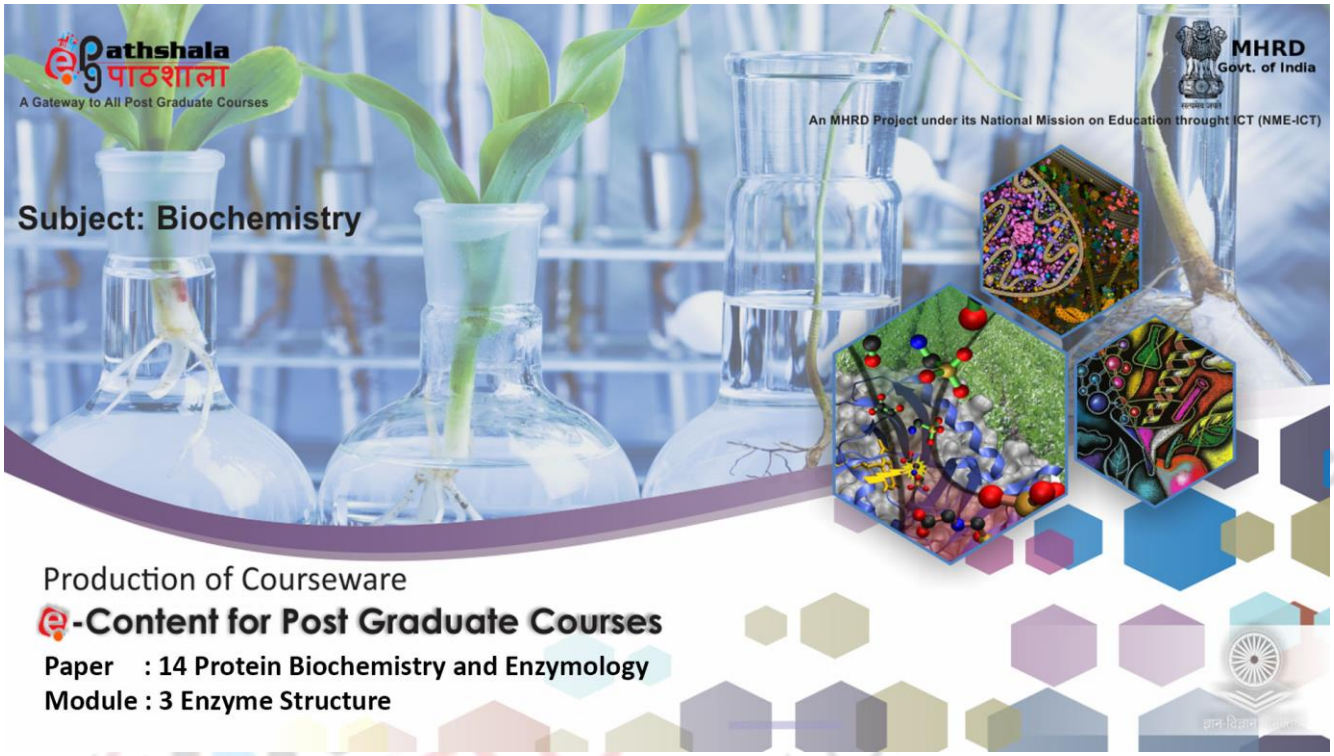

Production of Courseware

e-Content for Post Graduate Courses

Paper : 14 Protein Biochemistry and Enzymology

Module : 3 Enzyme Structure

athshala पाठशाला

MHRD Govt. of India

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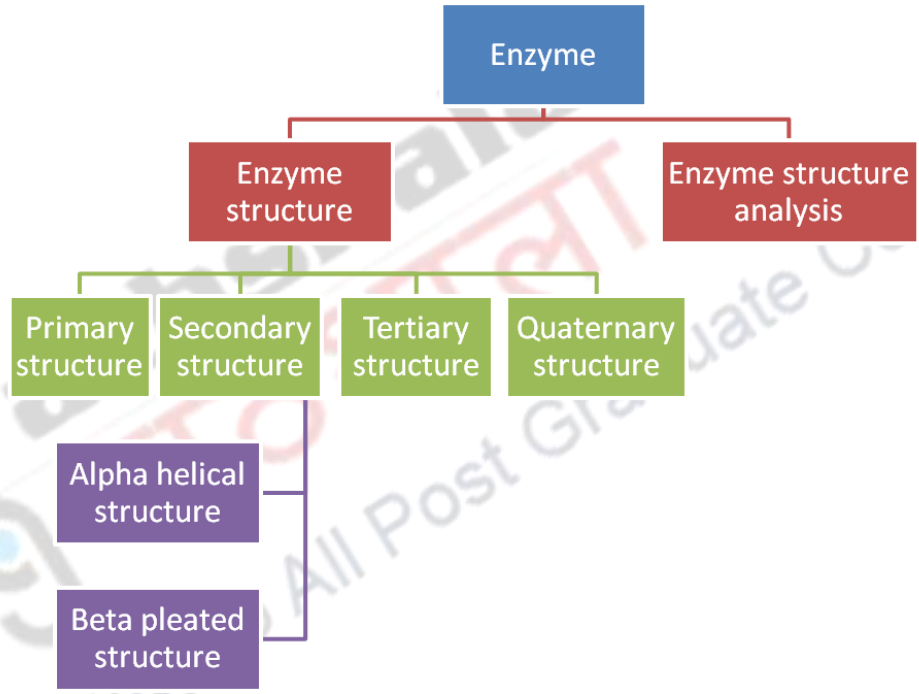
Description of Module	
Subject Name	Biochemstry
Paper Name	14
Module Name/Title	3 Enzyme Structure

1. Objectives

- Look at the various components of enzyme structure
- Understanding the types of enzyme structures in detail

2. Concept Map



3. Description

3.1 Enzymes

Enzymes are biological catalysts that increase the rate of reaction without affecting the reaction equilibrium. They work by lowering the activation energy (E_a) for a reaction, which leads to an increase in reaction rate and faster product formation.

Enzymatic reactions are also characterized by high substrate and reaction specificity and fewer side reactions. Enzymes have had several applications in areas of research and development, food and feed industry, pharmaceutical industry and other industries like detergent, textile, leather etc.

3.2 Enzyme structure

Enzymes have **four levels of structure**s as shown in Fig 1. These are:

- **Primary structure**
- **Secondary structure**
- **Tertiary structure**
- **Quaternary structure**

The enzyme structure ranges from a basic amino acid sequence to a three dimensional (3D) structure in a folded protein. The amino acid sequence in polypeptide chains in each enzyme is distinct and determines the three-dimensional shape. Further, it is the 3D structure of an enzyme that determines the enzyme activities. We will look at these structures in detail in the sections below.

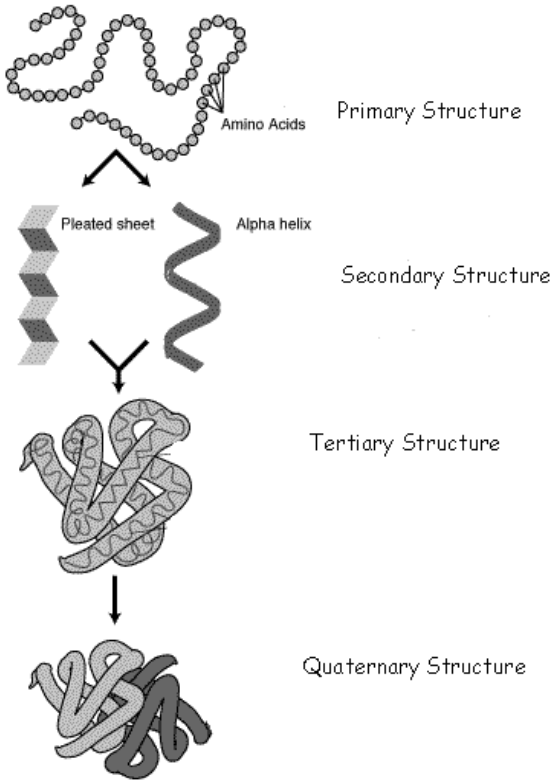


Fig 1

3.3.1 Primary structure

- The sequence of amino acids in an enzyme is the **primary structure**.

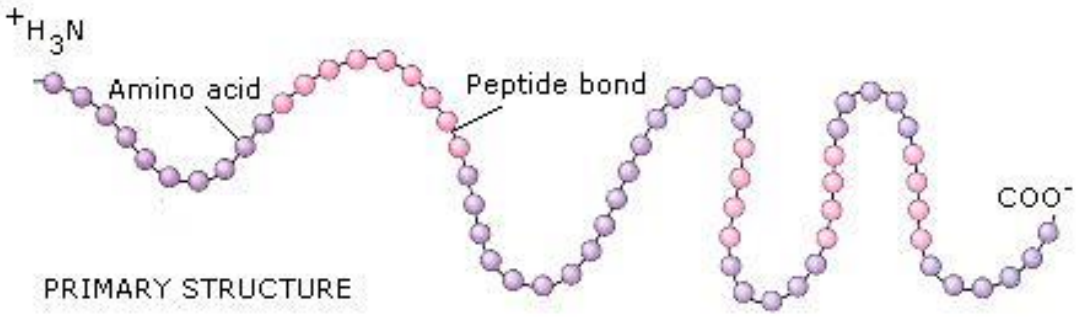


Fig. 2

- In the primary structure, the constituent amino acids are linked by peptide bonds (-CONH-) bonds (Fig 3).

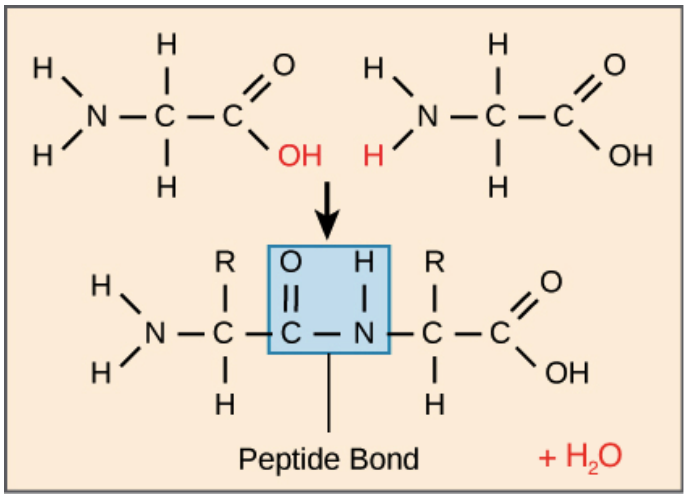


Fig. 3

- The peptide bond is formed between the amino group (-NH_2) of one amino acid and the carboxyl group (-COOH) of another, along with the release of water molecule.
- As mentioned above, the primary structure dictates three dimensional structures of the proteins. The different ways in which amino acids will be arranged in the chain will influence proper protein folding for the enzyme to be functionally active.

3.3.2 Secondary structure

The secondary structure in enzymes refers to the interaction of amino acids in a chain (primary structure) which are closely located. There are two types of secondary structures: helical (called **α helices**) and pleated sheets (called **β pleated sheets**).

Alpha helix

- The alpha helix is a helical structure, coiled around an axis. The helix is right-handed in nature.
- The alpha helix is characterized by intramolecular hydrogen bonds between the O atom of the C=O of each peptide bond in the strand and the N-H group of the peptide bond
- The side-chain substituents of the amino acids extend to the outside from the helix.

- The helix has about 3.6 amino acids per turn on an average, meaning that it will have 36 amino acids in 10 turns. The pitch is 5.4 Å

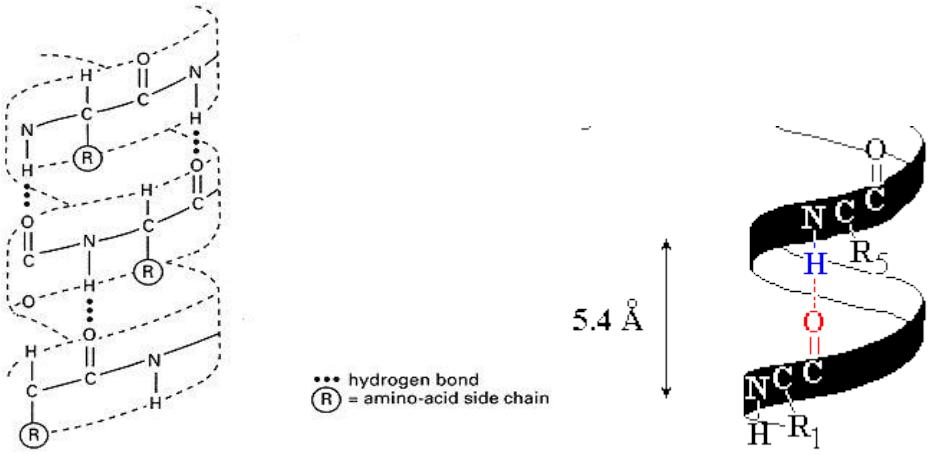


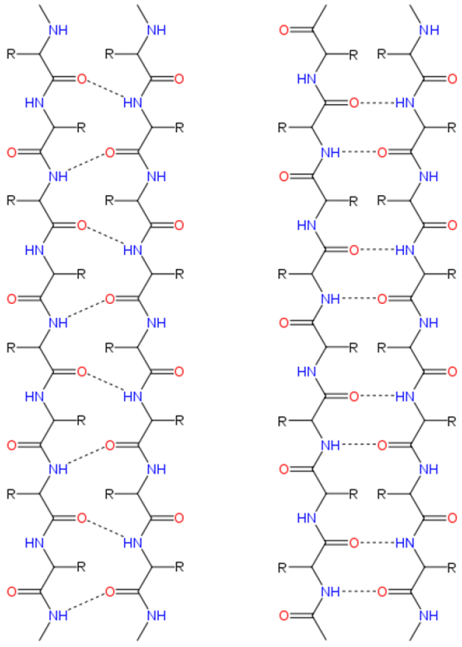
Fig. 4

Alpha helices form more readily in enzymes than any other possible conformations owing to the optimal use of internal hydrogen bonds is made in these arrangements for attaining stability.

Beta pleated sheet

The second form of secondary structure in enzymes is the beta pleated sheet. This structure is formed by intermolecular hydrogen bonding between two or more straight chains. The O atom of the C=O of peptide bond in one strand hydrogen bonds with the N-H group of the peptide bond in an adjacent strand.

Again, the two strands involved in the formation of beta pleated sheets can run either parallel to each other or anti-parallel to each other. If the amino groups of both chains are on the same side, the sheet are said to be parallel to each other. On the other hand, if the amino groups of both chains are on the opposite side, the chains are said to run in the opposite direction. In this case, the sheet is termed **antiparallel**. The anti-parallel ß-sheet is more stable than parallel sheet owing greater alignment in the hydrogen bonds.



Parallel **Anti-parallel**

Fig. 5

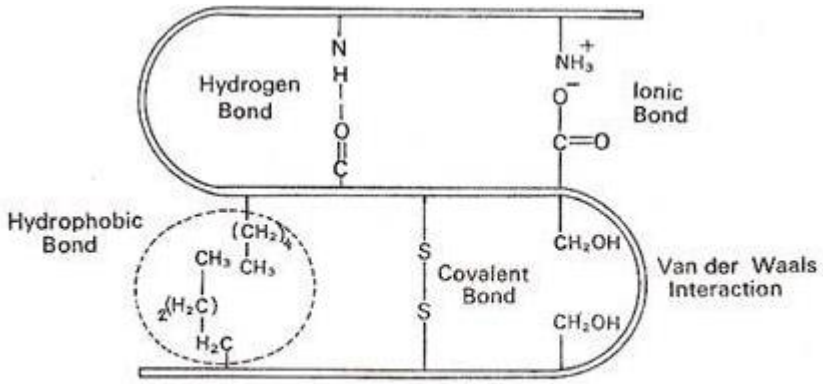
Difference between alpha helix and beta pleated sheet structure

Properties	**Alpha helix**	**Beta pleated sheet**
Structure	Right handed, helical	Sheet like
Formation	Formed by H bonds within the polypeptide chain	Formed by H bonds between two adjacent polypeptide chains
Side chains	Side Chains (R groups) orient out of the helix	Side chains (R groups) are directed both inside and outside the pleated structure
Types	Only one type	Can be of two types: parallel and antiparallel
Preferred amino acids	Ala, Leu, Met, Phe, Glu, Gln, His, Lys, Arg	Tyr, Trp, Phe, Met, Ile, Val, Thr, Cys

3.3.3 Tertiary structure

- The arrangement of amino acids in the three dimensional space defines the tertiary structure of enzymes.

- The protein molecule arranges itself three dimensionally in such a way as to achieve low energy and maximum stability.
- The various interactions involved in the formation/stabilization of a tertiary structure are Hydrogen bonds, polar-polar interaction, hydrophobic interaction, ionic interaction, formation of disulfide bonds, Van der Waals forces.



Various types of bonds or interactions found during the coiling of polypeptide.

Fig. 6

- Under physiologic conditions, the side chains of amino acids which are hydrophobic in nature such as phenylalanine or isoleucine, tend to remain buried within the protein/enzyme core, owing to their minimal affinity for the aqueous medium. The alkyl groups of Ala, Val, Leu, Ileu often form hydrophobic interactions between one-another. Acidic or basic amino acid side-chains are polar in nature, and therefore remain exposed on the enzyme surface, to allow for greater water solubility.

3.3.4 Quaternary structure

Sometimes, proteins or functional enzymes can be made up of more than one polypeptide chains, which are known as subunits. The interaction between these subunits is called the quaternary structure. Various

interactions, including H-bonding, disulfide-bridges and salt bridges are also involved in stabilizing the overall complex.

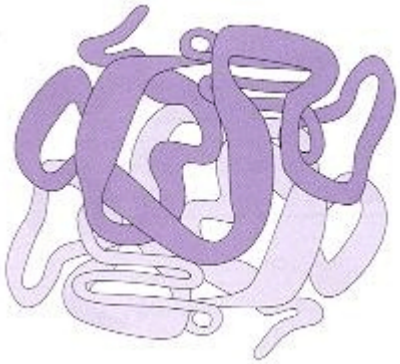


Fig. 7

4. **Enzyme Structure Analysis**

Analysis of enzyme/protein structure can be done with the help of following advanced analytical techniques/equipments.

- Determination of amino acids which are present in an enzyme and the molar ratios of each can be analyzed/determined by an **amino acid analyzer**.
- The sequence of amino acids in the enzyme can be analyzed by **peptide mapping, Edman degradation** or **mass spectroscopy**.
- The secondary structure of an enzyme can be determined by **circular dichroism spectroscopy** (CD).
- The tertiary structure of an enzyme can be determined by **fluorescence spectroscopy**.
- **X-ray crystallography** or **nuclear magnetic resonance** (NMR) analysis can be used to obtain a high-resolution analysis of the 3D structure of a enzyme.

4. Summary

In this lecture we learnt about:

- Enzyme structure has f**our levels** namely primary, secondary, tertiary and quaternary.
- The amino acid sequence of enzyme is called as its **primary structure.**
- The interaction of amino acids in a chain is the secondary structure in enzymes.
- The two types of secondary structures are helical (called **α helices**) and pleated sheets (called **β pleated sheets**).
- The arrangement of amino acids in three dimensional space is the **Tertiary structure**.
- **Quaternary structure refers to the interaction between protein subunits.**
- Analysis of enzyme structure can be done with the help of following advanced analytical techniques/equipments such as **amino acid analyzer, peptide mapping**, **Edman degradation** , **mass spectroscopy, circular dichroism spectroscopy**, **fluorescence spectroscopy, X-ray crystallography, nuclear magnetic resonance.**