River Valley High School
2025 JC1 H2 Biology

Lecture Topic 5: Proteins – Structure and Function

Name: _____ ( ) Class: 25J__ Date: _____

References

Titles	Authors
Biology (9th edition)	Campbell and Reece
Biological Science 1. Organisms, Energy and Environment (3rd edition)	Taylor, Green, Stout and Soper
Longman A-Level Course in Biology: Core Syllabus Volume 1	Hoh
Understanding Biology for Advanced Level (4th edition)	Toole and Toole
Biochemistry (3rd edition)	Voet and Voet

H2 Biology Syllabus 9477 (2025)

Candidates should be able to use the knowledge gained in the following section(s) in new situations or to solve related problems.

Related Topics	Content
Biomolecules of Life & Cellular transport	The structure of carbohydrates, lipids and proteins and their roles in living organisms Mode of action of enzymes The fluid mosaic model of membrane structure
The Structure of Nucleic Acids & Gene Expression	Central Dogma – DNA to RNA, RNA to protein

Learning Outcomes

1B. Biomolecules of life and cellular transport

g. Describe the structure and properties of the following monomers:
   - i. α-glucose and β-glucose (in carbohydrates)
   - ii. glycerol and fatty acids (in lipids)
   - iii. amino acids (in proteins) (chemical formulae of specific R-groups of different amino acids are not required)

h. Describe the formation and breakage of the following bonds.
   - i. glycosidic bond
   - ii. ester bond
   - iii. peptide bond

1C. Proteins

m. 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, disulfide bonds and hydrophobic interactions).

n. Explain the effects of temperature and pH on protein structure. *(KIV: Enzyme)*

o. Describe the molecular structure of the following proteins and explain how the structure of each protein relates to the function it plays:

- haemoglobin (globular; transport)
- collagen (fibrous; structural)

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

For practical, candidates should be able to:

- carry out the Biuret test for protein.

Lecture Outline

I. Introduction

II. Nature of Proteins

III. Formation of Polypeptides

IV. Proteins: Higher Orders of Structure

A. Primary structure
B. Secondary structure
C. Tertiary structure
D. Quaternary Structure

V. Relating Structure to Function of Proteins

A. Haemoglobin
B. Collagen
C. GPCR

VI. Biuret Test for Protein

Websites

URL	Description
http://proteopedia.org	3D encyclopaedia of proteins and other molecules with a focus on structure/function.
https://www.youtube.com/watch?v=O5uqdxQyJj8	Animation on protein structure and protein denaturation

I. Introduction

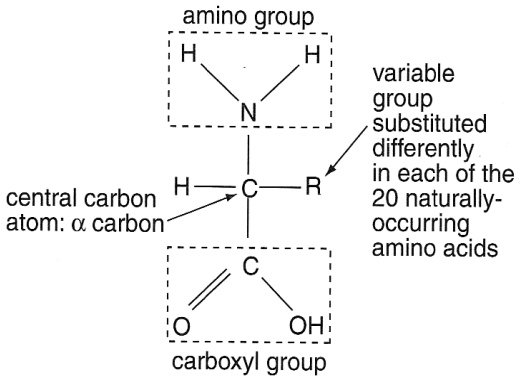
Proteins are physically and functionally complex macromolecules that perform diverse and critically important roles in living organisms:

Type	Function	Example
Structural	Maintains cellular shape and physical integrity	Collagen
Enzyme	Catalyse rate of metabolic reactions	Pepsin, DNA polymerase
Hormones	Carry information between cells to coordinate activities in an organism	Insulin
Transport	Facilitate transport of specific molecules across membranes or around the body	Haemoglobin
Receptor	Detect changes in environment to bring about changes in cell activities	Glucagon receptor
Defence	Recognise invading pathogens to combat infections	Antibodies
Source of energy	Oxidised after all carbohydrates and lipids are used up	-

II. Nature of Proteins

- Proteins are a group of organic compounds comprising the elements carbon, hydrogen, oxygen, nitrogen and sometimes sulfur.
- Despite their tremendous range of structures and functions, all proteins are made from the same type of monomer.
    - They are condensation polymers of **amino acids**.
    - Analysis of a vast number of proteins has shown that all proteins are composed of 20 'standard' amino acids. *(See Annex I)*

- Every amino acid comprises a central carbon atom **(α-carbon atom**) to which is bonded:
    i. an **amino group** ($-NH_2$)
    ii. a **carboxyl group** (-COOH)
    iii. a **hydrogen atom**
    iv. a variable **R-group** (or side chain)
    This can just be a hydrogen atom, a hydrocarbon chain or cyclic structure with functional groups like $–NH_2$, -COOH, -SH or -OH.
- The nature of the R-group determines the identity and properties of the amino acid.



- Amino acids can be categorised according to the polarities of their R groups:

  - **Neutral** amino acids are electrically neutral at physiological pH (overall sum of positive and negative charges is equal).

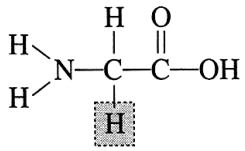
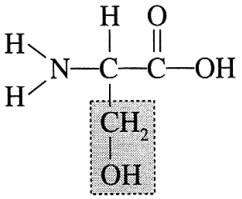
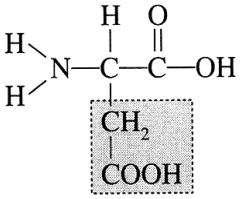
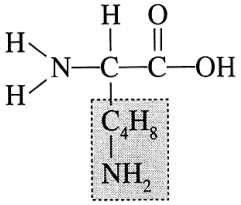
    They possess either

    - **Non-polar** R groups that are hydrophobic
    - **Polar** R groups that are hydrophilic

  - **Electrically charged** amino acids bear net positive or negative charges, and are thus hydrophilic.
    - **Acidic** amino acids have negatively charged R groups containing the **carboxyl group**, which usually dissociates to release H^+ at cellular pH.

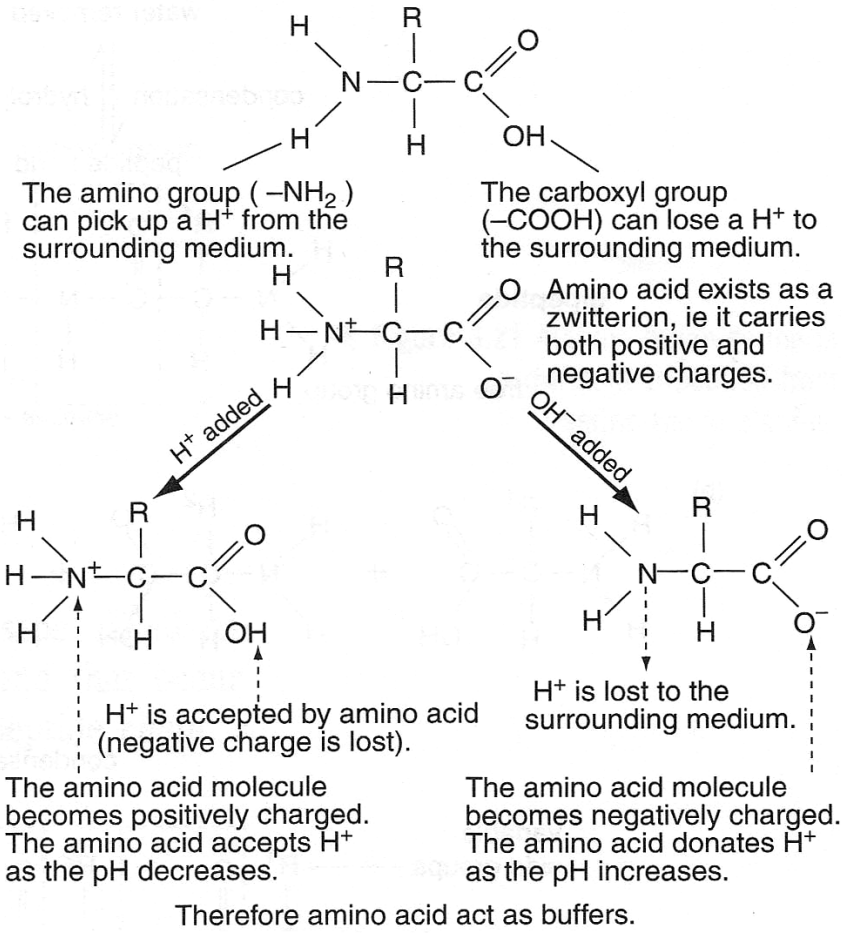
      Overall, the amino acid has more carboxyl than amino groups, thus giving rise to a net negative charge.
    - **Basic** amino acids have positively charged R groups containing the **amino group**, which usually accepts H^+ at cellular pH.

      Since the amino acid has overall more amino than carboxyl groups, it bears a net positive charge.

Amino acids with non-polar R group	*Amino acids with polar R group*	*Amino acids with acidic R group (negatively charged)*	*Amino acids with basic R group (positively charged)*
Example: glycine (Gly)	Example: serine (Ser)	Example: aspartic acid (Asp)	Example: lysine (Lys)
			
Other amino acids in this group are • alanine (Ala) • valine (Val) • leucine (Leu) • isoleucine (Ile) • tryptophan (Trp) • proline (Pro) • methionine (Met) • phenylalanine (Phe)	Other amino acids in this group are • asparagine (Asn) • glutamine (Gln) • tyrosine (Tyr) • cysteine (Cys) • threonine (Thr)	Other amino acids in this group are • glutamic acid (Glu)	Other amino acids in this group are • arginine (Arg) • histidine (His)

- Amino acids are soluble in water but insoluble in organic solvents.
  - Upon dissolving in water, they **ionise** to form ions.
  - In aqueous medium,
    - the basic amino group ($-NH_2$) picks up a H^+ and becomes NH_3^+.
    - the acidic carboxyl group (-COOH) dissociates, releasing a H^+ to the aqueous medium and becoming COO^-
    - the amino acid thus bears both positive and negative charges and is called a **zwitterion** *(German: zwitter, hybrid)*.
- In neutral aqueous solution, most amino acids exist as zwitterions and can act as either acids or bases, meaning they are **amphoteric**.
  - When an acid is added (i.e. as pH decreases), an amino acid takes up a H^+, thus has a net positive charge.
  - When an alkali is added (i.e. as pH increases), an amino acid donates a H^+, thus has a net negative charge.
- Being amphoteric allows amino acids to act as **pH buffers** in solution, which is useful in biological systems where sudden changes in pH could adversely affect enzyme performance.

  A buffer can resist changes in pH when an acid or alkali is added to it.



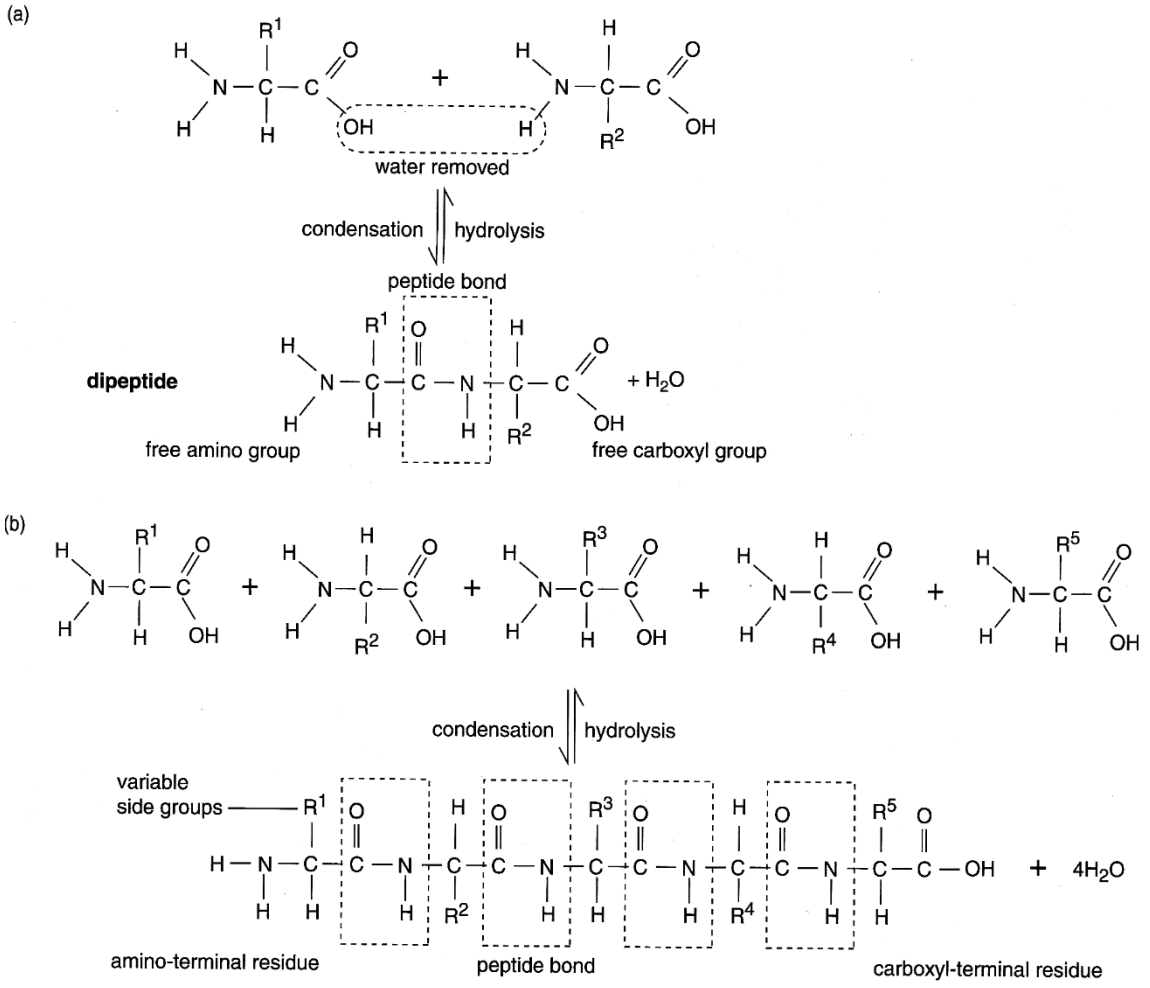
Therefore amino acid act as buffers.

III.Formation of Polypeptides

- Polypeptides are **condensation polymers** of amino acids.
  - A condensation reaction occurs between the **carboxyl group** of one amino acid and the **amino group** of another amino acid.
  - A <u>molecule of water is removed</u> in the condensation reaction.
  - The two amino acids are joined by a **peptide bond** to form a **dipeptide**.

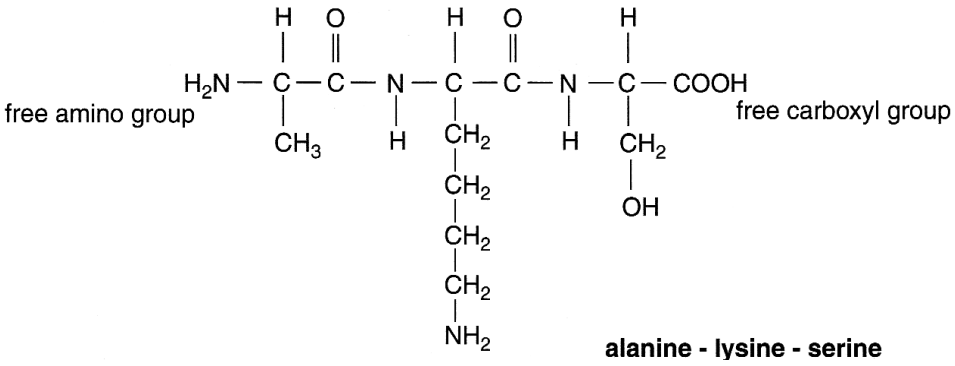
    This dipeptide has a <u>free amino group</u> at one end and a <u>free carboxyl group</u> at the other.
  - Amino acids present in peptides, having lost a hydroxyl group, are called **aminoacyl residues** and are named by replacing the *-ate* or *-ine* suffixes of free amino acids with *–yl*.

    E.g. alanine → alanyl, cysteine → cysteinyl



(a) Formation of a dipeptide. (b) Formation of a pentapeptide. R^1, R^2, R^3, R^4 and R^5 are the *R* groups of amino acid residues

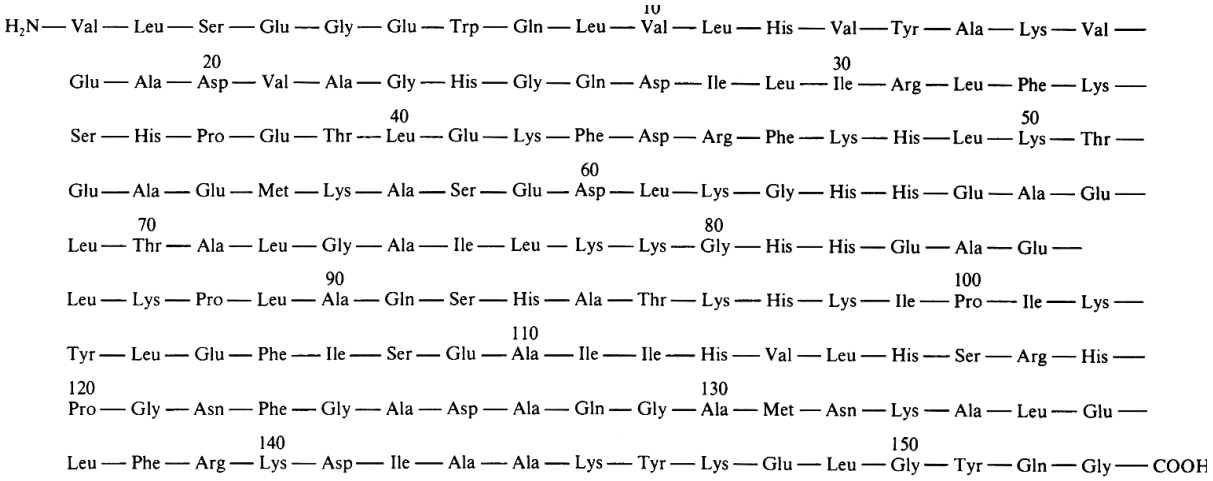
- Continued condensation leads to the addition of further amino acids and lengthening of the chain to form a **tripeptide** (3 residues), **oligopeptide** (3-10 residues) and eventually **polypeptide** (more than 10 residues).
- All polypeptide chains formed will have similar backbones, containing peptide bonds. The repeating order of atoms in this backbone is nitrogen, α-carbon and carbonyl carbon.
- A polypeptide chain has direction because its building blocks have different ends, namely the amino group and the carboxyl group.
    - By convention, the amino end (**N-terminus**) is taken to be the beginning of a polypeptide chain**,** while the carboxyl end (**C-terminus**) is the end of the chain. Therefore by convention, the sequence of amino acids in a polypeptide chain is written starting with the amino terminal residue at the left.
    - For example, in the tripeptide alanine-lysine-serine, _____ is the **N-terminal residue** and _____ is the **C-terminal residue**.



IV. Proteins: Higher Orders of Structure

- The term 'protein' is not quite synonymous with 'polypeptide'.
- A **functional protein** is not simply a polypeptide chain, it is one or more polypeptide chains precisely **twisted**, **folded** and **coiled** into a **unique molecular shape**. In proteins comprising multiple polypeptide chains, each polypeptide is referred to as a **subunit**.
- The specific three-dimensional shape of a protein molecule is called its **conformation**. This specific conformation in turn determines the specific function of the protein.
- There are four levels of organisation in the structure of proteins: primary, secondary, tertiary and quaternary.
    A. **Primary structure** refers to the amino acid sequence of the polypeptide chain.
    B. **Secondary structure** describes how segments of the peptide backbone orient into a regular pattern (without regard to the R groups)
    C. **Tertiary structure** describes how the entire polypeptide chain coils into an overall 3D conformation.
    D. **Quaternary structure** arises when a protein comprises two or more chains, loosely referred to as subunits. Quaternary structure describes the spatial arrangement of its subunits.

A. Primary Structure of Proteins



Myoglobin has a single polypeptide chain comprising 153 amino acid residues.

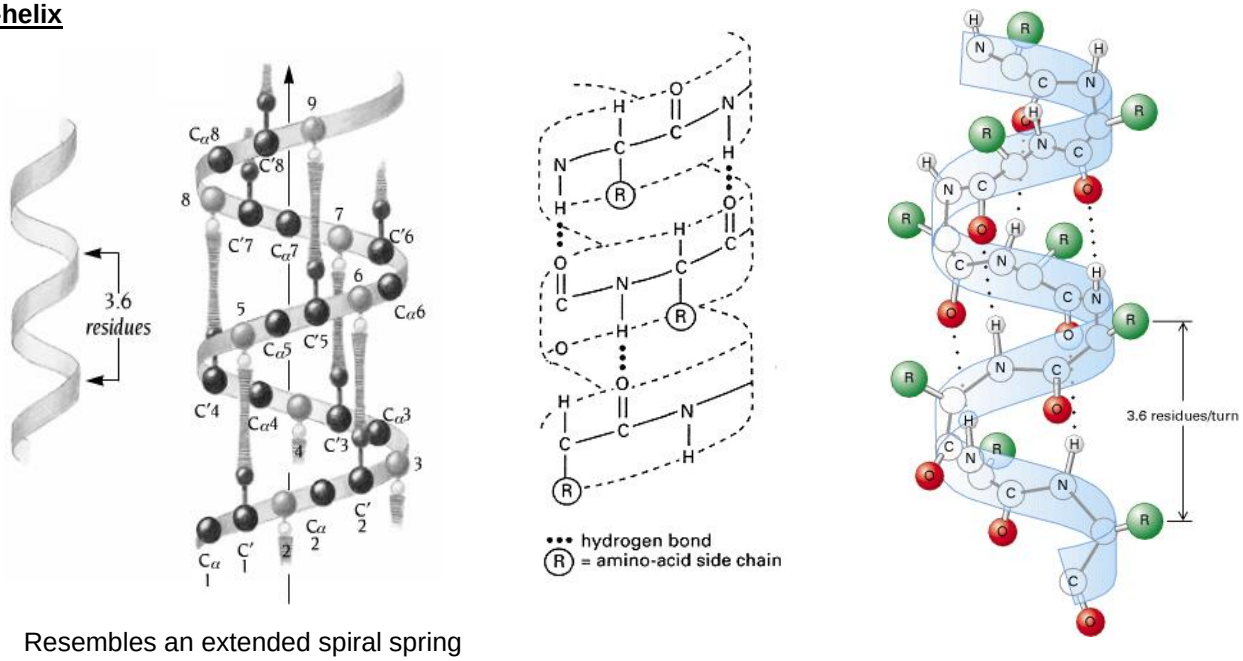
- The primary structure is the specific sequence of amino acids in a polypeptide.
- The only bonds responsible for maintaining the primary structure are the covalent **peptide bonds** between successive amino acid residues.
- The sequence of amino acids of a protein dictates its structure and hence, function(s). In turn, the amino acid sequence is strictly controlled by the DNA base sequence (gene).
    - Substitution of just one amino acid can cause a major alteration in a protein's function, as in the condition of sickle cell anaemia. *(KIV: Mutation)*

B. Secondary Structure of Proteins

- Most proteins have segments of their polypeptide chain(s) repeatedly coiled or folded in patterns that contribute to the proteins' overall conformation.
- These localised, repeated coils and folds collectively referred to as secondary structures[1], are the result of **hydrogen bonds** at regular intervals along the polypeptide backbone.
    - The hydrogen bond is formed between the electropositive hydrogen atom of NH group and the electronegative oxygen atom of CO group
    - Only the atoms of the backbone are involved in the formation of secondary structures (not the R-groups).
    - Each individual hydrogen bond is considered weak, but its frequent occurrence throughout each polypeptide chain results in extensive hydrogen bonding, thus is able to support a stable conformation.
- While several types of secondary structure have been elucidated, the most common examples are the **α-helix** and **β-pleated sheet**.

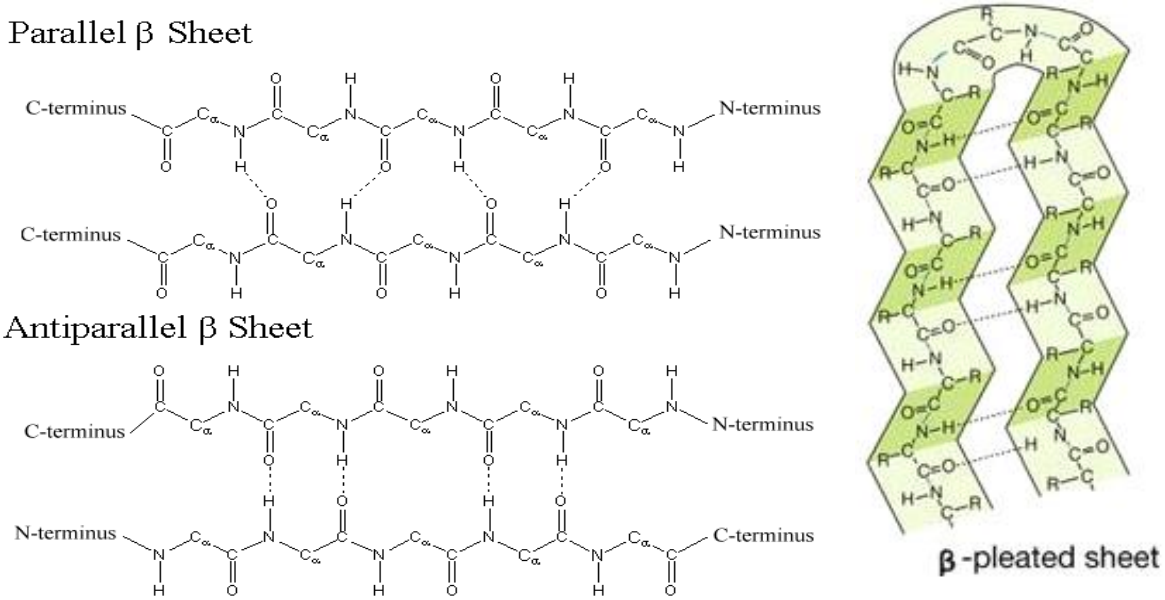
[1] Nucleic acids, especially single-stranded RNA molecules, also have secondary structures.

α-helix



- Resembles an extended spiral spring
- The **α-helix** structure is maintained by many **hydrogen bonds**, which are formed between nearby CO and NH groups of amino acid residues.
- The H atom of the NH group of one amino acid is bonded to the O atom of the CO group four amino acids away.
    - Hence, amino acid 1 would be bonded to amino acid 5; amino acid 2 would be bonded to amino acid 6; etc.
- Theoretically, all CO and NH groups can participate in hydrogen bonding as described, making α-helix a stable and rigid structure. However, hydrogen bonding could be disrupted by R-groups.
- X-ray diffraction data indicate that the α-helix makes one complete turn for every 3.6 amino acids.
- An example of a protein whose only structural motif is the α-helix is **keratin**. It is the structural protein of hair, wool and nails.

β-pleated sheet

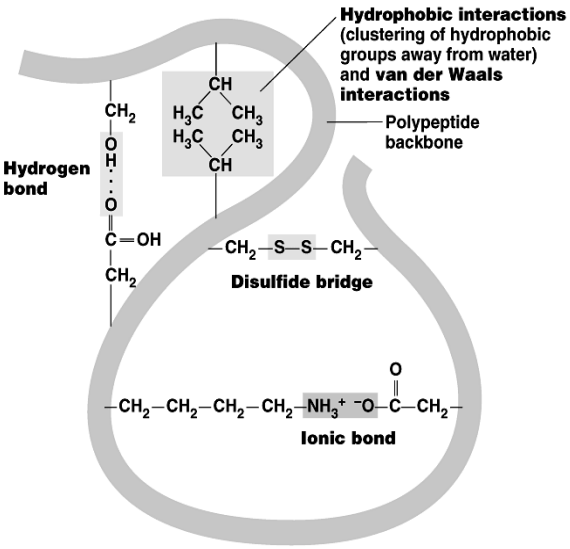


- Resembles a folded sheet with R groups projecting above and below the plane of the sheet.
- The **β-pleated sheet** structure is maintained by **hydrogen bonds**, which are formed between adjacent regions of a polypeptide chain that lie parallel to each other, either running the same or opposite direction.
- Hydrogen bonds are formed between the CO and NH groups of one region and the CO and NH groups of the adjacent region.
- Theoretically, all CO and NH groups are involved in hydrogen bonding as described, making β-pleated sheet a stable structure
- An example of a β-pleated sheet protein is **fibroin**, the protein used by silkworms when spinning their cocoon threads, and by spiders when spinning their webs.

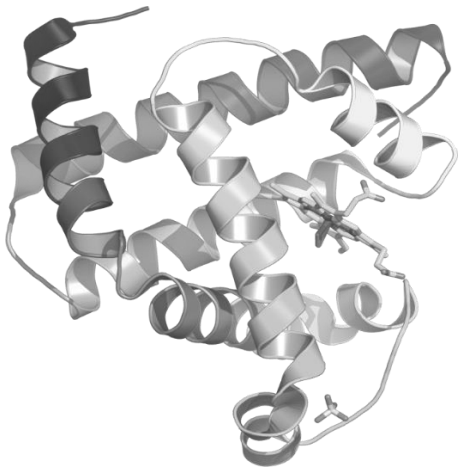
  The β-pleated sheet structure of silk has high tensile strength, thus cannot be stretched.

C. Tertiary Structure of Proteins

- The polypeptide (secondary) chain usually bends and folds extensively, forming a precise, compact, globular shape, which is the protein's **tertiary structure**.
- Tertiary structures are maintained by four types of bonds,
  i. disulfide bonds
  ii. ionic bonds
  iii. hydrogen bonds
  iv. hydrophobic interactions
- These interactions are formed between the **R-groups** of amino acid residues that are far apart in the linear sequence of the polypeptide chain.
- Since different polypeptides have a specific order of R-groups, the bonds are formed in specific places, leading to polypeptides taking on specific conformations and thus specific functions.



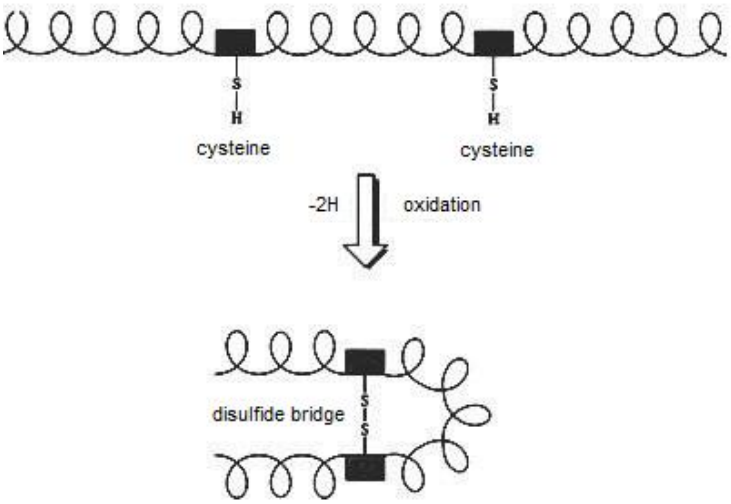
- An example of a protein with tertiary structure is **myoglobin**, which stores oxygen for aerobic respiration in muscles.
  - Primary structure:
    Single polypeptide chain of 153 amino acids
  - Secondary structure:
    About 75% of the polypeptide chain is α-helical, i.e. there are 8 helical sections
  - Tertiary structure:
    Non-uniform folding of the α-helical chain into a compact shape
  - Prosthetic group:
    Haem group (contains iron) that reversibly binds oxygen



- The specific conformation of a protein is stabilised by <u>four types of interactions</u> that occur <u>between the various amino acid residues</u> in the polypeptide chain (unlike peptide bonds that occur within the backbone of the polypeptide chain):
    i. **disulfide bonds/bridges**
    ii. **ionic (electrovalent) bonds**
    iii. **hydrogen bonds**
    iv. **hydrophobic interactions**

R-group interactions in tertiary structure:

<u>i. Disulfide bonds/bridges</u>

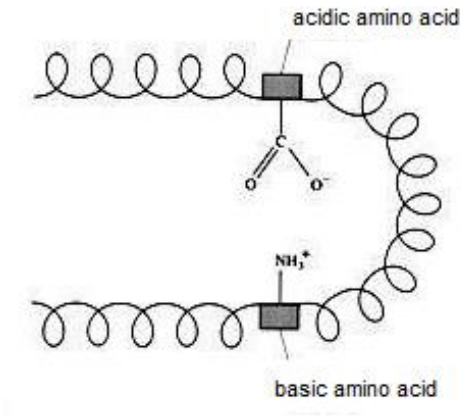


- The amino acid cysteine contains a **sulfhydryl group**, -SH, in its <u>R-group</u>.
- When two cysteinyl residues line up alongside each other, neighbouring –SH groups can be oxidised to form a disulfide bond.
- Disulfide bonds may be formed <u>between different amino acid chains</u> or <u>between different parts of the same chain</u>.
  In the latter, the disulfide bond makes the molecule <u>fold</u> into a particular shape.
- Disulfide bonds are <u>strong covalent bonds</u> and are not easily broken.

<u>ii. Ionic / electrovalent bonds</u>

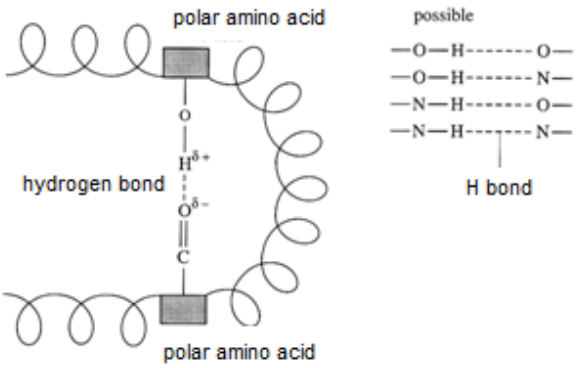
- Acidic (e.g. COOH) and basic R-groups (e.g. NH_2) exist in an <u>ionised state</u> at certain pHs.
- Acidic R-groups are negatively charged whilst basic R-groups are positively charged.
- They can therefore be attracted to each other, forming **ionic bonds**.
- In an aqueous environment, the ionic bond is easily broken by <u>changing the pH</u> of the medium.

  e.g. adding acid to milk produces curds due to precipitating of milk protein casein



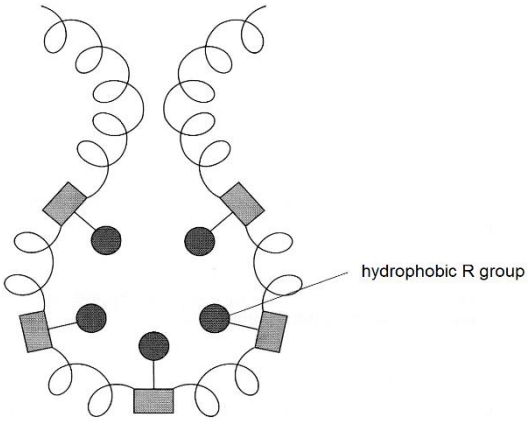
iii. Hydrogen bonds

- When a hydrogen atom is part of –OH or –NH groups, it becomes slightly positively charged since O and N are electronegative.
- The electrons that are shared in the O-H or N-H bond are attracted more towards the O or N atoms.
- The electropositive H atom may then be attracted towards a neighbouring electronegative O or N atom, such as the O of a C=O group or the N of an N-H group.
- Hydrogen bonds may also be formed between R-groups at different parts of the same chain, allowing the molecule to fold into a particular shape.

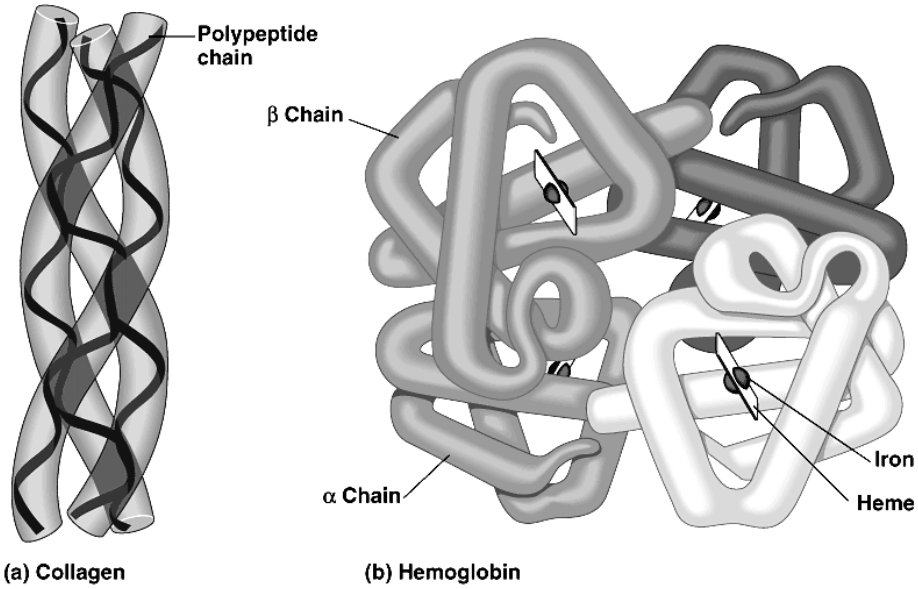


iv. Hydrophobic interactions

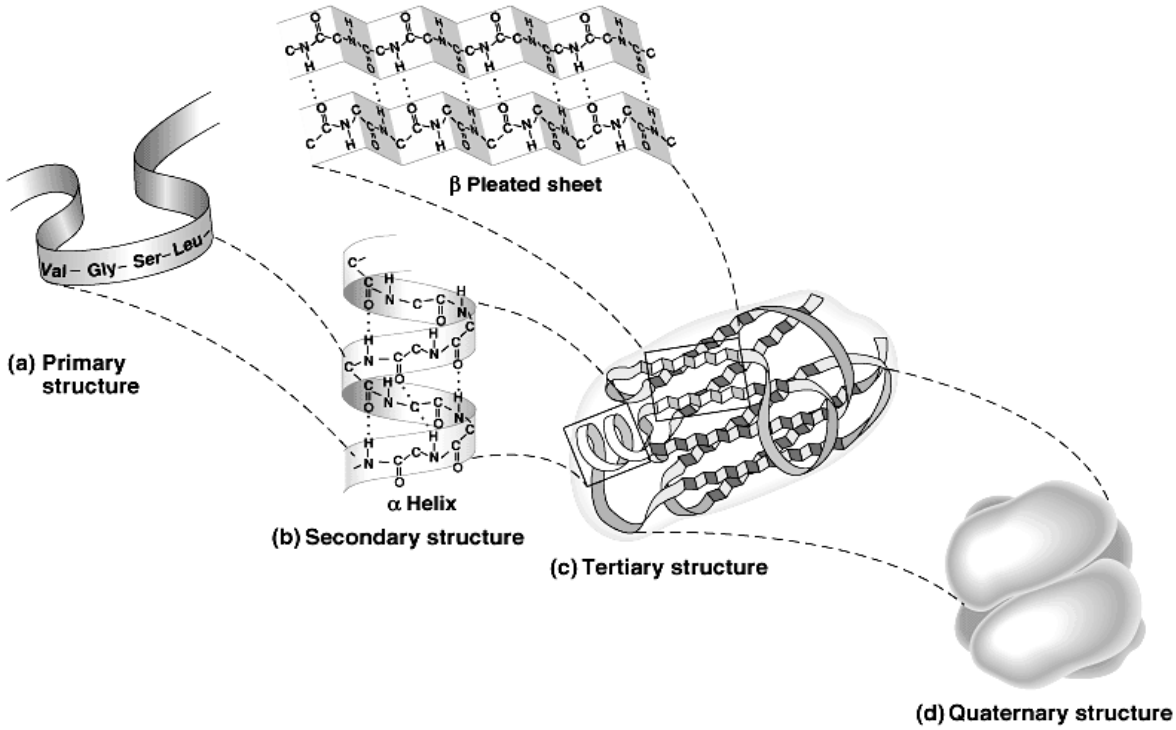
- Non-polar R-groups are hydrophobic, such as those on tyrosine and valine.
- If a polypeptide chain contains a number of these groups and is in an aqueous environment, the chain will tend to fold so that the maximum number of hydrophobic groups come into close contact and exclude water.
- In **globular proteins**, the hydrophobic groups tend to project inwards towards the centre of the roughly spherical molecule, while the hydrophilic groups face outwards into the aqueous environment, rendering the protein soluble.



D. Quaternary Structure of Proteins



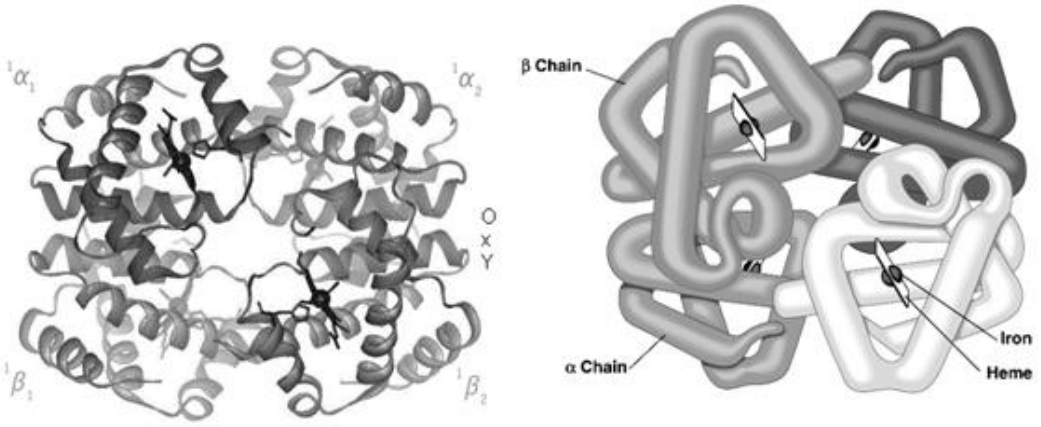
- Many proteins consist of <u>more than one polypeptide chain</u> (i.e. **multimeric** proteins).
- The <u>subunits</u> are held together by <u>R-group interactions</u> such as hydrophobic interactions, disulfide, hydrogen and ionic bonds.
- The overall protein structure resulting from the aggregation of the polypeptide subunits is known as the protein's **quaternary structure**.
- Constituent chains of a multi-subunit protein can be <u>identical or distinct</u>.
- Examples of proteins with quaternary structure are **collagen** (a fibrous protein) and **haemoglobin** (a globular protein).



V.Relating Structure to Function of Proteins

A. Haemoglobin

Haemoglobin is a **globular protein** adapted for transport of oxygen in the red blood cells of vertebrates. Its main function is to transport oxygen from the lungs to the capillaries of respiring tissues.



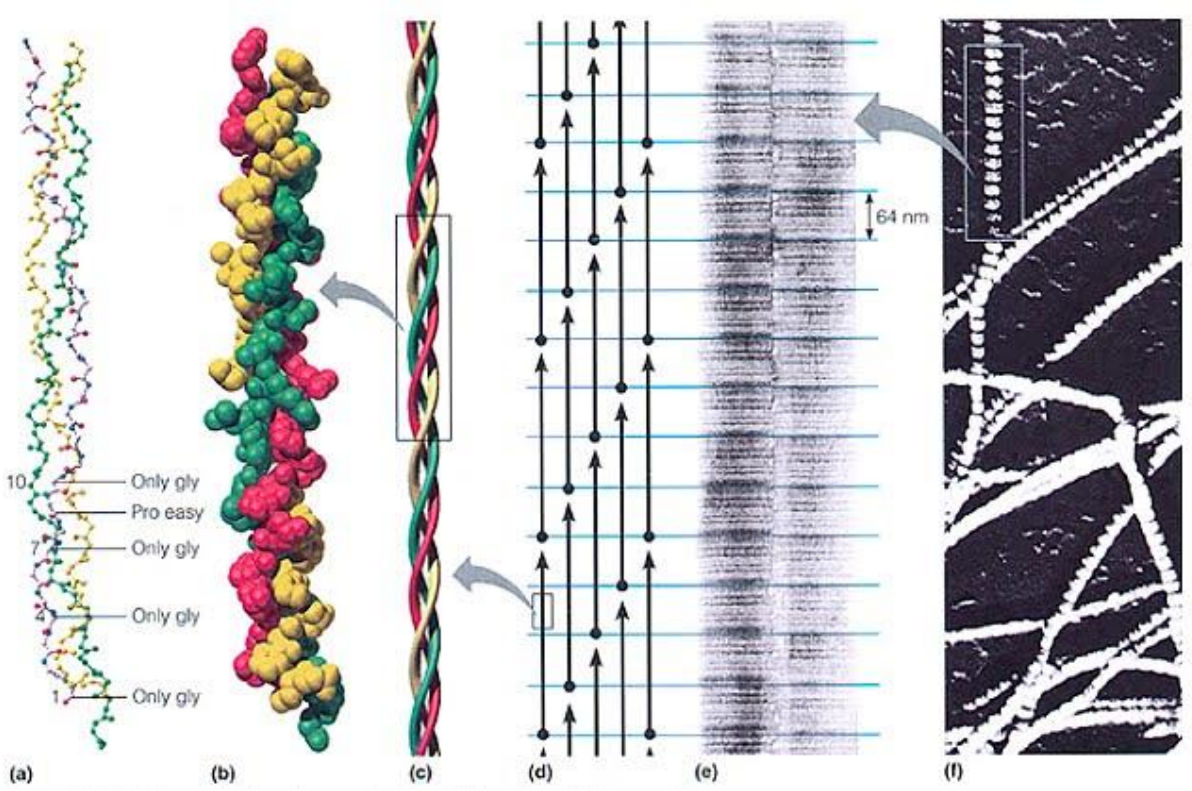
Structure:

- Haemoglobin molecule has a quaternary structure.
- It is a tetramer comprising four separate subunits, namely two α-chain subunits and two β-chain subunits.
- The two α-chain subunits each contain 141 amino acids, while the two β-chain subunits each contain 146 amino acids.
- The subunits are held together by R-group interactions such as ionic bonds, hydrogen bonds and hydrophobic interactions, forming a 3-dimensional conformation.
- Each subunit in haemoglobin consists of a protein component (**globin**) and a non-protein component or prosthetic group (**haem**).

Structure	Significance
♦ The haemoglobin molecule is globular and compact in shape.	♦ Many haemoglobin molecules can be _____ into a red blood cell for the transport of oxygen.
♦ Each haemoglobin molecule consists of four subunits, each capable of binding one O_2 molecule.	♦ A haemoglobin molecule can carry up to 4 oxygen molecules and this greatly _____ _____.
♦ Haemoglobin is an allosteric protein that exhibits **cooperative binding** of O_2 molecules.	♦ Cooperative binding _____ both the amount of O_2 loaded at the lungs and the amount of O_2 released at the tissues.
♦ The polypeptide chain of the subunit is folded such that the bulk of the hydrophobic amino acids are buried in the interior of the globular structure whilst the hydrophilic amino acid residues are on the outside.	♦ The haemoglobin molecule is _____ in red blood cells and hence is a good transport protein for oxygen in the blood.
♦ Globin contains a deep hydrophobic cleft, i.e. the haem-binding site.	♦ The haem-binding site provides a hydrophobic environment for the _____, which is largely hydrophobic.
♦ The **haem group** consists of a porphyrin ring and an iron (II) ion, Fe^{2+}.	♦ The Fe^{2+} can combine _____ and hence enhances the release of O_2 in metabolically active tissues such as muscle.

B. Collagen

- **Collagen** *(Greek: kolla, glue)* is a **fibrous** protein adapted for structural support.
- The basic structural unit of collagen is **tropocollagen**, which is a **triple helix** comprising three polypeptide chains.
- It is an essential component of connective tissue in skin, bone, tendon, ligament, blood vessels and teeth.

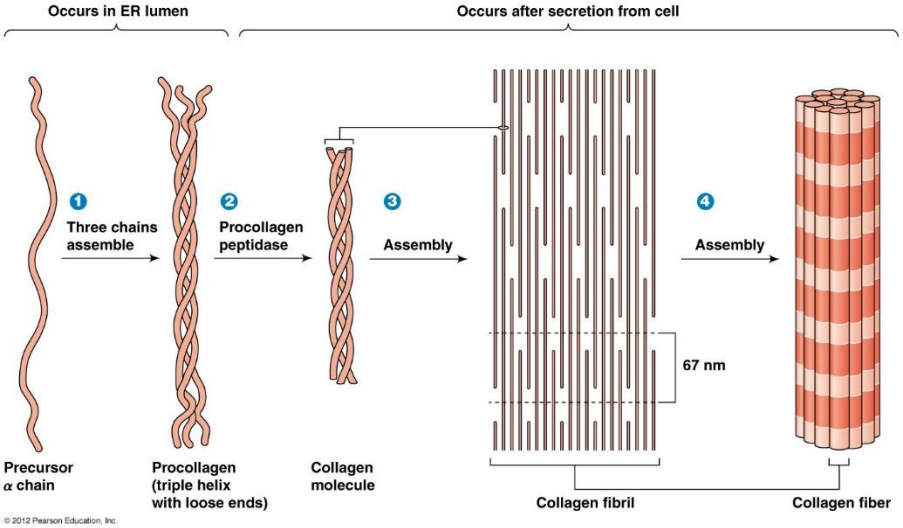


Structure of collagen (a-c): three polypeptide chains coil together to form a tropocollagen; (d-f): collagen fibrils
Source: http://web.mit.edu/3.082/www/team1_f02/collagen.htm

Structure:

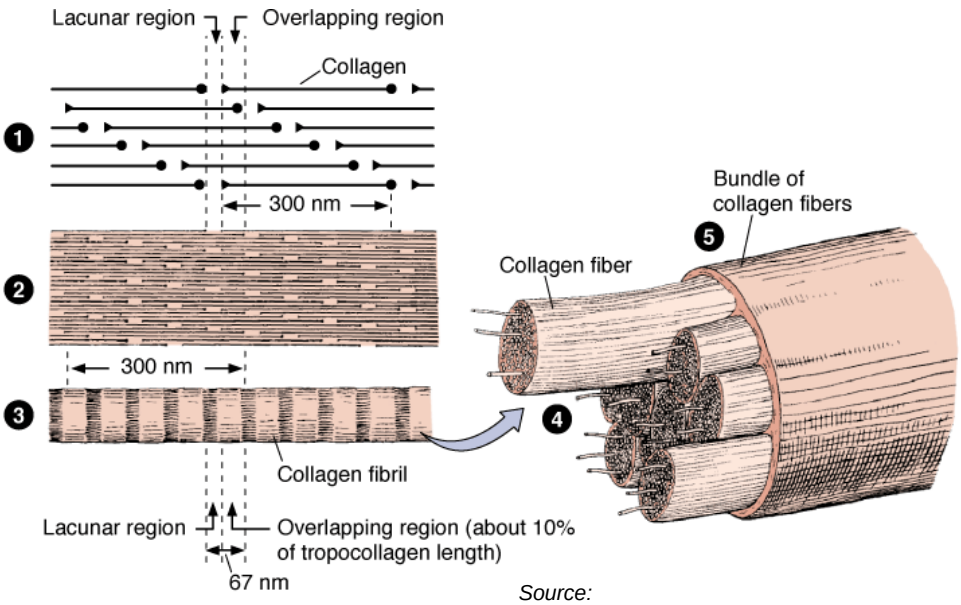
- The basic structural unit of collagen is **tropocollagen** which has a quaternary structure.
- Tropocollagen consists of three polypeptide chains, each about 1000 amino acid residues long.
- Each of the three polypeptide chains is in a helical conformation, and the three helical chains wind around each other via hydrogen bonds to form a **triple helix**.
- Collagen is unusually rich in **glycine** and **proline**. It also contains two amino acids that are present in very few other proteins, namely **hydroxyproline** and **hydroxylysine**.
- Each chain contains repeats of a tripeptide sequence gly-X-Y where X is often proline, and Y is often hydroxylysine or hydroxyproline.
- Many tropocollagen molecules can cross-link via covalent bonds to form **fibrils**, which further associate to form **collagen fibres**.

Structure	Significance
♦ Tropocollagen molecule has a large molecular size. ♦ The polypeptide chains also consist largely of glycine and proline which are hydrophobic in nature.	
♦ Every third amino acid of each polypeptide chain is a glycine.	♦ Glycine's R-group, a H atom, is small enough to fit within the central core of tropocollagen, allowing the three polypeptide chains to lie close together to form a **tight coil**.
♦ Each polypeptide chain contains many proline and hydroxyproline residues.	♦ The bulky and inflexible proline and hydroxyproline [2] residues contribute to the **rigidity** of the molecule.
♦ Within the tropocollagen molecule, extensive cross linking of **hydrogen bonds** between -NH group of glycine and -CO group of hydroxylysine holds the three polypeptide chains together to form the triple helix. ♦ Many tropocollagen molecules can lie parallel to each other in a staggered arrangement and cross-linked via **covalent bonds** between the carboxyl end of one molecule and the amino end of another. The tropocollagen bundled to form **fibrils**, which further assemble to form **collagen fibres**.	



Source: http://www.mun.ca/biology/desmid/brian/BIOL2060/BIOL2060-17/CB17.html

[2] Hydroxyproline is synthesised from adding proline, and hydroxylysine is synthesised from lysine. There is no DNA code for these amino acids and they are made from their parent amino acids *after* incorporation into collagen. The biological significance of these modifications is evident in the disease scurvy: a deficiency of vitamin C results in insufficient hydroxylation of collagen and the abnormal collagen fibers that result are unable to maintain normal tissue strength.



Source: http://histonano.com/books/Junqueira's%20Basic%20Histology%20PDF%20WHOLE%20BOOK/5.%20Connective%20Tissue.htm

VI. Biuret Test for Protein

- Principle:

  The Biuret test detects **peptide bonds**, and thus all proteins would yield a positive result.

- Method:

  1. Add an equal volume of 5% sodium hydroxide to 2 cm^3 of the solution being tested. Shake the tube to mix the contents.
  2. Add 1% copper sulfate solution dropwise, shaking the tube after every drop.

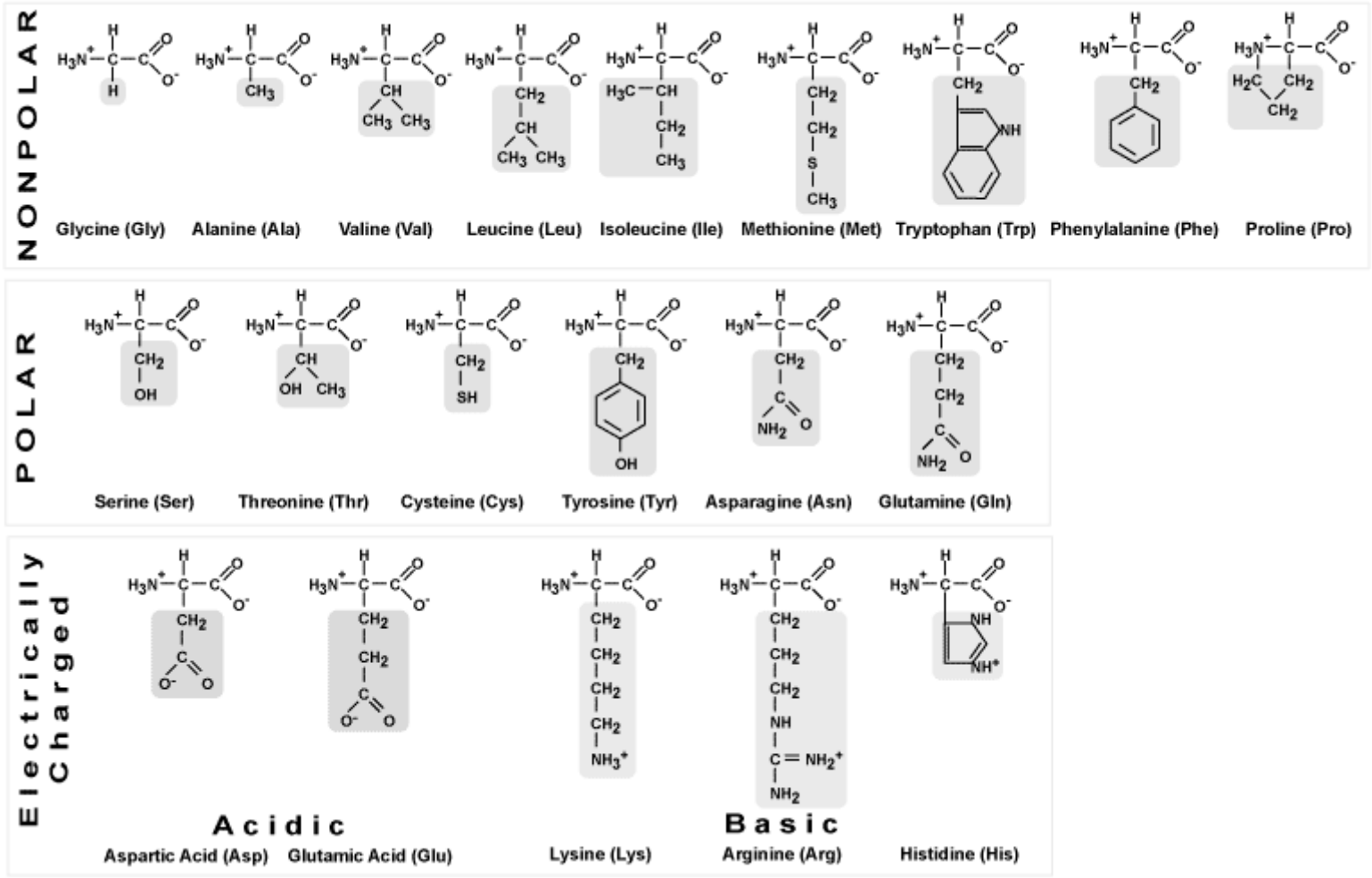
- Observations:

  If protein is present, a violet colouration is observed.

  A light blue colour, due to the presence of copper sulfate solution, indicates the absence of protein.

Annex I

Structures of the 20 standard amino acids



Annex II

Keratin in Hair and How Hair Permanents Work

At the molecular level, hair is composed mostly of chains of keratin molecules. In addition to intra- and intermolecular hydrogen bonds, keratins have large amounts of the sulfur-containing amino acid *cysteine*, required for the *disulfide bridges* that confer additional strength and rigidity by permanent, thermally-stable cross-linking—a role sulfur bridges also play in *vulcanized rubber*. The pungent smells of burning hair and rubber are due to the sulfur compounds formed.

Every time you wash your hair or go swimming, you generate a small chemical reaction. Hydrogen-rich water molecules snap the *weak hydrogen bonds* between your hair's keratin chains, prompting even the curliest of locks to straighten temporarily when wet. As the hair dries, the *hydrogen bonds are re-established*, and waves or curls return.

The opposite occurs with straight hair that is dampened and then wound around pins or rollers so that different parts of the keratin chains are adjacent to one another. When the hair gets wet, water molecules intrude into the keratin strands. The sheer numbers of water molecules are able to disrupt some of the hydrogen bonds which also help to keep the *alpha-helices* aligned. The helices are able to slip past each other and will retain a new shape in the hair drying process as new hydrogen bonds are formed. The hair strands are able for a short time to maintain the new curl in the hair. Blow dryers, electric rollers, and curling irons act along the same principle, but use *heat energy* to *reinforce the new bonding pattern.*

But as people whose hair style depends on a curling iron or a blow dryer know, their efforts can be undone in minutes. *All it takes is a little water* in the form of a sprinkling of rain or a moist sea breeze to send your hair's hydrogen bonds scrambling back into their normal alignments.

For more lasting changes to your hair style—and your hair chemistry—you must turn to *permanent waving (perming) or straightening*. These processes not only alter hair's hydrogen bonds but also split apart stronger chemical bonds that are unaffected by water. Although waving and straightening (also called *relaxing*) produce opposite results, the two procedures employ the same chemical tricks.

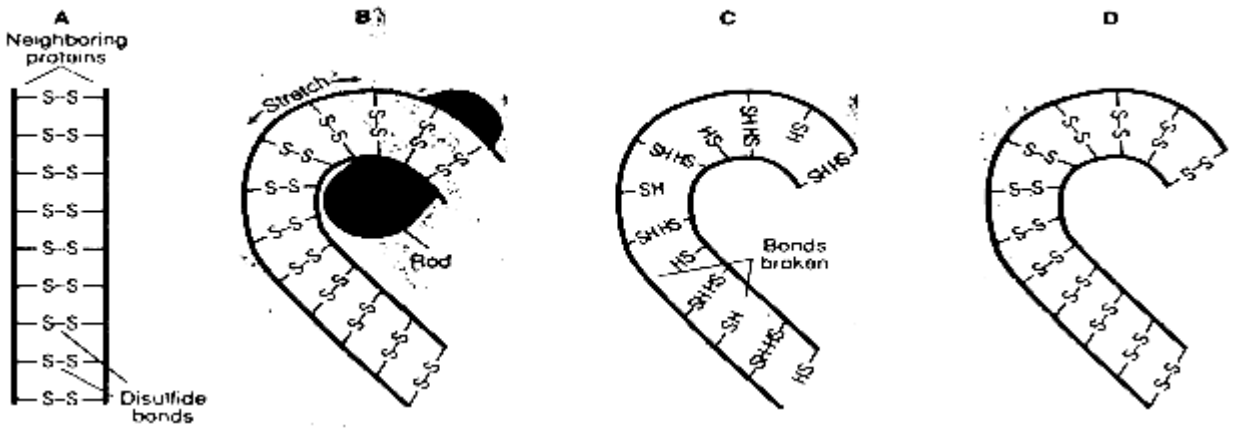


Diagram showing general steps of hair perming

Whether hair is permed or relaxed, the first step, called *softening*, involves *reduction*. In the permanent wave or straightening process, a basic reducing substance (usually ammonium thioglycolate) is first added to *reduce* and *rupture* some of the *disulfide cross-links*.

In the next step of the process, called *rearrangement*, the keratin chains are moulded into the desired configuration. This is accomplished by winding the softened hair on rods to produce curls or holding it flat to straighten it. Since the alpha-helices are no longer tightly cross-linked to each other, the alpha-helices can shift positions in relation to each other.

The final step, *hardening*, makes the rearrangement permanent by rebuilding the sulfur-to-sulfur bonds and other water-stable molecular links that hold hair strands together. This is accomplished through *oxidation*. For perms and relaxers, the chemicals that initiate oxidation are either sodium bromate or hydrogen peroxide solutions. Disulfide bonds are reformed in their new positions. The permanent will hence hold these new disulfide bond positions until the hair grows out, since new hair growth is of course not treated.