

Quadrant II – Transcript and Related Materials

Programme: Bachelor of Science (Second Year)

Subject: Zoology

Paper Code: ZOC 104

Paper Title: Animal Physiology and Biochemistry

Unit: 09 – Proteins

Module Name: level of organization in protein

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Notes

Introduction

Proteins are polymers of amino acids and made up of one or more polypeptide chains. The **number** and **sequence** of these amino acids in the protein are different in different proteins. Every protein in its native state has a unique three dimensional structure which is referred to as its **conformation**. The function of a protein arises from its conformation. Proteins can have **four** levels of structural organization.

They are designated as:

1. **Primary structure**
2. **Secondary structure**
3. **Tertiary structure**
4. **Quaternary structure**

All functional proteins will have up to 3 (tertiary level) structural level. Some proteins will have all the 4 levels (up to quaternary level).

Primary Structure

Primary structure of a protein gives the detail of the Amino acid sequence of a protein. The primary structure will tell you 2 main things

1. **The number of amino acid residues in the protein**
2. **The sequence of amino acids.**

The sequence information contains the correct order of amino acids in the protein starting from N- terminal to C- terminal. The primary structure of a protein will determine all levels of structural organisation of protein structure (secondary tertiary and quaternary). The primary structure is stabilized by peptide bonds. The first sequence of protein is insulin by Frederick sanger.

Secondary Structure

Secondary structure is confirmation of some part of a polypeptide chain. It is the folding pattern of the regular polypeptide backbone. The secondary structures are stabilized mainly by **hydrogen bonds**. Three most important secondary structure in protein are

1. **Alpha helix**
2. **β confirmations or beta plates / sheets**
3. **β turns**

α helix

The Alpha helix is the most common secondary structure. They are regular structures that repeat every 5.4 Armstrong. It is the simplest arrangement of a polypeptide chain. The Alpha helical structure of the protein was proposed by Pauling and Corey in 1951. Each helical Turn in Alpha helix contains 3.6 amino acids. The helical Twist of the Alpha helix in all protein is right handed. All hydrogen bonds together provide considerable stability to the Alpha helix.

β - plates

The β plates organise the polypeptide chain in two sheets. It is an extended form of a polypeptide chain forms a zigzag structure. The zigzag polypeptide chain can be arranged side by side to form a structure resembling a series of plates called β sheets. Also the structure is stabilized by hydrogen bonds. Based on this the β plates are classified into two types

1. **Antiparallel β plates**

2. Parallel β plates.

β turns

The β turns are very common in proteins where the peptide make a turn or loop. In globular protein nearly one-third of the amino acid Residues are in turns. The β turn structure is in 180 degree turn involving 4 amino acid Residues.

Tertiary structure

Tertiary structure of protein tertiary structure the overall three dimensional arrangement of all atoms in protein is referred to as the tertiary structure. The tertiary structure will have a single polypeptide backbone with one or more secondary structures. Tertiary structures in protein are stabilized by both covalent and non covalent bonds. **Covalent bond** : disulfide bonds. **Non covalent interactions**: ionic interactions, hydrophilic interactions, hydrophobic interactions. A protein with a single subunit only has up to the tertiary structure.

Quaternary Structure

The arrangement of protein monomers in three-dimensional complexes in a multisubunit protein is called quaternary structure. For a protein to have a quaternary structure it should fulfil two conditions

1. It should have more than one polypeptide subunits.

2. They should not have permanent covalent interactions between the subunits like disulfide Bond.

Bond stabilizing quaternary structure: hydrogen bonds and hydrophilic interactions, hydrophobic interactions.

