



**Raffles Institution**  
**Year 6 H2 Chemistry 2014**  
**Tutorial 17b**  
**Nitrogen Compounds II – Proteins**

Prepared by: Ms Lee Mei Yin

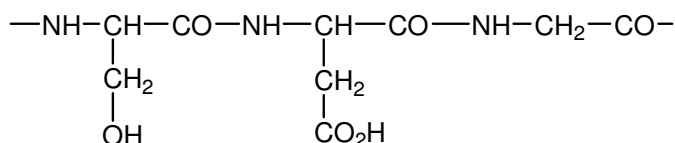
**Self-Check Questions**

1. Define the following terms:

- |                                    |                                     |
|------------------------------------|-------------------------------------|
| (a) peptide bond                   | (d) tertiary structure of protein   |
| (b) primary structure of protein   | (e) quaternary structure of protein |
| (c) secondary structure of protein | (f) denaturation of protein         |

2. [N99/I/7]

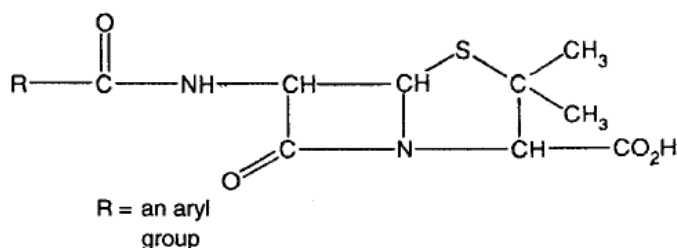
The following structure shows part of a protein molecule.



- (a) What reagents and conditions are needed to break the protein into its constituent amino acids? [2]
- (b) What is the name given to the type of reaction you have described in (a), and what type of bond is broken during it? [2]
- (c) Draw the structural formula of each of the three amino acids produced by the reaction, labelling any chiral centres in the molecules. [5]
- (d) In solution, amino acids exist as *zwitterions*.  
Choose **one** of the amino acids you have drawn in (c) to illustrate what is meant by this term. [1]
- (e) Amino acids act as buffers in solution. By means of equations, show how your chosen amino acid can act as a buffer when:  
(i) dilute HCl  
(ii) dilute NaOH  
is added to its solution. [2]

3. [N95/III/5]

- (a) Draw a displayed formula of aminoethanoic acid. [1]
- (b) Penicillin is widely used to kill bacteria. The general structure of a penicillin molecule is given below.



(i) Mark with an asterisk \* on the above structure any carbon atoms which are chiral centres. [2]

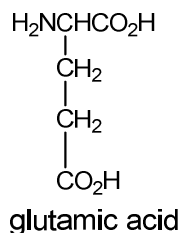
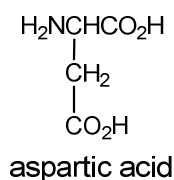
(ii) Bacteria mistake penicillin for protein molecules and bond on to the amino acid sequence present in penicillin. This sequence is also present in the skeleton of the aminoethanoic acid molecule you have drawn in (a).

Draw a ring around the part of the penicillin molecule which bacteria mistake for an amino acid. [1]

(c) Would you expect penicillin to be acidic, neutral or basic? Explain your answer as fully as you can. [2]

4. [N98/III/28]

The amino acids aspartic acid and glutamic acid can react with each other to form amide linkages.



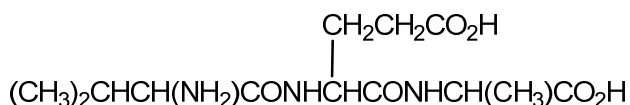
What is the maximum number of different compounds, each containing one amide linkage, that can be formed from one molecule of aspartic acid and one molecule of glutamic acid?

A 1  
B 2

C 4  
D 6

5. [J99/III/29]

Partial hydrolysis of insulin, the hormone essential for carbohydrate metabolism, gives the following tripeptide.



Which compound could be obtained by further hydrolysis of this tripeptide?

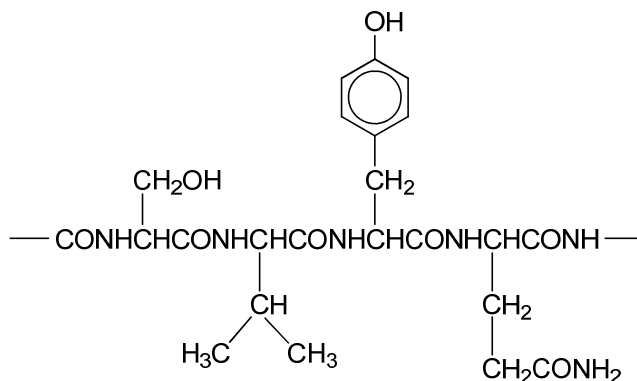
A  $\text{CH}_3\text{CH}(\text{CO}_2\text{H})_2$

B  $(\text{CH}_3)_2\text{CHCH}(\text{NH}_2)\text{CONH}_2$

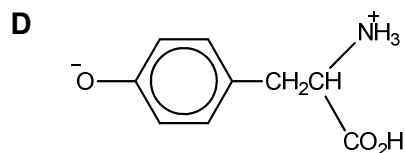
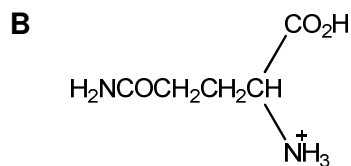
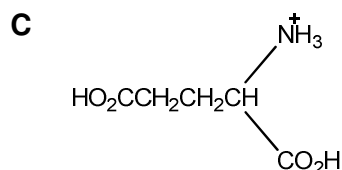
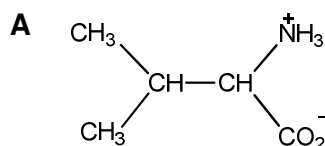
C 
$$\begin{array}{c} \text{CH}_2\text{CH}_2\text{CO}_2\text{H} \\ | \\ \text{H}_2\text{NCONHCHCO}_2\text{H} \end{array}$$

D 
$$\begin{array}{c} \text{CH}_2\text{CH}_2\text{CO}_2\text{H} \\ | \\ \text{H}_2\text{NCHCONHCH}(\text{CH}_3)\text{CO}_2\text{H} \end{array}$$

6. Part of the chain of the hormone insulin is shown below.



When insulin is heated in  $6 \text{ mol dm}^{-3} \text{ HCl}$  for a prolonged period, what is a product that is obtained?



7. [N12/I/27]

Which stabilizes the  $\alpha$ -helix of proteins?

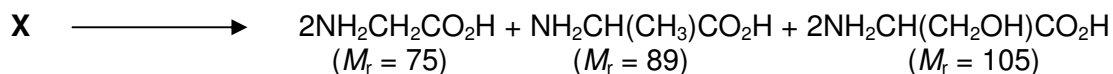
- A** disulfide bridges and hydrogen bonding
- B** disulfide bridges only
- C** hydrogen bonding only
- D** van der Waals' forces only

The responses **A** to **D** should be selected on the basis of

<b>A</b>	<b>B</b>	<b>C</b>	<b>D</b>
1, 2 and 3 are correct	1 and 2 only are correct	2 and 3 only are correct	1 only is correct

8. [N09/I/30]

A small peptide **X** is hydrolysed according to the following reaction.



What is the  $M_r$  of **X**?

- A** 359
- B** 377
- C** 431
- D** 449

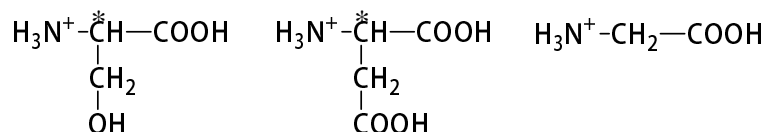
## Suggested Solution to Self-Check Questions

1	(a)	peptide bond	This bond is formed when two amino acids are joined together. It is formed between $\text{--COO}^-/\text{--COOH}$ group of one amino acid and the $\text{--NH}_3^+/\text{--NH}_2$ group of another amino acid.
	(b)	primary structure of protein	The <u>sequence of the amino acids</u> in a polypeptide chain or polypeptide chains.
	(c)	secondary structure of protein	The way in which segments of the polypeptide backbone orientate into a regular pattern through <u>hydrogen bonding</u> between the <u>N-H</u> and <u>C=O</u> groups of the <u>peptide linkages</u> in the <u>polypeptide backbone</u> (rather than between the side chains/R groups).
	(d)	tertiary structure of protein	This refers to the <u>3D arrangement</u> due to the folding of the $2^\circ$ structural elements ( $\alpha$ -helix or $\beta$ -pleated sheet) together with the spatial disposition of the side chains. Folding is due to <u>R group interactions</u> .
	(e)	quaternary structure of protein	The quaternary structure of proteins refers to the <u>spatial arrangement and association of the polypeptide subunits</u> . It is the combination of several protein chains into a larger 3-dimensional structure held together by <u>side chain/R group interactions</u> .
	(f)	denaturation of protein	Disruption of secondary, tertiary, or quaternary structure of proteins by breaking the <u>non-covalent interactions</u> (but including disulfide links) that hold these structures in their native conformations, resulting in the loss of biological function.

- 2 (a) HCl(aq), prolonged heating for a few hours  
**OR** NaOH(aq), prolonged heating for a few hours

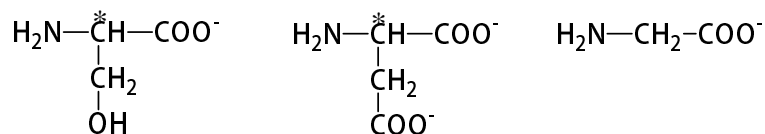
(b) Acidic / Alkaline hydrolysis. Peptide bonds are broken.

(c) Acidic hydrolysis



**OR**

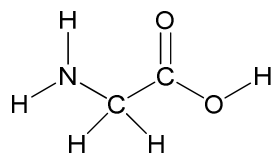
Alkaline hydrolysis



(d)  $^+\text{H}_3\text{N} - \text{CH}_2 - \text{COO}^-$

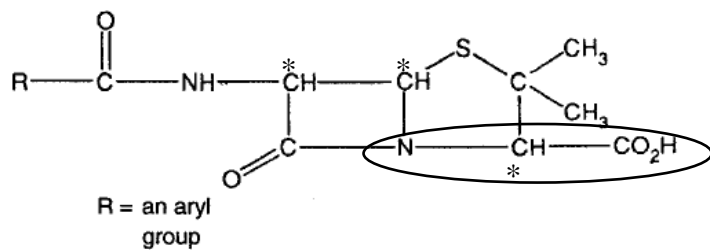
- (e) (i)  $\text{H}_3\overset{+}{\text{N}} - \text{CH}_2 - \text{COO}^- + \text{H}^+ \longrightarrow \text{H}_3\overset{+}{\text{N}} - \text{CH}_2 - \text{COOH}$   
(ii)  $\text{H}_3\overset{+}{\text{N}} - \text{CH}_2 - \text{COO}^- + \text{OH}^- \longrightarrow \text{H}_2\text{N} - \text{CH}_2 - \text{COO}^- + \text{H}_2\text{O}$

3 (a)



aminoethanoic acid

(b)



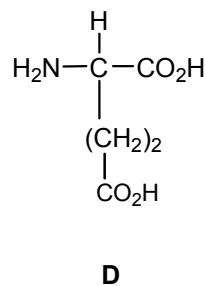
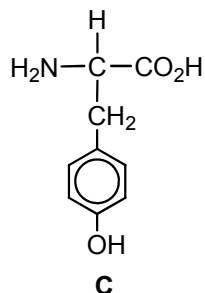
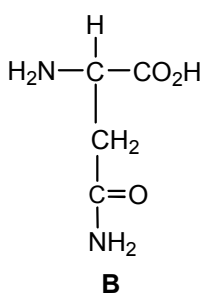
(c) Acidic as penicillin contains the acidic  $\text{-COOH}$  group while the amide groups are neutral.  
There is also the absence of basic groups in penicillin.

Q4	Q5	Q6	Q7	Q8
C	D	C	C	B

## Discussion Questions

### 1. [J91/III/9]

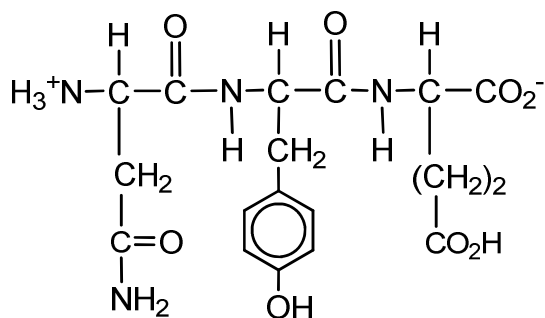
On hydrolysis, a tripeptide produced the following amino acids in equimolar amounts:



- (a) In how many different ways can these three amino acids be coupled by peptide bonds to form a tripeptide? [1]

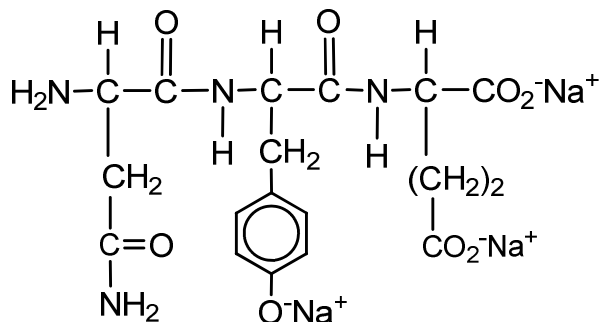
Assuming each tripeptide is formed from the three different amino acids, there are 6 ways of forming the tripeptide.

- (b) Draw the structural formula of one such tripeptide.



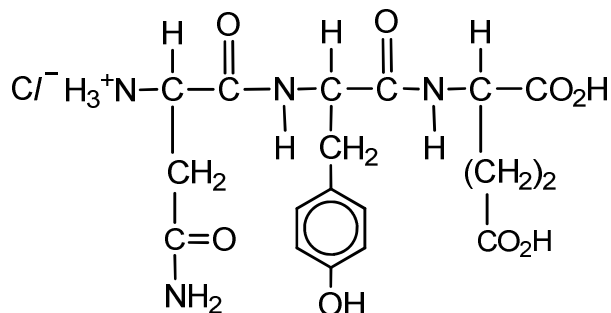
- (c) Give the structural formula of the product(s) formed when the tripeptide in (b) is dissolved **without hydrolysis** in

- (i) dilute aqueous sodium hydroxide, and

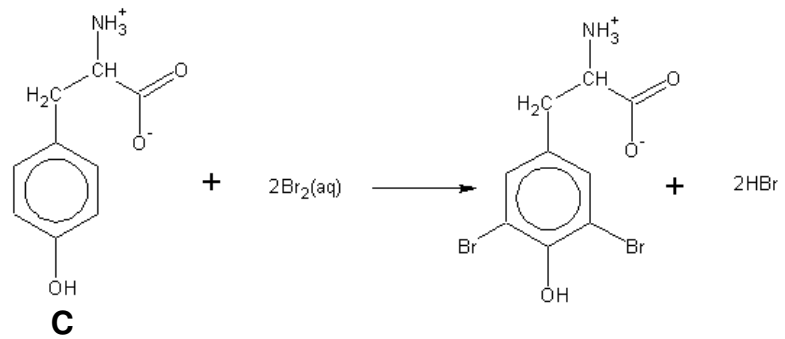


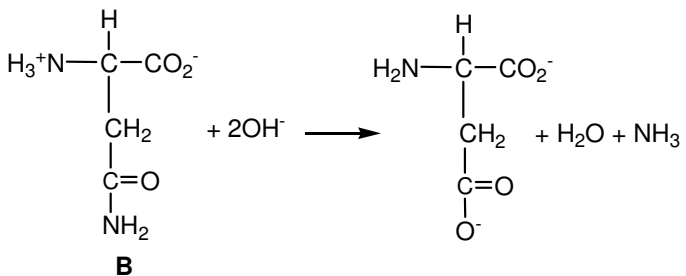
(ii) dilute hydrochloric acid.

[6]



(d) For each of the amino acids, **C** and **D**, describe a simple test by which its pure aqueous solution can be distinguished from that of **B**. [3]

<b>Test</b>	Add Br <sub>2</sub> (aq) to each of the solutions of <b>B</b> and <b>C</b> separately.
<b>Observation</b>	<b>C</b> : Decolourisation of orange Br <sub>2</sub> (aq) and white ppt formed. <b>B</b> : No decolourisation of orange Br <sub>2</sub> (aq)/ Solution remains orange. No white ppt formed.
<b>Equation:</b>	 <p>The reaction shows tyrosine (labeled <b>C</b>) reacting with 2Br<sub>2</sub>(aq) to produce 3,5-dibromotyrosine and 2HBr. The tyrosine molecule is shown as a benzene ring with a para-hydroxyl group and a side chain containing an amino group and a carboxylate group. The product is a benzene ring with a para-hydroxyl group and two ortho-bromo substituents, with the same side chain.</p>

<b>Test</b>	Add NaOH(aq) to each of the solutions of <b>B</b> and <b>D</b> separately and heat.
<b>Observation</b>	<b>B</b> : Colourless and pungent NH <sub>3</sub> gas evolved turns moist red litmus blue. <b>D</b> : No pungent NH <sub>3</sub> gas evolved.
<b>Equation:</b>	 <p>The reaction shows aspartic acid (labeled <b>B</b>) reacting with 2OH<sup>-</sup> to produce aspartate, H<sub>2</sub>O, and NH<sub>3</sub>. The aspartic acid molecule is shown as a central carbon bonded to H<sub>3</sub>N<sup>+</sup>, H, CO<sub>2</sub><sup>-</sup>, and a CH<sub>2</sub> group which is further bonded to a C(=O)NH<sub>2</sub> group. The product aspartate has the same structure but with H<sub>2</sub>N instead of H<sub>3</sub>N<sup>+</sup> and the side chain is CO<sub>2</sub><sup>-</sup>.</p>

## 2. [Modified from N01/I/7(d) and N11/III/4(d)]

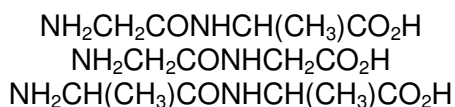
Complete hydrolysis of a protein produces individual amino acids, but partial hydrolysis can break the protein down into dipeptide or tripeptide fragments.

- (a) How could proteins be hydrolysed in the laboratory to form a mixture of their constituent amino acids?

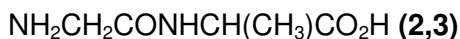
Prolonged heating with  $\text{HCl(aq)}$  /  $\text{NaOH(aq)}$  for a few hours.

(The actual conditions should be  $6 \text{ mol dm}^{-3} \text{ HCl}$ , warm for 10-36 hrs in a sealed tube for complete hydrolysis)

- (b) Partial hydrolysis of a tetrapeptide (containing four amino acid residues) produces the following three dipeptides, as well as the individual amino acids.



Deduce the order in which the amino acids are bonded together in the tetrapeptide, explaining your reasoning.



Correct Sequence: **(1234)**  $\text{NH}_2\text{CH}_2\text{CONHCH}_2\text{CONHCH}(\text{CH}_3)\text{CONHCH}(\text{CH}_3)\text{CO}_2\text{H}$

## 3. [J01/IV/1]

The enzyme chymotrypsin digests proteins or polypeptides at the carboxylic acid end of the amino acid phenylalanine. The following peptides were identified after digestion of the polypeptide **P** with chymotrypsin, and subsequent separation.

asp-lys-gly-phe  
lys-val-arg  
val-phe

Another enzyme trypsin digests at the carboxylic acid end of lysine. The following peptides were identified after digestion of the same polypeptide **P** with trypsin, and subsequent separation.

gly-phe-lys  
val-arg  
val-phe-asp-lys

Use the above information to determine the primary structure of polypeptide **P**. Justify your answer.

Overlapping regions are underlined.

Chymotrypsin	Trypsin	Sequence of fragments in P
asp-lys- <u>gly-phe</u>	<u>gly-phe</u> -lys	asp-lys- <u>gly-phe</u> -lys
lys- <u>val-arg</u>	<u>val-arg</u>	lys- <u>val-arg</u>
<u>val-phe</u>	<u>val-phe</u> -asp-lys	<u>val-phe</u> -asp-lys

Based on sequences of fragments (last column), find overlapping regions again.

asp-lys-gly-phe-lys

lys-val-arg

val-phe-asp-lys

**Complete sequence:** val-phe-asp-lys-gly-phe-lys-val-arg

#### 4. [Modified from N07/III/5]

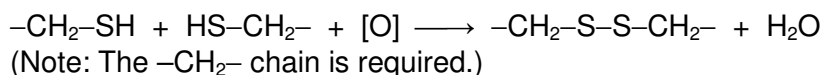
The human serum albumin, HSA, molecule is a single chain of 570 amino acids. 67% of the amino acids are held in an  $\alpha$ -helix. The molecule is roughly spherical in water.

The table shows some of the most common amino acids in the HSA molecule.

Amino acid	Formula of side chain (R in $RCH(NH_2)CO_2H$ )	Number of amino acid residues per molecule of HSA
Glutamic acid	$-CH_2CH_2CO_2H$	80
Leucine	$-CH_2CH(CH_3)_2$	58
Lysine	$-(CH_2)_4NH_2$	58
Valine	$-CH(CH_3)_2$	45
Cysteine	$-CH_2SH$	36
Phenylalanine	$-CH_2C_6H_5$	33
Threonine	$-CH(OH)CH_3$	27
Serine	$-CH_2OH$	22

(a) The cysteine residues in the HSA molecule form *disulfide bridges*.

Show the process using a chemical equation. If all the disulfide bridges are intramolecular, how many bridges can form in each HSA molecule.

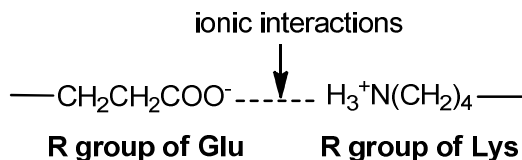


$$\text{Total number of disulfide bridges possible} = \frac{36}{2} = 18$$

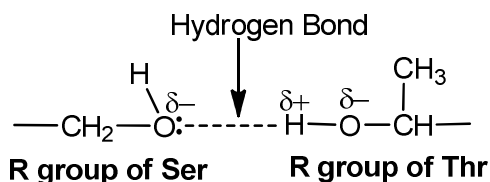
(b) The attractions between the various side chains of the HSA molecule account for its roughly spherical shape. Other than disulfide bridges, describe **two** other types of side-chain interactions. Use suitable pairs of amino acids to illustrate your answer.

- Ionic interactions (e.g. lys-glu)

(Note: Hydrogen bonding **NOT** accepted between lys and glu)



- Hydrogen bonding (e.g. lys-ser or thr-glu or thr-ser)



(c) The HSA molecule transport long chain fatty acids such as stearic acid ( $n = 17$  in the general formula,  $\text{H}-(\text{CH}_2)_n-\text{CO}_2\text{H}$ ) within its structure. Suggest **two** amino acids in HSA which can interact with stearic acid.

Any two of the three non-polar amino acids (leu, val or phe)

(d) Suggest **three** amino acids from the table which are likely to interact with water.

Any three of the polar amino acids (glu, lys, thr, ser)

5. [Modified from N09/III/1(a)(b), N12/III/4(d)]

- (a) With reference to the haemoglobin (Hb) molecule, describe and explain what is meant by the terms primary, secondary, tertiary and quaternary structures of proteins. In each case you should state the type of bonding or interactions involved. [8]

[Note: Two marks were allocated to each type of structure: one for a description of the structure and one for the bonding involved]

**Primary Structure**

- Refers to sequence of the amino acids in a polypeptide chain or polypeptide chains.
- These amino acid residues are held together by covalent amide (peptide) bonds.

**Secondary Structure**

- Refers to the way in which segments of the polypeptide backbone orientate into a regular pattern through hydrogen bonding between the C=O and N-H groups of the peptide linkages in the polypeptide backbone.
- These structures are called  $\alpha$ -helices and  $\beta$ -pleated sheets.

**Tertiary Structure**

- Refers to the 3-dimensional arrangement due to the folding of the secondary structural elements ( $\alpha$ -helix or  $\beta$ -pleated sheet) together with the spatial disposition of the side chains.
- The native 3D conformation is held by side chain / R group interactions, namely ionic attractions, van der Waals' interactions, hydrogen bonds and disulfide bonds.

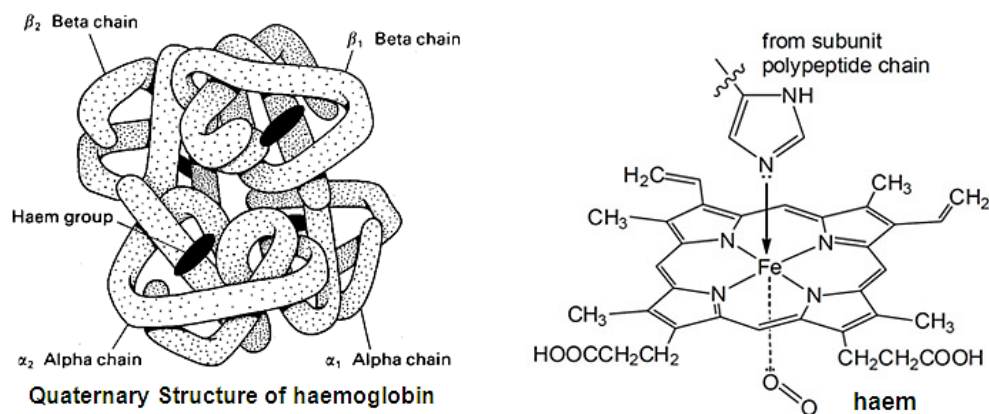
**Quaternary Structure**

- Refers to the spatial arrangement and association of more than one polypeptide subunit to form proteins.
- The polypeptide subunits are held together by side chain / R group interactions, namely ionic attractions, van der Waals' interactions, hydrogen bonds and disulfide linkage.

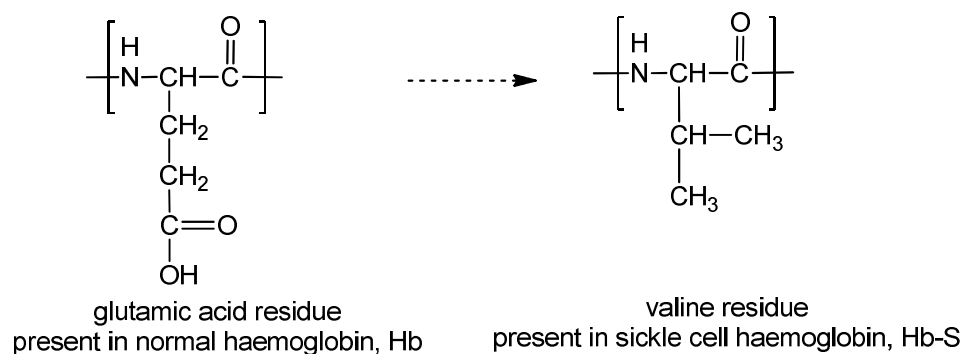
**Example: Haemoglobin**

- consists of four associated polypeptide chains (two  $\alpha$ -subunits and two  $\beta$ -subunits) fitting together to form a compact, globular assembly of considerable stability.
- considerable amount of R group interactions (hydrogen bonds, van der Waals' forces, ionic interactions and disulfide bridges) between the subunits.
- Each subunit is dative covalently bonded to a haem residue. (A histidine of each globin subunit forms a dative bond to the Fe centre in a haem residue)

(Note: The iron in the haem group binds to oxygen.)

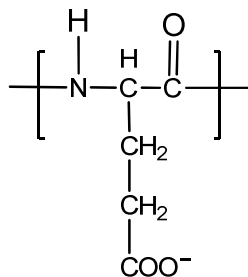


- (b) In patients suffering from sickle cell anaemia, the  $\beta$ -chains of their haemoglobin (abbreviated as Hb-S) differ from those of normal haemoglobin through the replacement of a glutamic acid residue by a valine residue.



This substitution has the effect of making the deoxygenated Hb-S molecules attract each other and aggregate, resulting in the formation of insoluble fibres.

- (i) Draw the structural formula of a glutamic acid residue in its most stable form at pH 7. Glutamic acid has a  $\text{p}K_a$  of 4.3.



- (ii) Suggest, in terms of the intermolecular forces present, a reason for the aggregation of Hb-S molecules.

- The R group (negatively charged  $\text{COO}^-$  group) of glutamic acid residue is changed to the non-polar R group of valine residue.
- This substitution enables aggregation of Hb-S molecules via van der Waals' (id-id) interactions of the non-polar R groups.

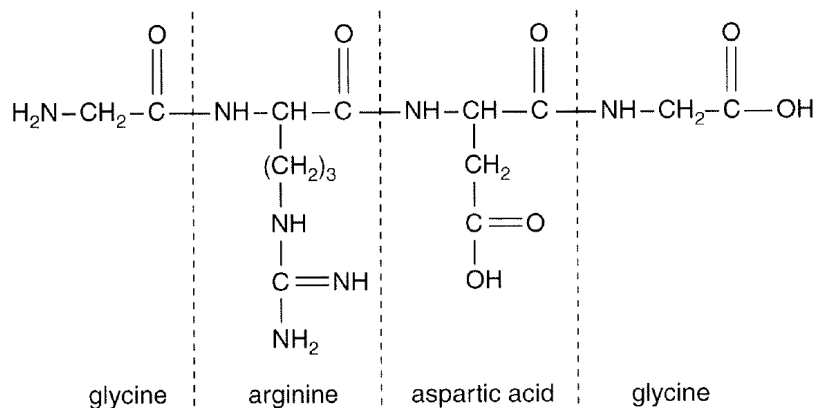
(Note: hydrophobic interactions are not acceptable.)

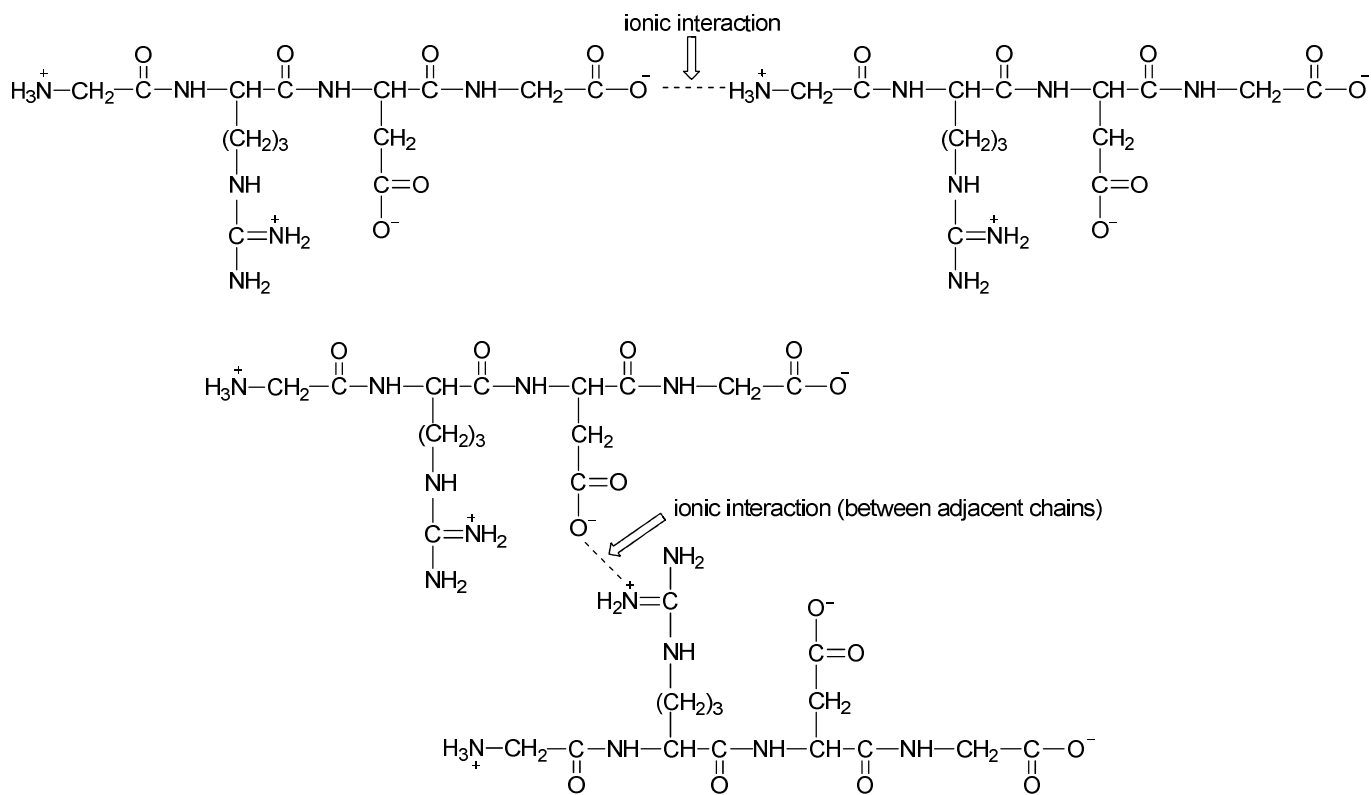
- (iii) Suggest a reason why molecules of normal haemoglobin do **not** attract each other. [4]

Normal haemoglobin do not have favourable interactions with each other due to repulsion of the negatively charged  $\text{COO}^-$  group, thus they do not attract each other.

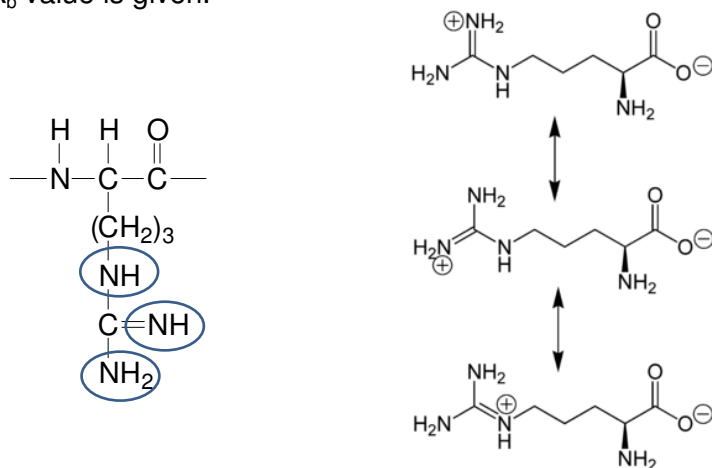
- (c) Ionic charges are important in determining the 3-dimensional structure of the haemoglobin molecule. The four protein chains of deoxyhaemoglobin are held in position by 8 ionic 'salt' links. Some of these interactions are between the C-terminal end of one chain and the N-terminal end of another chain, whereas other interactions are between aspartic acid residues on one chain and arginine residues on another chain.

- (i) Using the tetrapeptide whose structure is given below, and taking account of the ionic forms that the amino acid residues exist in at pH7, draw the structures of two of these tetrapeptide chains to illustrate both of the ionic interactions mentioned above.





Note: For the arginine residue, you can protonate at ANY of the 3 N atoms circled below in the side chain since no  $pK_b$  value is given.



However, in reality, the proton would attach itself to the =NH group to produce a cation that is stabilized by resonance as shown above.

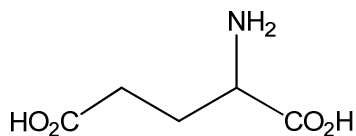
(ii) Describe two further ways, other than ionic linkages, by which the tertiary structures of proteins can be stabilized. [5]

Any two of the following:

- Hydrogen bonds between polar R groups (e.g.  $-\text{OH}$ )
- Van der Waals' (not hydrophobic) attractions between non-polar R groups.
- Disulfide (not disulfite) linkages between the SH groups of the side chains

6. [Modified from N10/III/2(a)(b)]

- (a) Soy sauce is produced by the fermentation of soybeans by the mould *Aspergillus oryzae*. The distinctive salty taste of the sauce is due to salts of glutamic acid formed during fermentation.

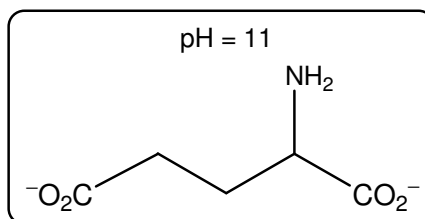
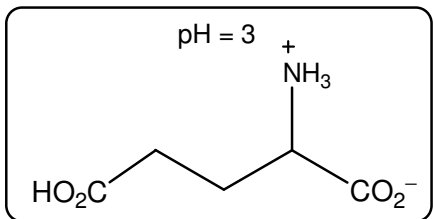
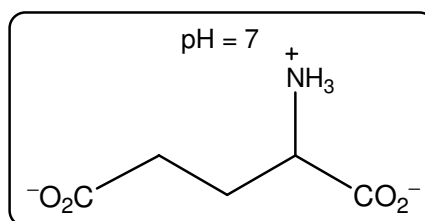
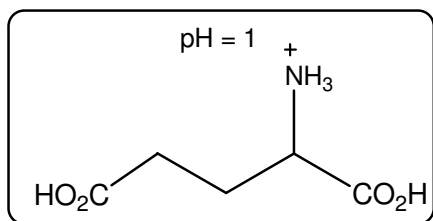


glutamic acid

There are three  $pK_a$  values associated with glutamic acid: 2.1, 4.1 and 9.5.

Make use of these  $pK_a$  values to suggest the major species present in solutions of glutamic acid with the following pH values.

- pH 1
- pH 3
- pH 7
- pH 11

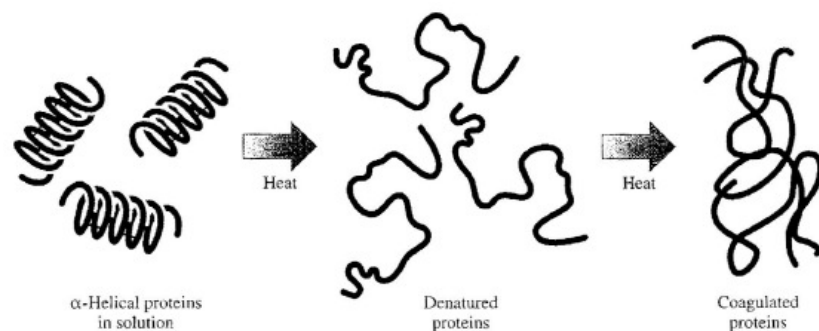


(b) Dofu is made by coagulating soy milk and then pressing the curds between fine cloth to extrude most of the moisture. Coagulating agents that have been used include certain salts, acids or enzymes. Coagulation is due to the denaturation of the proteins in the soy milk.

[You may find that including suitable sketches or diagrams will help you in your answers to parts (i), (ii) and (iii).]

(i) What aspect of a protein's structure is altered during coagulation, and why does this occur?

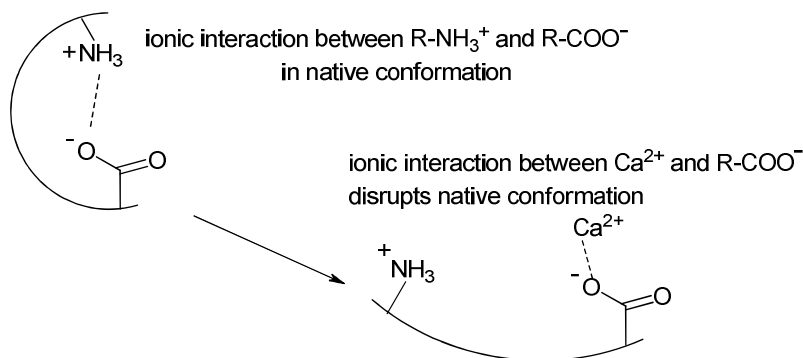
- The tertiary and quaternary structure or 3D arrangement due to folding of the protein is altered.
- The folding or native conformation of the protein is held by side chain / R group interactions.
- During denaturation, these R group interactions are broken or disrupted.
- Upon denaturation, the globular proteins unfold and the non-polar side chains / R groups are exposed.
- The unfolded protein can then aggregate with each other via side chain / R group interactions such as van der Waals' interactions between the non-polar R groups.
- This leads to the formation of a large insoluble mass which is observed as coagulation.



The calcium salts  $\text{CaSO}_4$  and  $\text{CaCl}_2$  are often used to produce dofu.

(ii) Suggest how  $\text{Ca}^{2+}(\text{aq})$  ions can interact with a protein to bring about denaturation.

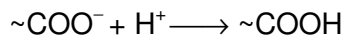
- $\text{Ca}^{2+}(\text{aq})$  cations compete with positively charged groups for attraction to negatively charged groups (e.g.  $\text{COO}^-$ ), hence disrupting the original ionic bonds, thereby bringing about the unfolding and denaturation of the protein.



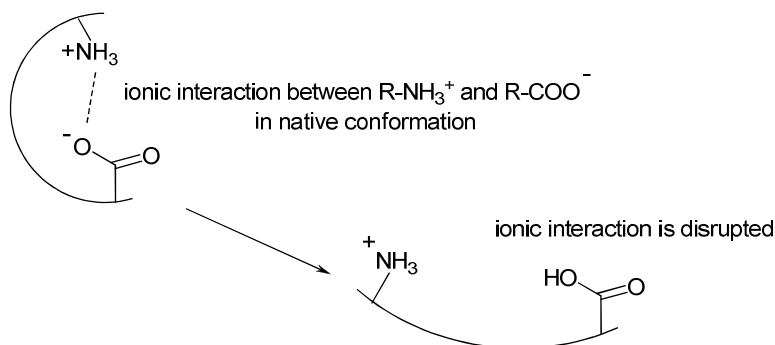
(iii) Suggest how a weak acid might interact with a protein to bring about denaturation.

[8]

Weak acid disrupt ionic interactions by protonating ionic side chain R groups containing carboxylate anions:



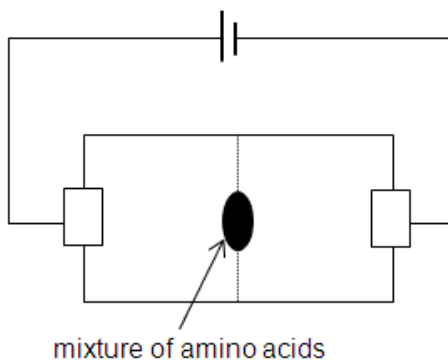
The protonated carboxyl groups are then unable to participate in ionic interactions with side chains containing  $-\text{NH}_3^+$ , bringing about denaturation of the protein.



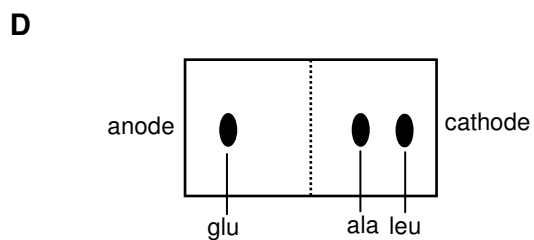
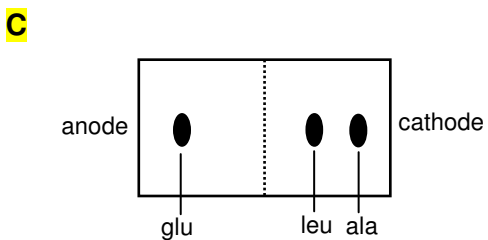
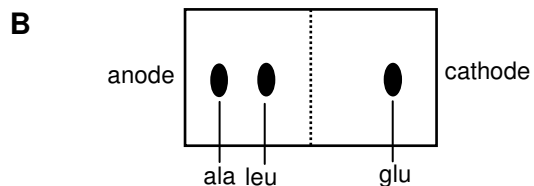
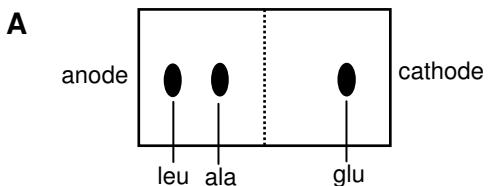
7. The table below gives some information pertaining to three amino acids.

amino acid	structure	isoelectric point
alanine (ala)	$\begin{array}{c} \text{H} \\   \\ \text{H}_2\text{N}-\text{C}-\text{COOH} \\   \\ \text{CH}_3 \end{array}$	6.0
leucine (leu)	$\begin{array}{c} \text{H} \\   \\ \text{H}_2\text{N}-\text{C}-\text{COOH} \\   \\ \text{CH}_2\text{CH}(\text{CH}_3)_2 \end{array}$	6.0
glutamic acid (glu)	$\begin{array}{c} \text{H} \\   \\ \text{H}_2\text{N}-\text{C}-\text{COOH} \\   \\ \text{CH}_2\text{CH}_2\text{CO}_2\text{H} \end{array}$	3.2

A mixture of these three amino acids can be separated by electrophoresis.



Which of the following diagram shows the result of the separation of the amino acid mixture at pH 5.0?

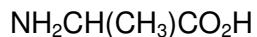


The responses **A** to **D** should be selected on the basis of

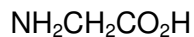
<b>A</b>	<b>B</b>	<b>C</b>	<b>D</b>
1, 2 and 3 are correct	1 and 2 only are correct	2 and 3 only are correct	1 only is correct

**8. [N11/I/40]**

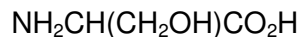
Spider silk is a protein composed mainly of the three amino acids alanine, glycine and serine.



alanine



glycine



serine

Which type of bonding can occur in the tertiary structure of spider silk?

- 1** van der Waals' forces
- 2** hydrogen bonding
- 3** ionic bonding

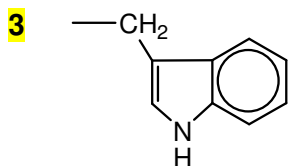
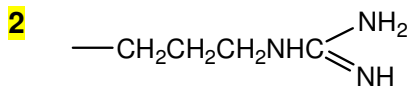
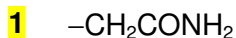
**9. [Specimen Paper 2007/I/Q40]**

The protein albumin (egg white) is precipitated from its aqueous solution when it is poured into **X**. What could **X** be?

- 1** A saturated aqueous solution of  $(\text{NH}_4)_2\text{SO}_4$
- 2**  $0.1 \text{ mol dm}^{-3}$  sulfuric acid
- 3**  $0.1 \text{ mol dm}^{-3}$   $\text{Pb}(\text{NO}_3)_2$

**10. [N08/I/40]**

Which groups within an amino group are able to form a cross-chain link to stabilise the tertiary structure of a protein?



**Assignment Question [Modified from RI 2011 CT2]**

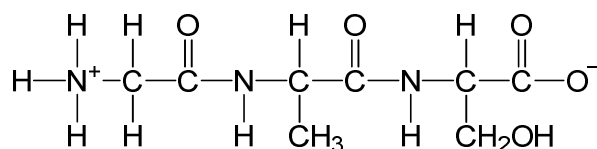
Spider silk is a natural polypeptide, polymeric protein and is in the scleroprotein group which also includes collagen (in ligaments) and keratin (in nails and hair). These are all proteins which provide structural support.

The exact composition of the proteins in spider silk depends on factors such as species and diet. It largely consists of glycine and alanine. The remaining components are mostly glutamine, serine, leucine, valine, and aspartic acid. One particular spider silk protein has the following composition.

Amino Acid	Formula of side chain (R in $\text{RCH}(\text{NH}_2)\text{CO}_2\text{H}$ )	Composition in spider silk (mole %)
Glycine	$-\text{H}$	42.0
Alanine	$-\text{CH}_3$	25.0
Serine	$-\text{CH}_2\text{OH}$	15.1
Glutamine	$-\text{CH}_2\text{CH}_2\text{CONH}_2$	9.2
Leucine	$-\text{CH}_2\text{CH}(\text{CH}_3)_2$	3.8
Aspartic Acid	$-\text{CH}_2\text{CO}_2\text{H}$	3.1
Valine	$-\text{CH}(\text{CH}_3)_2$	1.8

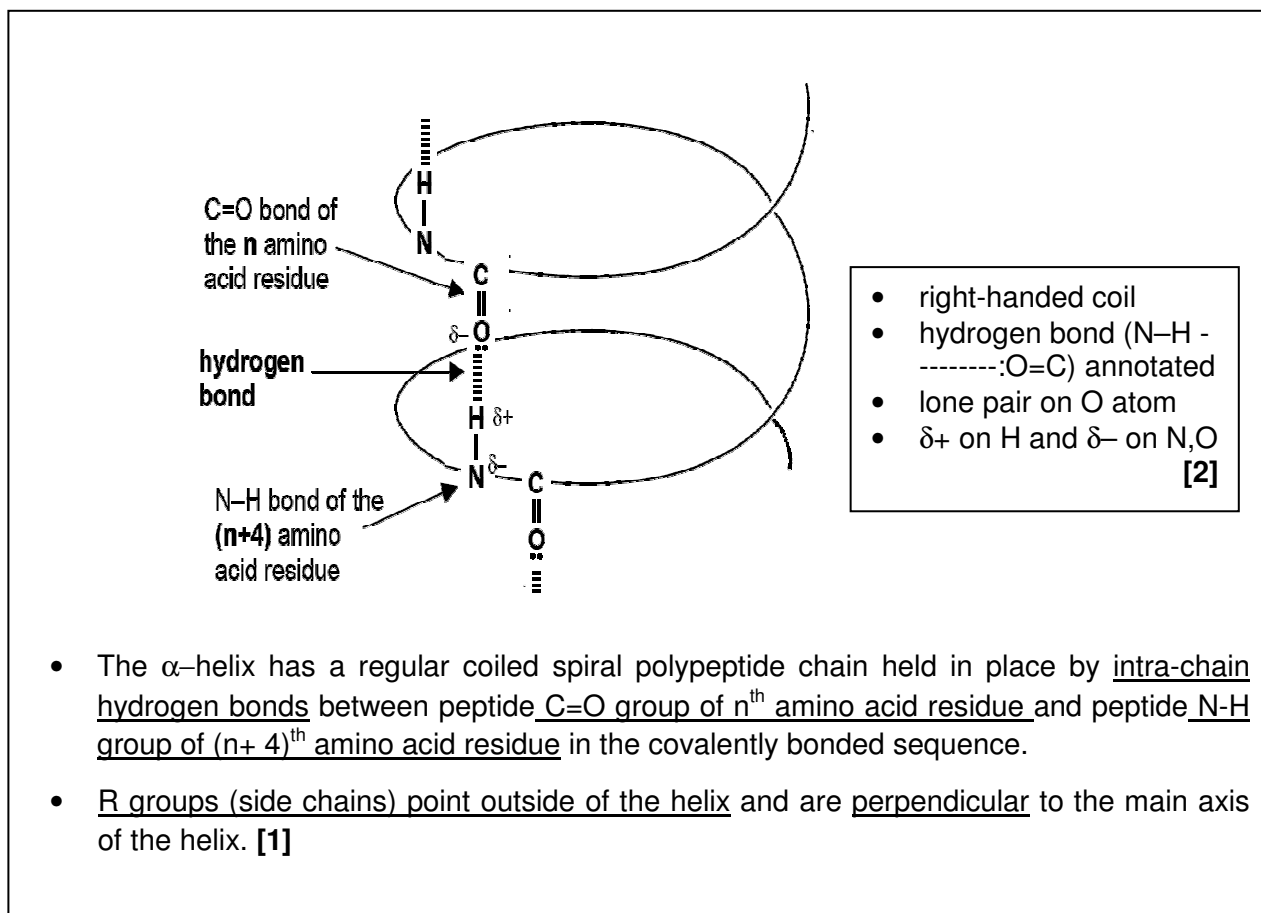
- (a) Draw the structure of the tripeptide, gly-ala-ser, showing the dominant form which it would exist at pH 3 and the displayed structure of the peptide linkages, given the following data. [2]

Amino Acid	Glycine	Alanine	Serine
$\text{p}K_{\text{a}1}$	2.35	2.34	2.19
$\text{p}K_{\text{a}2}$	9.78	9.87	9.21



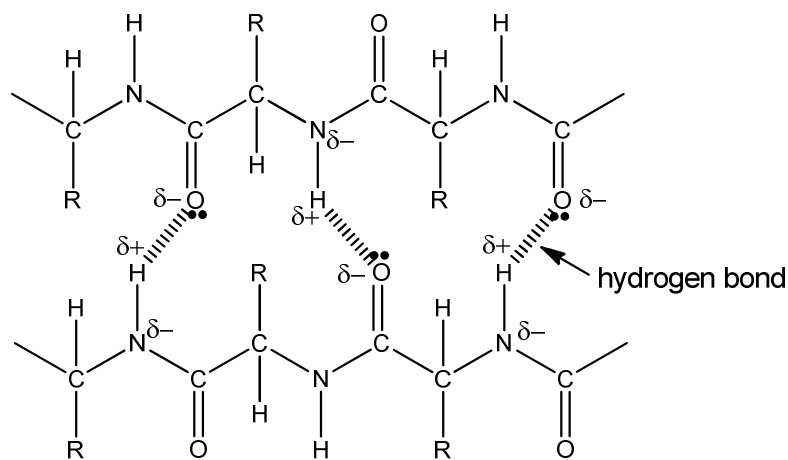
Displayed structure of peptide linkages shown [1]  
 Protonation at N terminal & deprotonated at C terminal [1]

- (b) With the aid of a diagram, describe how a polypeptide chain is held in the shape of an  $\alpha$ -helix. [3]



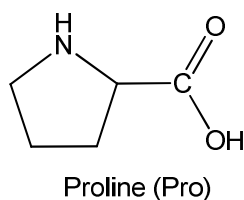
- (c) The tensile strength of spider silk is comparable to that of steel. This property can be attributed to the  $\beta$ -pleated sheets present in the secondary structure of the silk protein.

With the aid of a suitable diagram, describe the structure of the  $\beta$ -pleated sheet of the silk protein. [3]



- All peptide linkages are involved in intra-chain hydrogen bonding.
- It is stabilised by hydrogen bonds between the C=O group of a peptide in one strand and the N-H group of another peptide in the adjacent strand. [1]
- R groups (side chains) project above and below the sheet and are 90° to the plane of the pleated sheet. [1]

(d) Explain briefly why proline residues are known as 'structural disruptors' in the middle of regular secondary structures such as  $\alpha$ -helices or  $\beta$ -pleated sheets.



Proline does not fit into the regular secondary structures such as  $\alpha$ -helices or  $\beta$ -pleated sheets because

- the peptide bond formed by proline does not have N-H (since it forms a tertiary amide) and thus cannot form hydrogen bonding to stabilize the secondary structure. [1]
- of steric hindrance posed by the alicyclic structure. [1]

- (e) Apart from its high tensile strength, spider silk was also found to be rather flexible due to the glycine-rich regions in the structure.

Explain why glycine-rich regions of the protein structure give rise to its flexibility. [1]

Only van der Waals' forces of attraction present between the side chains of glycine which can be easily overcome allowing that region of the protein structure to be more flexible. [1]

- (f) Describe two types of side-chain interaction present in silk which may be broken during denaturation, illustrating your answer with suitable pairs of amino acids from the table above. [2]

Van der Waals' forces of attraction (e.g. between R groups of glycine & alanine) [1]  
Hydrogen bonds (e.g. between serine and glutamine) [1]