Lecture :.....6.....

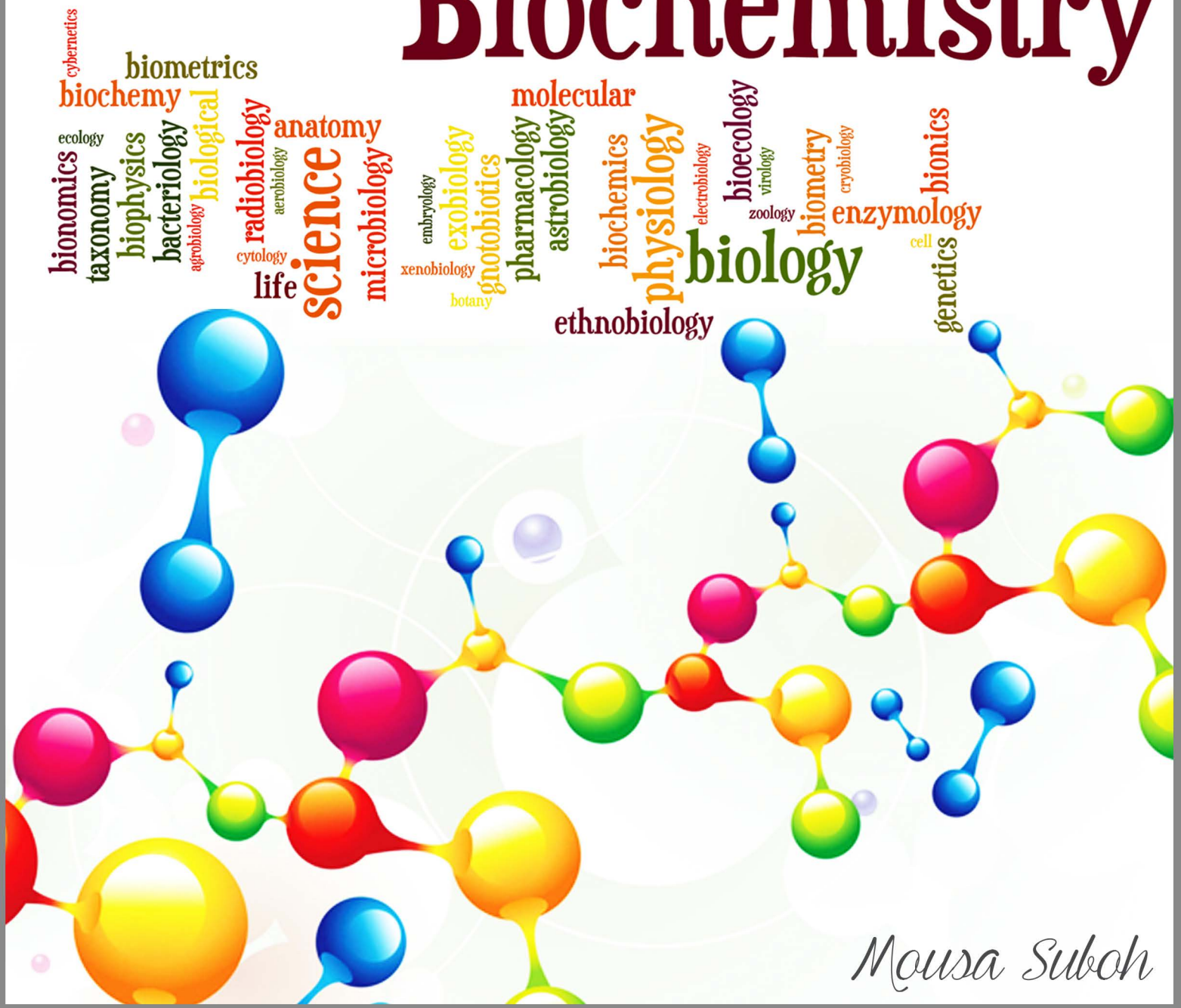
Dr. Name :.....Nafez Abu-Tarboosh.....

Done By :.....Ousama Samawi.....

☐ Slide ■ Sheet

Medical Committee
The University of Jordan

Biochemistry



Mousa Suboh

Poly peptide and protein

-protein conformation

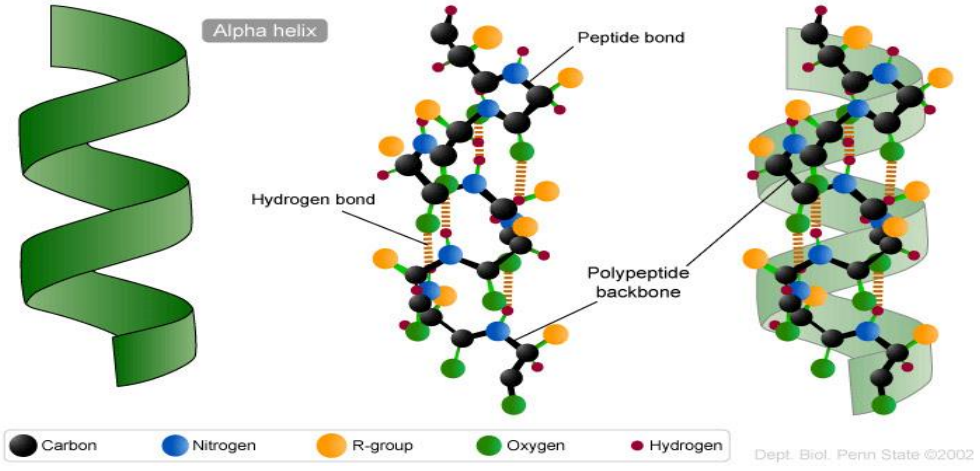
*As we have known from the last lecture:

Proteins can exist in a huge number of conformations, at least there is one only active conformation, its name is native conformation

- There are levels for the protein structure: (primary, secondary, tertiary, quaternary) and we've stopped at the secondary structure.

- There are two main kinds for the protein's secondary structure: 1- α-helix 2- β- pleated sheet.

- ### 1- The α-helix :
  - When the close (adjacent) regions in the α-helix gather around themselves they will spin in a spiral form because of the hydrogen bonding.
  - The secondary structure is formed due to the hydrogen bonding between the back bone of the amino acids.
  - There are few ways where this hydrogen bonding can make linkages.
  - There are a lot of linkages (hydrogen bonding) but the ways of making these linkages are few, one of these ways is the folding in a spiral form to make the α-helix.



-Depending on the cable, which represents the sequence of the amino acids, the doctor used this cable to explain some points (please check the picture above so you can understand):
-Imagine a complete turn of this cable:
- At the head of the cable, amino acid number one.
- At the end of the circle, amino acid number four.
- The hydrogen bonding is formed between the back bones.
- H-bonds are parallel to the helix axis (parallel to the long axis).
-Each turn includes around 3.6 amino acids. (Why it's not 4 because the bond is formed between 1 and 4 and that means there are some parts of 1 are not included in the turn and some parts of 4 are not included in the turn).
- The pitch (complete turn), (linear distance between corresponding points on successive turns) is 5.4 Å (angstrom).
- The R groups in the α-helix are extended to outside.

-Amino acids NOT found in α-helix:

1-Glycine: it's too small & entropically expensive. It also has high flexibility, and the α-helix must be stable, so you need to spend more energy to keep it in place and stable in the α-helix).
2- Proline: it can't form Hydrogen bonding, and Hydrogen bonding is one of the most important properties of the secondary structure.

a- There is no rotation around psi bond (C-N bond has no rotation) but in α-helix there must be a rotation around the α-carbon, so Proline is not found in the α-helix.
b- In the backbone there are carboxyl group, and Nitrogen which is engaged in another bond so it can't participate in hydrogen bonding.

3- Amino acids that have similar charges and are close to each other (close proximity of a pair of charged amino acids with similar charges). If you have 2 amino acids with similar charges, repulsion will occur between them.

-Amphipathic α helices:

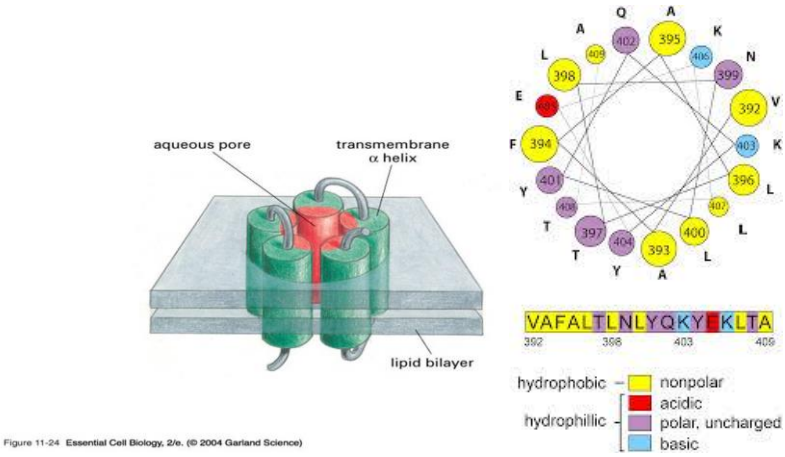


Figure 11-24 Essential Cell Biology, 2/e. (© 2004 Garland Science)

- You all know the channels which are found in the membranes that pass Na, K, etc... And you also know that the membranes are lipophilic (contains cholesterol and fatty acids). How could you put a protein inside the membrane and it could transport materials which are hydrophilic? As you can see in the picture there are some cylinders, the part of the cylinder which is directed towards the pore consists of polar amino acids and the other part of the cylinder which is directed towards the membrane (towards outside) consists of nonpolar amino acid so the hydrophilic materials can pass through these channels.

2- The β-sheets:

- Every β-sheet has 4-5 strands and sometimes it can have 10 strands. If you have for example two strands, they'll be anti-parallel to each other, these two strands are connected to each other in a small region, it's called a "turn". If you have one more strand it will be parallel to the first strand, and it will be connected to it by a long amino acid sequence, its in name is "loop"

- Backbone is almost completely extended

- R groups extend above and below the sheets, because if they were inside or between the sheets, repulsion will happen.

- H-bonds are intra-chain or inter-chain bonds

- Perpendicular to the direction of the protein chain

-Such β sheets can be purely antiparallel, purely parallel, or mixed

- How we can connect the strands with each other? By using turns or loops.

- The loop is a long amino acids sequence.

- What is the difference between the turn and the loop? Turns are short while loops are long.

- the R groups in the alpha helix is directed outside the helix in the β-sheets they are directed above and below the sheets that's what makes it zigzag structure (why they are not directed between the strands ? sterogenicly not favorable) .

- Proline tends to disrupt β sheets (same story with α-helix, for the same reasons)

- The turn consists of 4 amino acids and it connects the sharp areas (sharp angles in the protein)

-Turns' properties:

1- Compact, U-shaped secondary structures. What makes it stabilized in this shape? Because there are bonds between amino acid no.1 and amino acid no.4)

5- Glycine and Proline are commonly present in turns (why glycine and proline? because Glycine is a small amino acid which can exist in the sharp areas (turns) and Proline because it connects the amino acids in sharp areas so we need kinks which are present in the proline)

6- the structure of the turn is regular

-Loops' properties:

- They are similar to the turns however they are longer

- The structure of the turn is regular however the loop's structure is more irregular.

- More flexible.

-Super-secondary structures: Motifs & Domains:

-Higher structures than the secondary structures, more complex structures than the secondary structures, that's why they're called super secondary structures.

-Motifs: sequence of amino acids (typically less than 20 amino acids)

-In general, motifs may provide us with information about the folding of proteins, but no biological function

-to connect heme with proteins there should be a sequence of amino acids, this sequence of amino acids is called motif.

Examples: Helix loop helix, Helix turn helix.

-Domains:

-They are longer that motifs (100-200 amino acids). Domains usually have certain functions.

Examples:

-Leucine zipper (it's specific for DNA binding)

-Immunoglobulin fold (when you see it you know that this structure must bind with antigen "foreign body")
- An important point: they fold independently of the protein.

-Other Super-secondary structures: (Reading only) α–α unit, β–β unit, β–meander, Greek key, and β–barrel.

If there are 5 α-helix and 5 β-sheets in the protein, do you think that the shape of the protein would be compact (very tight) or loose? It would be loose because the protein has different shapes (α-helix and β-sheets).

*If we create a protein consists of α-helix, what would the structure be?

*If we create a protein consists of β-sheets, what would the structure be?

→The answer of these two questions: those proteins which consist of one type of secondary structures are called fibrous proteins, they are compact and mechanically strong, they are insoluble because there is no space for water to pass through them.

➔ The functions of these proteins are: 1-Support 2-Protection 3-They play an important structural role.

Examples: Keratin (hair, nails), Collagen(everywhere in the body), fibroin (spider webs, silk).

-Globular Proteins:

➔ They have spherical shape, these proteins consist of more than one type of secondary structure that means they contain α-helix and β-sheets together.
➔ they have spaces inside, they are not compact
➔ They do functions other that support and protection. They work as enzymes or transporters
➔ Examples: Myglobin & hemoglobion (these two examples don't have β-sheets. They have just α-helix) but usually globular proteins contain α-helix and β-sheets together.

Tertiary structure

➔ 3˚ Structure: The 3-dimensional arrangement of all amino acids in a protein
➔ 3˚ Structure: Is the end of the protein conformation unless the protein contains more than one polypeptide chain (quaternary structure). If the protein has just one polypeptide chain it'll stop at the tertiary structure.
➔ We have two types of 3˚ Structure: simple vs. conjugated

- ➔ Conjugated: something is attached to the protein, and this “thing” is not a protein
- ➔ Simple 3˚ Structure will do there function in their amino acids sequence.
- ➔ The conjugated 3˚ Structure can’t do their function using their amino acid sequence alone, it needs another thing from outside. Examples: Hemoglobin and myoglobin

  Globin is a protein, heme is not a protein. The heme will be added to the Globin and we end up with Hemoglobin, and heme could be added to Globin and we end up with myoglobin. Examples of these non proteinous structures: iron, heme, any other metals: calcium.

-Forces That Stabilize (determine) Protein Structure

Mainly: Hydrophobic interactions (Non-covalent interactions):
- Hydrogen bonds: amino acids, aqueous medium
- Charge-charge interactions (salt bridges)
- Charge-dipole interactions: charged R groups with partial charges of water

Van der Waals Forces are weak however they are significant, why? They are presented in a large number.

If you have a globular protein (like a ball), is it possible to have a hydrophilic (polar) amino acids in the core (inside the ball)? Yes, you might find polar amino acids in the core, and it’s designed to do certain and specific function in that place. How polar amino acids in the globe could be stabilized? By hydrogen bonding with the back bone.

Done by: Ousama Samawi