CHAPTER 6
PROTEIN

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6.1 INTRODUCTION

Proteins have diverse functions such as essential parts of organisms, transport of other substances, structural support, storage and signaling from one part of the organisms to another. Proteins are organic compound made from amino acids arranged in linear form (polypeptides) and folded into specific conformation. Each type of protein has a unique three-dimensional conformation or shape.

6.2 FOUR LEVEL OF PROTEIN STRUCTURE

There are four distinct levels of protein structure which are primary, secondary, tertiary and quaternary.

6.2.1 Primary Structure

Primary structure of protein is its unique sequence of amino acids forming its polypeptide chains. Every polypeptide has a specific amino acids sequence. Primary structure of a protein start from the amino-terminal (NH_3^+) end to the carboxyl-terminal (COO^-) end. **Figure 6.1** below show the primary structure of protein.

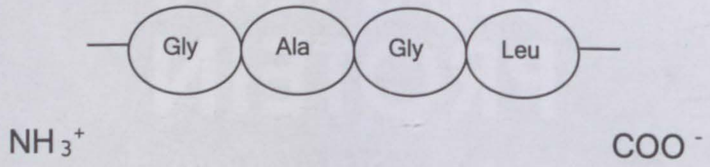

Figure 6.1: Primary structure of protein.

6.2.2 Secondary Structure

The secondary structure of a protein is the coiling or folding of its polypeptide chains. There are two types of secondary structure which are α helix and β-pleated sheet. Both patterns are stabilized by hydrogen bonding between carbonyl and amino group along the polypeptide's backbone.

- α-**helix** is a rigid, rod like structure. It is formed when polypeptides coiled into right-handed conformation. The alpha helix is stabilized by hydrogen bonds between the carbonyl oxygen of one amino acid and the backbone nitrogen of a second amino acid located four positions away. There are 3.6 amino acid residues per turn of the helix, and the pitch is 54nm. Amino acid R groups extend outward from the helix.

- **β-pleated sheet** formed when two regions of polypeptide chain lie parallel to each other. Each individual region is called β-strand. Hydrogen bond between the polypeptide backbone N-H and carbonyl groups of adjacent chains stabilized the structure.

There are two types of β-pleated sheets, which are parallel and antiparallel. In parallel β-pleated sheet structures, the polypeptide chains were arranged in same direction. While in antiparallel β-pleated sheets, the polypeptide chains arranged in opposite direction. Antiparallel β-pleated sheets are more stable than parallel β-pleated sheets because fully collinear hydrogen bonds form. Usually, mixed parallel and antiparallel β-pelated sheets can be observed in protein structure.

Many globular proteins contain combination of α-helix and β-pleated sheet structure. It is called supersecondary structure. There are 5 types of supersecondary structure: βαβ units, β-meander units, αα units, β-barrel and Greek key. βαβ unit formed when two parallel β-pleated sheets connected by a α-helix fragment. While β-meander unit formed when two antiparallel β-sheets are connected by polar amino acids and glycines to effect an abrupt change in direction of the polypeptide chain (reverse or β-turns). In αα unit, two α-helices separated by loop or nonhelical segment. β-barrel pattern form when various β-sheet configurations fold back on themselves. When antiparallel β-sheet doubles back on itself in a pattern that resembles a common greek pottery design, the pattern is called Greek key.

6.2.3 Tertiary structure

Tertiary structure is the three-dimensional conformation of a single protein molecule. The α-helices and β-pleated sheets are folded into compact globule. Protein folding occurs as consequence of interactions between the side chains in their primary structure. The following types of interactions stabilize tertiary structure **(Figure 6.2)**:

1. **Hydrophobic interactions**. As polypeptide folds, amino acids with hydrophobic (nonpolar) side chain are brought close to each other and congregate in clusters at the core of the protein, out of contact with water.
2. **Electrostatic interactions**. The strongest electrostatic interaction in proteins occurs between ionic groups of opposite charge. Referred as salt bridge.
3. **Hydrogen bonds**. A large number of hydrogen bonds form within a protein's interior and on its surface.