Biomolecules of Life (Part 2)- Proteins

1. Overview of Topic

Compounds that contain carbon atoms are said to be organic and the branch of chemistry that specializes in the study of carbon compounds is called **organic chemistry**. This set of lecture notes covers the topic of **Proteins**. Nucleic acids will be covered in the Core Idea 2: **Genetics and Inheritance**.

These four major classes of biomolecules function as molecular building blocks for macromolecules to be assembled. Macromolecules are often called polymers because each polymer molecule is a long molecule consisting of many similar or identical building blocks linked by covalent bonds. Each repeating unit of a smaller molecule is called a monomer.

2. Learning Outcomes

a. Describe the structure and properties of the following monomers:
   i. amino acids (in proteins) (knowledge of chemical formulae of specific R-groups of different amino acids is not required).

b. Describe the formation and breakage of the following bonds:
   i. peptide bond

c. Explain primary structure, secondary structure, tertiary structure and quaternary structure of proteins, and describe the types of bonds that hold the molecule in shape (hydrogen, ionic, and disulfide bonds, and hydrophobic interactions).

d. Explain the effects of temperature and pH on protein structure.

e. Describe the molecular structure of the following proteins and explain how the structure of each protein relates to the function it plays:
   i. haemoglobin (transport)
   ii. collagen (structural)
   iii. G-protein linked receptor (signalling) – *to be covered in cell signalling*

   (knowledge of details of the number of amino acids and types of secondary structures present is not required.)

3. References

Campbell, N.A. and Reece, J.B. (2011), ***Biology*** (9th edition), Pearson Benjamin-Cummings, San Francisco

Brooker, R.J., Widmaier, E.P., Graham, L. and Stiling, P. (2008), ***Biology***, Mc-Graw-Hill, New York

Contents

4. Introduction

Notes to self

As compared to biomolecules such as carbohydrates, the number of proteins is found in the natural world is enormous. Proteins are **specific to each species** unlike carbohydrates. For example, haemoglobin, a protein found in the red blood cells of vertebrates has a different structure in crocodiles as compared to humans. These differences have their implications too. Have you ever wondered why crocodiles can hold their breaths longer, when they are underwater, than humans? The answer is likely to lie in the differences in the structures of their haemoglobin proteins which are responsible for oxygen transport in their bodies. This is just one example of how structures of proteins can influence their functions. Indeed, it is the proteins rather than fats or carbohydrates which determine characteristics of a species.

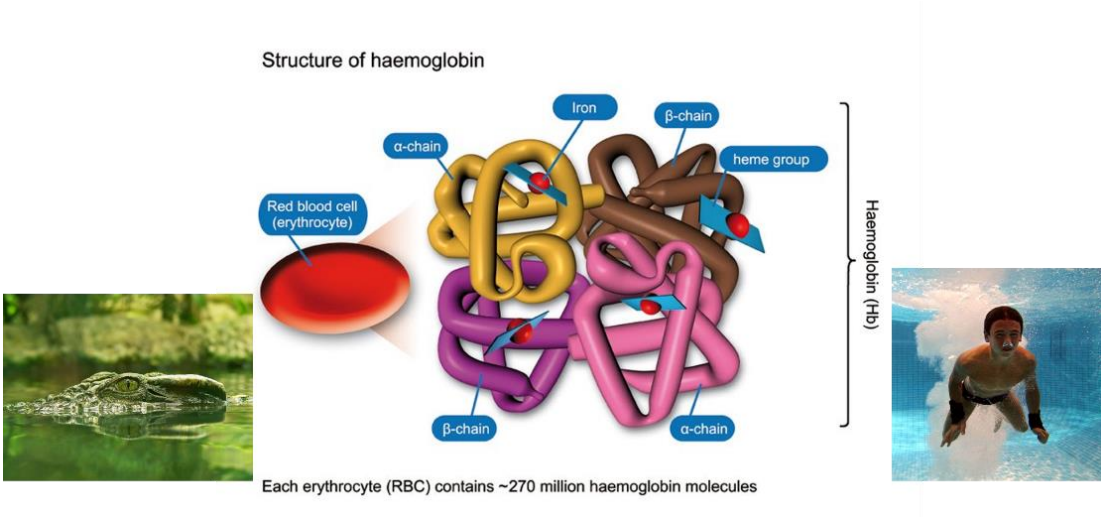

Fig.4.1: The crocodile haemoglobin differs from its human counterpart by just 14 amino acids & but has better oxygen delivery capacity.

As you might have learn previously, the DNA sequence in our genes ultimately determine the number and sequence of amino acids of all the proteins in our bodies. As such, different genes lead to differences in the proteins found in organisms of different species. You will learn about gene expression in greater detail in subsequent chapters.

Notes to self

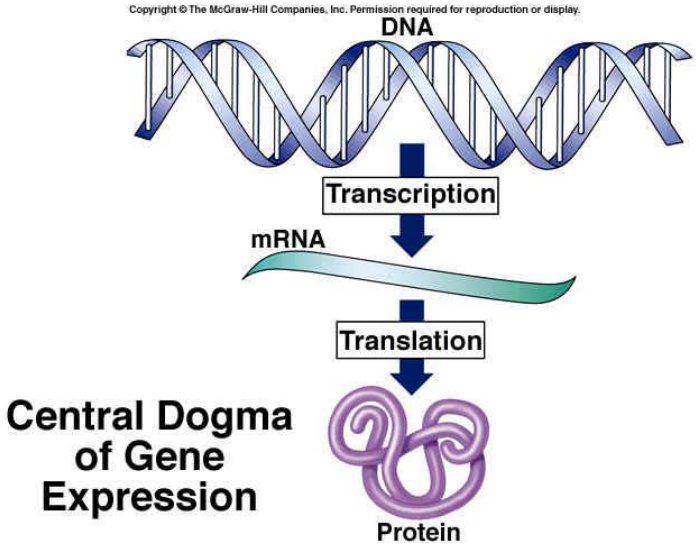

Fig.4.2: The Central Dogma of Gene Expression

5. Components of proteins

Notes to self

Proteins consist of the following elements: Carbon, Hydrogen, Oxygen, Nitrogen & Sulphur (in some proteins).

The basic structural units or monomers of proteins are called **amino acids**.

6. Structure of amino acids

There are **20 amino acids** that are used in the biosynthesis of proteins in cells.

An amino acid consists of an **α-carbon atom** that is covalently bonded to 4 groups (Fig. 6.1):

(i) a **hydrogen atom**
(ii) an **amino group** ($-NH_2$)
(iii) a **carboxyl group** (-COOH) and
(iv) a **variable R group**, also called a side chain.

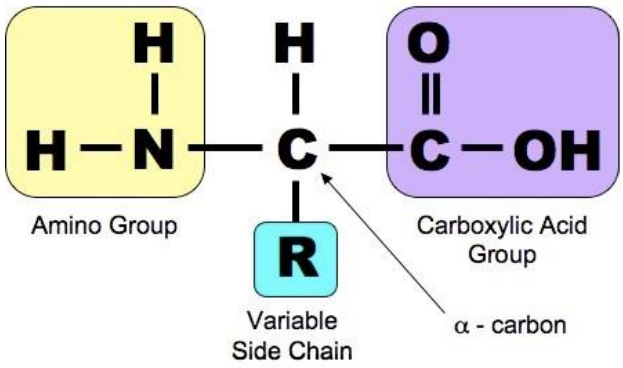

Fig.6.1: General structural formula of an amino acid

Each amino acid has at **least one amino group ($-NH_2$)** and **one carboxyl group (-COOH)**, with the exception of proline, which results in it having a cyclic conformation.

The 20 different amino acids, each has a different R group which leads to variations in charge, chemical reactivity, ability to form hydrogen bonds, size and shape between them.

Amino acids differ from each other only in the nature of their R groups. Therefore, the **physical and chemical properties** of the R groups determine the uniqueness of each amino acid and subsequently that of the polypeptide it makes.

7. The classification of amino acids

Notes to self

Classification according to human nutrition

Essential amino acids

These amino acids cannot be synthesised from simple substances by humans and must be obtained from their diet. Continuous deprivation of just 1 or 2 essential amino acids can eventually cause death.

Non-essential amino acids

These amino acids can be synthesised from simpler substances by humans.

Classification based on R group properties

Neutral amino acids

These amino acids have **non-polar R groups** are **hydrophobic** or **polar R groups** which are **hydrophilic**. They are electrically neutral as the sum of positive and negative charges are equal.

Electrically-charged amino acids

- **Acidic** amino acids have R groups that are negatively-charged due to the presence of a **carboxyl group**, which usually dissociates to form COO^- at cellular pH.
- **Basic** amino acids have R groups that are generally positively-charged due to the presence of an **amino group**, which accepts H^+ to form NH_3^+.
- *Do note that all amino acids have carboxyl and amino groups; the terms acidic and basic in this context refer only to the groups within the R groups/side chains.*
- As they are charged, acidic and basic amino acids are **hydrophilic**.

<table>
<tr><th colspan="2">Neutral amino acids</th><th colspan="2">Electrically-charged</th></tr>
<tr><td colspan="2" rowspan="2">Uncharged at physiological pH at pH 7.2 because they have 1 amino group and 1 carboxyl group</td><td>Acidic amino acids</td><td>Basic amino acids</td></tr>
<tr><td>Charged at physiological pH because they have more carboxyl than amino groups (R group contains –COOH)</td><td>Charged at physiological pH because they have more amino than carboxyl groups (R group contains –NH_2)</td></tr>
<tr><td>Non-polar, Hydrophobic R group</td><td>Polar, Hydrophilic R group</td><td>Negatively-charged, Hydrophilic R group</td><td>Positively-charged, Hydrophilic R group</td></tr>
<tr><td>R group does not form hydrogen bonds with water</td><td>R group forms hydrogen bonds with water</td><td>R group forms interactions with water</td><td>R group forms interactions with water</td></tr>
<tr><td>Alanine
Glycine
Isoleucine
Leucine
Methionine
Phenylalanine
Proline
Tryptophan
Valine</td><td>Asparagine
Cysteine
Glutamine
Serine
Threonine
Tyrosine</td><td>Aspartic acid
Glutamic acid</td><td>Arginine
Histidine
Lysine</td></tr>
</table>

Summary table of amino acids based on their R-group properties.

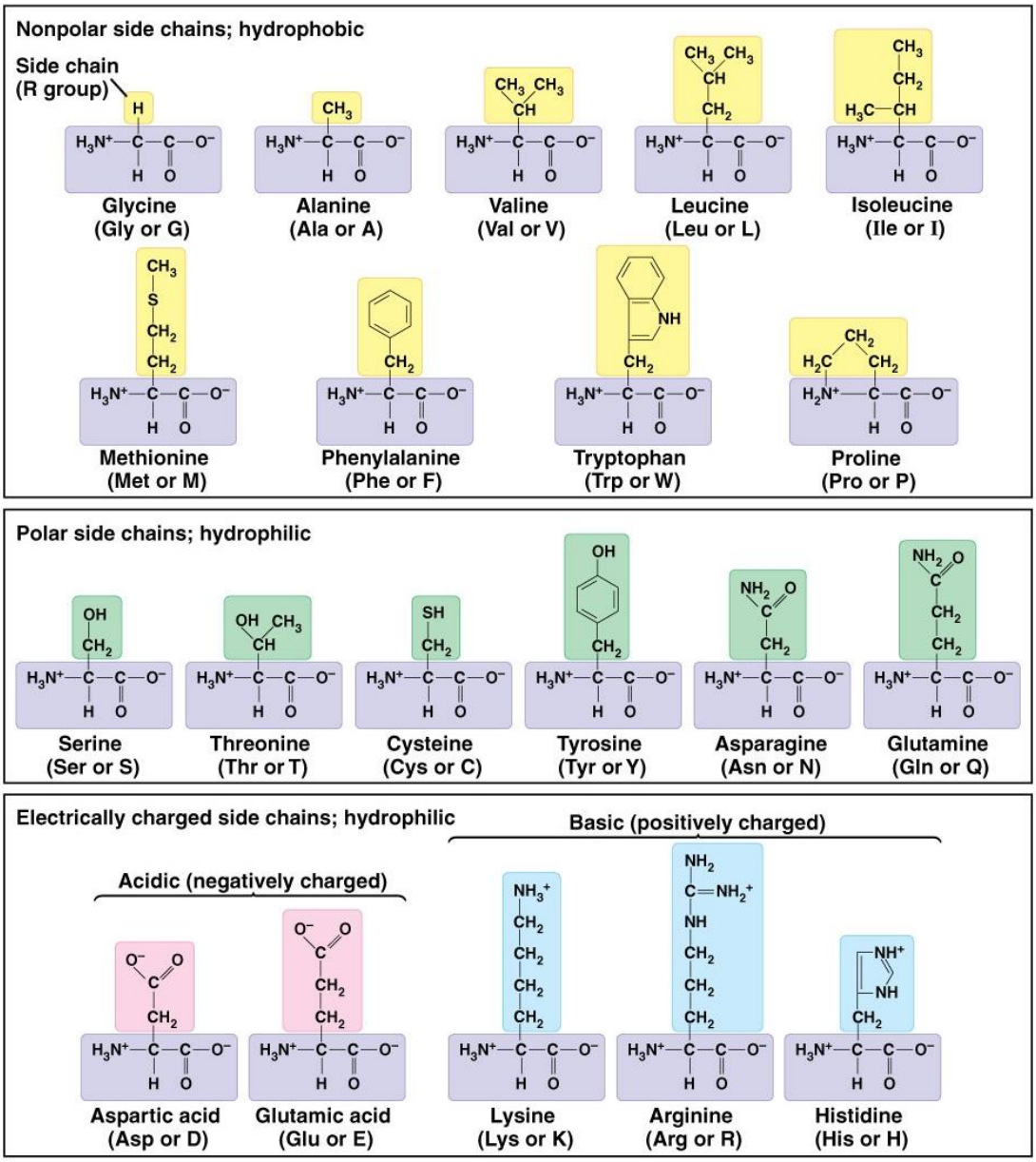

Fig. 7.1: The classification of the 20 common amino acids according to their R group (side chains) properties.

8. Properties of amino acids

Notes to self

Amino acids exist in the form of zwitterions

Amino acids are **generally soluble in water** and **become ionized** (Fig. 8.1).

In solution, the un-ionised amino group (-NH_2) receives an H+ and becomes positively-charged (-**NH_3^+**). The carboxyl group (-COOH) dissociates, releasing an H+ and becomes negatively-charged (-**COO^-**).

Zwitterions ($^+H_3NRCHCOO^-$) refer to ionised amino acids in solution which **carry both positive and negative charges**. They are also referred to dipolar ions. In this dipolar form, an amino group is protonated (-NH_3^+) and the carboxyl group is deprotonated (COO^-).

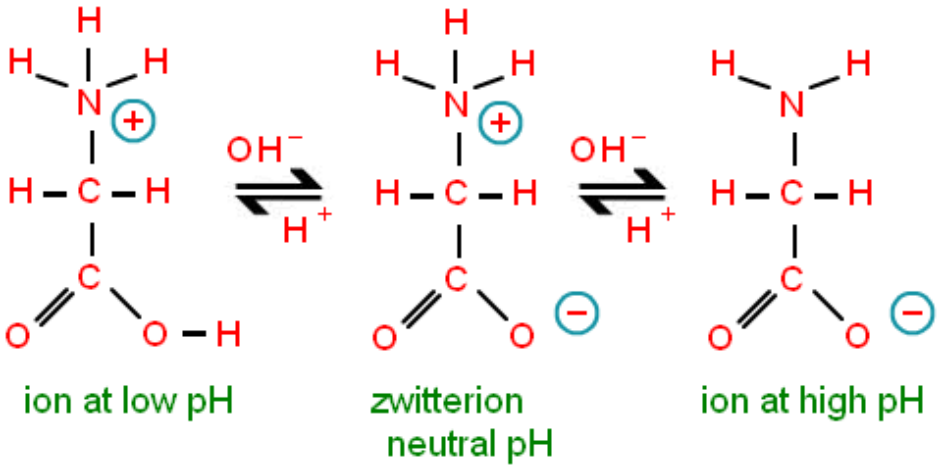

Fig. 8.1: In neutral solutions, amino acids often exist as zwitterions. This allows amino acids to act as buffers in biochemical reactions.

Amino acids act as buffers in biochemical reactions

When amino acids are dissolved in water, the amino and carboxyl groups act as bases and acids respectively. Therefore, amino acids are considered to be **amphoteric** i.e. able to act as an acid or as a base.

The amphoteric nature of amino acids allows them to act as buffers in biochemical reactions. Amino acids in a solution can accept or donate H^+ ions, thus allowing them to buffer any changes in the pH of their environment when a small amount of acid or alkali is added.

This property of amino acids is important in biological systems where a sudden change in pH can adversely affect the activity of proteins such as enzymes.

9. The formation of polypeptides

Notes to self

Amino acids are the **monomers** that join to form **polypeptides** during the process of translation in cells.

Polypeptides have different names depending on the number of amino acid residues which make them up. Dipeptide (2 amino acid residues), Tripeptide (3 amino acid residues), Oligopeptide (~3 to 10 amino acid residues) & Polypeptides (> 10 amino acids to a thousand or more).

Amino acids are joined via a **condensation reaction** that links the carboxyl group (-COOH) of one amino acid to the amino acid group ($-NH_2$) of another, with the **elimination of one water molecule (H_2O)** (Fig. 9.1)

This results in the formation of a **peptide bond** which joins the 2 amino acids and each amino acid monomer is then known as a residue.

The reverse reaction which results in the breaking of the peptide bond is known as a hydrolysis reaction and it requires a water molecule.

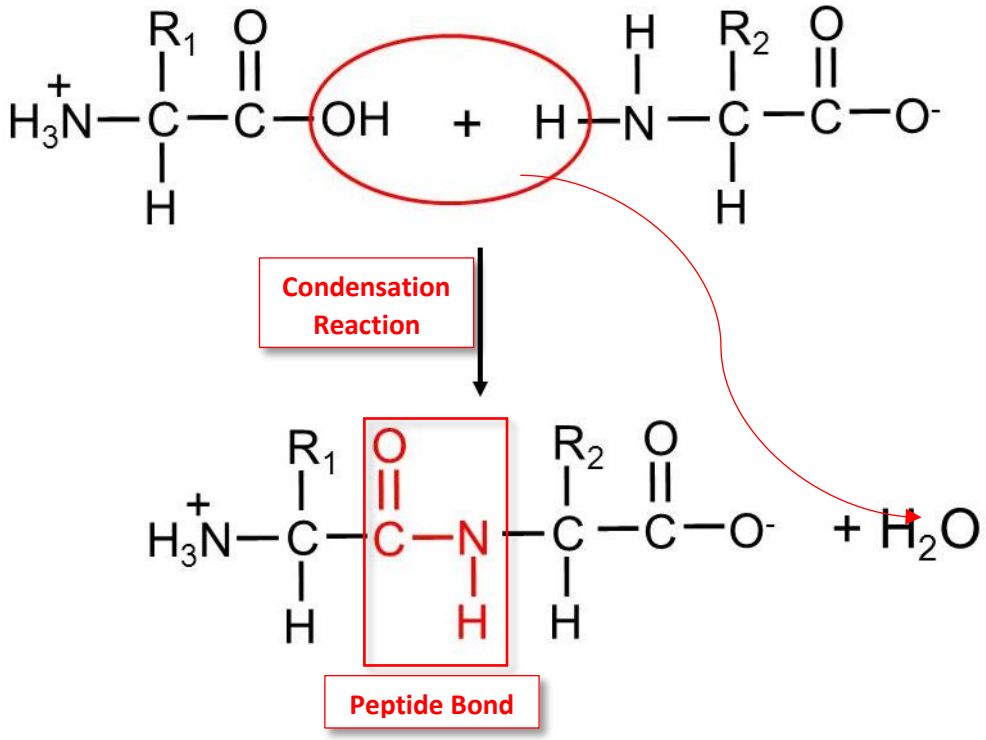

Fig.9.1: The formation of a peptide bond between 2 amino acids via a condensation reaction, which results in the removal of 1 water molecule.

Further additions of amino acids result in the formation of a linear polymer molecule called a polypeptide.

Notes to self

The regular repeating part, the main chain, is referred to as the **polypeptide backbone**. The variable regions comprise of the **distinct, variable R groups** of the amino acid residues.

The polypeptide chain has **directionality** i.e. 2 different ends.

- *Amino-terminus* (N-terminus) has a free amino group at the start of polypeptide chain.
- *Carboxyl-terminus* (C-terminus) with a free carboxyl group at the **end** of the polypeptide chain.

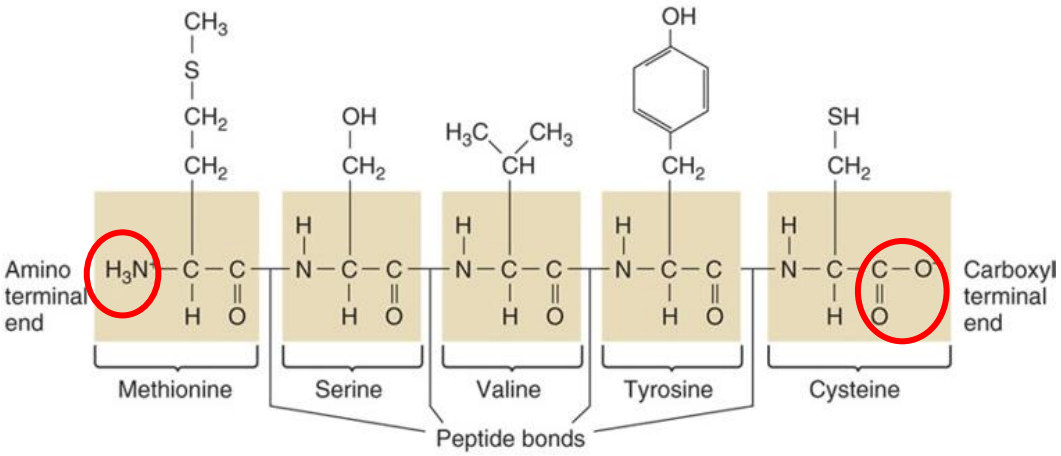

Fig. 9.2: The terminal ends of a polypeptide chain

A polypeptide folds into a **specific three-dimensional shape/ conformation.** ('Conformation' refers to the three-dimensional arrangement of atoms of a protein molecule.)

When proteins fold into specific 3D conformation, there are complementary surfaces and clefts that can fit only with specific molecules. On these surfaces and clefts, different R groups enable proteins to form bonds with other molecules – controlling precisely the orientation, strength and duration of these interactions. e.g. enzyme-substrate interaction, ligand-receptor interaction. Thus, a protein interacts only with specific molecules.

Hence, a protein's function is determined by its conformation, which is dictated by its amino acid sequence.

Strengthen your Synapses!

Can you recall the other two types of condensation reactions involving biomolecules? Can you draw annotated diagrams to show the formation of the products involved?

Notes to self

10. Levels of Organisation of Proteins

Notes to self

There are 4 levels of organisation in the structure of proteins –

Primary, **Secondary**, **Tertiary**, and **Quaternary**.

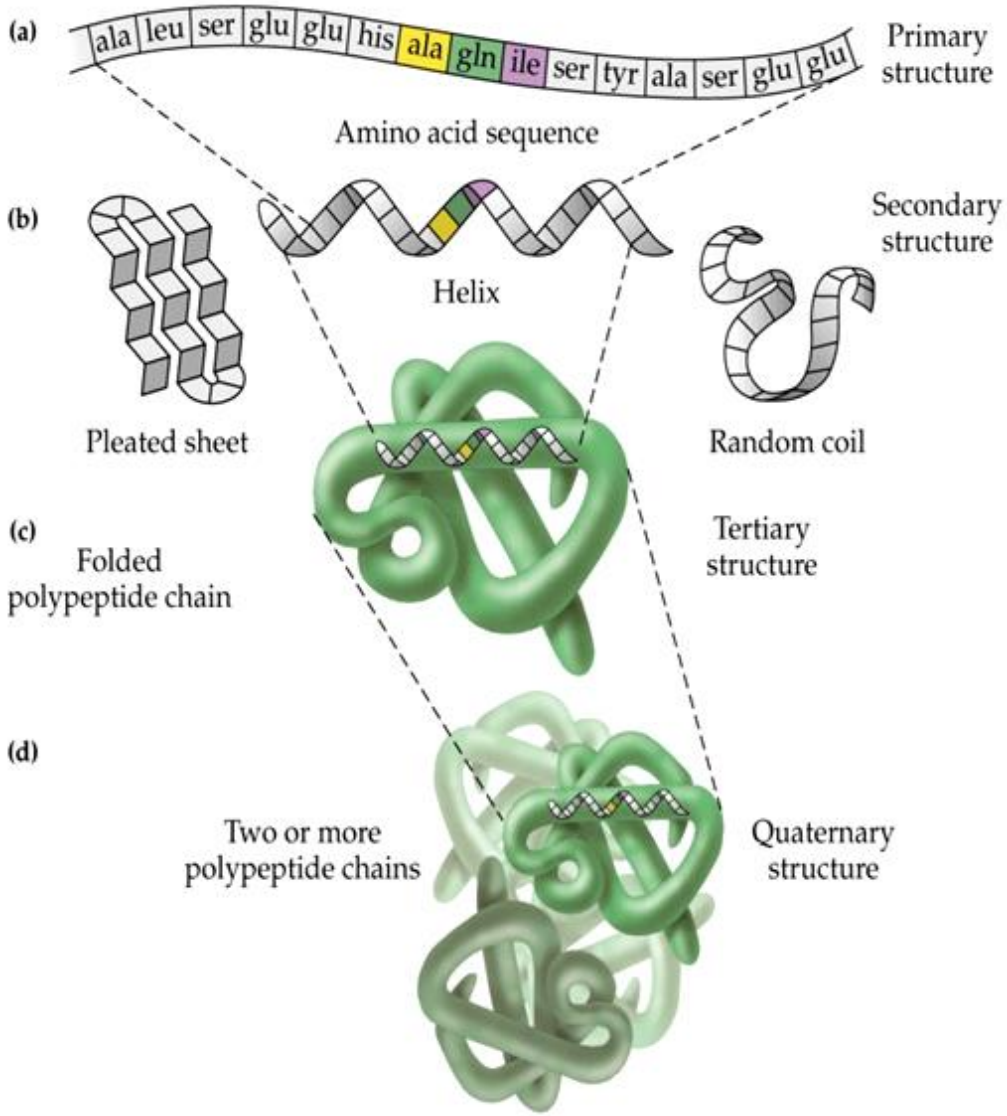

Fig. 10.1: Structural organisation of a polypeptide

A. Primary Structure

Primary structure refers to the **number, sequence and type of amino acids** in a **single polypeptide chain**.

The primary structure is maintained by **peptide bonds** between adjacent amino acid residues. The peptide bonds are the only bonds found in the primary structure of polypeptides.

It is this sequence of amino acids (and their distinct R groups) of the polypeptide chain which determine the type and location of the chemical interactions, and hence the **pattern of folding** of the polypeptide to achieve more complex levels of organisations.

The primary structure of a protein is specified by nucleotide sequences in **genes**.

Assume a polypeptide has a length of *n* residues. Each of the n positions can be occupied by one of the *20* amino acids. Thus, the number of different combinations of synthesising the polypeptide chain is 20^n.

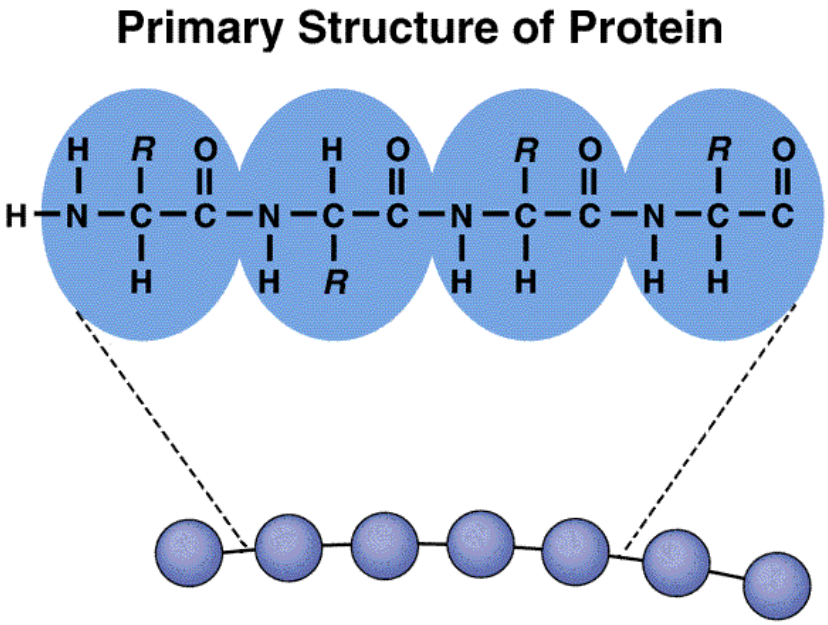

Fig. 10.2: Primary structure of a protein

B. Secondary Structure

Notes to self

The secondary structure refers to the spatial arrangement formed by regular coiling or pleating of a single polypeptide chain.

The secondary structure of proteins is maintained by **hydrogen bonds** at regular intervals. These hydrogen bonds are **formed between the CO and NH groups of the polypeptide backbone**.

The R groups are NOT involved in the formation of hydrogen bonds in the secondary structure of polypeptides.

Example: α-helix

Made of a single polypeptide chain which is wound into a regularly coiled helical structure.

Turns of the helix are linked together by **hydrogen bonds between** the **CO groups** of one turn and the **NH groups** of the next turn.

These hydrogen bonds are formed between groups **at every 4th peptide bond** (i.e. amino acid 1 would be bonded to amino acid 5, amino acid 2 to amino acid 6 and so on).

In other words, the lone pair of electrons on the oxygen atom of a C=O group forms a hydrogen bond with the hydrogen atom of the N-H group, **four amino acids away** in a single polypeptide chain.

In the α-helix, all main-chain CO and NH groups are involved in hydrogen bond formation. This results in considerable stability in the secondary structure. In the α-helix, there are **3.6 amino acid residues in every turn** of the helix.

An example of a protein which consists of α-helices is **keratin**, a structural protein which is found in hairs, wool and nails.

Notes to self

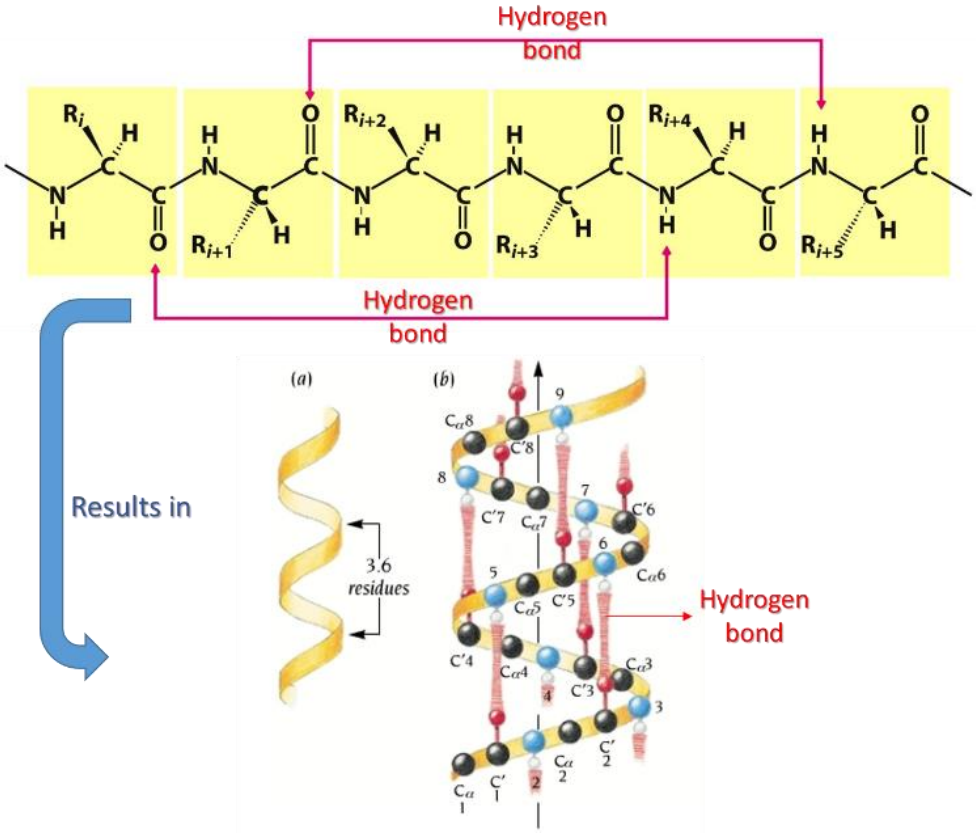

Fig. 10.3: Formation of a regularly coiled alpha helix

Example: β-pleated sheet

Notes to self

The β-pleated structure is formed when **two or more regions/segments** of a single polypeptide chain lying **side by side** are linked by **hydrogen bonds**.

The hydrogen bond is formed between the CO (or NH) group of one region/segment and the NH (or CO) group of an adjacent region/segment of the polypeptide backbone of a single polypeptide chain.

The segments of the chain may run parallel (same direction) or anti-parallel (opposite directions), which result in the formation of a flat sheet, which becomes folded.

An example of a protein which has β-pleated sheet structures is **fibroin**, which is found in the silk produced by silkworms and spiders.

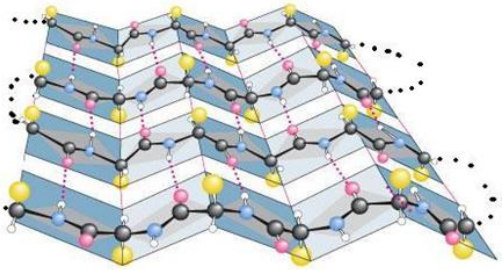

Fig. 10.4a. β-pleated sheet – 4 regions of a single polypeptide chain are linked by hydrogen bonds.

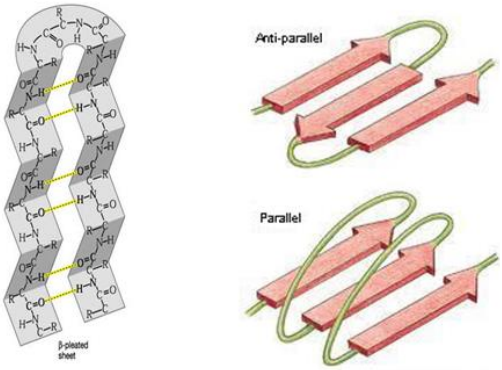

Fig. 10.4b. Hydrogen bonds between CO & NH groups of adjacent regions of polypeptide backbone. Anti-parallel & parallel segments in a polypeptide, forming a β-pleated sheet

C. Tertiary structure

Notes to self

Tertiary structure refers to the structure formed by further extensive folding and bending of a single polypeptide chain, usually forming a compact, **globular/spherical molecule**, giving rise to the **specific 3D conformation** of a protein.

As a result of the folding and bending, residues that are far apart on the polypeptide chains as well as those that are adjacent can be brought closer together.

Structure is maintained by 4 types of intramolecular interactions (hydrogen bonds, ionic bonds, hydrophobic interactions and disulfide bonds) formed between R groups of amino acid residues.

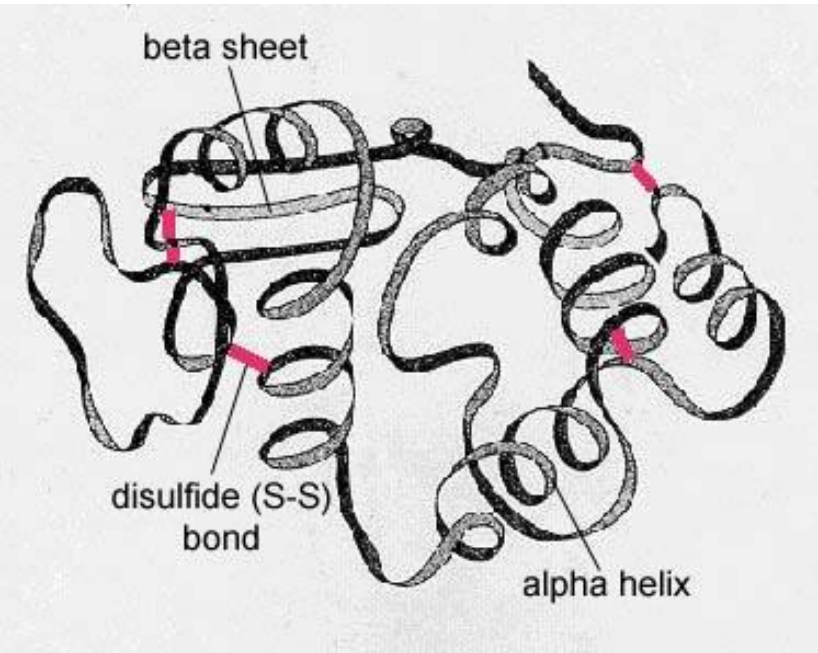

Fig. 10.5: The tertiary structure of a protein may also consist of regions which are made of secondary structures e.g. alpha helices & beta-pleated sheets.

The 4 types of interactions which help stabilise the 3D conformation of a protein, at a tertiary level, are (in order of strength of association):

Notes to self

a. Disulphide bond/bridge:

- Formed **between two cysteine amino acid residues** by oxidation of sulfydryl (-SH) groups.
- Disulfide bonds are **strong covalent bonds**. Strongest of these 4 interactions, they **contribute to the stability of many proteins**.
- Increase in number of disulfide bonds increases stability of a protein to heat denaturation.

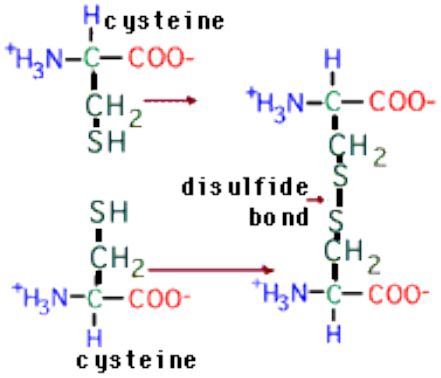

Fig.10.6: A disulphide bond between R-groups of 2 cysteine amino acid residues.

b. Ionic bond:

- Formed **between oppositely-charged R groups** of amino acids.
- **COO^-** and **NH_3^+** are found on **R groups** of **acidic and basic amino acids** respectively.
- They are also found at the ends of a polypeptide chain.
- A change in pH of surrounding medium can alter these charges and hence affect the stability of ionic bonds with a protein.

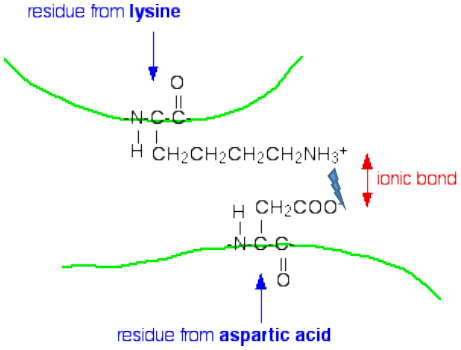

Fig. 10.7: An ionic bond between opp. charged R groups of two amino acid residues

Notes to self

c. Hydrogen bond:

- Oxygen (e.g. O of C=O group) and nitrogen (e.g. N of -NH group) are electronegative (δ-). Hydrogen of -NH or -OH group is electropositive (δ+). The **electropositive and electronegative atoms** form hydrogen bonds.
- Formed between **R groups of polar amino acids** at the tertiary structure or between -CO and -NH groups of the peptide bonds at the secondary structure.
- Individually the hydrogen bond is weak, but collectively strong and is able to support the conformation of a polypeptide chain.

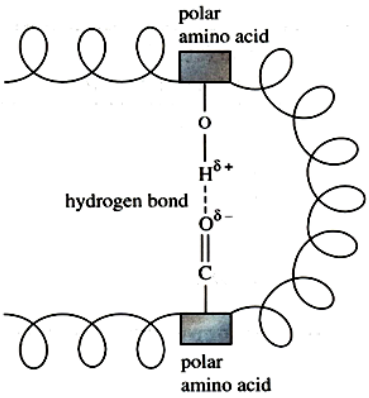

Fig.10.8: Formation of a hydrogen bond

d. Hydrophobic interactions:

- Formed between **non-polar R groups** which are **hydrophobic**. They interact and cluster at core of the protein to avoid water.
- This causes the polypeptide to fold such that as many of the hydrophobic R groups are shielded from the aqueous environment as possible:
- Most hydrophobic R groups tend to point inwards towards the centre of the roughly spherical molecule. Most hydrophilic R groups face outwards into the aqueous environment, making the protein soluble.

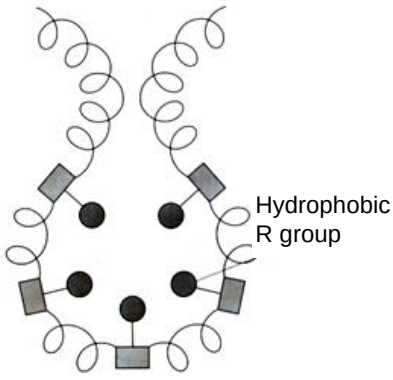

Fig.10.9: Hydrophobic interactions

Fig. 10.10 shows a summary of the 4 different types of intramolecular interactions which aid in the folding of a protein to achieve its tertiary conformation.

Notes to self

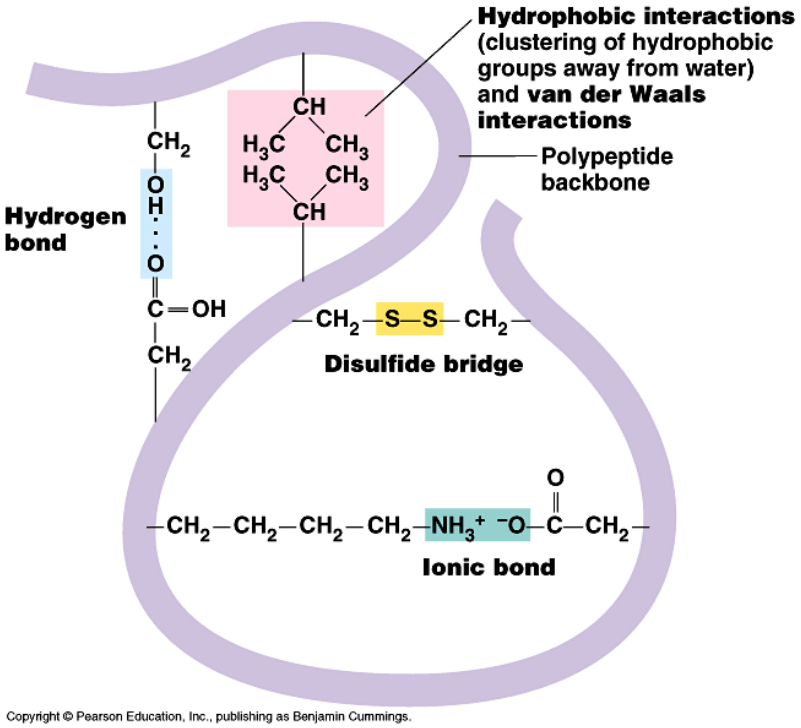

Fig. 10.10: The intramolecular interactions/bonds in a tertiary level protein

D. Quaternary structure

Notes to self

Quaternary structure refers to the association of **two or more polypeptide chains** into one functional protein molecule.

Each polypeptide is referred to as a subunit and the subunits are held together by hydrogen bonds, ionic bonds, hydrophobic interactions and disulfide bonds.

Proteins with 2 subunits are dimers, others with more than two are oligomers. Constituent chains of a multimeric protein (has more than 2 or more subunits) can be identical or different.

Example of a protein that has a quaternary structure is **haemoglobin**.

Not all proteins have a quaternary structure e.g. lysozymes & myoglobin are functional proteins which only have tertiary level of organisation i.e. they consist of a single polypeptide chain which is extensively folded.

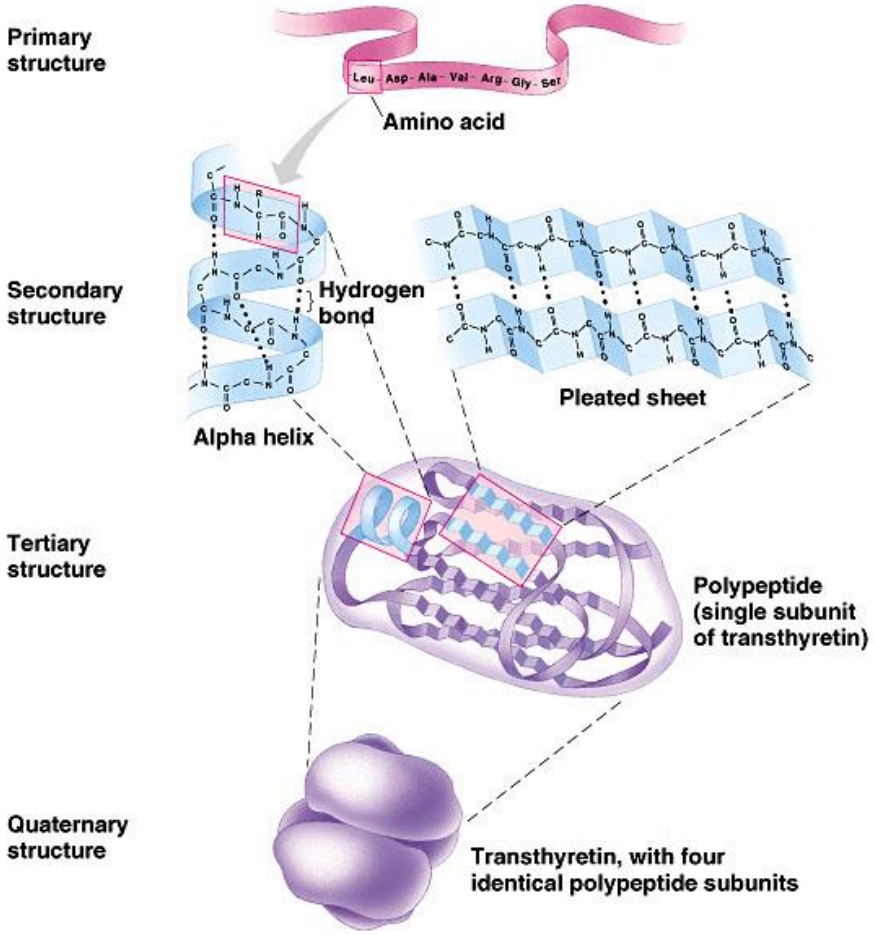

Fig.10.11: Levels of structural organisation in transthyretin protein

11. Classification & Example of Proteins

Notes to self

Proteins can be classified into fibrous or globular proteins. In general, **fibrous proteins** have **structural roles** while **globular proteins** have **metabolic roles**. The structural make-up of these proteins often relate to the functions they play in cells.

A. Haemoglobin – A Globular Protein

Haemoglobin is a transport protein which is involved in the **transport of oxygen** in blood. It is found in the **red blood cells of vertebrates**.

Each typical human red blood cell contains about 270 million haemoglobin proteins within it!

In an adult, a haemoglobin molecule has a **quaternary structure** as it is made up of 4 polypeptides, namely **2 α-globin subunits** and **2 β-globin subunits**.

As with proteins with a quaternary structure, each subunit is arranged so that most of its **polar/charged, hydrophilic amino acid R-groups** are on the **external surface** while most of the **non-polar, hydrophobic** R-groups of amino acids are pointed towards the interior, shielded away from the aqueous environment.

Each subunit is made up of two components:

- A polypeptide chain called **globin** &
- A prosthetic (non-protein) component called **haem group.** Each haem group consists of a porphyrin ring and an iron ion (Fe^{2+}).

The Fe^{2+} ion of the haem group binds reversibly to oxygen, so 1 haemoglobin molecule can carry up to 4 oxygen molecules, at the same time, forming oxyhaemoglobin.

Notes to self

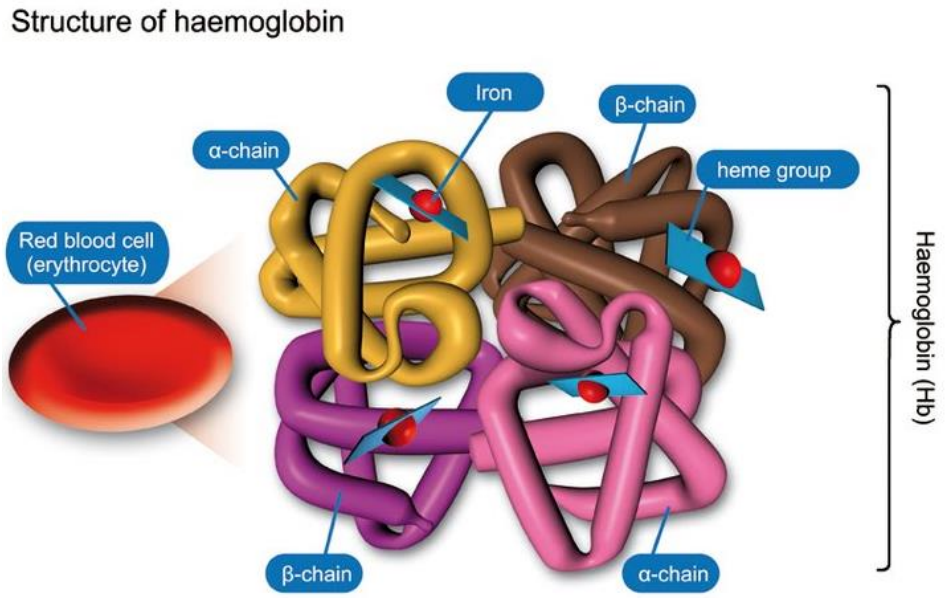

Fig.11.1: Structure of a haemoglobin protein

In the case of haemoglobin, the **4 polypeptide subunits** are held together by **ionic bonds**, **hydrophobic interactions** and **hydrogen bonds**. There are no disulphide linkages in haemoglobin.

This allows for the **subunits to move relative to each other**, allowing for a change in structure that **influences its affinity for oxygen**.

Binding of one oxygen molecule to 1 haemoglobin subunit induces a structural change in the other 3 subunits. This leads to an increase in their affinity for oxygen.

Thus, the initial 'hesitant' loading of the 1st oxygen molecule results in the rapid loading of the other 3 oxygen molecules. This is known as the **cooperative binding of oxygen**.

Conversely, when one subunit unloads its O_2, the other 3 quickly follow suit, as conformational changes reduce their affinity for oxygen.

Notes to self

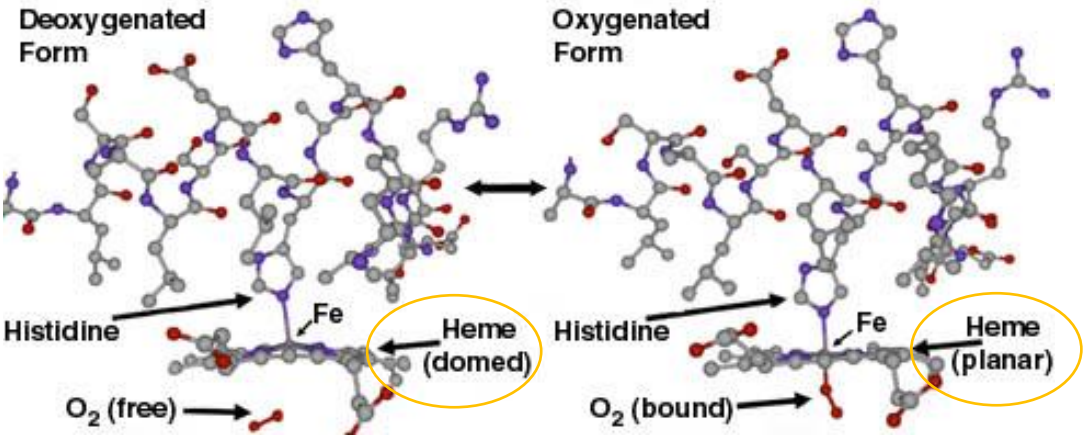

Fig.11.2: The binding of oxygen to the haem group causes a change in the conformation of the subunit

A genetic disease which involves a mutation in the β-globin gene is sickle cell anaemia. This disease will be covered in detail in subsequent lectures.

B. Collagen – A Fibrous protein

Notes to self

Collage is a structural protein. It is the most abundant fibrous protein in the human body and is an essential component of connective tissue in tendons, bones, skin and teeth.

A collagen molecule (referred to as **tropocollagen**) consists of **three helical polypeptide chains** (called loose helices, not α-helices!) wound around each other like a rope.

Hence, collagen is said to have a **quaternary** structure.

- **Each individual loose helix:**
  - Each of the three helical polypeptide chains contains about 1000 amino acids and forms a **loose helix**.
  - Intramolecular **hydrogen bonds** are formed within each helical polypeptide chain. This stabilises each polypeptide chain.
  - The amino acid sequence is usually a repeating tripeptide unit: **glycine-X–Y,** where X is usually **proline** and Y is usually **hydroxyproline**.

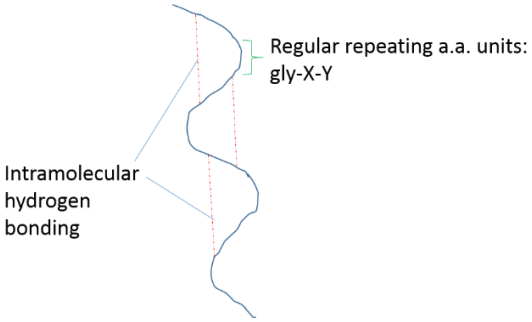

Fig.11.3: Loose helix – Primary structure

- **Tropocollagen (triple helix):**
  - The tropocollagen molecule can form a **compact coil** as almost every third amino acid in each polypeptide chain is a **glycine**, the **smallest amino acid** → this allows it to fit into the tight spaces in the centre of the triple helix.
  - **Hydrogen bonds** are also formed **between adjacent polypeptide chains**: This increases **tensile strength** and also makes the molecule **insoluble in water** as the amino acid residues in the different helices are already **extensively involved in intermolecular hydrogen bonding**. Hence, interaction with water are limited.
  - The **bulky** and **relatively inflexible** proline and hydroxyproline residues confer **rigidity** to the molecule.

Notes to self

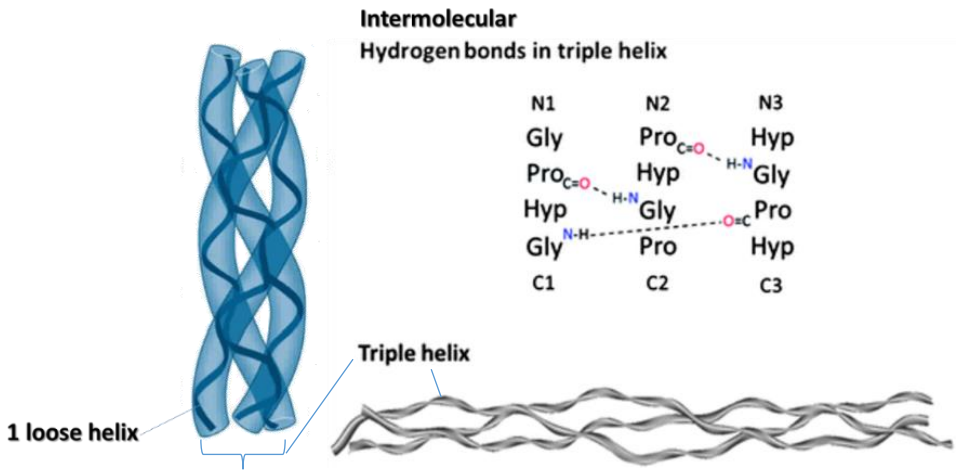

Fig.11.4: Three helical polypeptides coil to form tropocollagen due to intermolecular hydrogen bonding.

- **Assembly to form collagen fibrils:**
  - Each tropocollagen molecule **cross-links with neighbouring tropocollagen molecules** running parallel to it. **Cross-linking** (i.e. covalent bonds between **lysine residues**) of adjacent tropocollagen molecules results in the formation of a collagen fibril.
  - → This arrangement greatly **increases tensile strength**.
  - → Furthermore, the staggered/overlapping arrangement of tropocollagen in the fibrils **minimises the points of weakness** along the length of fibrils and contributes to the **tensile strength** as well.

- **Assembly to form collagen fibres:**
  - Collagen fibrils then come together to form bundles of **collagen fibres**. This increases tensile strength of collagen.
  - Collagen fibres have a **banded appearance** due to the offset/staggered arrangement of the tropocollagen.

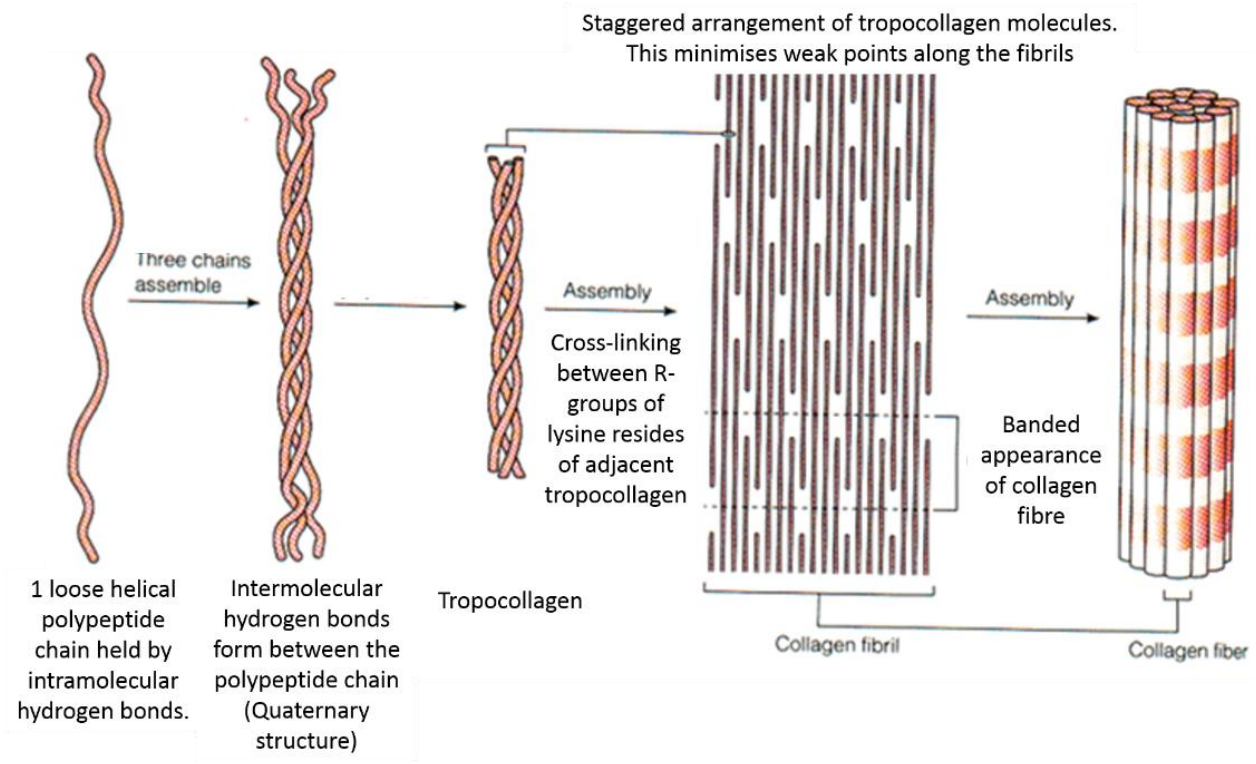

Fig.11.5: Organisation of collagen

Did you know?

Proteins can have bizarre names. For example, the protein Pikachurin is a retinal protein that was named after a Pokémon character Pikachu. The protein Sonic Hedgehog was named after Sonic the Hedgehog. A blue protein is named Ranasmurfin, after the Smurfs!

Now Try This!

Question: Compare the differences in the features between a fibrous protein and a globular protein

Point of comparison	Fibrous protein e.g. collagen	Globular protein e.g. haemoglobin
Shape of protein	They are usually made up of long polypeptides forming long **straight** strands/fibres.	They are usually made up of polypeptide chains folded into a roughly **spherical** shape.
Solubility in water	Proteins are **insoluble** in water as they are **large** and are **limited in their ability to form hydrogen bonds** with water molecules. There are extensive hydrogen bonds already formed between residues in different polypeptides.	Proteins are **soluble** in water as the **polar/charged R groups** are exposed to water molecules in the aqueous environment. These are soluble as the polar R groups can **form hydrogen bonds** with the water molecules and the charged R groups can **associate with the water molecules**.
Variety of amino acids	There is **less variety of amino acids** are used to construct the proteins. (e.g. repetitive regular sequences of amino acids e.g. gly-X-Y repeats in collagen	There is **a greater variety of amino acids** are used to construct the proteins.
Length of polypeptide	The lengths of polypeptides and sequences of amino acids **may vary slightly** between two samples of the same protein, yet the protein is still functional.	The lengths of polypeptide and sequence of amino acids are **always identical** between the two samples of the same protein, or else protein may not be functional.
Functions	Proteins such as collagen & keratin have **structural roles**.	Proteins such as haemoglobin and enzymes are functional in a variety of **metabolic roles**.

Tease Your Brain!

Explain how the structures of the following proteins are related to their functions.

(i) Haemoglobin

Structure	Function

(ii) Collagen

Structure	Function

12. Properties of Proteins

Notes to self

a) Solubility of proteins

Solubility of protein is dependent on both its **size** and its **ability to interact with water molecules.**

Globular proteins are **soluble in water** but **fibrous proteins are not**. This is because globular proteins have mostly polar/charged, hydrophilic R groups on the exterior of the molecules, which form hydrogen bonds/interact with water but fibrous proteins have mainly non-polar, hydrophobic R groups on their exterior. Fibrous proteins also tend to be large and are cross-linked with each other, thus reducing their capacity to form hydrogen bonds/interactions with water molecules.

b) Denaturation

Denaturation is the **loss of conformation** of a protein molecule which causes the protein to **lose its function**.

Occurs as a result of **disruptions of interactions** (hydrogen bonds, ionic bonds, hydrophobic interactions and disulphide bonds) that maintain secondary or higher level structure of proteins. **Primary structure remains unaffected**. Some factors which can lead to denaturation include heat and changes in pH (these will be covered in more detail in the enzymes lecture)

c) Identification of proteins

Food Test: Biuret Test	Observation	Basis of test
$2cm^3$ protein solution + equal volume of 5% KOH. Mix the solutions. Then, add 2 drops of $CuSO_4$ & mix.	A purple colour develops slowly.  negative biuret test results positive biuret test results	This is a test for the **presence of peptide bonds**. In the presence of peptide bonds, nitrogen atoms in the peptide chain form a purple complex with copper (II) ions. Biuret is a compound derived from urea, which also contains the –CONH- group and gives a positive result.

Practices of Science

If a polypeptide chain has many amino acids, how can scientists figure out its folding which gives rise to its 3D conformation?

One way, beyond the conventional use of computational power, is to utilise the idea of 'Citizen Science'.

Created by various departments and labs from the University of Washington, 'Foldit' explores the process by which living beings create the primary structure of proteins. The protein biosynthesis is reasonably well understood, as is the means by which proteins are encoded as DNA. Determining how the primary structure of a protein turns into a functioning three-dimensional structure – how the molecule "folds" – is more difficult; the general process is known, but predicting protein structures is computationally demanding.

Foldit is an attempt to apply the human brain's natural three-dimensional pattern matching abilities to this problem. Current puzzles are based on well-understood proteins; by analyzing the ways in which humans intuitively approach these puzzles in the game, researchers hope to improve the algorithms employed by existing protein-folding software. As more players complete more puzzles, the researchers can create a better understanding of these protein structures and craft new medicines to promote better health and cure disease. The success of Foldit comes from the constant feedback between developers and the community and the constant stream of new puzzles.

Interested in trying out 'Foldit'? Visit this website: https://fold.it/portal/