FACULTY OF ENGINEERING AND TECHNOLOGY

Department of Biotechnology

PROTEIN CAN BE CLASSIFIED BY:

- Structure
- Biological function
- Shape and solubility
- Composition
- Nutritional basis

Protein structure prediction is the inference of the three-dimensional structure of a protein from its amino acid sequence—that is, the prediction of its folding and its secondary and tertiary structure from its primary structure. Structure prediction is fundamentally different from the inverse problem of protein design. Protein structure prediction is one of the most important goals pursued by bioinformatics and theoretical chemistry; it is highly important in medicine (for example, in drug design) and biotechnology (for example, in the design of novel enzymes).

CLASSIFICATION BY STRUCTURE

PRIMARY STRUCTURE

- The primary structure of proteins is defined as a linear sequence of amino acids joined together by peptide bonds.

- Peptide bonds and disulfide bonds are responsible for maintaining the primary structure.

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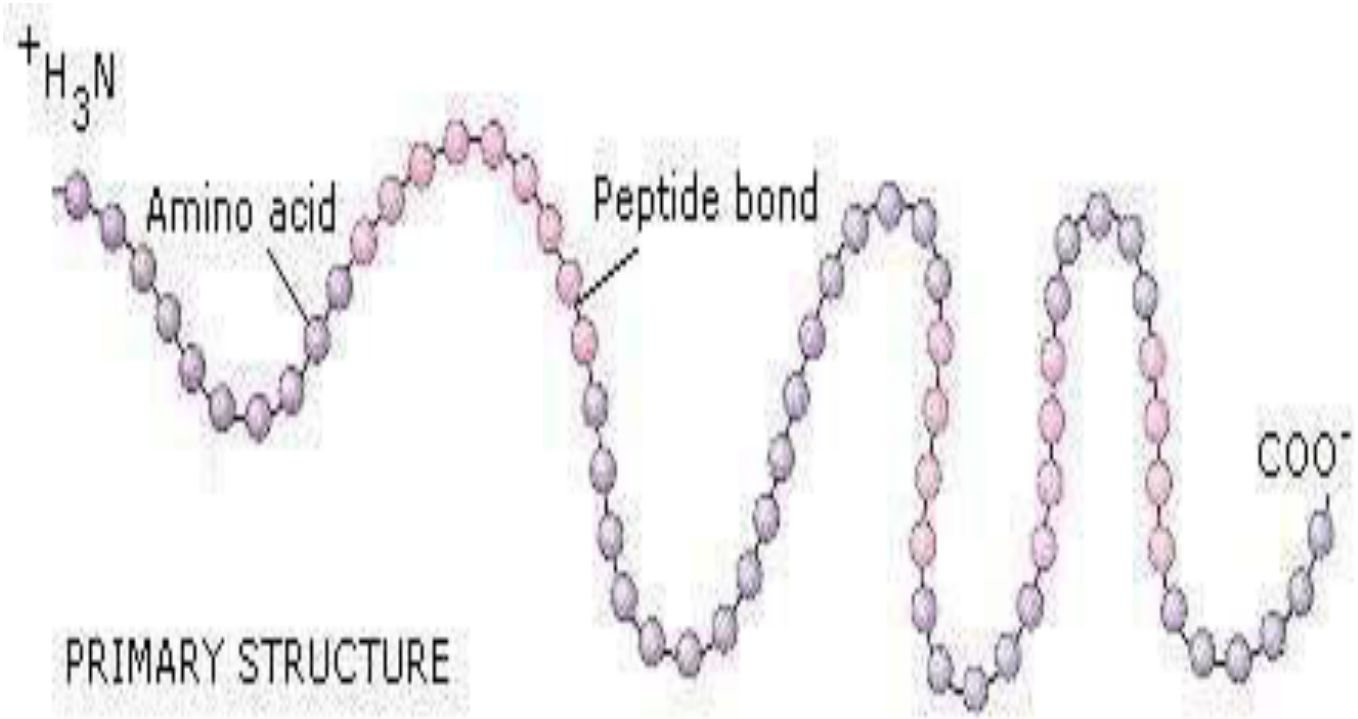
$^{+}H_3N$
Amino acid
Peptide bond
COO^{-}
PRIMARY STRUCTURE

SECONDARY STRUCTURE

- **The secondary structure of a protein is defined as a local spatial structure of a certain peptide segment, that is, the relative positions of backbone atoms of this peptide segment.**
- **H-bonds are responsible for stabilizing the secondary structure.**
- **Repeating units of Ca-C(=O)-N(-H)-Ca constitute the backbone of peptide chain.**
- **Six atoms, Ca-C(=O)-N(-H)-Ca, constitute a planer peptide unit.**

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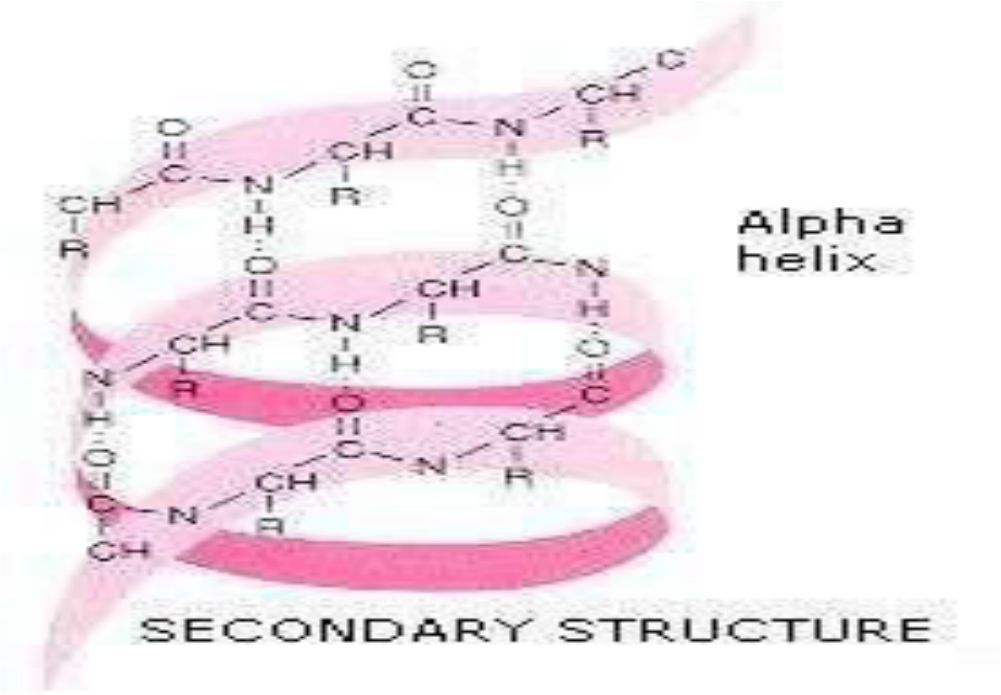
Alpha
helix
SECONDARY STRUCTURE

TERTIARY STRUCTURE

- **The tertiary structure is defined as the three-dimensional arrangement of all atoms of a protein.**

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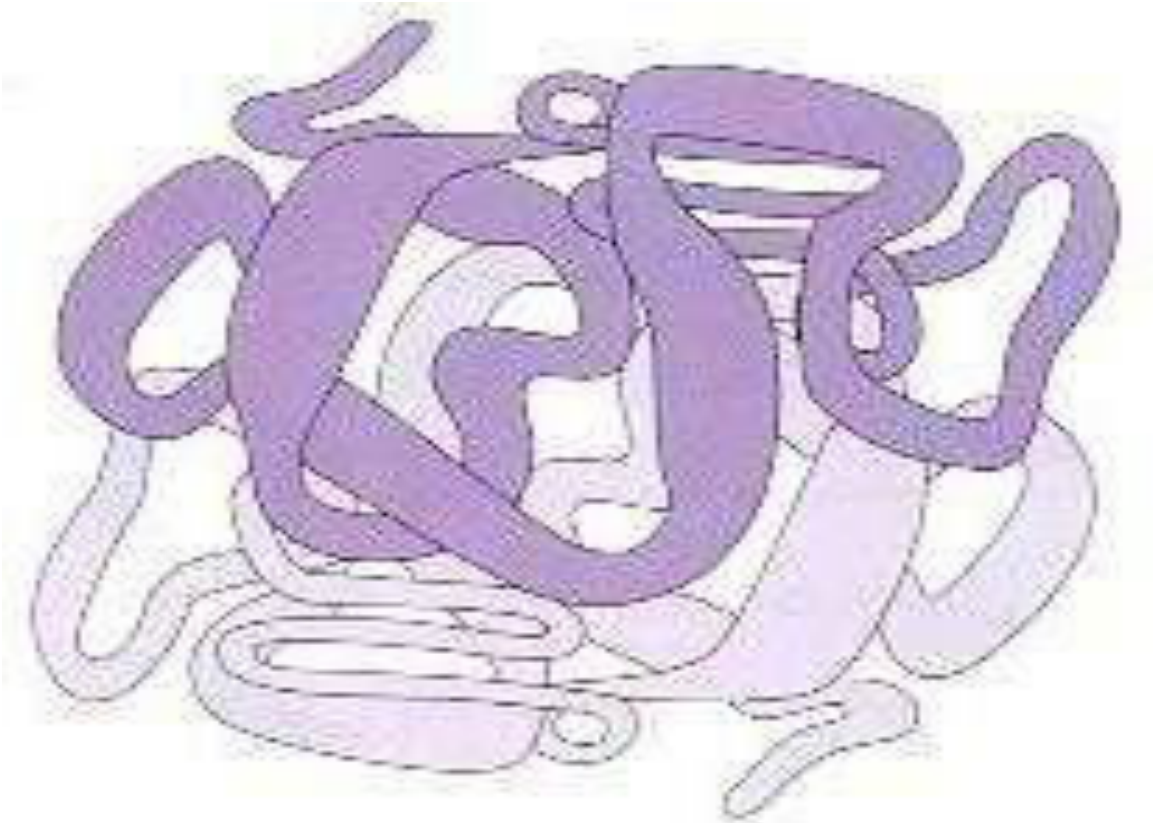

QUATERNARY STRUCTURE

The prediction of protein three-dimensional structure from amino acid sequence has been a grand challenge problem in computational biophysics for decades, owing to its intrinsic scientific interest and also to the many potential applications for robust protein structure prediction algorithms, from genome interpretation to protein function prediction.

More recently, the inverse problem — designing an amino acid sequence that will fold into a specified three-dimensional structure — has attracted growing attention as a potential route to the rational engineering of proteins with functions useful in biotechnology and medicine.

Methods for the prediction and design of protein structures have advanced dramatically in the past decade. Increases in computing power and the rapid growth in protein sequence and structure databases have fuelled the development of new data-intensive and computationally approaches for structure prediction.

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XYZ

abc

XYZ

abc

XYZ

abc

XYZ

abc

MCQs

1. A
2. A
3. A
4. A
5. A
6. A
7. A
8. A
9. A
10. A

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