# Enzyme structure

## 1. Protein structure :

Proteins are polymers of amino acids linked by a peptide bond.

**1. 1. Primary structure :**

This is the description of the polypeptide chain that forms the protein. It is determined by :

- Number of polypeptide chains.
- Number and nature of the constituent amino acids.
- Sequence of amino acids in each chain, starting from the N-terminal amino acid to the C-terminal.
- Location of inter- and intra-chain disulfide bridges.

*Example :*

Bovine insulin consists of two polypeptide chains of 21 and 30 amino acids. It contains three disulfide bridges : one intra-chain bridge linking amino acids 6 and 11, and two inter-chain bridges between amino acids A7–B7 and A20–B19.

**1. 2. Secondary structure :**

It is a regular form adopted by part of the protein (β-sheet, α-helix, turn). In other words, it is the conformation of the peptide bonds.

The α-helix structure is characterized by :

- ✓ The cohesion of the structure is due to hydrogen bonds between the C=O and N-H atoms of two superimposed peptide bonds. Van der Waals interactions, established by the tightly packed atoms at the core of the helix, give it additional stability.
- ✓ The helix turn contains 3.6 amino acids.
- ✓ The side chains of the amino acids (radicals) are located outside the helix.

The β-sheet structure is characterized by :

- ✓ The cohesion of this structure is due to hydrogen bonds between C=O and N-H atoms between two elongated polypeptide chains or between two regions of the same chain.
- ✓ Formation of parallel sheets and other antiparallel sheets.
- ✓ The side chains of amino acids (radicals) are located on either side of the sheet.

**1. 3. Tertiary structure :**

This is the final form of the protein. The assembled protein folds into a precise three-dimensional structure :

*Globular proteins :* most proteins have a compact form (like a small cloud).

*Fibrous protein s*: these are long and thread-like. They are formed from a single α-helix and can bind together to form strong fibers.

This structure is stabilized by hydrogen bonds, hydrophobic interactions, salt interactions, disulfide bridges, and Van der Waals forces.

### *1.4. Quaternary structure :*

The quaternary structure describes the association of several protein subunits by non-covalent bonds (hydrogen, ionic, and very often hydrophobic) to form the final protein.

The assembly of subunits occurs spontaneously and is highly specific. It is more stable than each isolated subunit.

The association between subunits is achieved through contact zones between protomers or monomers. These zones must be mobile in order for the oligomer to perform its functions.

## 2. Enzyme types :

### 2.1. Monomeric enzymes :

Some enzymes consist of a single subunit or a single polypeptide chain. These are most often secreted enzymes such as chymotrypsin and pancreatic ribonuclease (proteases).

### 2.2. Oligomeric enzymes :

Other enzymes, which are more numerous, consist of several polypeptide chains or subunits that are either identical (homo-oligomer) or different (hetero-oligomer) and linked by non-covalent bonds.

**Oligomeric protein :**

Has a globular form and comprises few subunits (2-8) (Oligo: few).

**Multimeric (polymeric) protein :**

Is often fibrillar and contains several subunits; more than 12.

## 3. Multi-enzymatic system :

Enzymes that catalyze a series of reactions in the same metabolic pathway can combine within a multienzyme complex whose molecular mass can reach several thousand units. These systems generally include a key enzyme that can be activated or inhibited by specific effectors (negative feedback, feedback control).

## 4. Allosteric enzymes :

### *4. 1. Generalities :*

This is a special category of enzymes that play a fundamental role in regulating metabolic pathways in all living organisms.

**Example :**

In the metabolic pathway : **A** ⟶ **B** ⟶ **C** ⟶ ……. ⟶ **Z**

The enzyme that catalyzes the first reaction is inhibited by product Z (feedback inhibition).

In fact, the enzyme reversibly binds Z at a site other than the catalytic site. In this case, Z is called an effector or allosteric ligand of the enzyme.

## *4. 2. Allostery :*

The term allostery (allos: Greek for “other,” “different”) comes from the fact that these enzymes are inhibited or activated by effectors, inhibitors, or activators that are sterically different from the substrate(s).

These effectors bind to sites distinct from the active site, called allosteric sites, through non-covalent bonds. Thus, the enzyme-effector complex is dissociable (reversible).

Effectors are therefore regulators of allosteric enzyme activity, since their binding results in a decrease or increase in the initial speed.

## *4. 3. Properties of allosteric enzymes :*

- They have a quaternary structure.
- They exhibit kinetic behavior that does not conform to the Michaelis function.
- They are subject to conformational changes without loss of biological activity. These changes are detectable by various physical or kinetic measurements.
- They generally have a regulatory function in metabolism, particularly in synthesis pathways.

## *4. 4. Cooperativity :*

Allosteric interactions between subunits of the same enzyme are cooperative interactions caused by the binding of a ligand (effector or modulator) to a specific site, modifying the binding of a second ligand to another site on the enzyme protein. In other words, the binding of a substrate molecule to one subunit may or may not promote the binding of other molecules to the remaining subunits.

This cooperativity is reflected in the sigmoidal curve that links the initial speed ($V_0$) to the ligand concentration ([S]).