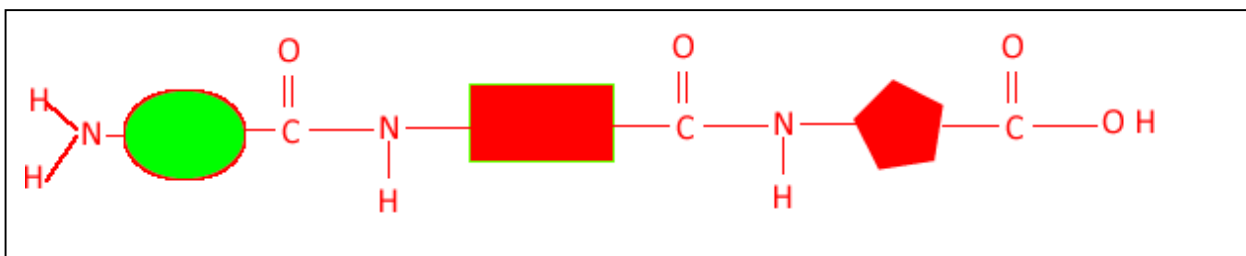
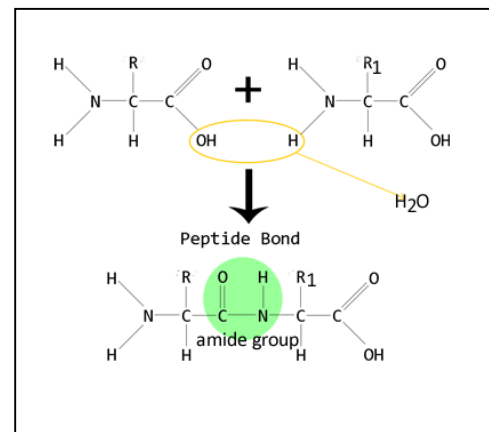


## Lesson 2 –proteins

[Click](#) to revise amino acids and protein structure.

Proteins are formed during condensation polymerisation reactions between amino acids. Amino acids react in a condensation reaction to form an amide link which results in the expulsion of one water molecule for every amide group formed.

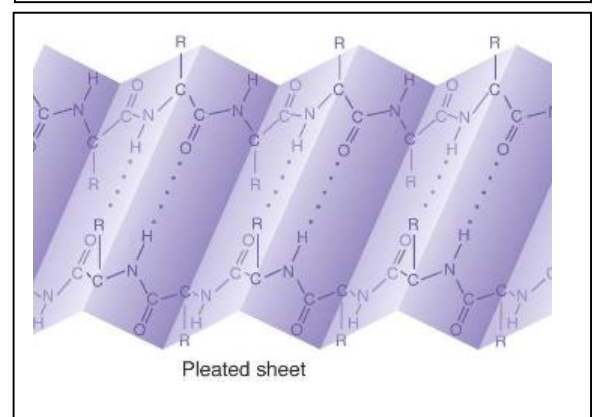
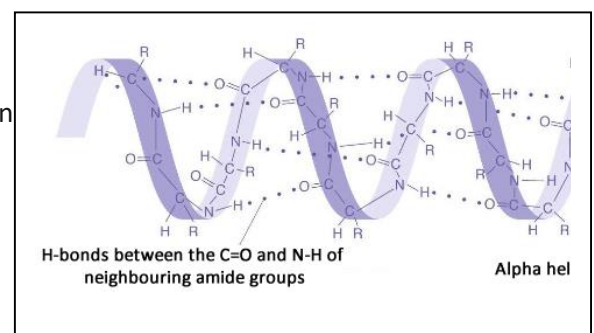
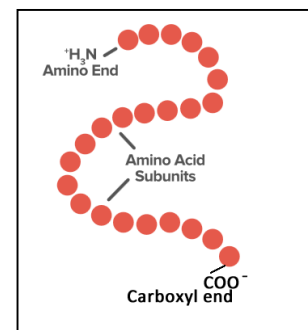
The resulting peptide structure consists of amino acids covalently linked by amide groups to each other, as shown below.



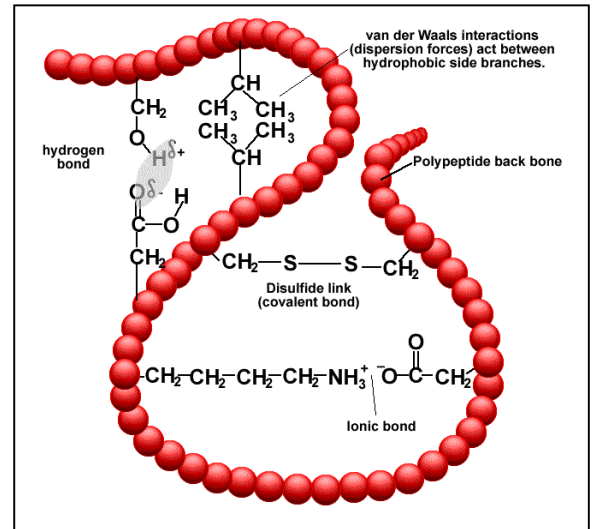
Proteins are complex molecules with unique structures and functions. The shape of the molecule is critical to its role in the body and it is the sequence of amino acids in the protein chain that determine how the protein folds.

Proteins have a number of levels of structure.

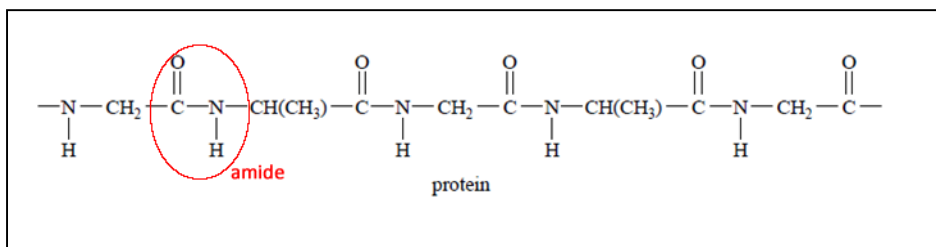
- The primary structure- the sequence of covalently bonded amino acids.
- The secondary structure- which is formed by hydrogen bonding between amide groups along sections of the primary structure. On average it is every fourth amide group that undergoes hydrogen bonding. This results in two types of structures known as an alpha helix or beta pleated sheet.



- c) Further interactions between several secondary structures along the protein chain form the **tertiary structure**. This comes about due to bonding between the side groups of amino acids. The type of bonding taking place is summarised in the diagram on the right.
- d) A **quaternary structure** occurs when several tertiary structures come together.

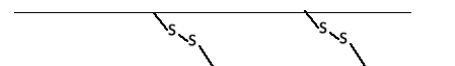


Heat and changes in pH can severely disrupt and destroy the secondary and tertiary structures of proteins, which are primarily, held together by weaker bonding forces, such as hydrogen bonding and van der waals interactions. The primary structure is not broken down by heat or pH changes as covalent bonds holding the amino acids together are too strong.



- 1) Consider a small section of protein chain shown above.
- Circle and name a common functional group.
  - Name the amino acids present. *Glycine and alanine*

- 2) A protein is made up of 80 amino acids and has the structure shown on the right.



- a) How many amide links are present in this protein?

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- b) The image shown on the right represents structures associated with proteins.

- i. Which structures are likely to be disrupted by heat?

*ii and iv*

- ii. Which represents a primary structure of a protein?

*iii*

- iii. Which represents a structure most likely to involve a disulphide bond?

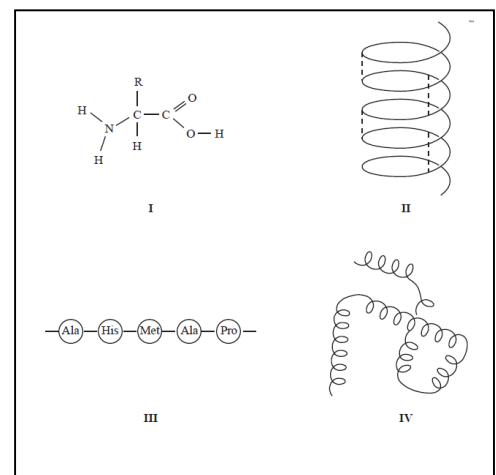
*iv*

- iv. Which represents a structure formed primarily from the hydrogen bonding between amide groups.

*ii*

- v. Which structure can form a zwitterion at a given pH?

*i*



3) Denaturation of proteins results in significant structural unfolding of the protein structure. Which of the following comments relate to protein denaturation? Explain

- i. It could result from a temperature change and disrupts the secondary and tertiary structures of the protein.  
*True. The bonds responsible for the secondary and tertiary structures are relatively weak and easily broken by heat .*
- ii. It may be caused by a pH change and disrupts the primary structure of the protein.  
*False. The primary structure involves the amino acids covalently bonded to each other. Covalent bonds holding the amino acids residues in place are not easily disrupted by changes in pH*
- iii. It alters the primary structure as well as the tertiary structure of the protein.  
*False. The primary structure is not altered during denaturation as the covalent bonds are strong enough to resist heat and pH changes.*
- iv. It results in a change in the shape of the protein.  
*True Significant changes occur to the shape of the molecule when the secondary and tertiary structures are disrupted.*

4) Australian jellyfish venom is a mixture of proteins for which there is no antivenom. Jellyfish stings are painful, can leave scars and, in some circumstances, can cause death. Some commercially available remedies disrupt the interactions between the side chains on amino acid residues. These products most likely

- A. disrupt the primary structure of the protein.
- B. disrupt the secondary structure only of the protein.
- C.** disrupt the tertiary structure only.
- D. secondary and tertiary structures as well as the covalent bonds between amino acid residues.

5) Consider the following statements about the structure of proteins.

I The primary structure of a protein is determined by the sequence of amino acid residues.

II The secondary structure of a protein is the result of hydrogen bonding between –NH and –CO groups.

III The tertiary structure of a protein involves bonding between the side chains on the amino acid residues.

IV Heat and pH disrupt both the primary and tertiary structures.

Of these statements

A. only I and III are true.

B. only I and IV are true.

C. only II and III are true.

**D.** I, II and III are all true.

6) A protein has the amino acid sequence shown below

Tyr – Ala – Gly – Phe – Gly

a) How many amide links are present? **4**

b) How many carboxyl groups are present? **1**

c) How many amino groups are present? **1**

d) What is the name of the reaction that formed this protein? *Condensation polymerisation*

e) What is the formula mass of the protein if the formula mass of each amino acid is given below.

Tyr = 181, Ala = 89, Gly = 75, Phe = 165.

*$(181 + 89 + 75 + 165 + 75) - 4 \times 18 = 513 \text{ amu}$*

7) Enzymes are proteins that catalyse chemical reactions in living organisms. Which one of the following statements about enzymes is/are true? Explain

- i. Enzymes can only be denatured by an increase in temperature.

*False. They can also be denatured by a change in pH.*

- ii. The tertiary structure of an enzyme may be altered if a small number of amino acids in its primary structure are altered.

*True. The shape of the protein is highly dependent on the sequence of the amino acids in its primary structure. Any modifications in this sequence will alter the interaction of the amino acid side chains and cause a change in the tertiary structure and hence the shape of the protein.*