Instructor: Dr Jimoh MO

Content: Proteins and amino acids

Proteins

Proteins are polymers of amino acids, arranged in a linear sequence. They are one of the most abundant organic molecules in living systems and have the most diverse range of functions of all macromolecules. Proteins may be structural, regulatory, contractile, or protective; they may serve in transport, storage, or membranes; or they may be toxins or enzymes. Each cell in a living system may contain thousands of proteins, each with a unique function. Their structures, like their functions, vary greatly.

Proteins have different shapes and molecular weights; critical to its function, and this shape is maintained by many different types of chemical bonds. Some proteins are globular in shape while others are fibrous in nature. Exposure to chemicals, changes in temperature and pH may lead to permanent changes in the shape of the protein, causing denaturation. Proteins are marginally stable, they achieve stability within narrow ranges of temperature and solvent conditions. Protein structure is dictated by the amino acid sequence. All proteins are made up of different arrangements of the same 20 types of amino acids.

Amino Acids

Amino acids are the monomers that make up proteins. Each amino acid has the same fundamental structure, which consists of a central carbon atom, also known as the alpha (α) carbon, bonded to an amino group (NH_2), a carboxyl group (COOH), and to a hydrogen atom. Every amino acid also has another atom or group of atoms bonded to the central atom known as the R group.

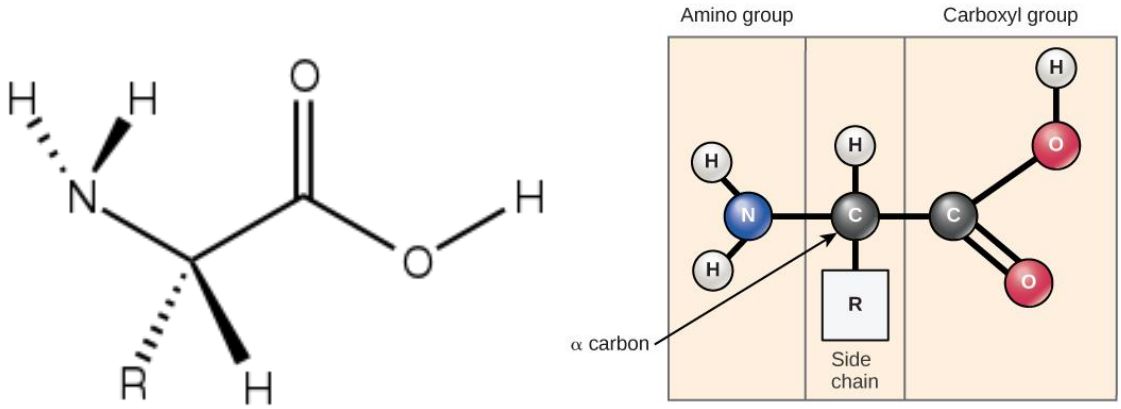

Figure 1. Generic structure of amino acids

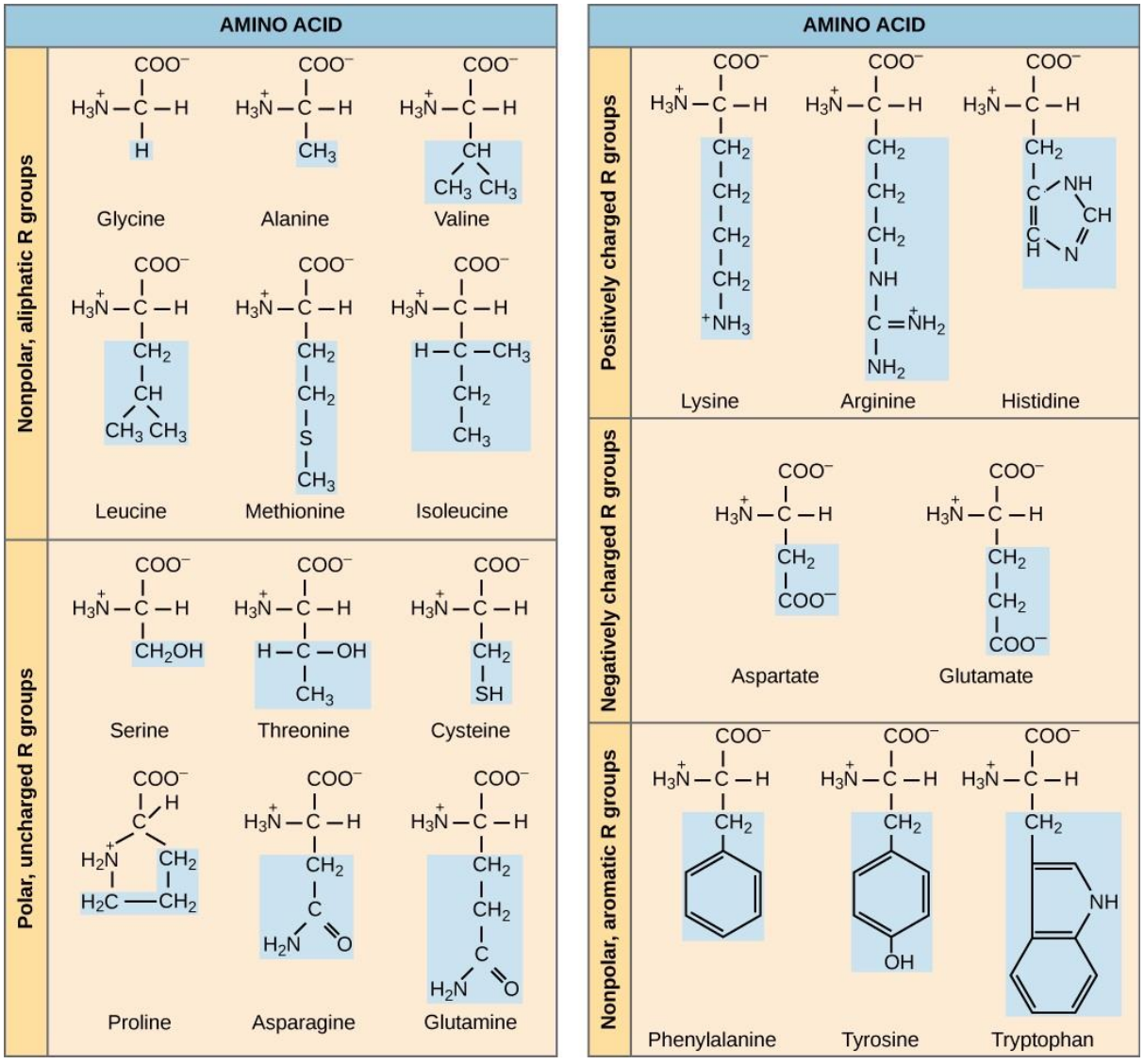

Figure 2. The 20 amino acids commonly found in proteins and their structures

Peptide bond

Peptide bond formation is a dehydration synthesis reaction or condensation reaction between amino acids. The carboxyl group of one amino acid is linked to the amino group of the incoming amino acid. In the process, a molecule of water is released. The resulting four-atom functional group -C(=O)NH- is called an amide group or (in the context of proteins) a peptide group.

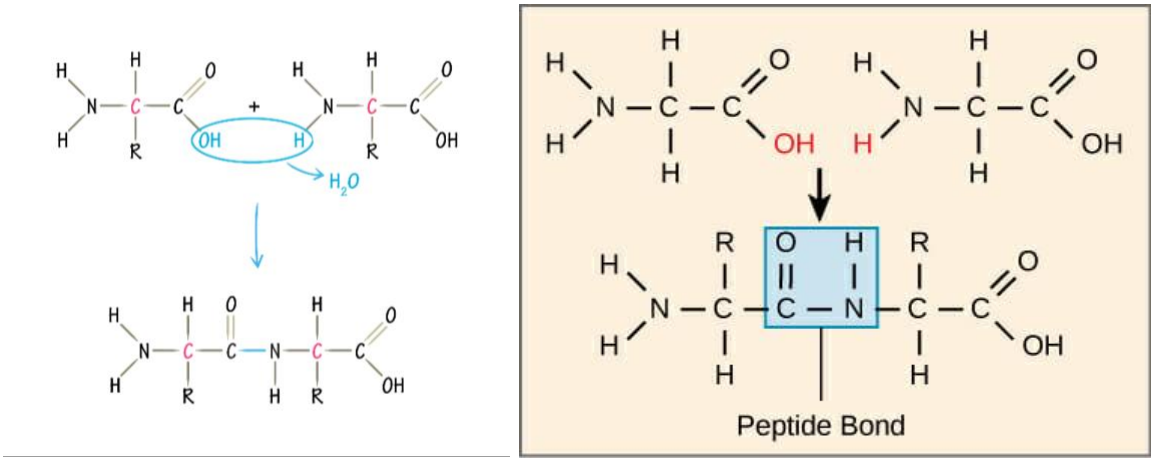

Figure 3. Peptide bond formation

Protein Structure

There are four levels in proteins structure: primary, secondary, tertiary, and quaternary.

Primary Structure of Proteins

The primary structure of a protein is the linear sequence of the side chains that are connected to the protein backbone. Each protein has a unique sequence of amino acid residues that cause it to fold into a distinctive shape that allows the protein to function properly. An example of proteins with primary structures are insulin.

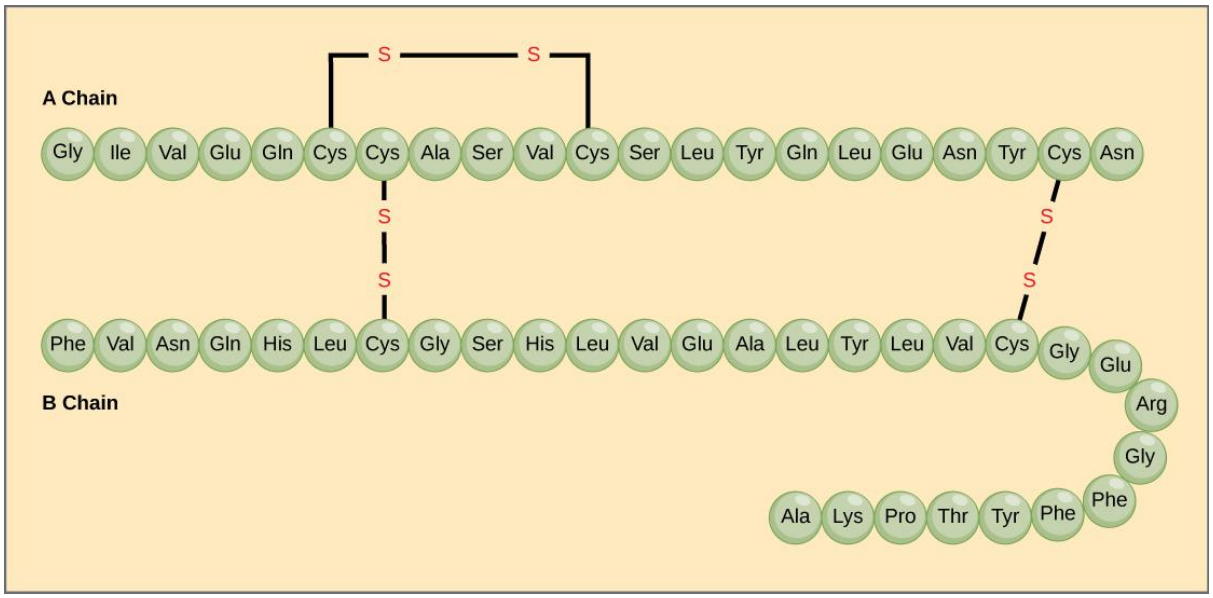

Figure 4: Primary structure of human insulin

Secondary Structure

Hydrogen bonding causes protein chains to fold and align to produce orderly patterns called secondary structures.

- The **α-helix** is a single protein chain twisted to resemble a coiled helical spring.
- The **α-helix** is held in this shape by hydrogen bonding interactions between amide groups, with the side chains extending outward from the coil.
- The amount of **α-helix** coiling in proteins is highly variable.
- The **β-pleated sheet** is another secondary structure is, in which several protein chains lie side by side, held by hydrogen bonds between adjacent chains.
- The **β-pleated sheet** structure is less common than the **α-helix.**
- It is found extensively only in the protein of silk.

Tertiary Structure of Proteins

- The tertiary structure of a protein refers to the bending and folding of the protein into a specific three-dimensional shape.
- These structures result from four types of interactions between the R side chains of the amino acids residues:

    1. **Disulfide bridges** can form between two cysteine residues that are close to each other in the same chain, or between cysteine residues in different chains. These bridges hold the protein chain in a loop or some other 3D shape.

    2. **Salt bridges** are attractions between ions that result from the interactions of the ionized side chains of acidic amino acids (—COO-) and the side chains of basic amino acids (—NH3 +).

    3. **Hydrogen bonds** can form between a variety of side chains, especially those that contain: Hydrogen bonding also influences the secondary structure, but here the hydrogen bonding is between R groups, while in secondary structures it is between the C=O and NH portions of the backbone.

    4. **Hydrophobic interactions** result from the attraction of nonpolar groups, or when they are forced together by their mutual repulsion of the aqueous solvent. These interactions are particularly important between the benzene rings in phenylalanine or tryptophan.

Quaternary Structure of Proteins

Quaternary structure is the arrangement of the subunits to form a larger protein.

- Two or more polypeptide chains are held together by disulfide bridges, salt bridges, hydrogen bond, or hydrophobic interactions, forming a larger protein complex.
- Each of the polypeptide subunits has its own primary, secondary, and tertiary structure.

Protein Denaturation

Protein denaturation occurs when the folded native structures break down into smaller units due to exposure to high temperatures or pH values, which disrupt the stabilizing structures. The structure becomes random and disorganized.

- Proteins can be denatured by heavy-metal ions such as Hg^{2+}, Ag^{+} , and Pb^{2+} that interact with -SH and carboxylate groups. Heavy metals form bonds to thiol groups and precipitate proteins as insoluble heavy-metal salts
- Heavy-metal poisoning is often treated with large doses of raw egg white and milk; the proteins in the egg (albumin) and milk (casein and whey) bind to the metal ions, forming a precipitate, which

- Most proteins are biologically active only over a temperature range of 0 °C to 40 °C.
  - **Heat and ultraviolet light**: Disrupt hydrogen bonds and ionic attractions by making molecules vibrate too violently; produce coagulation, as in cooking an egg.
- **Strong acids or bases**: Disrupt hydrogen bonds and ionic attractions; prolonged exposure results in hydrolysis of protein.
- **Detergents**: Disrupt hydrogen bonds, hydrophobic interactions, and ionic attractions