



Protein Structure

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Objectives

Understand the peptide bonding between amino acids.

- Explain the different levels of protein structure and the forces stabilizing these structures and what happens when the protein is denatured.
- Define the α-helix and β-sheet as the most commonly encountered secondary structures in a protein molecule.
- Correlate the protein structure with function with hemoglobin as an example.
- Understand how the misfolding of proteins may lead to diseases like Alzheimer's or prion disease.

What Are Proteins?

Proteins are large, complex molecules that play many critical roles in the body.

- Proteins are made up of hundreds or thousands of smaller units called amino acids, which are attached to one another in long Chains.
- There are mainly 20 different types of amino acids that can be combined to make a protein.
- The sequence of amino acids determines:
- Each protein's unique three dimensional (3D) structure.
 - The protein's specific function



What Are Proteins?

Proteins can be described according to their large range of functions in the body eg:

1- Antibody

2- Enzyme

3- Messenger

4- Structural component

5- Transport and storage

How to determine the primary structure Sequence?

• DNA sequencing (indirect)

• Direct amino acids sequencing

Primary structure

- It is the linear sequence of amino acids.
 - Covalent bonds in the primary structure of protein:
 - Peptide bond.
- Disulfide bond (if any) (connects 2 residues of cysteine).
- The primary structure is the simplest and first-level form of structure.
- Peptide bonds are very strong and they require enzymes to be broken.



Peptide Bond (Amide Bond)

- Each amino acid in a chain makes 2 peptide bonds.
- The amino acids at the two ends of a chain make only 1 peptide bond.
- The amino acid with a free amino group is called amino terminus or NH2-terminus.
- The amino acid with a free carboxylic group is called carboxyl terminus or COOH-terminus

Residue: the molecule after remove water molecule



Peptides

NOTE 438:

- Residue: amino acid in polypeptide chain
- We always read from N-terminus to C-terminus

Note:

 Tripeptide has 2 peptide bonds

Peptide bond=Amide bond



Peptides

Amino acids can be polymerized to form chains:

- Two amino acids \rightarrow dipeptide \rightarrow one peptide bond.
- Three amino acids \rightarrow tripeptide \rightarrow two peptide bonds.
- Four amino acids \rightarrow tetrapeptide \rightarrow three peptide bonds.
- Few (2-20 amino acids) \rightarrow oligopeptide.
- More (>20 amino acids) → polypeptide.

How to determine the primary structure sequence?

- DNA sequencing.
- Direct amino acids sequencing.



- It is regular arrangements of amino acids that are located near to each other in the linear sequence.
- Excludes the conformations (3D arrangements) of its side chains.
- α-helix, β-sheet and β-bend are examples of secondary structures frequently found in proteins.





α-helix:

- It is a right-handed spiral, in which side chains of amino acids extended outward.
- Hydrogen bonds: Stabilize the α-helix. form between the peptide bond carbonyl oxygen and amide hydrogen.
- Amino acids per turn: Each turn contains 3.6 amino acids.



Amino acids that disrupt an α -helix:

- Proline \rightarrow imino group, interferes with the smooth helical structure.
- Glutamate, aspartate, histidine, lysine or arginine → form ionic bonds.
- Bulky side chain, such as tryptophan.
- Branched amino acids at the β-carbon, such as valine or isoleucine.

β-sheet:

Composition:

- Two or more polypeptide chains make hydrogen bonding with each other
- Also called pleated sheets because they appear as folded structures with edges



Hydrogen bonds in parallel direction are less stable than in antiparallel direction

Other Secondary Structure Examples

1- β-bends (reverse turns)

- Reverse the direction of a polypeptide chain
- Usually found on the surface of the molecule and often include charged residues
- The name comes because they often connect successive strands of antiparallel β-sheets
- β-bends are generally composed of four amino acids residues, proline or glycine are frequently found in β-bends

2- Non-repetitive secondary

E.g. loop or coil conformation

Proline is in the β-bends frequently because it bends due to its imino group.

Glycine: is the smallest amino acids which makes it easier to bend.



Supersecondary Structure (Motifs) Supersecondary structure is a combination of secondary structural elements, such as: $\alpha \alpha$ motif: $\beta \alpha \beta$ motif:

Helix-loop-helix

two α helices together

β-α-β unit

a helix connecting two β sheets

β barrels:



rolls of β sheets

β hairpin:



B-Meander

reverse turns connecting antiparallel β sheets

Tertiary Structure

- Tertiary structure: the three-dimensional (3D) structure of an entire polypeptide chain including side chain (R).
- Domains: the fundamental functional and 3D structural units.
- Polypeptide chains that have >200 amino acids have 2 or more domains. The core of a domain: is built from combinations of supersecondary structural elements (motifs) and their side chain.
 - Domains can combine to form tertiary structure



Tertiary Structure

Interactions stabilizing tertiary structure:

- **Disulfide:** SS (Cysteine with Cysteine covalent bond).
- **Hydrophobic interactions:** between nonpolar amino acids in the interior of the polypeptide (most important interaction that stabilizes the tertiary structure)
- **Hydrogen bonds:** between polar and hydrophilic amino acids.
- **Ionic interactions:** oppositely charged side-chains groups reactions

Protein Folding



Primary structure



Secondary structure



Supersecondary Structure



Tertiary Structure

- Some proteins exist in quaternary structure (level of folding after tertiary)
- Chaperons are folded by other chaperons.

Chaperons:

- Specialized group of proteins, required for the proper folding of many species of protein
- Chaperons interact with polypeptides at various stages during the folding process
 - Also known as "heat shock" proteins لأنه يزداد عند وجود الحرارة
- They make sure that the folding process is done right

Quaternary Structure

- Some proteins contain two or more polypeptide chains that may be structurally identical or totally unrelated
- Each chain forms a 3D structure called **subunit**.
- According to the number of subunits: Dimeric, Trimeric, multimeric
- Subunits may either function independently of each other, or work cooperatively, e.g. hemoglobin

NOTE441:

- \bullet Protein has 1 polypeptide chain \rightarrow the protein has 3 levels of structure only (primary, secondary, tertiary).
- Protein has >1 polypeptide chains \rightarrow the protein has 4 levels of structure (primary, secondary, tertiary, quaternary).
- Nascent protein: the primary structure of a protein.
- Native protein: the mature protein that has been folded.
- The quaternary structure is the last complexity.

Quaternary Structure 441 Illustration



Hemoglobin

1- Globular protein (round/spherical)

2- α_2 and β_2 (4 subunits)

3- Oligomer (Multisubunit protein)

4- two identical subunits are called proteomes



Denaturation of Proteins

- Denaturation results in the unfolding and disorganization of the protein's secondary and tertiary structures.
- Most proteins, once denatured, remain permanently disordered
- Denatured proteins are often insoluble and, therefore, precipitate from the solution

E.g the protein in the egg "albumin" once we put it in "heat" it will be denatured and become insoluble.







Protein Misfolding

- Every protein must fold to achieve it's normal conformation and function
- Abnormal folding of proteins leads to a number of diseases in human, e.g. Alzheimer's and prion diseases

Alzheimer's disease	Creutzfeldt-Jacob (prion) disease
<mark>β amyloid</mark> protein is a misfolded protein. It forms fibrous deposits or plaques in the brain	Prion protein is present in normal brain tissues. In diseases brains, the same protein is misfolded. Therefore it forms insoluble fibrous aggregates that damage brain cells.





Summary

Take Home Messages

- Native conformation of the protein: functional, fully folded structure.
- Unique 3D structure of native conformation is determined by primary structure (amino acid sequence)
- Interactions between amino acids side-chains guide the folding of the polypeptide chain to form secondary, tertiary, and sometimes quaternary structures that cooperate in stabilizing the native conformation of the protein.
- Protein denaturation results in unfolding and disorganization of the protein's structure, which aren't accompanied by hydrolysis of peptide bonds.
- Diseases can occur when an apparently normal protein assumes a conformation that is cytotoxic, as in the case of Alzheimer's or Prion's disease.



there are .. different types of amino acids?





there are .. different types of amino acids?







The amino acid with a free amino group is Called carboxyl terminus?



The amino acid with a free amino group is Called carboxyl terminus?



Two or more polypeptide chains make hydrogen bonding with each other?



Two or more polypeptide chains make hydrogen bonding with each other?



Biochemistry Team

