Lec. 8 · By. Rofida Awwad.

Proteins 1

Peptide bond

is a chemical bond that is formed between two amino acids when the carboxyl group (تقدم ال OH) of one molecule reacts (تفاعل) with the amino group (تقدم ال H) of the other molecule, releasing a molecule of water [H_2O].

- This is a dehydration synthesis reaction [also known as a condensation reaction], and usually occurs between amino acids. (→ removal water molecules)

- The resulting CO-NH bond is called a peptide bond, and the resulting molecule is an amide.

*راجع الصورة في السلايد

- Di-peptides have two amino acids.
- Tri-peptides have three amino acids
- Polypeptide sequence of amino acids linked by peptide bonds.

[Polypeptides and Proteins are chains of amino acids held together by peptide bonds].

- C-terminal: the end amino acid
- N-terminal: the first amino acid

- Sequences of amino acids in a polypeptide are read from the amino terminal end to the carboxyl-terminal end.

* الصور في السلايد ادرسهم

- A polypeptide chain consists of a [constant backbone] (ثابتة) and variable (متغيرة) side chains. "R"
  → All polypeptide components except R-group or side chain.

~ characteristics of the peptide bond ~

1. It is a covalent bond.
2. Strong bond
3. peptide bond is uncharged but polar.
4. Lack of rotation around the bond: the peptide bond has a partial double-bond character - that is; it is shorter than a single bond and is therefore rigid and planar.

كأنها في نفس المستوى والسبب Partial double bond.

5. Trans configuration: the peptide bond is generally a trans bond [instead of Cis].

~ Trans form is strongly favoured because of steric clashes that occur in the Cis form.

← مراجعة الصور في السلايد.

~ PROTEIN ~

- Proteins are composed of one or more than one of poly peptide chains containing hundreds of amino acids.

- Each protein has its own unique amino acid sequence that is specified by the nucleotide sequence of the gene encoding this Protein.

- Protein builds, maintains, and replaces the tissues in your body.

- Your muscles, your organs, and your immune system are made up mostly of protein.

- Your body uses the protein you eat to make lots of specialized protein molecules that have specific jobs. for instance, your body uses protein to make hemoglobin, the part of red blood cells that carries oxygen to every part of your body:)

~Proteins are the chief actors within the cell, said to be carrying out the duties specified by the information encoded in genes~

المعلومات المشفرة في الجينات

Proteins Biomedical Importance

1- They provide (توفر) immune protection, antibodies search out foreign invaders. عبارة عن بروتينات تهاجم اي جسم غريب

2- They function as catalysts: enzymes catalyse reactions that generate energy, synthesize and degrade biomolecules, replicate and transcribe (نسخ) genes, etc. enzymes عبارة عن Proteins

3- They transport and store other molecules such as Haemoglobin transports oxygen.

4- They provide mechanical support, the internal protein network "cytoskeleton", maintains cellular shape and physical integrity (السلامة الجسدية).

5- They generate movement, actin and myosin filaments form the contractile machinery of muscle.

6- They work as receptors that enable (تمكن) cells to sense (الإحساس) and respond (الإستجابة) to hormones and other environmental cues. العوامل البيئية الأخرى

♥ Structure - function relationship in protiens ♥

[1] The function of aprotein is directly dependent on its three dimensional structure.

[2] Proteins contain [awide range of functional groups]. these functional groups accounts for the broad spectrum of protein function. for instance, the chemical reactivity associated with these groups is essential to the function of enzymes.

[3] Proteins can interact with oneanother and with other biological macromolecules to form complex assemblies. Example replication (تضاعف) of DNA, the transmission of signals within cells, and many other essential processes.

[4] Some proteins are quite rigid (صلبة تماماً), whereas others display limited flexibility (محدود المرونة). * Rigid units can function as structural elements or in connective tissue. * parts of proteins with limited flexibility may act as to assembly (تجميع) proteins with one another and with other molecules into complex units (وحدات معقدة), and to the transmission (نقل) of information within and between cells.

~ Protein structure ~

Primary structure.	Secondary structure.	Tertiary structure.	Quaternary Structure.
Amino acid sequence.	· α- helix · β- sheet · turns	Three-dimensional structure formed by assembly of secondary structure.	formed by more than one polypeptide chains.

+ الصورة في السلايد

• Primary structure of proteins

✓ is the sequence of residues (amino acids) in the polypeptide chain.

✓ Starting from the amino-terminal (N) end to the carboxy-terminal (C) end.

✓ The sequence of amino acids in a protein is determined by the genetic code for the protein.

genetic code :: is the set of rules by which information encoded in genetic material [DNA or mRNA sequences] is translated into proteins [amino acid sequences] by living cells.

نسخ → ترجمة

transcription → translation.

داخل النواة.

← الصورة في السلايد

AUG initiation codon — methionine ← أول كودون ← AUG; amino acid — متى يلتش تحضير البروتين ..

UAA, UAG, UGA Stop codon ⇐ آخر amino acid بيتحضر مسؤول عنه. ← تتوقف عملية التحضير.

• Secondary structure of proteins

✓ is a local regularly occurring structure in proteins and is mainly formed through hydrogen bonds between backbone atoms. (مالها علاقة بتكوينة (R group))

~ Two major types of stable secondary structure ~

- Alpha helices
- Beta-sheets

• are preferably (يفضل) located at the core of the protein, whereas loops prefer to reside in outer regions.

✓ Amino acids vary in their ability to form the various secondary structure elements. Proline and glycine are sometimes known as "helix breakers" because they disrupt, both have unusual conformational abilities and are commonly found in turns.

✓ By contrast, the large aromatic residues [tryptophan, tyrosine, and phenylalanine] prefer to adopt β - strand conformations. (β-sheet = نفسها)

α-helix

one backbone [same]

- is a right-handed coiled or spiral conformation, in which every backbone N-H group donates a hydrogen bond to the backbone C=O group of the amino acid four residues earlier.

- Right-handed α-helix :- is one of the most common secondary structures.

- Left-handed α-helix :- is rarely found in nature.

- the polypeptide chain is coiled tightly in the fashion of a spring. شكل زمرك

The "backbone" of the peptide forms the inner part of the coil while the side chains extend outward from the coil.

- The helix is stabilized by hydrogen bonds between the N-H of one amino acid and the C=O on the 4th amino acid away from it, One "turn" of the coil requires 3.6 amino acid units. طولها

* الصور في السلايد

Amino-acid propensities

Different amino-acid sequences have → Different propensities for forming α-helical structure.

بتحب تكوّن helix

- Have high helix-forming propensities : Methionine, alanine, leucine, uncharged glutamate, and lysine.
- Have poor helix-forming propensities : Proline and glycine.

بتحطم helix

(Proline) either breaks or kinks a helix, both because it cannot donate an amide-hydrogen bond [having no amide hydrogen], and also because its side chain interferes sterically with the backbone of the preceding turn - inside a helix, this forces a bend of about 30° in the helix axis.

- Large numbers of charged amino acids (for example, glutamate, aspartate, histidine, lysine, or arginine). also disrupt the helix.

- Amino acids with bulky side chains, such as tryptophan, can interfere with formation of the α-helix if they are present in large numbers.

* الصورة ع السلايد

lysine

* لمّا تكون اعداد قليلة بتكوّن α-helix بس لمّا تكون اعداد كبيرة وتكون charged ما بيصير

يكوّن α-helix

β-sheet [different backbone]

* [β-pleated sheet] is less common than the α-helix.
* Consist of beta strands connected laterally by at least two or three backbone hydrogen bonds, forming a generally twisted, pleated sheet.
* A beta strand is a strech of polypeptide chain typically [3 to 10] amino acids long with backbone in an almost fully extended conformation.

* The majority of β strands are arranged adjacent (جنب بعض) to other strands and form an extensive hydrogen bond network with their neighbors in which the N-H groups in the backbone of one strand establish hydrogen bonds with the C=O groups in the backbone of the adjacent strands.

* In the fully extended β strand, successive side chains point straight up, then straight down, then straight up, etc..

~ β-sheet ~

- Parallel: [Adjacent polypeptide chains running in the same direction.]
- Antiparallel: [When the adjacent polypeptide chains run in opposite direction.]

* راجع الصور في السلايد

Turns [short back bone only]

✓ is an element of secondary structure in proteins where the Polypeptide chain reverses its overall direction.

✓ is a structure motif where the C^{α} atoms of two residues separated by few [usually 1 to 5] (amino acid) peptide bonds are in close approach (< 7 A), while the corresponding residues don't form a regular secondary structure element such as an alpha helix or beta sheet.

Tight turns (classified according to the separation between the two end residues)

- **Alpha-turn** → the end residues are separated by four peptide bonds
- **Beta-turn or Beta-bend** → the most common form by three bonds.
- **Gamma-turn** → By two bonds.
- **Delta-turn** → By one bond.
- **π-turn** → By five bonds.

- **Beta-Bends** often found at sites where the peptide chain changes direction.
- β-Bends are stabilized by the formation of hydrogen bonds and by having a distance of less than 7 A (amino acid) between the C^{α} atoms of residues one and four.

• β- Bends are generally composed of four amino acids, one of which may be proline that causes a "kink" in the polypeptide chain. Glycine, the amino acid with the smallest R- group, is also frequently found in β-bends.

- Super secondary structures [also called motifs].

- are combinations of alpha-helices and beta- structures connected through loops. → turns اسم انواع

- These folding patterns are stabilized through the same kind of linkages than the tertiary level. Sometimes the term "motif" is used to describe these super secondary structures.

- These structures can be relatively simples, as alpha- alpha [two alpha helices linked by a loop], Beta - Beta [two beta - strands linked by a loop], Beta- alpha - Beta [Beta - strand linked to an alpha helix that is also linked to other beta strand, by loops]. or more complexes structures, like the beta - barrel