Proteins—Chapter Five

Structure:

Polypeptide Chain – Polymer of amino acids (20 possibilities) that are arranged in a specific linear sequence and are linked by peptide bonds.

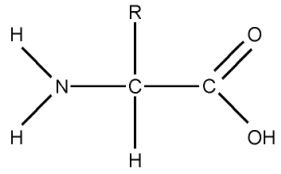
Function:

1. Structural support (keratin)
2. Storage (of amino acids)
3. Transport (ex. Hemoglobin)
4. Signaling (chemical messengers)
5. Cellular response to chemical stimuli (receptor proteins)
6. Movement (contractile proteins)
7. Defense against foreign substances and disease-causing organisms (antibodies)
8. Catalysts of biochemical reactions (enzymes)

Structure of Amino Acid Monomers:

Amino Acid – Building block molecule of a protein; most consist of an asymmetric carbon termed the alpha carbon, which is covalently bonded to:

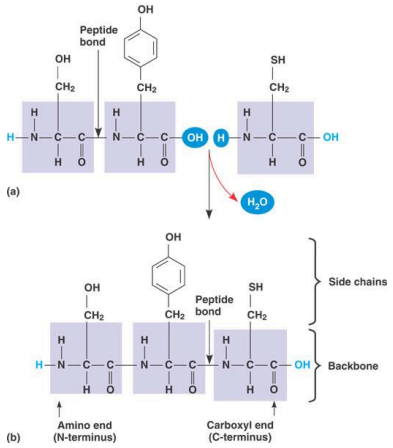
1. Hydrogen atom
2. Carboxyl group
3. Amino group
4. Variable R group (side chain) specific to each amino acid. Physical and chemical properties of the side chain determine the uniqueness of each amino acid.



Amino acids contain carboxyl and amino functional groups.

Peptide bond – Covalent bond formed by a condensation reaction that links the carboxyl group of one amino acid to the amino group of another.

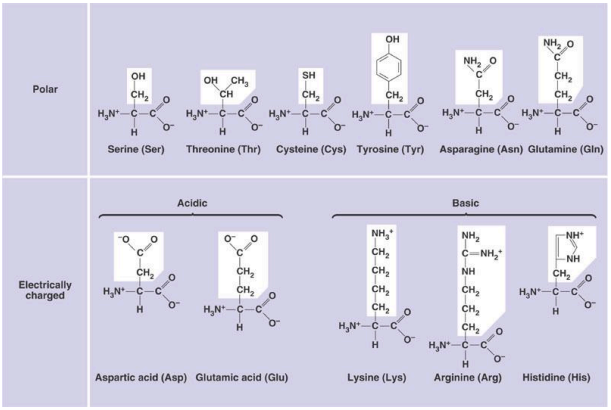
- Has polarity with an amino group on one end (N-terminus) and a carboxyl group on the other (C-terminus).
- Has a backbone of the repeating sequence
- -N-C-C-N-C-C-

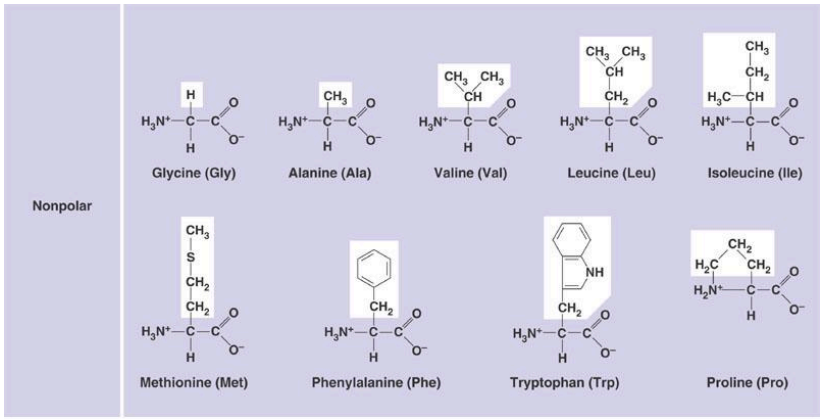


The twenty common amino acids can be grouped by properties of side chains

1. Nonpolar side groups (hydrophobic). Amino acids with nonpolar groups are less soluble in water.
2. Polar side groups (hydrophilic). Amino acids with polar side groups are soluble in water.

- Acidic side groups. Dissociated carboxyl group gives these side groups a negative charge
- Basic side groups. An amino group with an extra proton gives these groups a net positive charge

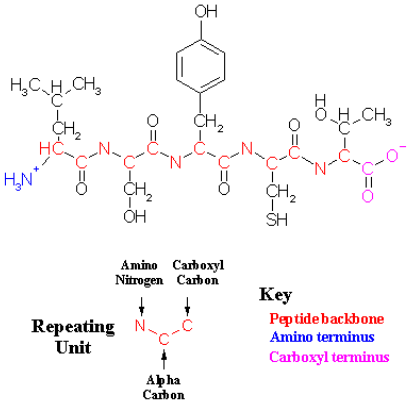




Protein Conformation & Function:

Polypeptide chains:

- Range in length from a few monomers to more than a thousand
- Have unique linear sequences of amino acids



A protein's function depends on its specific conformation

A protein's function depends upon its unique conformation.

Protein conformation – 3 dimensional shape of a protein

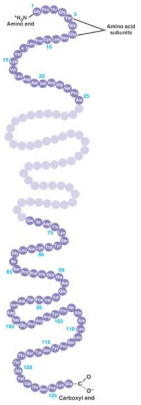
Four Levels of Protein Structure

The correlation between form and proteins is an emergent property resulting from superimposed levels of protein structure:

1. Primary structure
2. Secondary structure
3. Tertiary structure

When a protein has two or more polypeptide chains, it also has:

4. Quaternary structure



Primary Structure – Unique sequence of amino acids in a protein

- Determined by genes
- Slight change can affect a proteins conformation and functions

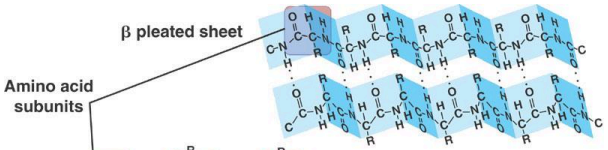
(ex sickle cell)

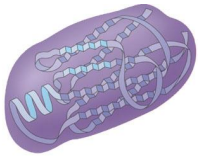
Secondary structure – Regular, repeated coiling and folding of a proteins polypeptide backbone.

- Stabilized by hydrogen bonds between peptide linkages in the protein's backbone

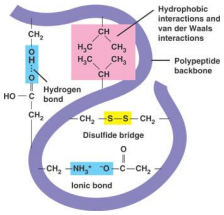
(carbonyl and amino groups)

- The major types of secondary structure are alpha helix (spiral) and beta pleated sheet



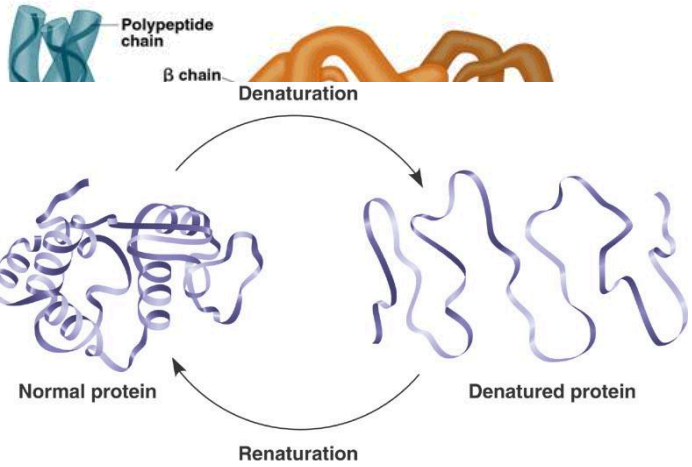


Tertiary structure – Irregular contortions of a protein due to bonding between R groups

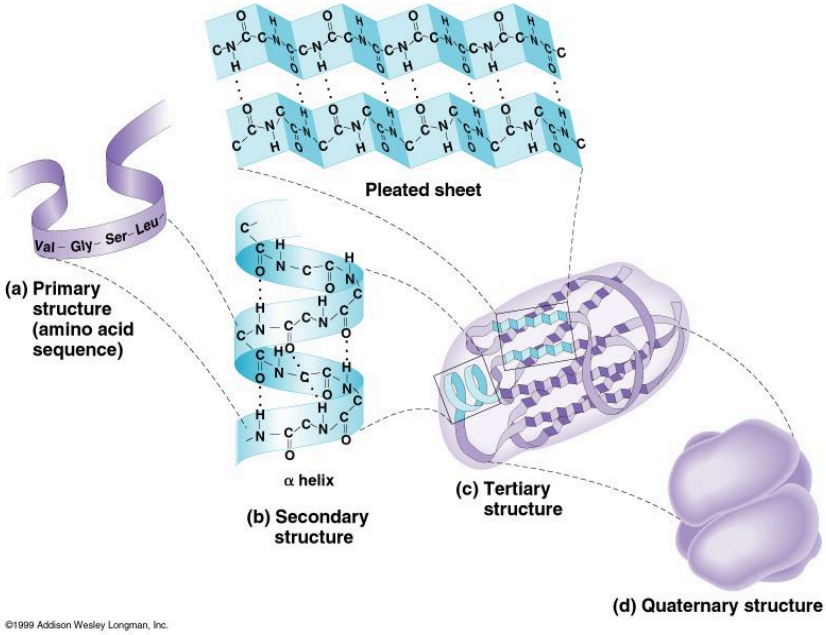


- H bonding between polar side chains
- Ionic bonding between charged side chains (between acidic and basic a.acids)
- Hydrophobic – nonpolar a.acids move to center away from water
- Disulfide bridges from strong covalent linkages (two sulfhydryl groups)

Quaternary Structure: results from interactions among 2 or more polypeptides



Factors that determine Protein Conformation:
Occurs during protein synthesis within cell
Depends on physical conditions of environment
pH, temperature, salinity, etc.
change in environment may lead to denaturation of protein
denatured protein is biologically inactive
can renature if primary structure is not lost



***Building a protein activity:**

In groups of 3-4, get a 4 foot tuber and 15 push pins (amino acids), as outlined below.

Blue (2) – basic (+)
Red (2) – acidic (-)
Yellow (6) – hydrophobic
White (3) – polar
Green (2) – cysteine (each with a sulfhydryl group)

Assemble a protein and run through the four levels of protein structure. You need to interact with another group when modeling quaternary structure.