

**Aim: Predict the secondary structure of a given amino acid sequence and mark Beta-pleated and alpha helix.**

**Theory:** Proteins are macromolecules and have four different levels of structure – primary, secondary, tertiary and quaternary.

### **Primary Structure**

There are 20 different standard L- $\alpha$ -amino acids used by cells for protein construction. Amino acids, as their name indicates, contain both a basic amino group and an acidic carboxyl group. This difunctionality allows the individual amino acids to join in long chains by forming peptide bonds: amide bonds between the -NH<sub>2</sub> of one amino acid and the -COOH of another. Sequences with fewer than 50 amino acids are generally referred to as peptides, while the terms, protein and polypeptide, are used for longer sequences. A protein can be made up of one or more polypeptide molecules. The end of the peptide or protein sequence with a free carboxyl group is called the carboxy-terminus or C-terminus. The terms, amino-terminus and N-terminus, describe the end of the sequence with a free  $\alpha$ -amino group. The amino acids differ in structure by the substituent on their side chains. These side chains confer different chemical, physical, and structural properties to the final peptide or protein. Depending on the side-chain substituent, an amino acid can be classified as being acidic, basic or neutral. Although 20 amino acids are required for synthesis of various proteins found in humans, we can synthesize only ten. The remaining 10 are called essential amino acids and must be obtained in the diet. The amino acid sequence of a protein is encoded in DNA. Proteins are synthesized by a series of steps called transcription (the use of a DNA strand to make a complimentary messenger RNA strand - mRNA) and translation (the mRNA sequence is used as a template to guide the synthesis of the chain of amino acids which make up the protein). Often, post-translational modifications, such as glycosylation or phosphorylation, occur which are necessary for the biological function of the protein. While the amino acid sequence makes up the primary structure of the protein, the chemical/biological properties of the protein are very much dependent on the three-dimensional or tertiary structure.

### **Secondary Structure**

Stretches or strands of proteins or peptides have distinct, characteristic local structural conformations, or secondary structure, dependent on hydrogen bonding. The two main types

of secondary structure are the  $\alpha$ -helix and the  $\beta$ -sheet. The  $\alpha$ -helix is a right-handed coiled strand. The side-chain substituents of the amino acid groups in an  $\alpha$ -helix extend to the outside. Hydrogen bonds form between the oxygen of each C=O bond in the strand and the hydrogen of each N-H group four amino acids below it in the helix. The hydrogen bonds make this structure especially stable. The side-chain substituents of the amino acids fit in beside the N-H groups. The hydrogen bonding in a  $\beta$ -sheet is between strands (inter-strand) rather than within strands (intra-strand). The sheet conformation consists of pairs of strands lying side-by-side. The carbonyl oxygens in one strand bonds with the amino hydrogens of the adjacent strand. The two strands can be either parallel or anti-parallel depending on whether the strand directions (N-terminus to C-terminus) are the same or opposite. The anti-parallel  $\beta$ -sheet is more stable due to the more well-aligned hydrogen bonds.

Suggested readings: <https://www.nature.com/scitable/topicpage/protein-structure-14122136/>

<https://www.ncbi.nlm.nih.gov/books/NBK26830/>

<https://drive.google.com/file/d/1dnTZcl-Oq1V8BuR8Kio61ycWPTA9KvYf/view>