH₂CH₂COOCH₂CH₂CO–*
*or –CH₂CH₂COOCH₂CH₂COO–*
*ignore ( ) or n*
*NB answer has a total of 6 carbons and 4 oxygens*

1

(ii) condensation (polymerisation)

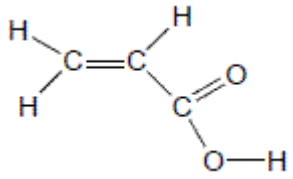
*Allow close spelling*

**1**

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

**1**

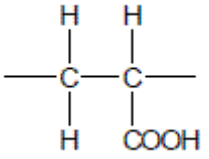
(ii)



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

**1**

(iii) must show trailing bonds

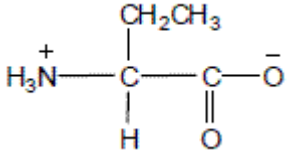


*allow polyalkene conseq on their c(ii)*

*ignore n*

**1**

(d)

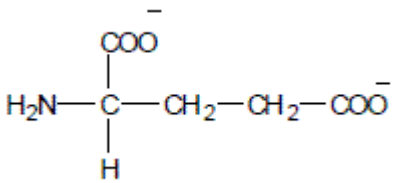


*allow $NH_3^+$—*

*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*

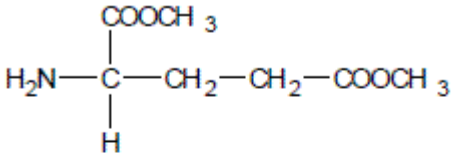
*NB two carboxylate groups*

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

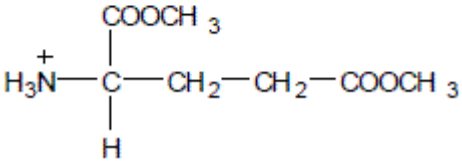
*allow $NH_2$–*

**1**

(ii)



**OR**



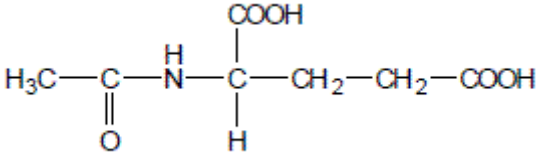
*In (e), do not penalise a slip in the number of carbons in the -$CH_2CH_2$- chain, but all must be bonded correctly*

*NB two ester groups*

*allow $NH_2$– or $^+NH_3$–*

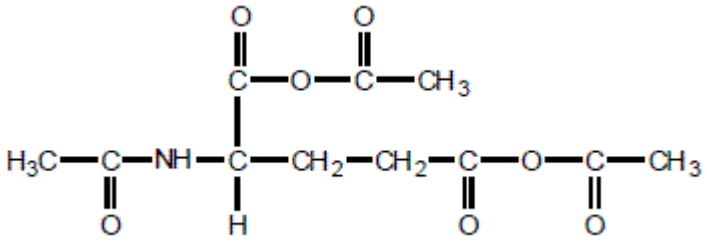
**1**

(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

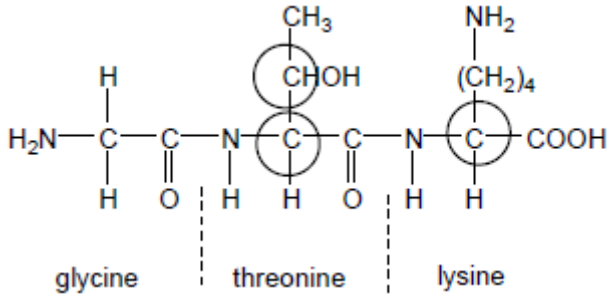
1

**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

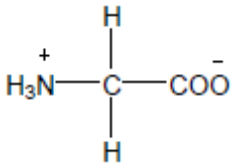
**[13]**

**M4.**(a)



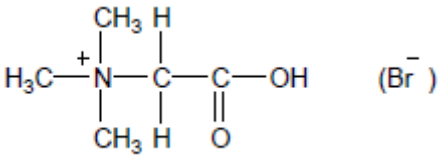

1

(b)

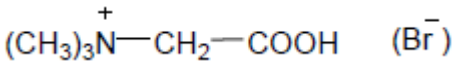


1

(c)



*Allow*

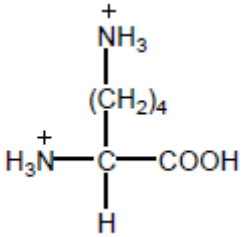


1

(d) 2-amino-3-hydroxybutanoic acid

1

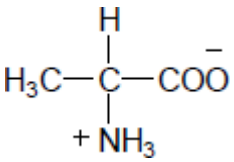
(e)



1

**[5]**

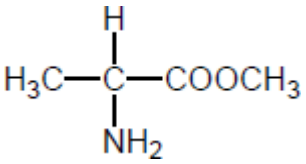
**M5.**(a)



*Allow* $-NH_3^+$ *and* $^+NH_3-$

1

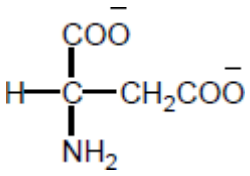
(b)



*Allow protonated form, i.e. $-NH_3^+$ or $^+NH_3-$*

**1**

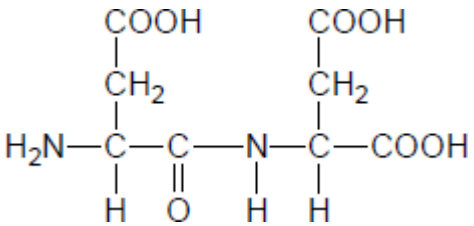
(c)



*Allow – $CO_2^-$*

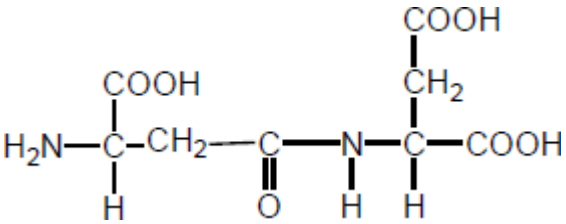
**1**

(d)



*Allow zwitterion with any $COO^-$*

*Allow use of "wrong" COOH*



**1**

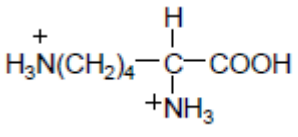
**[4]**

**M6.**(a) 2,6-diaminohexanoic acid

*Ignore additional , or – or spaces.*

**1**

(b) (i)



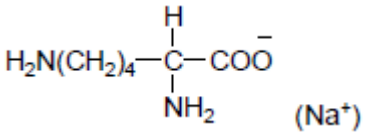

*NB both N must be protonated.*

*Allow $-NH_3^+$ allow $CO_2H$ Allow $-^+H_3N$.*

*Penalise – $C_4H_8$ – here.*

**1**

(ii)



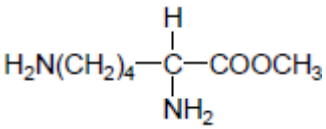

*Allow $CO_2^-$.*

*Allow $-H_2N$.*

*Allow –COONa but penalise O–Na bond shown.*

**1**

(iii)

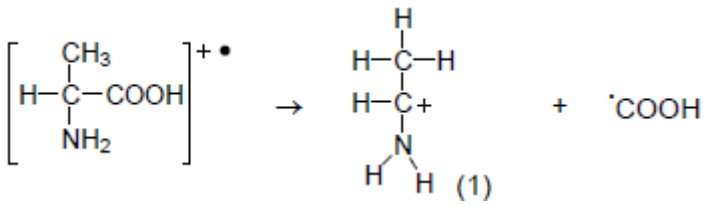



*Allow $CO_2CH_3$.*

*Allow $-NH_3^+$ or $-H_2N$.*

**1**

(c)




*1 for <u>displayed formula</u> of fragment ion.*

*1 for molecular ion of alanine AND radical.*

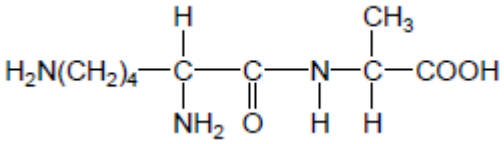
*Allow molecular ion without brackets and fragment ion in brackets with outside +.*

*Allow dot anywhere on radical.*

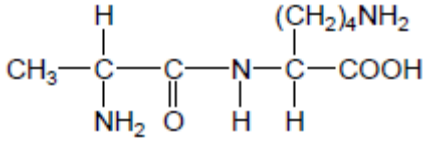
*Allow $[C_3H_7NO_2]_+^{\bullet}$ for molecular ion.*

**2**

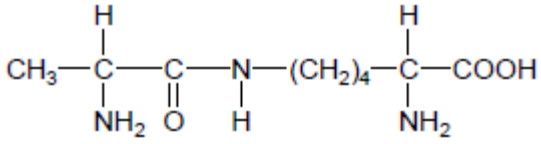
(d)



**OR**



**OR**



*Dipeptide, not repeating unit /.*

*Allow $CO_2H$ Allow $–H_2N$.*

*Allow –CONH–.*

**1**

(e) M1 In acid lysine has double positive or more positive charge

**1**

M2 sticks (Lysine ion) has greater affinity / greater attraction / adheres better / better to polar / stationary phase

*M2 only scores after a correct M1.*

*Ignore greater retention time.*

**1**

**[9]**

**M7.**(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]**