AL-MUSTAQBAL UNIVERSITY COLLEGE

Department of Biomedical Engineering

Biochemistry
(Primary, secondary, tertiary structure of protein)

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Protein Stability

Due to the nature of the weak interactions controlling the three-dimensional structure, proteins are very sensitive molecules. The term native state is used to describe the protein in its most stable natural conformation *in situ*. This native state can be disrupted by several external stress factors including temperature, pH, removal of water, presence of hydrophobic surfaces, presence of metal ions and high shear. The loss of secondary, tertiary or quaternary structure due to exposure to a stress factor is called denaturation. Denaturation results in unfolding of the protein into a random or misfolded shape

The primary structure
is its amino acid sequence Amino acids, held together by peptide bonds, form proteins. In total, there are 20 different amino acids, but these amino acids can be arranged in many different orders and lengths to create the many proteins needed in the body.

Primary structure is the simplest level of protein structure. The amino acid sequence of a protein determines its shape, structure, and therefore its function.

The specific sequence is very important, as a small change (called a change) may cause a disorder. For example, sickle cell anemia is a disorder in which hemoglobin in the body contains only two amino acid differences.
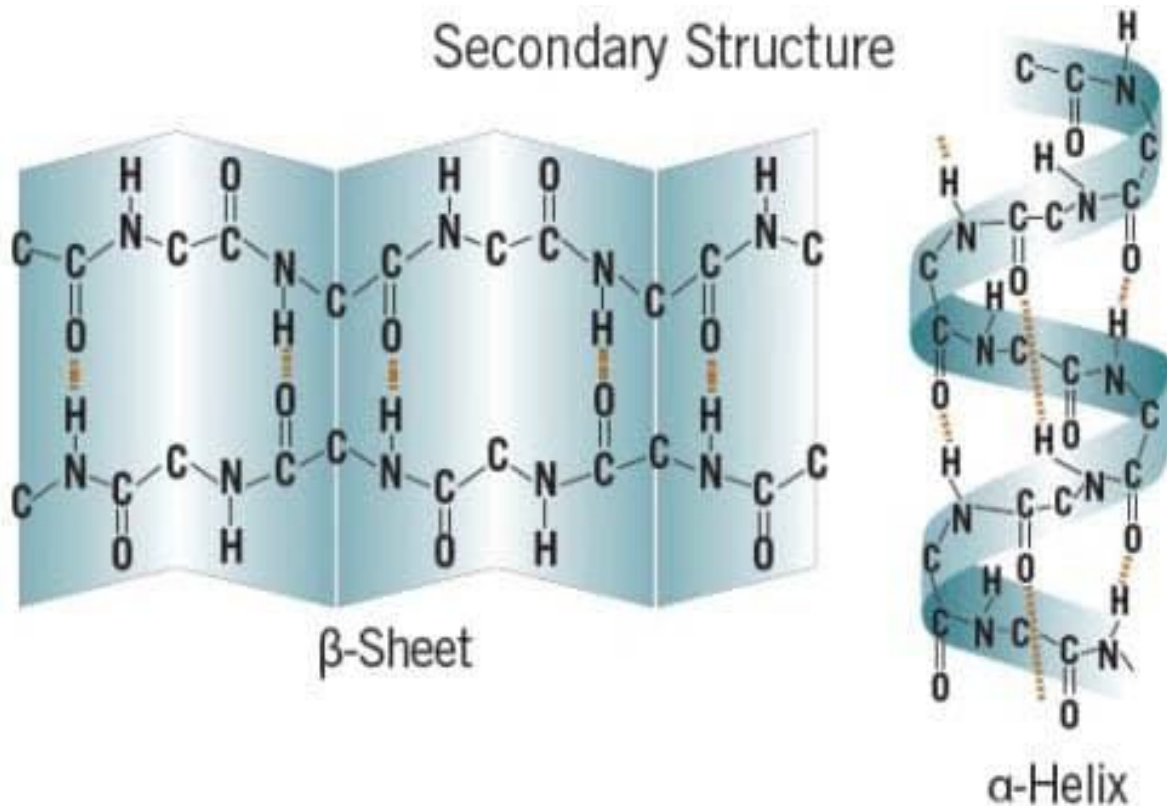
Primary Structure

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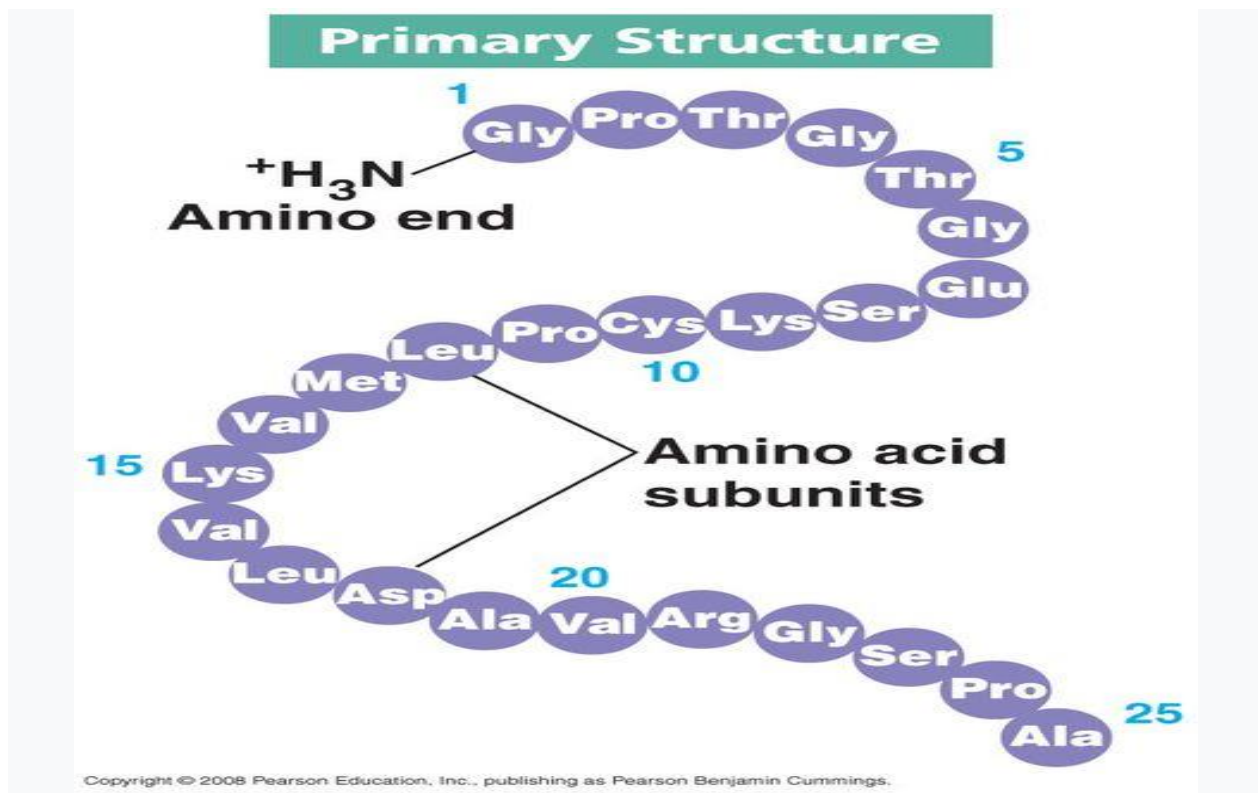
Protein Primary Structure Determination Proteins play important roles as the "building blocks of life"

(1) enzyme: catalyze biochemical reaction which would not be thermodynamically feasible.

(2) Hormone and receptor for those hormones

(3) Generate coordinated mechanical motion when present in the form of muscle fibers

(3) Sensing device: such as rhodopsin.

(4) Essential roles in immune system such as immunoglobins..

(5) Expression of genetic information (transcription)

(6) Constitute of important body part: such as collagen which provides bones, tendons, and ligaments
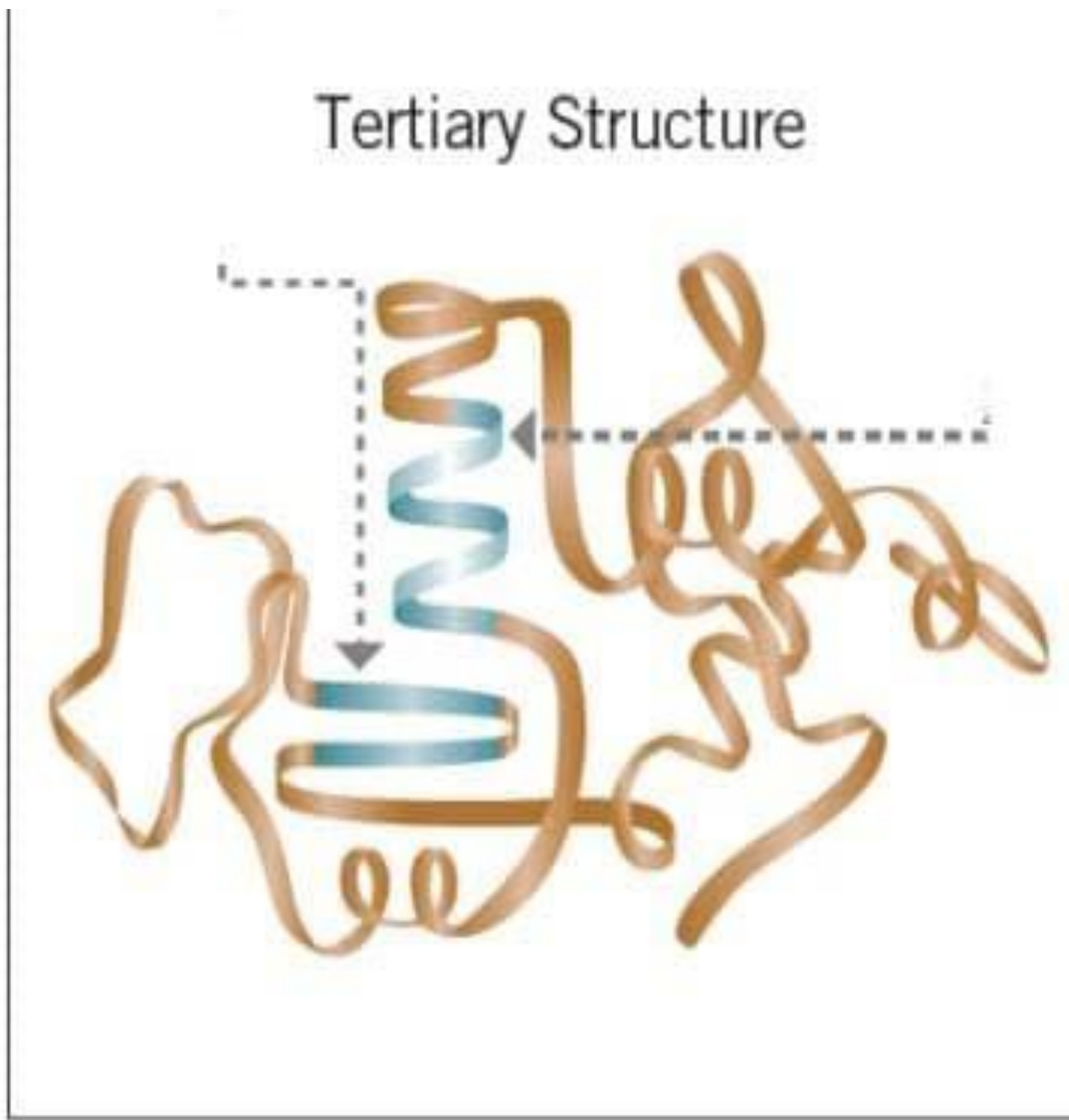
Secondary Structure:

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 α-helix and the ß-sheet. The *α-helix* is a right-handed coiled strand. The side-chain substituents of the amino acid groups in an α-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.

Secondary Structure

β-Sheet

α-Helix

Tertiary Structure:

The overall three-dimensional shape of a protein molecule is the tertiary structure. The protein molecule will bend and twist in such a way as to achieve maximum stability or lowest energy state. Although the three-dimensional shape of a protein may seem irregular and random, it is fashioned by many stabilizing forces due to bonding interactions between the side-chain groups of the amino acids.

Tertiary Structure

What forces determine the structure?

• Primary structure - determined by covalent bonds

• Secondary, Tertiary, Quaternary structures - all determined by weak forces Weak forces - H-bonds, ionic interactions, van der Waals interactions, hydrophobic interactions