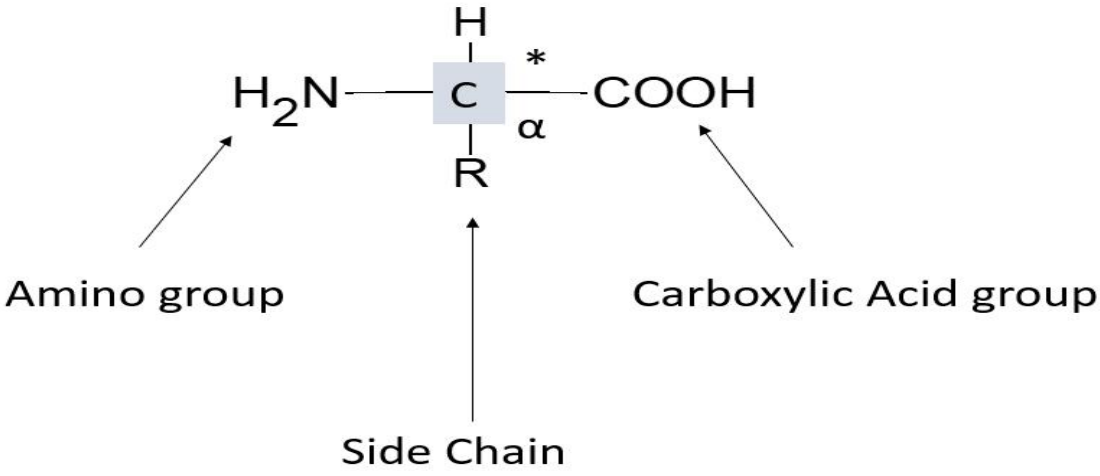
AMINO ACIDS AND PROTEINS

α-Amino acids

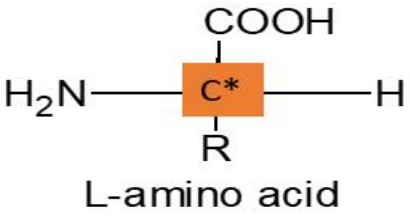


Chiral if R- is not H-, i.e. glycine In α-amino acids, amino group is in alpha position.

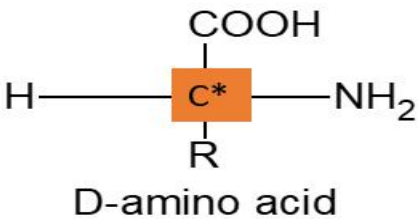
Amino acids are grouped on the basis of the chemical nature of the side chains

Amino acids

- All are primary amino acids except proline which is a secondary amino acid.
- Also found in enantiomeric form, D- and L-:



L-amino acid

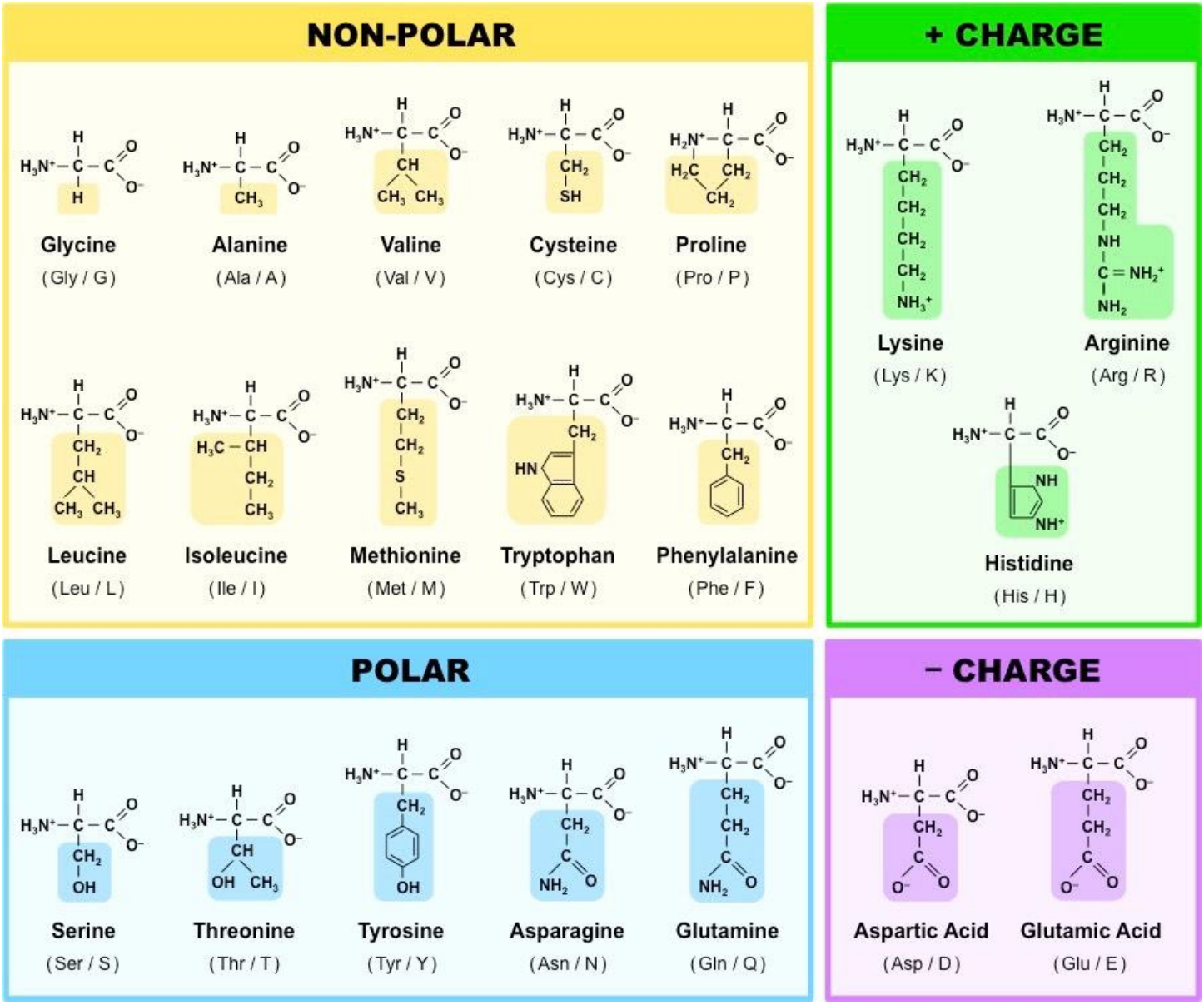


D-amino acid

- Amino group on the left (L-amino acid), similar to OH- on the left of sugars
- Most natural amino acids are in L- configuration.
- Most protein consist of 20 amino acids

Amino acid classification

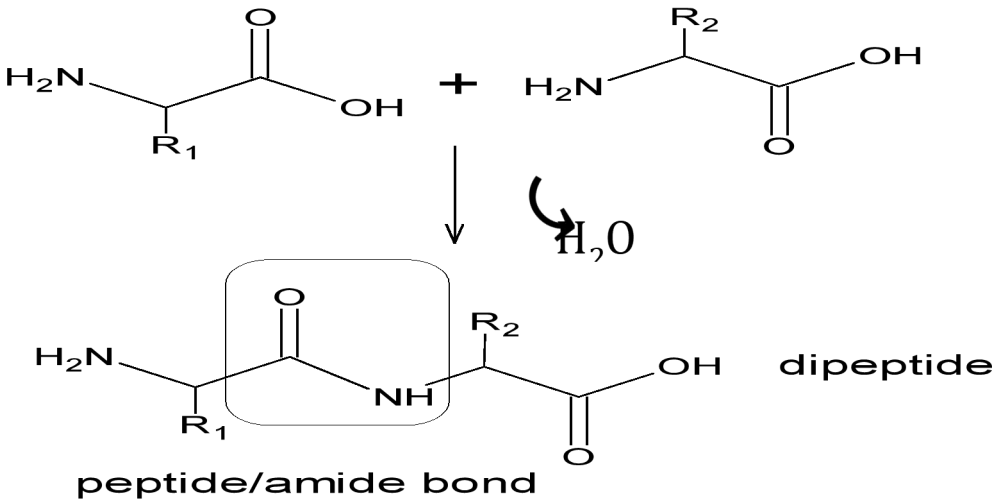
- Amino acid side chains: hydroxyl, aromatic, alkyl, carboxylic acid, amino, amide or sulfur containing.
- Hydrophilic, hydrophobic or amphiphilic.
- Polar or non-polar. High levels of polar groups increase water solubility



Proteins

Proteins are polymers of amino acids. Subunits of 20 common amino acids. Molecule with less than 50 amino acids is called peptide. Dipeptide = 2 units of amino acids. Tripeptide = 3 units of amino acids.

Peptide bond is the special name given to the amide bond between the α-carboxyl group of one amino acid and the α-amino group of another.



Protein classification based on functionality

-Enzymes

-Structural

-Contractile (myosin, actin)

-Hormones (insulin, growth hormone)

-Transfer proteins

-Antibodies (immunoglobulins)

-Storage proteins (egg albumen, seed proteins)

-Protective proteins (toxins, allergens)

Protein classification based on solubility

-Albumins: soluble in neutral salt free water

-Globulins: soluble in neutral salt solutions

-Glutelins: soluble in dilute acid or base solutions

-Prolamins: soluble in 50-90 % ethanol

-Scleroproteins: Insoluble in water. Structural proteins.

-Histones: Basic proteins, high content in lysine and arginine. Soluble in water.

-Protamines: Strongly basic, low MW proteins.

2- Classification of proteins based on shape and size:

a- Fibrous proteins:

In fibrous proteins, the polypeptide chains are long, thin fiber or needle shaped. These proteins often serve structural roles in cells. Typically, they are insoluble in water or in dilute salt solution. Like ∝-keratin (from hair, nail wool and skin), silkfibroin (fibroin, the protein of silk, is produced by insects and spiders), collagen (found in connective tissue such as tendons, cartilage, the organic matrix of bone, and the cornea of the eye.), and elastin (a component of some connective tissues).

2- Globular proteins:

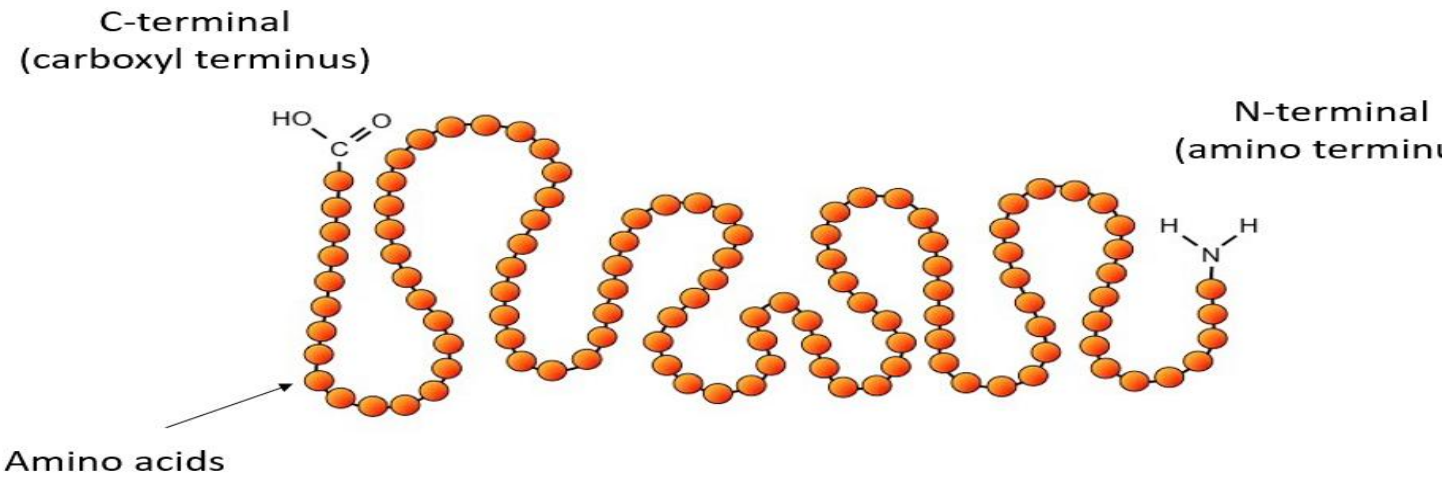
Globular proteins also called sphero proteins are spherical in shape. Globular proteins are soluble in aqueous solution. This group includes albumin, many enzymes, protamines, globulin, histones and actin…..

Protein structure

Proteins have four levels of structure: primary, secondary, tertiary and quaternary

1-Primary Structure of Protein

Sequence of amino acids in the polypeptide chain, Peptide bonds stabilized this structure (amide covalent bond).



2-Secondary Structure

spatial arrangement of the polypeptide chain along one axis due to hydrogen bonding between amino acids

This is to minimise hydrophobic sites of protein to water and maximise hydrophilic sites exposure to water

Major types of secondary structure

α-helix

β-pleated sheets

β-turns

α-helix

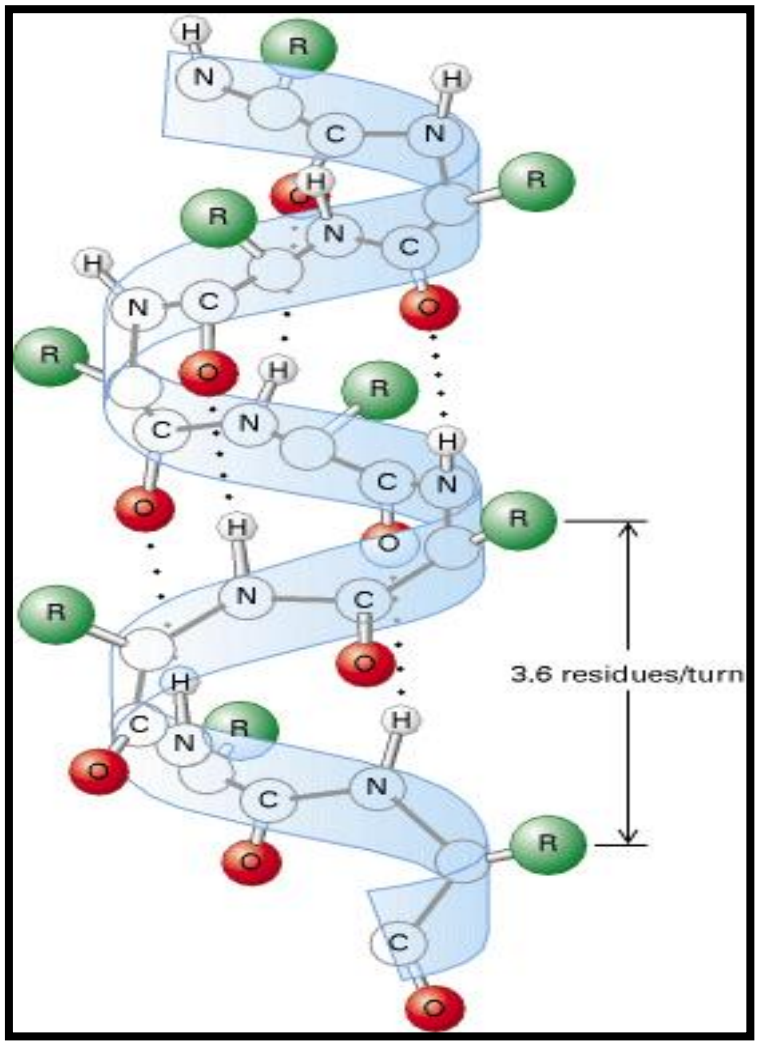
-Fibrous proteins are regularly coiled to form a structure called the α -helix

-Structures are stabilized by H-bonding to neighboring molecules

-Right- or left- hand orientation

-Amphiphilic nature: One side of the helical surface is hydrophobic and the other hydrophilic

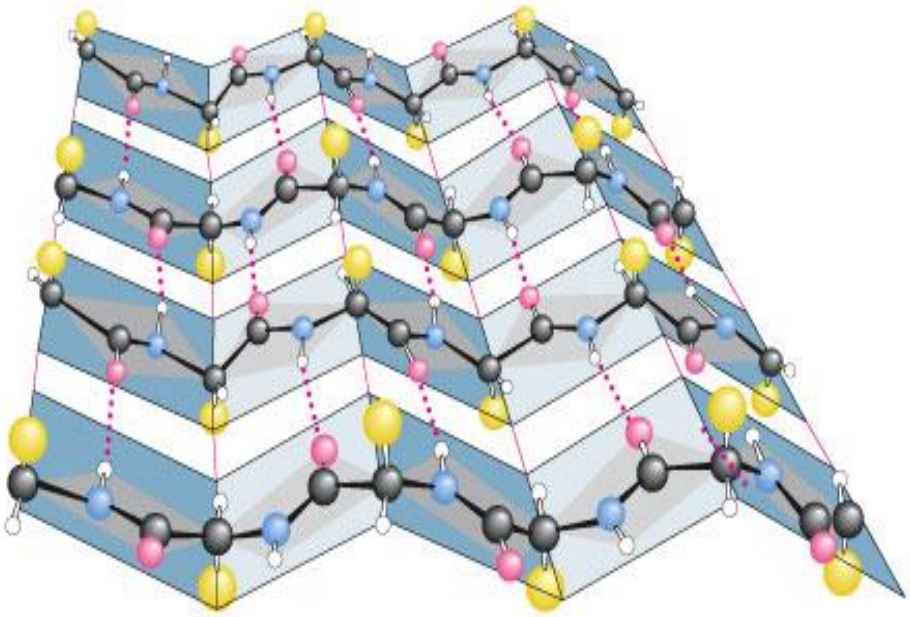
-R groups extend outward from the backbone of the coiled polypeptide chain

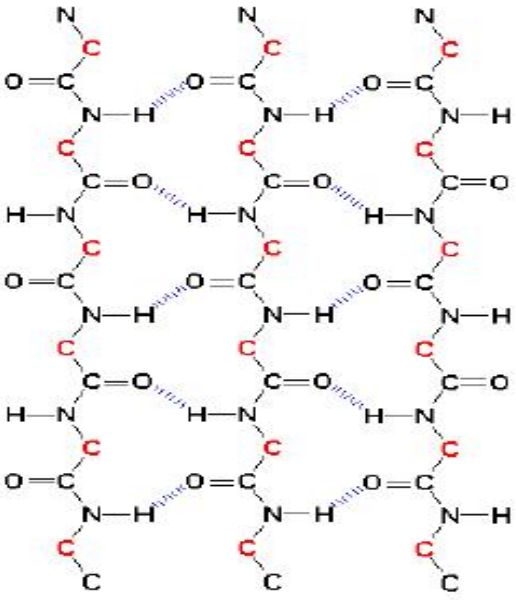


pleated sheet

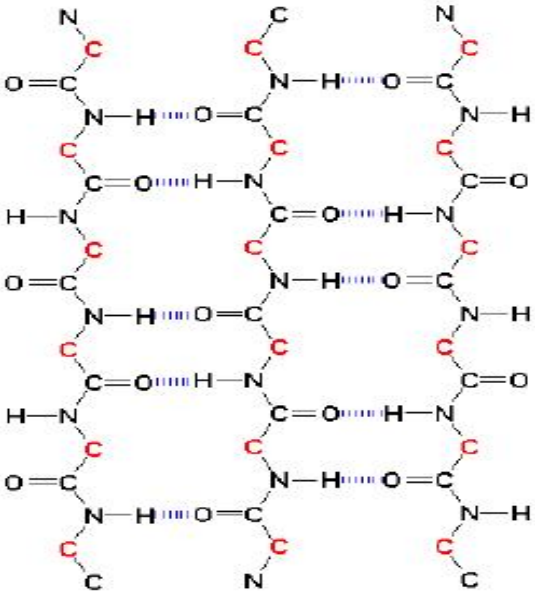
Polypeptide chains can also be in an extended zig-zag configuration, the β-pleated sheet Such chains are arranged alongside each other to form a structure called a pleated sheet, in which the adjacent polypeptide chains run in opposite directions

The adjacent chains of the pleated sheet are held together by hydrogen bonding





Parellel form



Anti-parellel

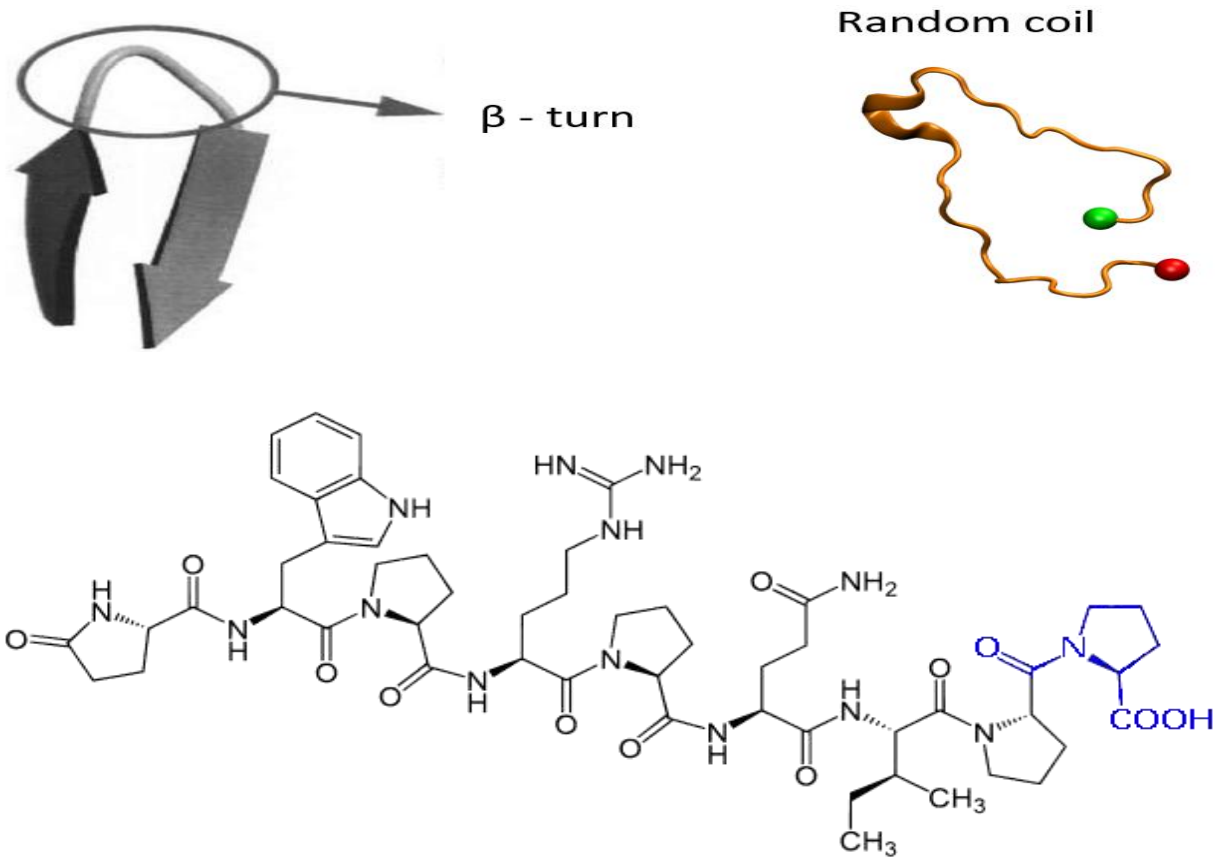
-May join distance peptide chain through H-bonding

-More stable than α-helix. High β-sheet content higher thermal denaturation temperature

-May be parallel or anti-parallel. Anti-parallel more stable.

β-turns and random coils

β-turns in proteins causes a change in direction of the polypeptide chain. Proline (imino acid) is responsible for β-turns. Random coils do not have structure and are oriented randomly in space.



The conformation of caseins is much like that of denatured globular proteins. The high number of proline residues in caseins causes particular bending of the protein

chain and inhibits the formation of close-packed, ordered secondary structures. When proline is in a peptide bond, **it does not** have **a hydrogen** on the α amino group, it cannot **donate a hydrogen bond to stabilize an α helix**.

- proline led to produce partially folding α helix or naturally un folded protein (naturally denatured proteins) with high resistant against heat treatment this is cause why **casein is very resistant against heat treatment.**

3-Tertiary Structure

The three-dimensional structure of globular proteins, in which the polypeptide chain is tightly folded and packed into a compact spherical form.

1. Hydrophobic attraction: the close association/attraction of amino acids with non-polar groups

2. Ionic bonds: between positively charged groups and negatively charged groups

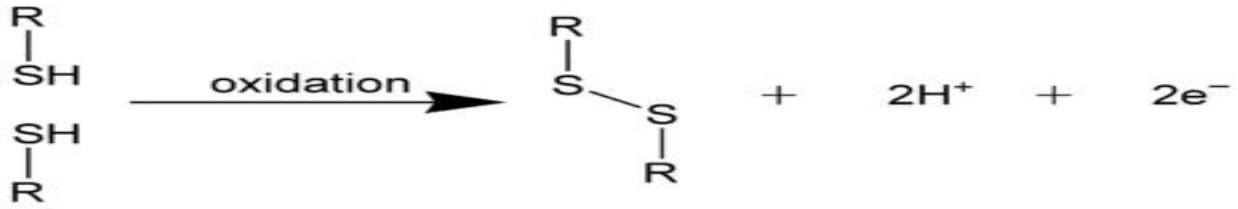
3. Hydrogen bonds

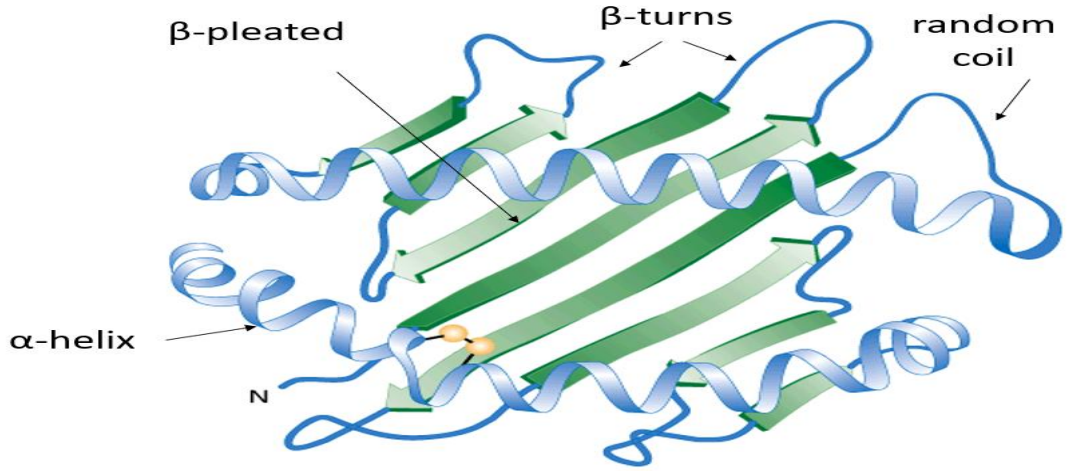
4. Disulfide bonds

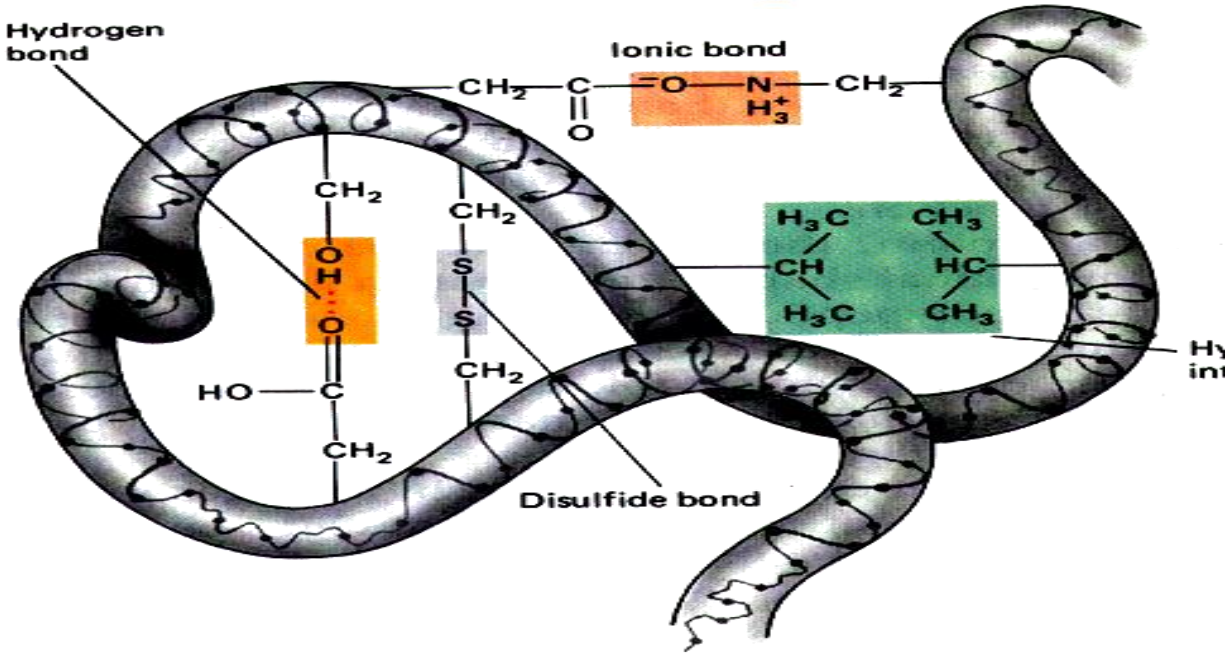
Due to spontaneous folding of protein to minimize exposure of hydrophobic amino acid side chains and maximize hydrophilic chains to water

Disulfide bonds

Chemical bonds between cysteines due to oxidation of sulfhydryl group (-SH). The only covalent side-chain cross link.

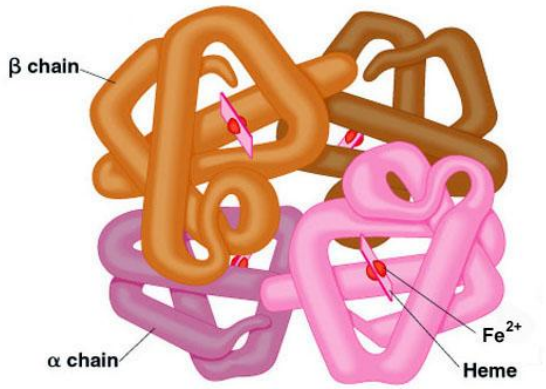






4-Quaternary Structure

Only proteins with more than one chain have quaternary structure.



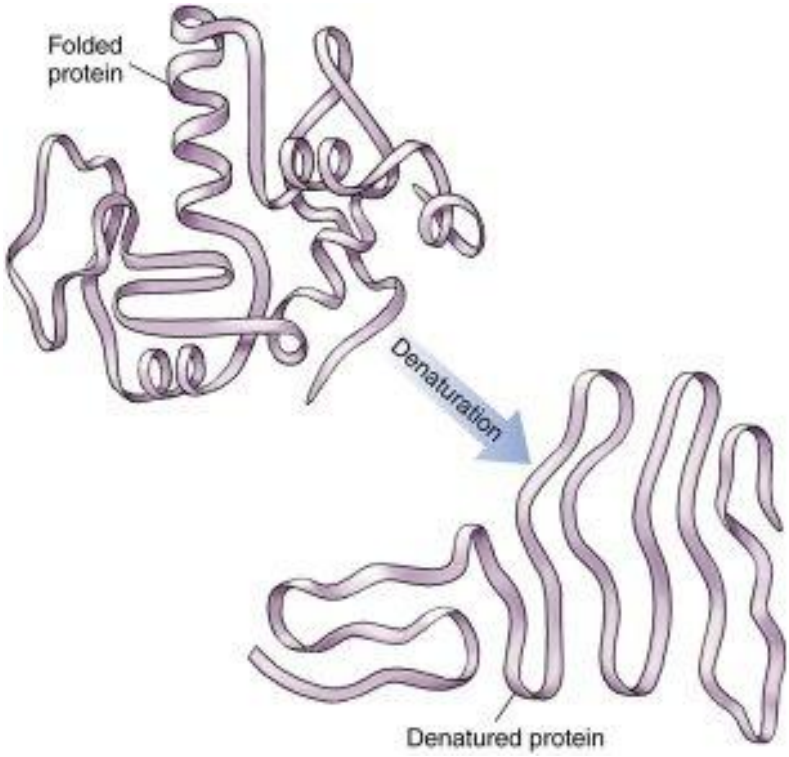
Haemoglobin

Protein Denaturation

- Major changes in secondary, tertiary or quaternary structure of protein leading to a change in **3D** spatial arrangement of the molecule.
- Denaturation is regarded the loss of secondary, tertiary or quaternary structures. Loss of ordered structure.
- In denaturation there is no peptide bond cleavage
- Caused by:
    - pH change
    - Increase in temperature
    - Salts
    - Agitation
    - Solvent

Results of denaturation:

- Changes of physical properties e.g. coagulation, gelation.
- Increase in emulsification capacity
- Inactivation e.g. loss of enzymic properties
- Improvement of digestibility/bioavailability



Temperature Change

- Increase of temperature causes increased vibration that breaks intramolecular interactions (does not break peptide bonds) of protein causing denaturation.
- Hydrophobic interactions are strengthened.
- Protein molecules starts to interact with each other causing coagulation, e.g. egg white.
- Irreversible if interactions after denaturation cannot be removed.
- Amino acid composition affects thermal stability. More hydrophobic amino acids, more stable protein
- Water facilitates thermal denaturation. Dry powders are stable
- Preservation by heating is one of the most common food processing technologies

Mechanical Shear and Pressure

- Agitation such as blending, whipping, shaking and kneading
- Destabilize protein structure leading to the stretching of protein molecule and denaturation
- Denaturation due to whipping is important in foam formation.
- Pressure affects protein structure (1-12 kbar)
- Occurs due to make compressibility of protein structure
- It is mostly reversible
- Important in processing HHPP (high hydrostatic pressure processing) using high pressures.
- HP is applied to food products with the following goals:
- Inactivation of microorganisms, such as bacteria, viruses, and parasites of human health concern,
- Shelf-life extension (inactivation of organisms and partial inactivation of enzymes),
- Physical and chemical modification of food matrix (e.g., cold cooking)

pH and denaturation

Proteins are most stable at their isoelectric point

Proteins unfold at extreme pH values.

Unfolding is greater at extreme alkaline pH values than at extreme acid.

pH-induced denaturation is mostly reversible if there is no peptide bond cleavage.

Organic Solvents – Solutes

Affect the stability of hydrophobic interactions, hydrogen bonding and electrostatic interaction in multiple ways.

Hydrophobic interactions are weakened. Hydrogen bonding can be weakened or enhanced.

Electrostatic interactions between oppositely charged groups are enhanced.

Repulsions between charged groups with the same charge are enhanced.

The overall effect depends on protein-solvent pair

Ethanol: important “edible solvent” during processing and fermentation denatures proteins

Small molecules

Urea, guanidine hydrochloride weakens the strength of hydrogen bonding. It can be reversible by removing the denaturant.

Sugars tend to stabilise the proteins.

Detergents are powerful denaturing agents.

Salts may cause denaturation

Compete with protein for interactions with water molecules.

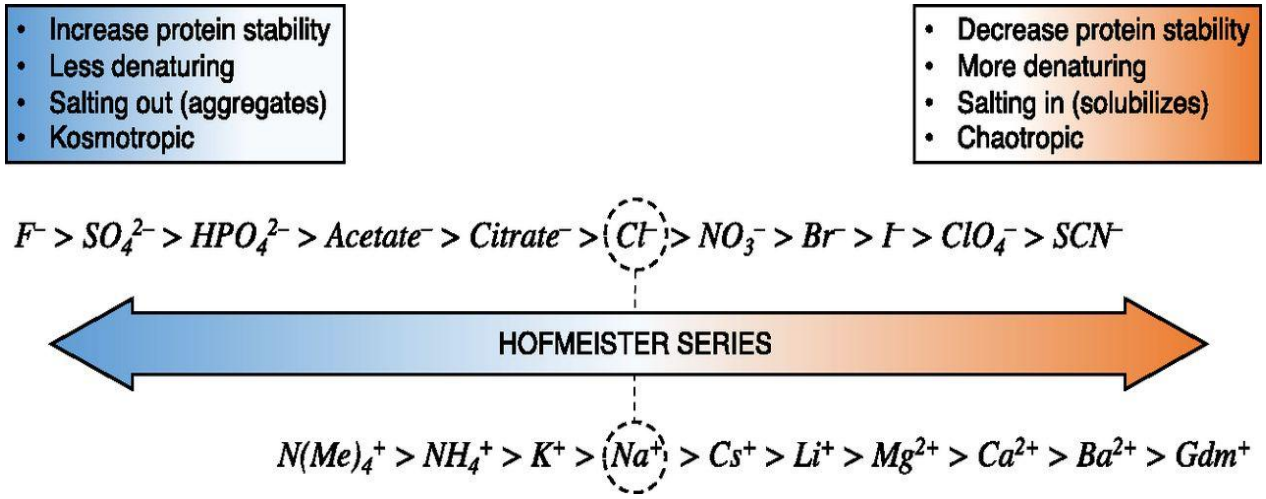
Protein structure is influenced more by anions than by cations

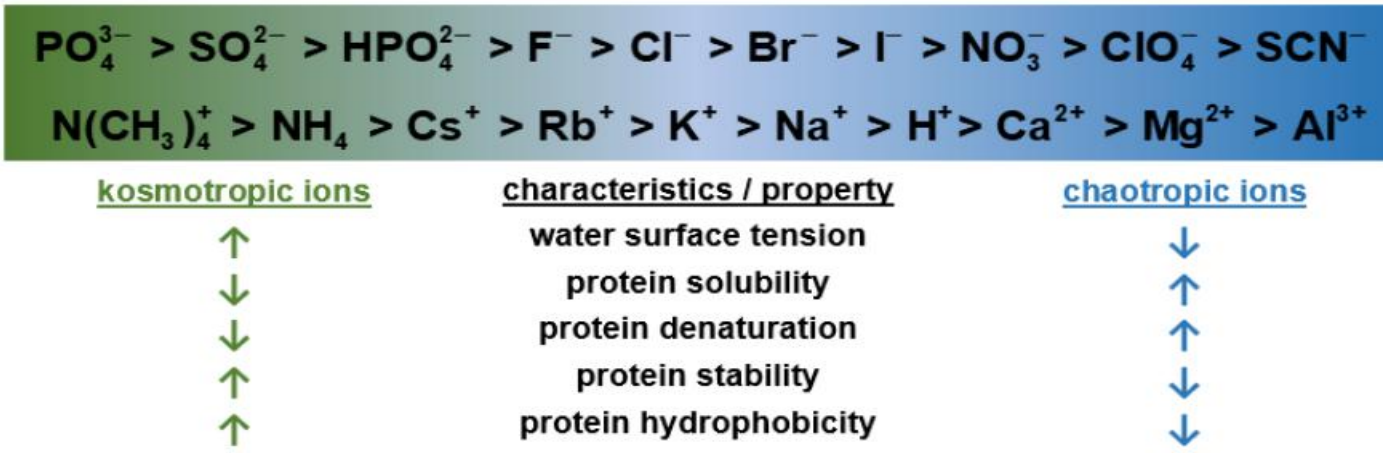
Salting out = Protein precipitation

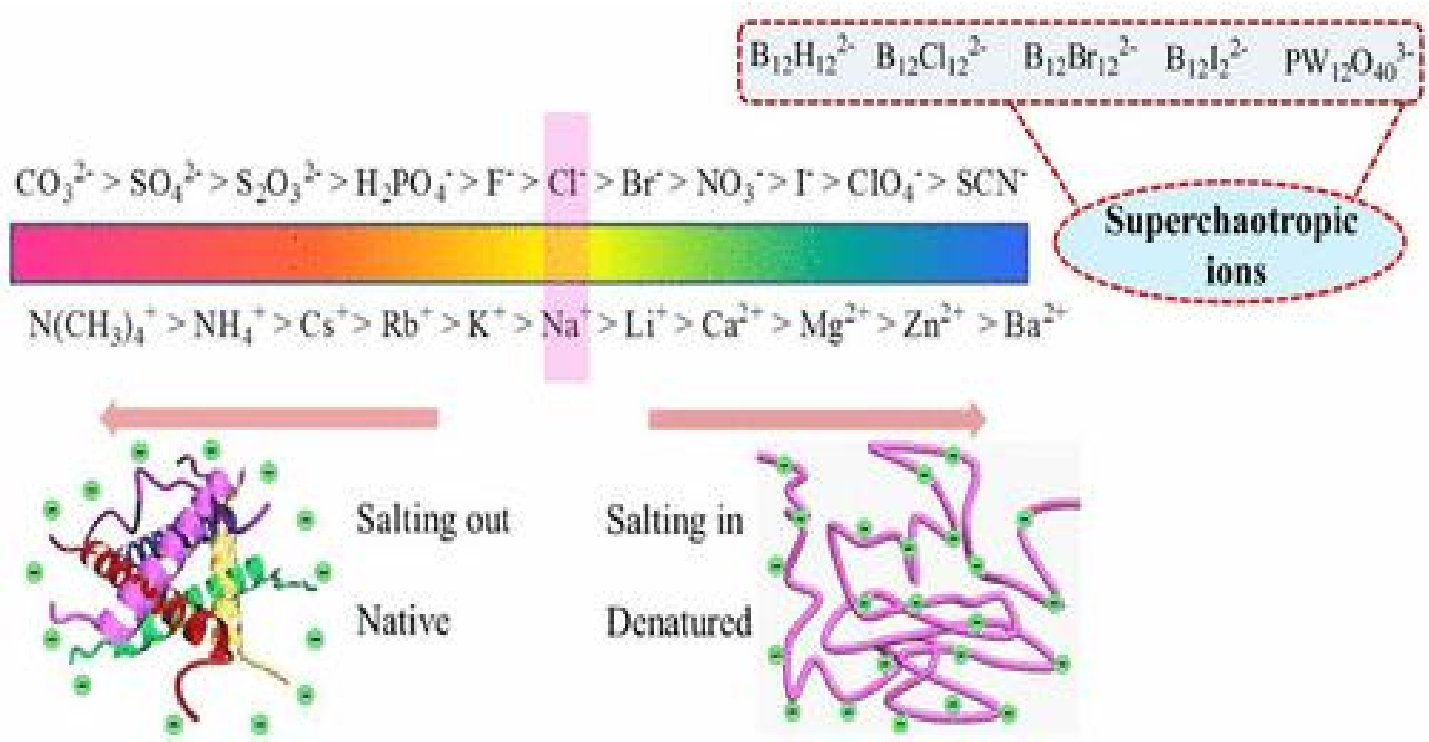
Salting in = Protein solubilization

HOFMEISTER series of salts

The Hofmeister series or lyotropic series is a classification of salts in order of their ability **to precipitate (or solubilise) proteins**.







Normal arrangement of protein components is maintained by the provision of energy (ATP); which is not available after death and the protein tend to denature.

It is accompanied by an increase in the reactivity of various chemical groups, a loss of biological activity (enzymic or hormonal properties), a decrease in solubility in aqueous solutions and a change in molecular shape and size.

It has a major effect on the structure and characteristics of meat, affecting its appearance and ability to hold or bind water.

Factors that can induce denaturation are the temperature (cooking <60°C), pH values (acidification), high concentration of salt (salting) or low levels of water-activity.

Hydrolysis

Hydrolysis involves breaking peptide bonds yielding smaller peptide chains or amino acids. Is achieved by acid or proteolytic enzymes**.**