Amino Acids (a.a.)

More than 300 different amino acids have been described in nature, only twenty are commonly found as constituents of mammalian proteins. Each amino acid (except for proline) has a carboxyl group, a primary amino group, and a distinctive side chain (R group) bonded to the α-carbon atom.

At physiological pH (approximately pH 7.4), the carboxyl group is dissociated, forming the negatively charged carboxylate ion (\(-\text{COO}^-\)), and the amino group is protonated (\(-\text{NH}_3^+\)). In proteins, almost all of these carboxyl and amino groups are combined in peptide linkage, and in general are not available for chemical reaction except for hydrogen bond formation.
Classification of α. α.:
It is useful to classify the a.a. according to the properties of their side chains, that is, whether they are nonpolar or polar.

A- Amino acids with nonpolar side chains:
These amino acids do not bind or give off protons or participate in hydrogen or ionic bonds.

\[
\begin{align*}
\text{Glycine} & \quad H_2N-C-CO2H \\
\text{Ala} & \quad H_2N-C-CO2H \\
\text{Val} & \quad H_2N-C-CO2H \\
\text{Leucine} & \quad H_2N-C-CO2H \\
\text{Isoleucine} & \quad H_2N-C-CO2H \\
\text{Tryptophan} & \quad H_2N-C-CO2H \\
\text{Methionine} & \quad H_2N-C-CO2H \\
\text{Proline} & \quad H_2N-C-CO2H \\
\end{align*}
\]
Location of nonpolar amino acids in proteins:
The side chains of the nonpolar amino acids tend to cluster together in the interior of protein, this phenomenon is the result of the hydrophobicity of nonpolar R-groups which give the proteins its three-dimensional shape.

Sickle cell disease is a pathology that results from the substitution of polar glutamate by nonpolar Valine in the β subunits of hemoglobin.

Proline: proline differs from other a.a. in that proline's side chain and α-amino N form a rigid five membered ring structure.

β-Amino acids with uncharged polar side chains:
These amino acids have zero net charge at neutral pH, the side chain of cysteine and tyrosine can lose a proton at an alkaline pH.

\[
\begin{align*}
\text{Serine} & : & +H_2N-C-CO2H & \quad & \text{Threonine} & : & +H_2N-C-CO2H & \quad & \text{Tyrosine} & : & +H_2N-C-CO2H \\
& & H & \quad & H & \quad & H_2 & \quad & H_2 & \quad & H & \\
& & H-C-OH & \quad & H-C-OH & \quad & CH_2 & \quad & CH_2 & \quad & \text{O} & \\
& & H & \quad & H & \quad & \text{O} & \quad & \text{O} & \quad & \text{SH} \\
\text{Asparagine} & : & +H_2N-C-CO2H & \quad & \text{Glutamine} & : & +H_2N-C-CO2H & \quad & \text{Cysteine} & : & +H_2N-C-CO2H \\
& & CH_2 & \quad & CH_2 & \quad & CH_2 & \quad & \text{O} & \quad & \text{O} & \\
& & \text{N} & \quad & \text{N} & \quad & \text{N} & \quad & \text{SH} & \quad & \text{SH} & \\
\end{align*}
\]
C- Amino acids with acidic side chains:
These a.a. are proton donors at physiological pH. The side chains of these a.a. are fully ionized containing a negatively charged carboxylate group (\(-\text{COO}^\)).

\[
\begin{align*}
\text{Aspartic acid} & : & \text{H}_3\text{N} & -\text{C} - \text{COOH} & \text{H} & + \\
\text{CH}_2 & & \text{O} & \text{C} - \text{O} & \text{H} & \text{H} \\
\text{CH}_2 & & & & & + \text{H}_3\text{N} - \text{C} \text{COOH} \text{CH}_2 \\
\text{O} & \text{C} & \text{OH} & & & \text{CH}_2 \\
\text{CH}_2 & & & & & \text{CH}_2 \\
\text{CH}_2 & & & & & \text{CH}_2 \\
\text{N-H} & & & & & \text{NH}_3 \\
\text{N-H} & & & & & \text{NH}_2 \\
\text{N-H} & & & & & \text{NH}_2 \\
\end{align*}
\]

D- Amino acid with basic side chains:
The side chain of the basic amino acids accept protons at physiological pH and fully ionized and positively charged.

\[
\begin{align*}
\text{Histidine} & : & \text{H}_3\text{N} & -\text{C} - \text{COOH} & \text{H} & + \\
\text{CH}_2 & & \text{C} - \text{C} & \text{H} & \text{H} & \text{H} \\
\text{C} = \text{NH} & & & & & + \text{H}_3\text{N} - \text{C} \text{COOH} \text{CH}_2 \\
\text{CH}_2 & & & & & \text{CH}_2 \\
\text{CH}_2 & & & & & \text{CH}_2 \\
\text{N-H} & & & & & \text{NH}_3 \\
\end{align*}
\]

\[
\begin{align*}
\text{Lysine} & : & \text{H}_3\text{N} & -\text{C} - \text{COOH} & \text{H} & + \\
\text{CH}_2 & & \text{C} - \text{C} & \text{H} & \text{H} & \text{H} \\
\text{CH}_2 & & & & & + \text{H}_3\text{N} - \text{C} \text{COOH} \text{CH}_2 \\
\text{CH}_2 & & & & & \text{CH}_2 \\
\text{CH}_2 & & & & & \text{CH}_2 \\
\text{N-H} & & & & & \text{NH}_3 \\
\end{align*}
\]

\[
\begin{align*}
\text{Arginine} & : & \text{H}_3\text{N} & -\text{C} - \text{COOH} & \text{H} & + \\
\text{CH}_2 & & \text{C} - \text{C} & \text{H} & \text{H} & \text{H} \\
\text{CH}_2 & & & & & + \text{H}_3\text{N} - \text{C} \text{COOH} \text{CH}_2 \\
\text{CH}_2 & & & & & \text{CH}_2 \\
\text{CH}_2 & & & & & \text{CH}_2 \\
\text{N-H} & & & & & \text{NH}_3 \\
\text{N-H} & & & & & \text{NH}_2 \\
\end{align*}
\]
Optical properties of Amino acids:
The \(\alpha\)-Carbon of each a.a. is attached to four different chemical groups and is, therefore, a chiral or optically active carbon atom (Glycine is the exception? why).
Amino acids that have an asymmetric center at the \(\alpha\)-carbon can exist in two forms, designated D and L, that are mirror images of each other:

\[
\begin{align*}
\text{L-Alanine} & : & \text{D-Alanine} \\
\text{COOH} & & \text{HOOC} \\
\text{H} & & \text{H} \\
\text{H}_3N - C - \text{H} & & \text{H} - C - NH_2 \\
\text{CH}_3 & & \text{H}_3C \\
\end{align*}
\]

The two forms in each pair are termed stereoisomers, optical isomers, or enantiomers. All a.a. are found in proteins are of the L-configuration. However, D-a.a. are found in some antibiotics and plant and bacterial cell walls.
Amino acids did not participate in protein synthesis: these amino acids play an important role in biological operations of the human body but did not participate in protein synthesis. For example, Creatine, Ornithine, Citrulline, Phenytoxin, and Dihydroxy phenylalanine.

Essential Amino acids:
These amino acids did not produced by the body or produced in a little amounts and should be taken with dietary:
- Methionine, phenylalanine, Leucine, Valine, Lysine, Isoleucine, Threonine, Tryptophane.

Acidic and Basic properties of Amino acids:
Amino acids in aqueous solution contain weakly acidic α-carboxyl groups and weakly basic α-amino groups. In addition to an ionizable group in its side chain:

\[ HA \rightleftharpoons H^+ + A^- \]

strong acid \hspace{2cm} proton \hspace{2cm} or conjugate base

\[ K_a = \frac{[H^+][A^-]}{[HA]} \Rightarrow \text{p}K_a + \log \frac{[A^-]}{[HA]} = \text{pH} \]

Buffers: is a solution that resists change in pH following the addition of an acid or base and can created by mixing a weak acid (HA) with its conjugate base (A⁻) or weak base with its conjugate acid:

\[ +H_3N-C-COOH \quad \text{Alanine in acid solution} \quad \text{PH less than 2} \]

\[ H_3N-C-COO^- \quad \text{Alanine in neutral solution PH = 6} \]

\[ -H_3N-C-CO^- \quad \text{Alanine in basic solution PH > 10} \]
Primary structure

2. Secondary structure

3. Tertiary structure

4. Quaternary structure
د.الدلاء الإفتراض (1)

تشتت بين مجمور 1600 ق.م فراغا مع 1600 ك.م فضا 5

 diversos عند نجدة (2)
لا يوجد نص يمكن قراءته بشكل طبيعي من الصورة المقدمة.
لا يوجد نص يمكن قراءته بشكل طبيعي من الصورة المرفقة.
Globulins

A. 1. Antibodies

B. Histones

C. Prolamines

Globulins

1. Antibodies

2. Histones

3. Prolamines

Globulins

1. Antibodies

2. Histones

3. Prolamines

Hordon
Conjugated Proteins

Prostatic groups

Nucleo-proteins

Histone & Protamines

Glycoproteins

Chromoproteins
Derived proteins

Weakened proteins and partially denatured proteins

Denatured proteins are those proteins that have been altered in their structure, typically due to heat, pH changes, or other factors. This can lead to a loss of functionality and some denatured proteins may become insoluble.

Coagulated proteins

A type of protein that has undergone a heat-induced change in its structure. This can result in the formation of a solid mass, often referred to as a coagulum. Coagulated proteins can be found in various biological systems and are often associated with food processing and gel formation.
Proteins

The twenty amino acids commonly found in proteins are joined together by peptide bonds. The linear sequence of the linked a.a. contains the information necessary to generate a protein molecule with a unique three-dimensional shape.

Structure Of Proteins:

1. Primary Structure of Proteins

   The sequence of a.a. in a protein is called the primary structure of the protein. Many genetic diseases result in proteins with abnormal a.a. sequences which cause improper folding and loss or impairment of normal function.

   Peptide bond:

   In proteins, amino acids are joined covalently by peptide bonds which are amide linkage between the α-carboxyl group of one amino acid and the α-amino group of the other. 

   

   \[ \text{Primary Structure} \]

   - Peptide bonds are not broken by conditions that denature proteins such as heating or high concentration of urea.
   - The free amino end of the peptide chain (N-terminal) is written to the left and the free carboxyl end (C-terminal) to the right.

   

   [Diagram of peptide bond formation between Valine and Alanine]
2. Secondary Structure of Proteins:

The polypeptide backbone does not assume a random three-dimensional structure, but instead generally forms regular arrangements of units that are located near to each other in the linear sequence. These arrangements are termed the secondary structure of the polypeptide:

A. \( \alpha \)-Helix: is the most known helix. It is a spiral structure consisting of a tightly packed, coiled polypeptide backbone core with the side chain of the component amino acid extending outward from the central axis.

Hydrogen bonds stabilize an \( \alpha \)-helix, and extend up and are parallel to the spiral from the carboxyl oxygen of one peptide bond to the \(-NH-\) group of a peptide linkage four residues ahead in the polypeptide.

\[ \text{\( \alpha \)-Helix showing peptide backbone} \]
Each turn of an α-helix contains 3.6 amino acids.

β-sheets: is another form of secondary structure in which all of the peptide bond components are involved in hydrogen bonding. There are two types of β-sheets:

Parallel: Poly peptide chains are arranged parallel to each other.

Anti-parallel: Poly peptide chains are arranged anti-parallel to each other.

3. Tertiary Structure of Proteins:

The tertiary structure refers to the folding of domains (the basic units of structure and function), and to the final arrangement of domains in the poly peptide.

Domains: are the fundamental functional and three-dimensional structural units of poly peptides.

Interactions stabilizing tertiary structure:

1. Disulfide bonds: is a covalent linkage formed from the sulfhydryl group (–SH) of each of two cysteine residues.

2. Hydrophobic interactions: Amino acids with nonpolar side chains tend to be located in the interior of the polypeptide molecule, where they associate with other hydrophobic amino acids.


4. Ionic interactions: Negatively charged groups, such as the carboxyl group (–COO⁻) in the side chain of aspartate or glutamate can interact with positively charged groups such as the amino group (–NH₃⁺) in the side chain of lysine.
4. Quaternary Structure of Proteins:

Many proteins consist of single polypeptide chain and are defined as monomeric proteins. However, others may consist of two or more polypeptide chains. The arrangement of these polypeptide chains or subunits is called the quaternary structure of the protein.

Subunits are held together by noncovalent interactions (for example, $\alpha$-hydrogen bonds, ionic bonds, and hydrophobic interactions). Subunits may either function independently of each other, or may work cooperatively, as in hemoglobin.
Carbohydrates

1. Overview
Carbohydrates are the most abundant organic molecules in nature. They have a wide range of functions, including providing a significant fraction of energy in the diet of most organisms, acting as a storage form of energy in the body, and serving as a cell membrane component. Also a structural component of many organisms.

2. Classification and structure of Carbohydrates
Monosaccharides (simple sugars) can be classified according to the number of carbon atoms they contain.

<table>
<thead>
<tr>
<th>Generic names</th>
<th>examples</th>
</tr>
</thead>
<tbody>
<tr>
<td>3 carbons: Trioses</td>
<td>Glyceraldehyde</td>
</tr>
<tr>
<td>4 carbons: Tetroses</td>
<td>Erythrose</td>
</tr>
<tr>
<td>5 carbons: Pentoses</td>
<td>Ribose</td>
</tr>
<tr>
<td>6 carbons: Hexoses</td>
<td>Glucose</td>
</tr>
<tr>
<td>7 carbons: Heptoses</td>
<td>Sedoheptulose</td>
</tr>
<tr>
<td>9 carbons: Nonoses</td>
<td>Neuraminic acid</td>
</tr>
</tbody>
</table>

Carbohydrate with an aldehyde are called aldoses.
For example, glyceraldehyde is an aldose, whereas dihydroxyacetone is a ketose.

Disaccharides contain two monosaccharide units
Oligosaccharides contain from three to about ten monosaccharide units,
Poly saccharides contain about hundreds of sugar units.
Isomers and Epimers

Compounds have the same chemical formula but have different structures are called isomers. For example, fructose, glucose, mannose, and lactose are all isomers of each other, having the same chemical formula C6H12O6.

Carbohydrate isomers that differ in configuration around only one specific carbon atom (with the exception of the Carboxyl Carbon) are defined as epimers of each other. For example, glucose and galactose are C-4 epimers—their structures differ only in the position of the OH groups at Carbon 4. (Note: the carbons in sugars are numbered beginning at the end that contains the Carboxyl Carbon—that is, the aldehyde or ketone group.

Glycosidic bond

Lactose = galactosyl-β(1→4)-glucose
2. Enantiomers:
A special type of isomerism is found in the pairs of structures that are mirror images of each other. These mirror images are called enantiomers, and the two members of the pair are designated as D- and L-sugar.

\[
\begin{array}{c|c}
\text{CH}_3 & \text{CH}_2 \\
\text{H}_2\text{C}_\text{O} & \text{H}_2\text{C}_\text{O} \\
\text{H}_2\text{C}_\text{OH} & \text{H}_2\text{C}_\text{OH} \\
\text{H}_2\text{C}_\text{O} & \text{H}_2\text{C}_\text{O} \\
\text{CH}_2\text{OH} & \text{CH}_2\text{OH} \\
\text{L-Glucose} & \text{D-Glucose}
\end{array}
\]

The vast majority of the sugars in humans are D-sugar. Enzymes are able to convert D- to L-isomers called racemases.

3. Cyclization of monosaccharides
Less than one percent of each of the monosaccharides with five or more carbons exists in the open chain (acyclic) form. Rather, they are predominantly found in the ring (cyclic) form, in which the aldehyde or ketone group has reacted with an alcohol of the same sugar, making the carbonyl carbon asymmetric.

Pyranose refers to a six-membered ring consisting of five carbons and one oxygen.

a. Anomeric Carbon: Cyclization creates an anomeric carbon (the former carbonyl carbon), generating the \(\alpha\) and \(\beta\) configurations of the sugar, for example \(\alpha\)-D-glucopyranose and \(\beta\)-D-glucopyranose and that they are in equilibrium with each other in sugar solution.
Joining of monosaccharides:

Monosaccharides can be joined to form disaccharides, oligosaccharides, and polysaccharides.

Important disaccharides include lactose (galactose + glucose), sucrose (glucose + fructose) and maltose (glucose + glucose).

Important polysaccharides include branched glycogen (from animal sources) and starch (plant sources) and unbranched cellulose (plant sources) each is a polymer of glucose. The bond that link sugars are called glycosidic bonds, these are formed by enzymes called glycosyltransferases, that use nucleotide sugars such as UDP-glucose as a substrate.

Naming glycosidic bonds = according to the number of the connected carbons and also with regard to the position of the anomeric hydroxyl group of the sugar involved in the bond, if this anomeric hydroxyl is in the α-configuration, the linkage is an α-bond for example Lactose is synthesized by forming a glycosidic bond between carbon 1 of β-galactose and carbon 4 of glucose, the linkage therefore a β(1→4) glycosidic bond.
4. Complex Carbohydrates:

Carbohydrates can be attached by glycosidic bonds to non-carbohydrate structures including Purine, Pyrimidine bases found in nucleic acids, aromatic ring (such as those found in steroids and bilirubin), protein (found in glycoproteins), lipids (found in glycolipids).

N- and O-glycosides: If the group on the non-carbohydrate structure molecule to which the sugar is attached is an -NH₂ group, the structure is an N-glycoside and the bond is called an N-glycosidic link. If the group is an -OH, the structure is an O-glycoside, and the bond is an O-glycosidic link.
Digestion of Carbohydrates:

The principal sites of dietary carbohydrate digestion are the mouth and intestinal lumen.

A family of glycosidases that degrade carbohydrates into their reducing sugar components.

Further digestion of carbohydrates occurs in the small intestine by pancreatic enzymes.

When the acidic stomach contents reach the small intestine, they are neutralized by bicarbonate secreted by the pancreas, and pancreatic α-amylase continues the process of starch digestion.

Digestive Enzyme Deficiencies:

Alterations in disaccharide degradation can be caused by a variety of intestinal diseases, malnutrition, or drugs that injure the mucosa of the small intestine. For example, brush border enzymes are rapidly lost in normal individuals with severe diarrhea, causing a temporary acquired enzyme deficiency.
Racemic mixture

Dextrorotatory

Enantiomers

Levorotatory

Structural Formulas for monosaccharides

\( \text{Structural Formulas for monosaccharides} \)

\[ \begin{align*}
\text{D-} & \quad \text{L-}
\end{align*} \]

\( \text{D-} \quad \text{L-} \)

\[ \begin{align*}
\text{D-} & \quad \text{L-}
\end{align*} \]

\( \text{D-} \quad \text{L-} \)

\[ \begin{align*}
\text{D-} & \quad \text{L-}
\end{align*} \]

\( \text{D-} \quad \text{L-} \)

\[ \begin{align*}
\text{D-} & \quad \text{L-}
\end{align*} \]

\( \text{D-} \quad \text{L-} \)

\[ \begin{align*}
\text{D-} & \quad \text{L-}
\end{align*} \]

\( \text{D-} \quad \text{L-} \)

\[ \begin{align*}
\text{D-} & \quad \text{L-}
\end{align*} \]

\( \text{D-} \quad \text{L-} \)

\[ \begin{align*}
\text{D-} & \quad \text{L-}
\end{align*} \]

\( \text{D-} \quad \text{L-} \)

\[ \begin{align*}
\text{D-} & \quad \text{L-}
\end{align*} \]

\( \text{D-} \quad \text{L-} \)
6. Changes in the enzyme activity in the presence of X are shown in the pictures. 3. Add the following reagents:

- Fehling Solution: CuSO₄ + NaOH + Na₂K₄[Fe(CN)₆]
- Benedict's Solution: CuSO₄ + Na₂CO₃ + NaAc Citrate
- Barfoeds Solution: Cu(C₂H₃COO)₂ + acetic acid

u. Tollens test: ammonium Ag solution - Silver mirror
Derived lipids: produced from hydrolysis of simple and compounds lipids and addition to hydrophobic portion such as

1. FA
2. Terpenes
3. Steroids

1) Terpenes: Biological compounds consist of isoprene units such as carphor, 
β-carotene, lycopene, and provitamin A. Lycopene and phytol that occurs in chlorophyll.

2) Squalene: occurs in liver of shark and intermedial compound in biosynthesis of cholesterol and synthesis in body of human from acetic acid and converted by multisteps to cholesterol by joining six units of isoprene.
Transcription: The first step is to transfer the genetic code from DNA to tRNA inside the nucleus.

The genetic code, called Codon, consists of three nucleotides and is specific to an amino acid. Examples:

- **AUG** for methionine
- **CAU** for leucine