**WEEK 6**

| **UNIT 2_4 PROTEINS** | **Where? How long?** | ***Explanations /Questions*** |
|---|---|---|
| ***Introduction***<br>Proteins are of the primary importance in cellular life as they are found in all aspects of cell structure and function. Some are enzymes, hormones, storage proteins, contractile proteins, transport proteins, structural proteins, protective proteins and toxins. A protein is composed of one or more long chains composed of amino acids. The individual amino acid subunits are joined by amide linkages called **peptide bonds**.<br><br>***Expectation***<br>In this lesson, you'll learn about the primary structure, function, and sources of protein molecules while exploring some real-world examples and illustrations.<br><br>***Course outline***<br>Amino Acids<br>Peptide bonds<br>Proteins | 10 minutes | Where is this from?<br><br>Explain here what it is they are going to be learning and ***why*** they need to know about proteins<br><br>Also what the expectations are in terms of time commitment, tutor support and so on. |
| **Learning outcomes**<br>At the end of this unit, you should be able to:<br>• Recognize the chemical structure of each of the 20 standard amino acids<br>• Describe the two basic building blocks of protein structure (α-helix and β-sheet)<br>• Describe levels of protein structure<br>• Describe the forces and interactions that promote protein folding<br>• Define the process of protein denaturation | | |

| ACTIVITY AHEAD OF LESSON :PROTEINS | | | |
|---|---|---|---|
| **Purpose:** | All proteins in all living cells are constructed from the same set of 20 amino acids (AA). These are called standard amino acids. The diversity observed within living organisms is because cells can produce proteins with strikingly different properties and activities by joining the same 20 amino acids in many different combinations and sequences. | 30 minutes | **Amino Acids**<br><br>You must know:<br>Their names<br>Their structure<br>Their three letter code<br>Their one letter code |
| **Over to you:** | You will learn about the structure of AA and Proteins .Go to this open resource<br>**Be certain to note anything that you don't understand** | | |
| **Activity:** | Do the MCQ associated with this lesson . | | |

## The structure of an amino acid

An amino acid consists of amino group, a carboxyl group, hydrogen atom and a functional R-group, which are bonded to a α-carbon atom.

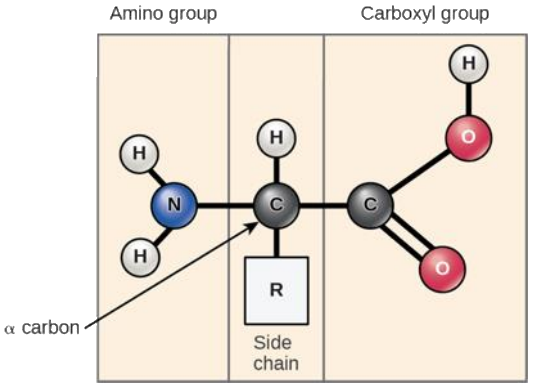


**Figure 2.18 : General structure for amino acids**
OpenStax Biology 2nd Edition, Biology 2e. OpenStax CNX. Feb 13, 2019,accessed February 15, 2019.
https://cnx.org/contents/jVCgr5SL@15.3:IRyJF0BE@11/3-4-Proteins

20 minutes

Notes to tutor

Explain that the R-group (side chain) is what makes each amino acid unique.
Each of the 20 amino acids has a different side chain structure.
Side chains contain mainly hydrogen, carbon, and oxygen atoms.
Some amino acids have sulfur or nitrogen atoms in their R-group

## Classification of amino acids

Each amino acid has unique chemical properties determined by the nature of the side group (indicated by R) covalently bonded to the central carbon atom. Each amino acid has the same chemical backbone, but differs in the side, or R, group it possesses. The 20 common AA are classified based on their side groups:

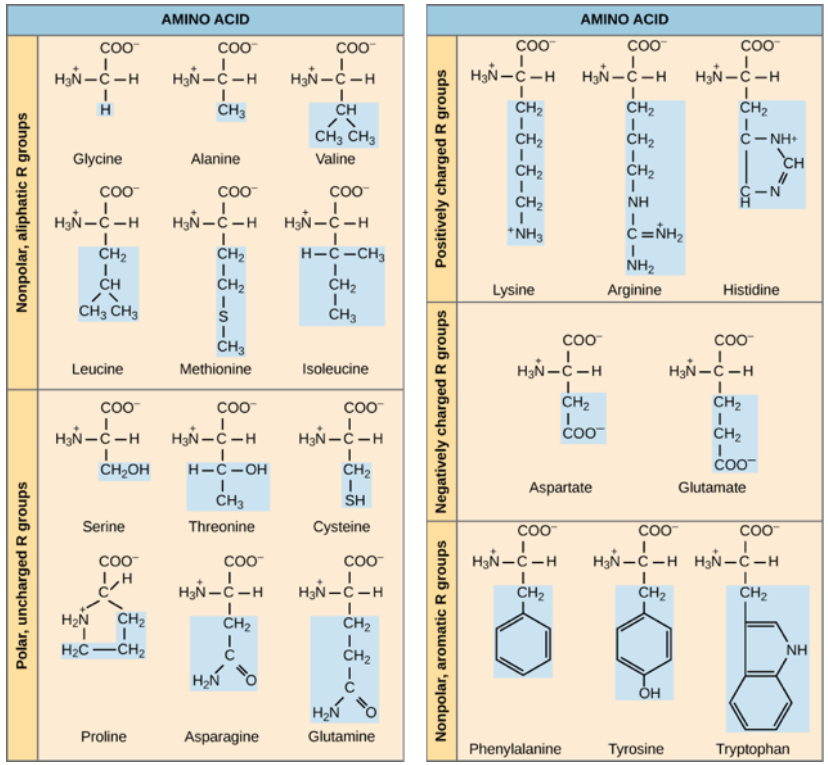


**Figure 2.18 : Classification of amino acids according to the polarity of their side chains**
OpenStax Biology 2nd Edition, Biology 2e. OpenStax CNX. Feb 13, 2019,accessed February 15, 2019.
https://cnx.org/contents/jVCgr5SL@15.3:IRyJF0BE@11/3-4-Proteins

20 minutes

## Properties of amino acids

**Acid base property**

Amino acids behave as acids and bases at the same time because they have both a basic amine group and an acidic carboxylic acid group. When dissolved in water at they form neutral hybrid ions (ones having equal number of negative and positive signs at the same time) called **zwitterions.**

The pH at which an amino acid has equal number of negative and positive signs is called isoelectric point abbreviated as **pl**

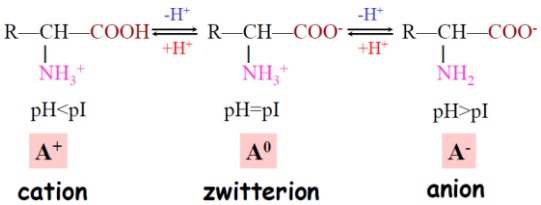


**Figure 2.19. In solutions, carboxylic and amine groups are in their ionic state.** The predominant charge depends on the pH of the solution.

## Types of Amino Acids

The 20 common amino acids are grouped into five chemical classes, based on their R group:

1. Nonpolar amino acids, such as leucine, often have R groups that contain —$CH_2$ or —$CH_3$.
2. Polar uncharged amino acids, such as threonine, have R groups that contain oxygen (or —OH).
3. Charged amino acids, such as glutamic acid, have R groups that contain acids or bases that can ionize.
4. Aromatic amino acids, such as phenylalanine, have R groups that contain an organic (carbon) ring with alternating single and double bonds. These are also nonpolar.
5. Amino acids that have special functions have unique properties. Some examples are methionine, which is often the first amino acid in a chain of amino acids; proline, which causes kinks in chains; and cysteine, which links chains together.

20 minutes

Notes to tutor

| IN CLASS ACTIVITY: AMINO ACIDS | | | |
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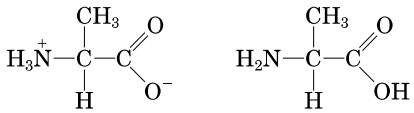
| **Purpose:** | To learn the 20 essential AAs. | 30 minutes | Do no to use the internet<br>Discuss in group. |
| **Over to you:** | Use the previous group of 4 , take a white paper and draw a table with 3 heading in the Columns: Amino Acid, Abbreviation and R-group Linea Formula | | |
| **Activity:** | Fill the table with the 20 essentials AAs, after the 10 minutes the group will exchange their answers sheet with other groups for marking.<br><br>Fills the table on the board for corrections.<br><br>**Answer these questions:**<br>What are the non-polar AA and polar AA?<br>What are the uncharged AA?<br>What are the Aromatic AA?<br><br>**Answer this problem:**<br>How Much Alanine Is Present as the Completely Uncharged Species? At a pH equal to the isoelectric point, the net charge on alanine is zero. Two structures can be drawn that have a net charge of zero (zwitterionic and uncharged forms), but the predominant form of alanine at its pI is zwitterionic.<br>  <br>Zwitterionic Uncharged<br>(a) Explain why the form of alanine at its pI is zwitterionic rather than completely uncharged.<br>(b) Estimate the fraction of alanine present at its pI as the completely uncharged form. Justify your assumption | | |

## PEPTIDE BOND

Two or more amino acid can form a bond between the carboxyl group of one amino acid and the -amino group of another with release of water. The formed bond is called **peptide bond**. When a few amino acids are joined in this fashion, the structure is called an **oligopeptide.** When many amino acids are joined, the product is called a **polypeptide.** Proteins may have thousands of amino acid residues.

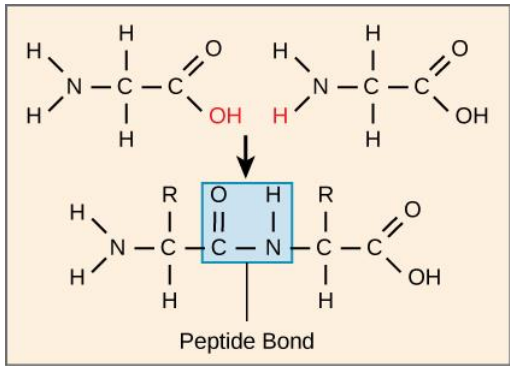



**Figure 2.20 : Peptide bond formation**
OpenStax Biology 2nd Edition, Biology 2e. OpenStax CNX. Feb 13, 2019,accessed February 15, 2019.
https://cnx.org/contents/jVCgr5SL@15.3:IRyJF0BE@11/3-4-Proteins

10 minutes

## PROTEIN STRUCTURE

The shape of a protein determines its function. The structure of proteins is usually discussed in terms of a hierarchy of four levels: *primary*, *secondary*, *tertiary*, and *quaternary* .

**Primary structure**: order of the amino acids joined together to make a protein. it includes all features of a protein which are a result of covalent bonds; peptide bonds & sulphur bridges.

**Secondary structure**: refers to particularly stable arrangements of amino acid residues by forming bond hydrogen between its backbone amide and carbonyl groups. Hydrogen bond can form in the same polypeptide so that all amide and carbonyl groups are engaged in bonding; the formed helical structure is called α helix. The helical twist of the α-helix found in all proteins is right-handed**.** Hydrogen bond can be formed between adjacent segments of polypeptide chain forming a sheet structure called β sheet.

**Tertiary structure**: the final three dimensional structure of an entire polypeptide chain (polypeptide backbone and amino acid side chain). A protein is initially driven into its tertiary structure by hydrophobic exclusion from water. Ionic bonds between oppositely charged R groups bring regions into close proximity, and disulfide bonds (covalent links between two cysteine R groups) lock particular regions together.

**Quaternary structure**: spacial arrangement of subunits for proteins composed of two or more polypeptide.

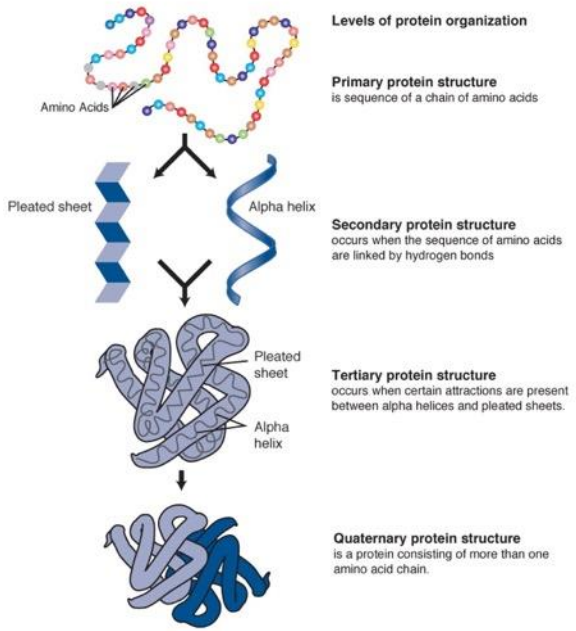



**Figure 2.21: Four levels of protein structure.** By Darryl Leja,NCBI Accessed February 24, 2019. https://www.genome.gov/glossary/index.cfm?id=169

20 minutes

Notes to tutor

Project this video about protein structure.

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| **PROTEIN FOLDING**<br>During protein synthesis, the sequence of nucleotides in DNA is converted into the sequence of amino acids in a polypeptide chain. But this polypeptide is not yet a functional protein. To be functional polypeptides must fold into distinct three-dimensional conformations, and in many cases multiple polypeptide chains must assemble into a functional complex.<br><br>Several types of non-covalent forces help maintain the folded structure. These include the **covalent peptide backbone** of a polypeptide, covalent **disulfide bond** that may form between pairs of cysteine side-chains, **hydrogen bonds** formed between hydrogens covalently bonded to oxygen or nitrogen and lone pairs on oxygen or and nitrogen, **hydrophobic interactions** between non-polar side chains, **electrostatic interactions** formed by either ionizable residue side-chains, or by the free ionized groups of the amino- and carboxy-termini and **van der Waals interactions** resulting from transient induced dipoles in the electron cloud surrounding an atom.<br><br>**Chaperones**<br>The proper folding of proteins within cells is assisted by specialized molecules (proteins) called **chaperones**. Chaperons **bind and stabilize unfolded** or partially folded polypeptides and help them to fold properly. In the absence of chaperones, unfolded or partially folded polypeptide chains would be unstable within the cell, frequently folding incorrectly or aggregating into insoluble complexes. Chaperons bind to a nascent polypeptide chains that are still being translated on ribosomes, thereby preventing incorrect folding or aggregation of the amino-terminal portion of the polypeptide before synthesis of the chain is finished.<br><br>**Mis folded proteins**<br>Mis folded proteins act as non-function or malfunction proteins which may result in disease process.<br>Example: Amyloid protein result in Alzheimer disease | 20 minutes | **Note to tutor**<br><br>Project this video about folding<br><br>Explain what is Alzheimer disease. |

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| **PROTEIN DENATURATION**<br>It is a change in native state (physical, chemical, and biological properties) of proteins due to the change of its surrounding solution. Proteins denaturation occurs without destruction of their peptide linkages, but destruction of secondary bonds leading to unfolding protein molecules.<br>Denaturating agents may be physical (High temperature, high pressure, X-ray, ultraviolet rays-mechanical agitation. organic alkalies) or chemical (Strong acids, strong alkalis, organic solvents and heavy metal)<br>Among these denaturating agents, the most common are heat and pH. Heat causes some proteins to coagulate. Example: egg albumin. When egg white is heated, the albumins unfold and coagulate to produce solid rubbery mas. | 10 minutes | |

| IN CLASS ACTIVITY: PROTEINS | | | |
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| **Purpose:** | These are review questions that will help you to assess if you understand the content of this lessons | 30 minutes | |
| **Over to you:** | Sit in groups and discuss following review questions: | | |
| **Activity:** | Answer and discuss following questions:<br>1. Which level of protein organization is the most important in determining the final conformation?<br>2. What is the difference between alpha-helix and beta-sheet protein conformations?<br>3. Do changes in the primary, secondary or tertiary structure of a protein normally have consequences for their function? | | |

| LABORATORY PRACTICALS : DETERMINATION OF TOTAL PROTEINS | | | |
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| **Purpose:** | Some functional groups in proteins can react to produce characteristically colored products.<br><br>The color intensity of the product formed by a particular group varies among proteins in proportion to the number of reacting functional or free groups present and their accessibility to the reagent. | 120 minutes | For lab this exercises make sure materials in the lab manual are available and the lab prepared.<br><br>In case the reagents are not available you can propose another method to determine total protein |
| **Over to you:** | This test is specific for the peptide bond. It allows to detect the presence of peptides or proteins in a sample. | | |
| **Activity** | Under alkaline conditions copper ions present in Biuret reagent interact with –CO-NH-groups present in adjacent dipeptide and form a purple coloured complex.<br><br>This can be measured spectrophotometrically at 540nm. The method is fairly specific and there is little interference with other compound containing – CO-NH-groups like urea and other like reducing sugar that can interact with cupric ions. | | |

**Anticipated time required for Unit 2.4 activities :**

Theory : 2h all activities + 2h self-learning

Practical : 2h