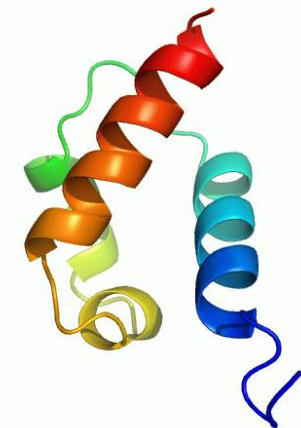
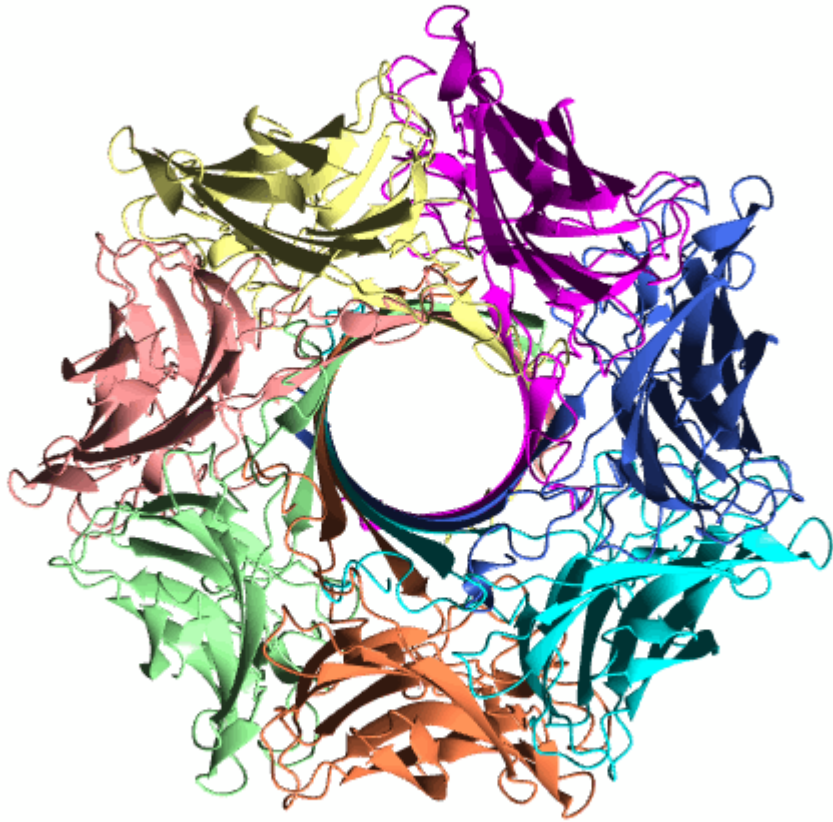
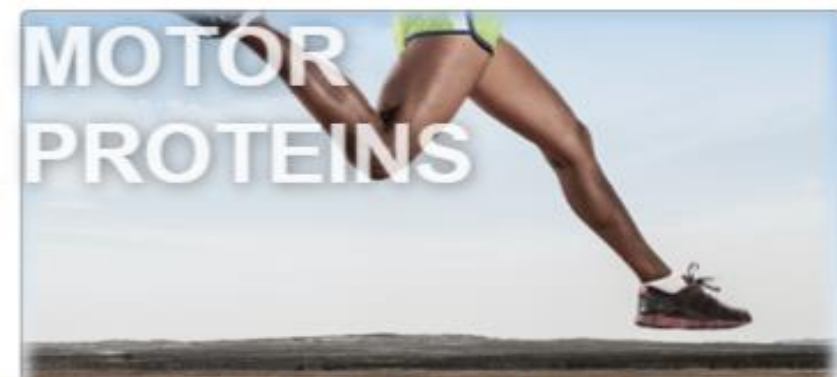
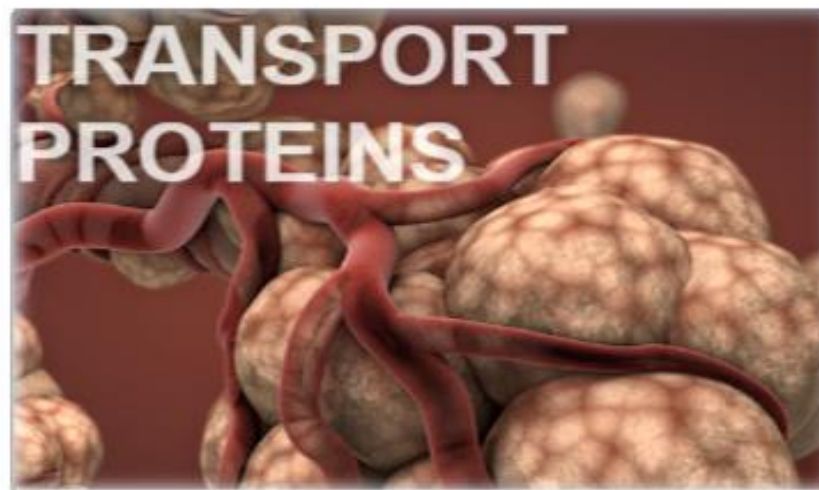
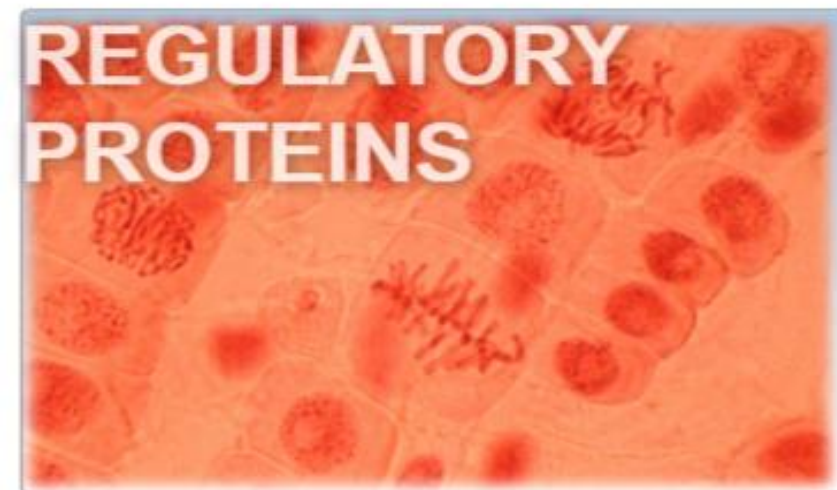
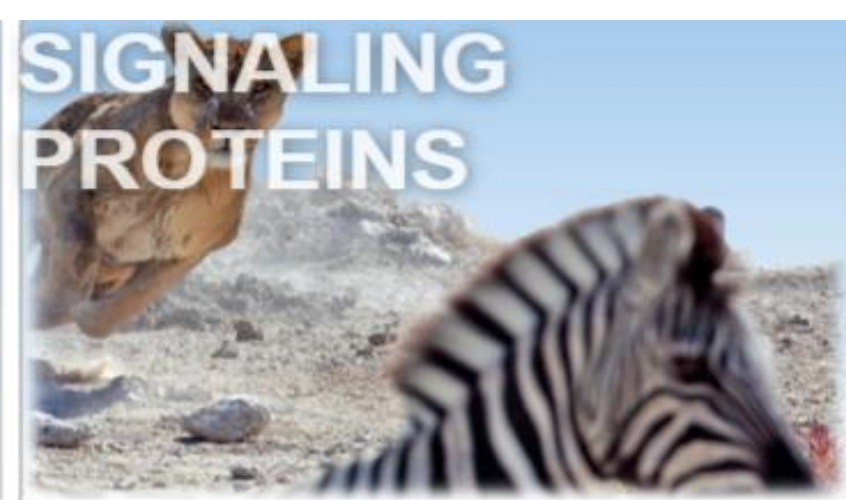
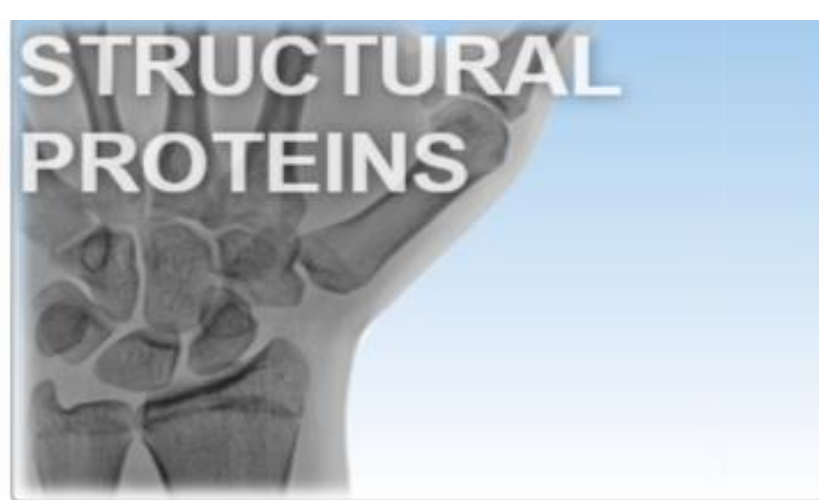


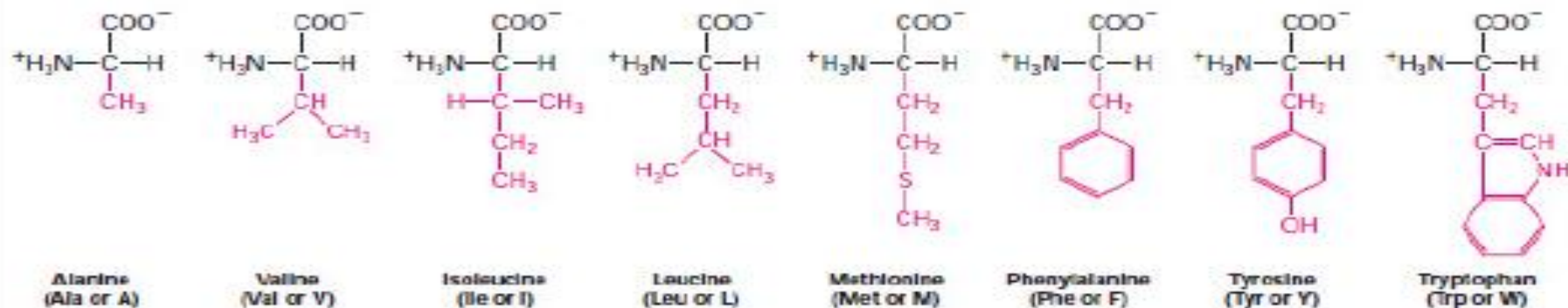
Proteins



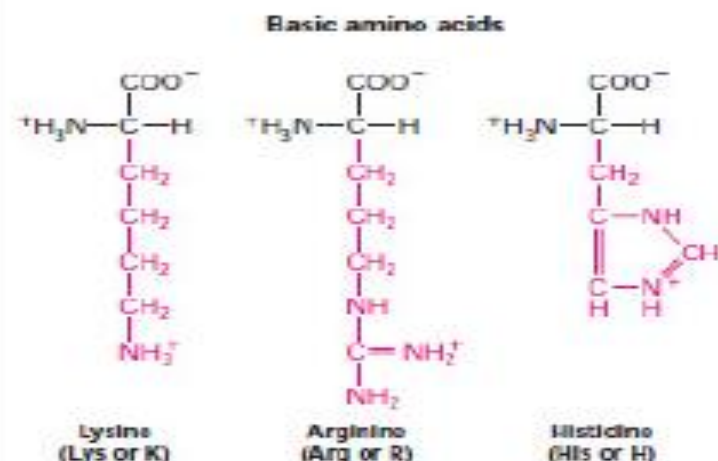
- ✓ Proteins are the most abundant biological macromolecules
- ✓ Occurrence, number, size
- ✓ Dynamic function
- ✓ Name & imp derived: *proteios*, meaning “first,” or “primary.”
- ✓ Protein Mass???
- ✓ Function: Catalysis, defense, storage, transport, cellular, communication, movement, or structural support
- ✓ Basic building blocks (amino acids)
- ✓ All 20 of the common amino acids are α -amino acids
- ✓ Possess a carboxyl group and an amino group bonded to the same carbon atom (α carbon).
- ✓ Only vary with side chain R which varies which vary in structure, size, and electric charge



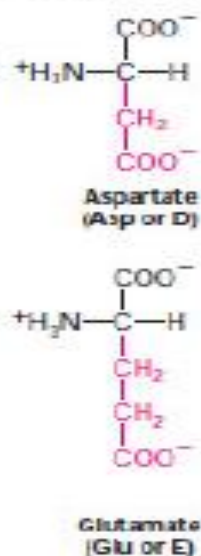
HYDROPHOBIC AMINO ACIDS



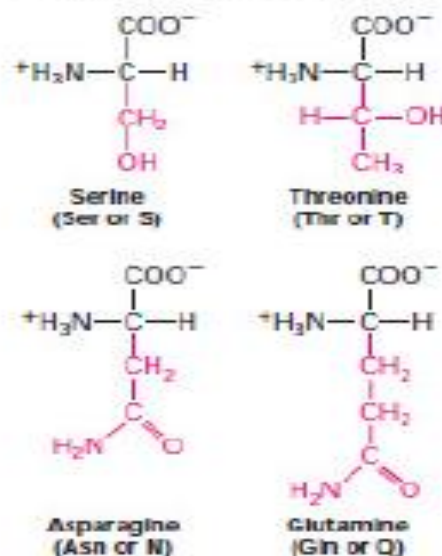
HYDROPHILIC AMINO ACIDS



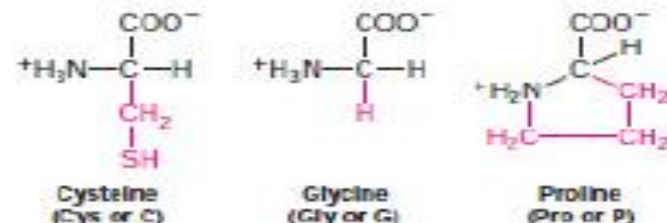
Acidic amino acids



Polar amino acids with uncharged R groups



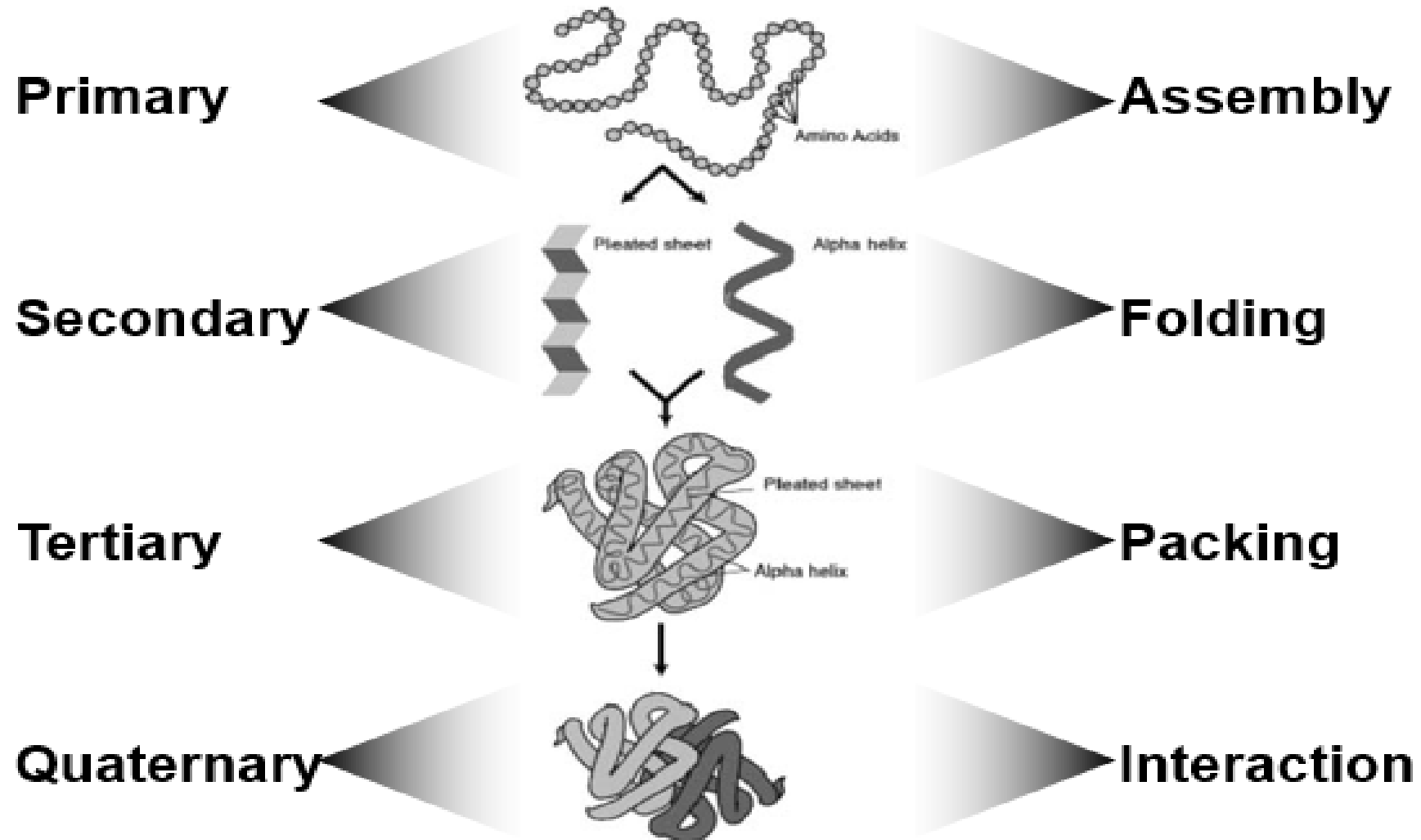
SPECIAL AMINO ACIDS



▲ FIGURE 2-13 The 20 common amino acids used to build proteins. The side chain (R group; red) determines the characteristic properties of each amino acid and is the basis for grouping amino acids into three main categories: hydrophobic, hydrophilic, and special. Shown are the ionized forms that exist at the pH (~7) of the cytosol. In parentheses are the three-letter and one-letter abbreviations for each amino acid.

Biology/Chemistry of Protein Structure

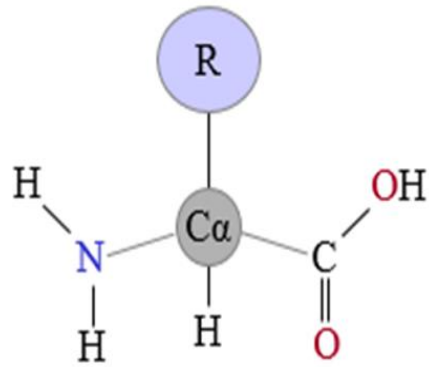
STRUCTURE



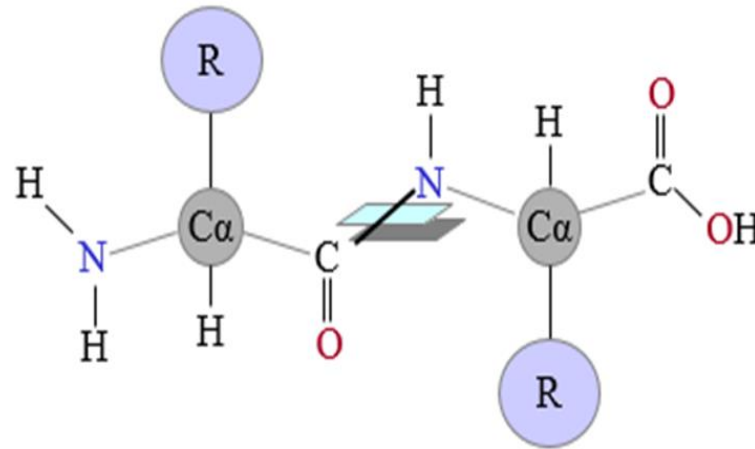
PROCESSES

Protein primary structure

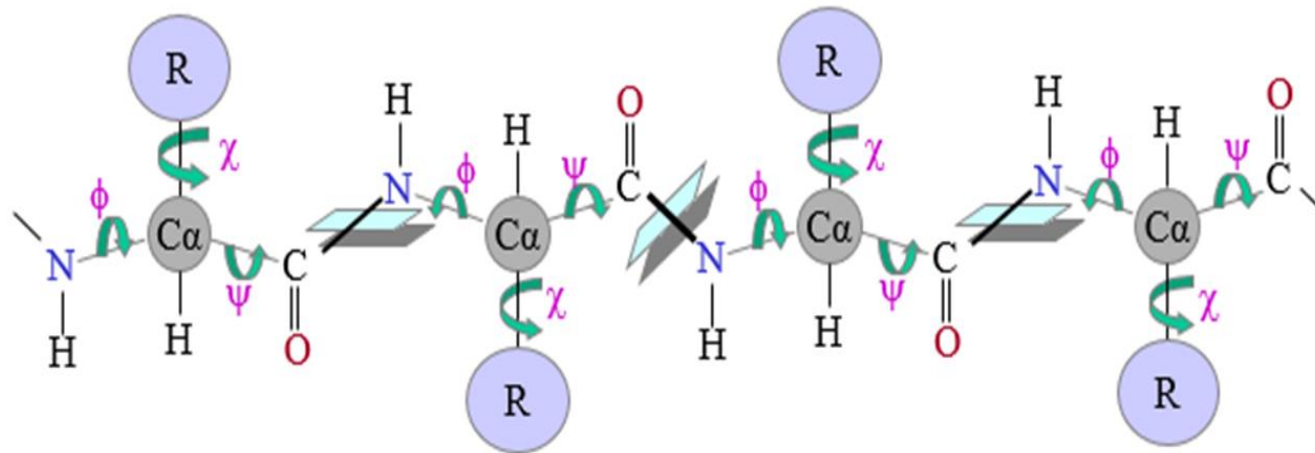
twenty types of amino acids



two amino acids join by forming a peptide bond



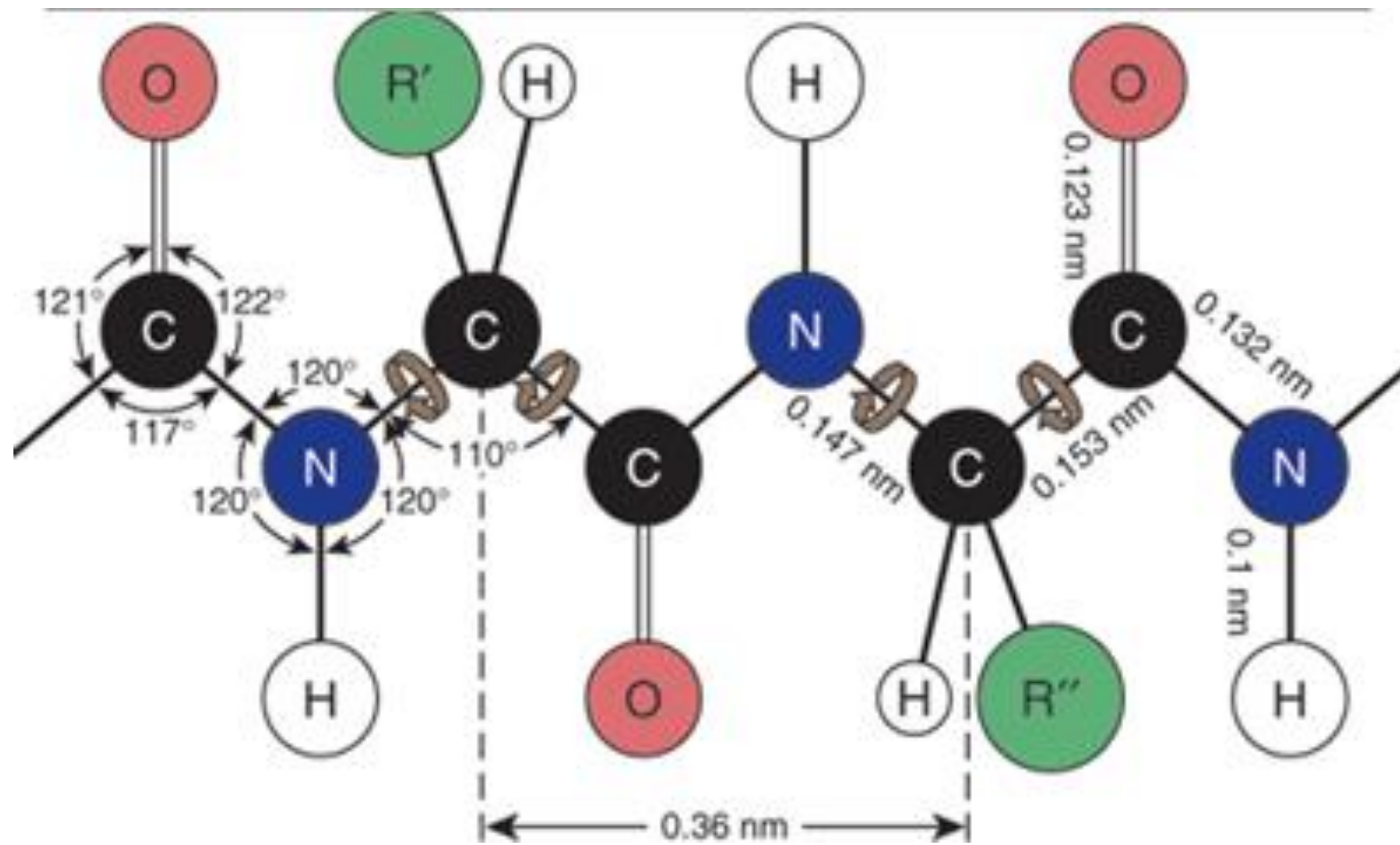
each residue in the amino acid main chain has two degrees of freedom (ϕ and ψ)



the amino acid side chains can have up to four degrees of freedom (χ_{1-4})

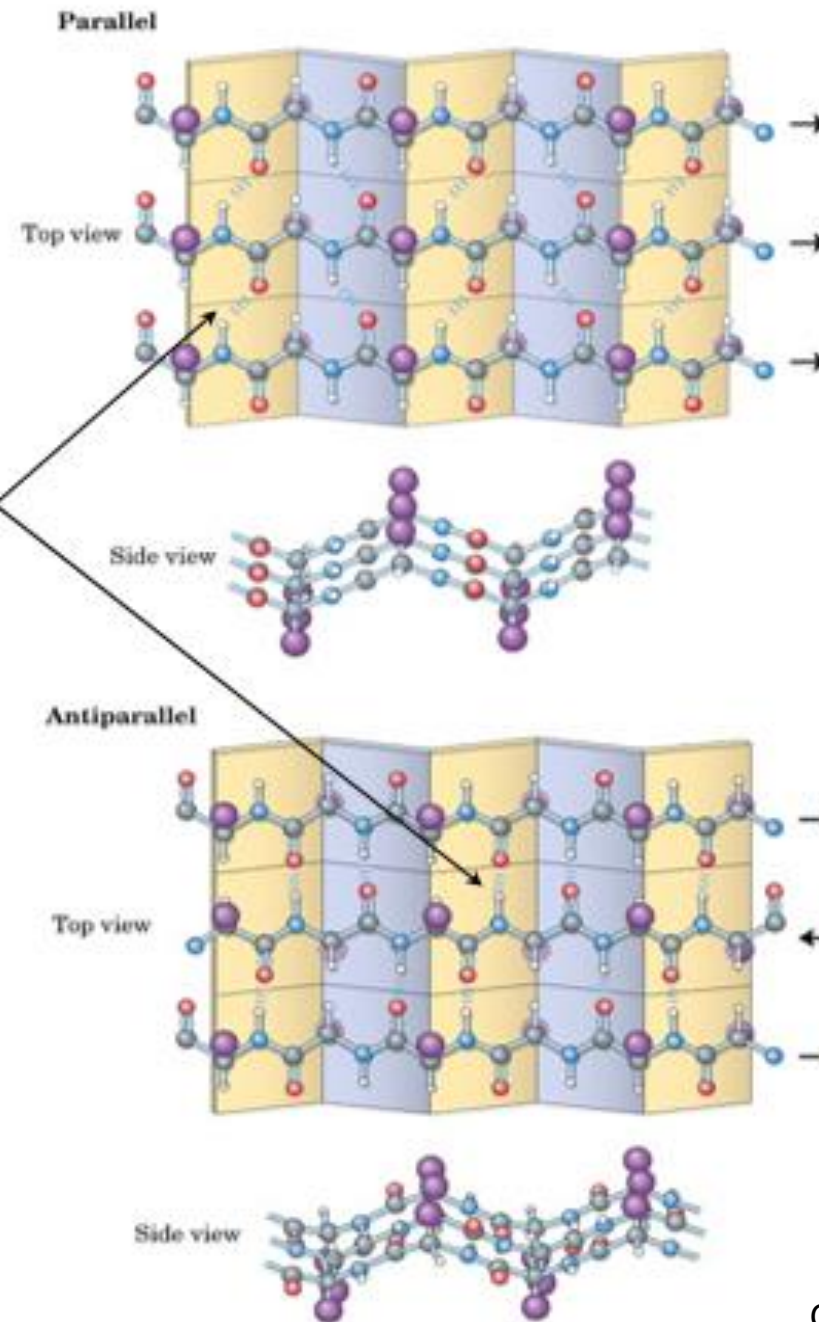
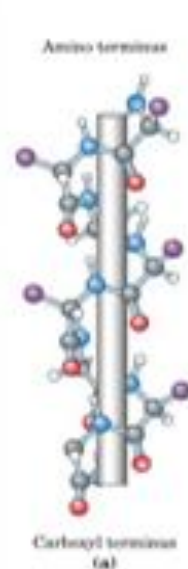
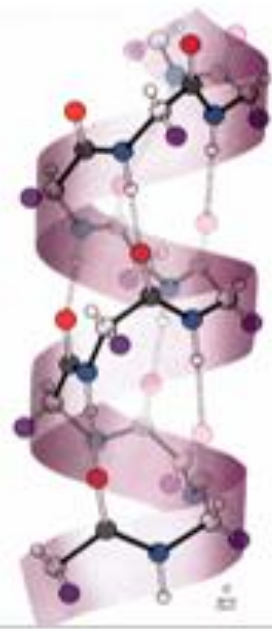
15

- linear
- ordered
- 1 dimensional
- sequence of amino acid polymer
- by convention, written from amino end to carboxyl end
- a perfectly linear amino acid polymer is neither functional nor energetically favorable → folding!

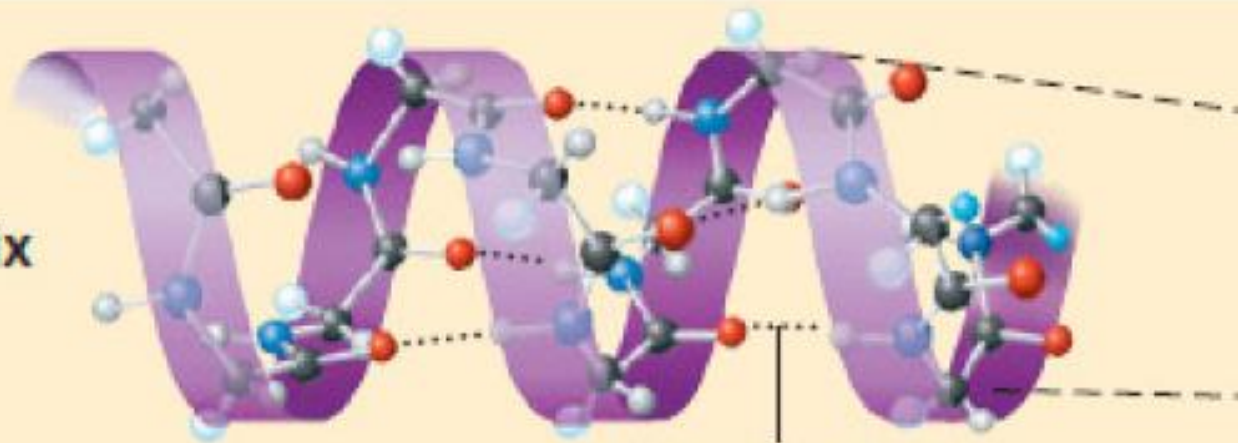


Secondary Structure

- non-linear
- 3 dimensional
- localized to regions of an amino acid chain
- formed and stabilized by hydrogen bonding, electrostatic and van der Waals interactions

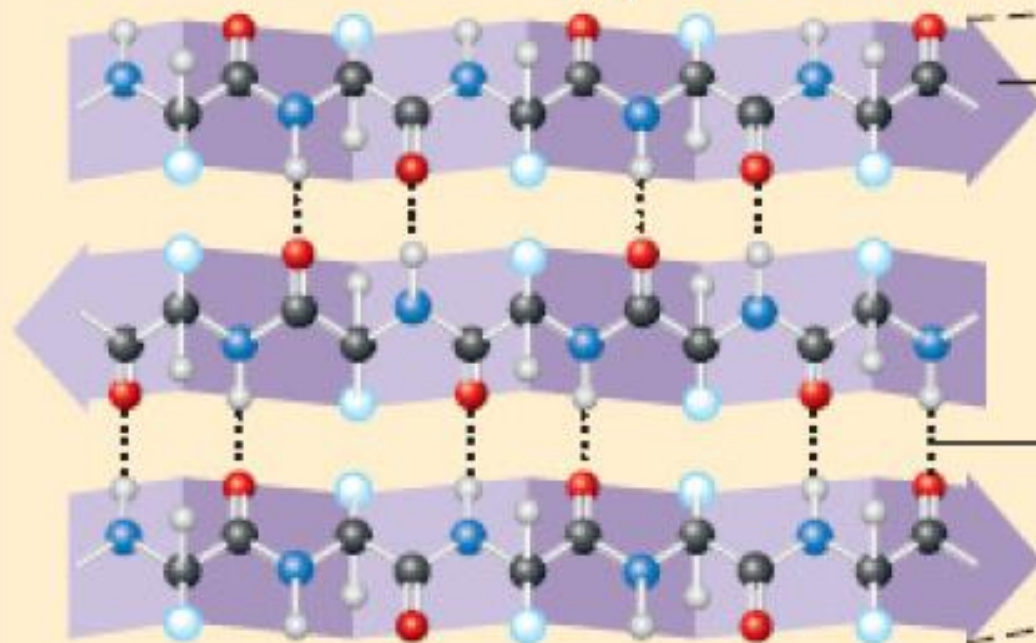


α helix



Hydrogen bond

β pleated sheet

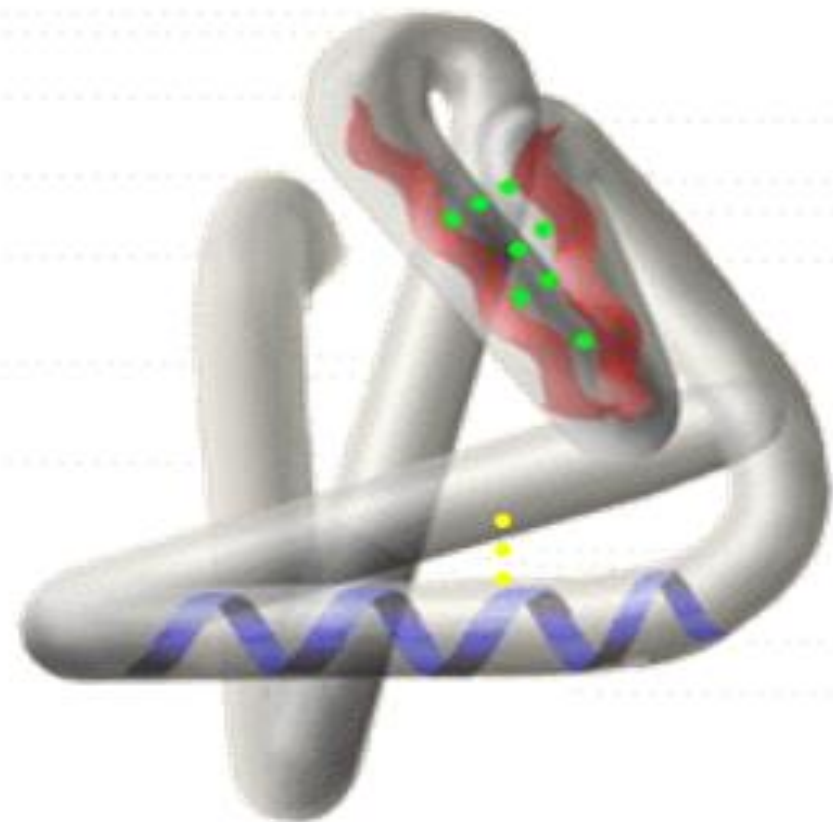


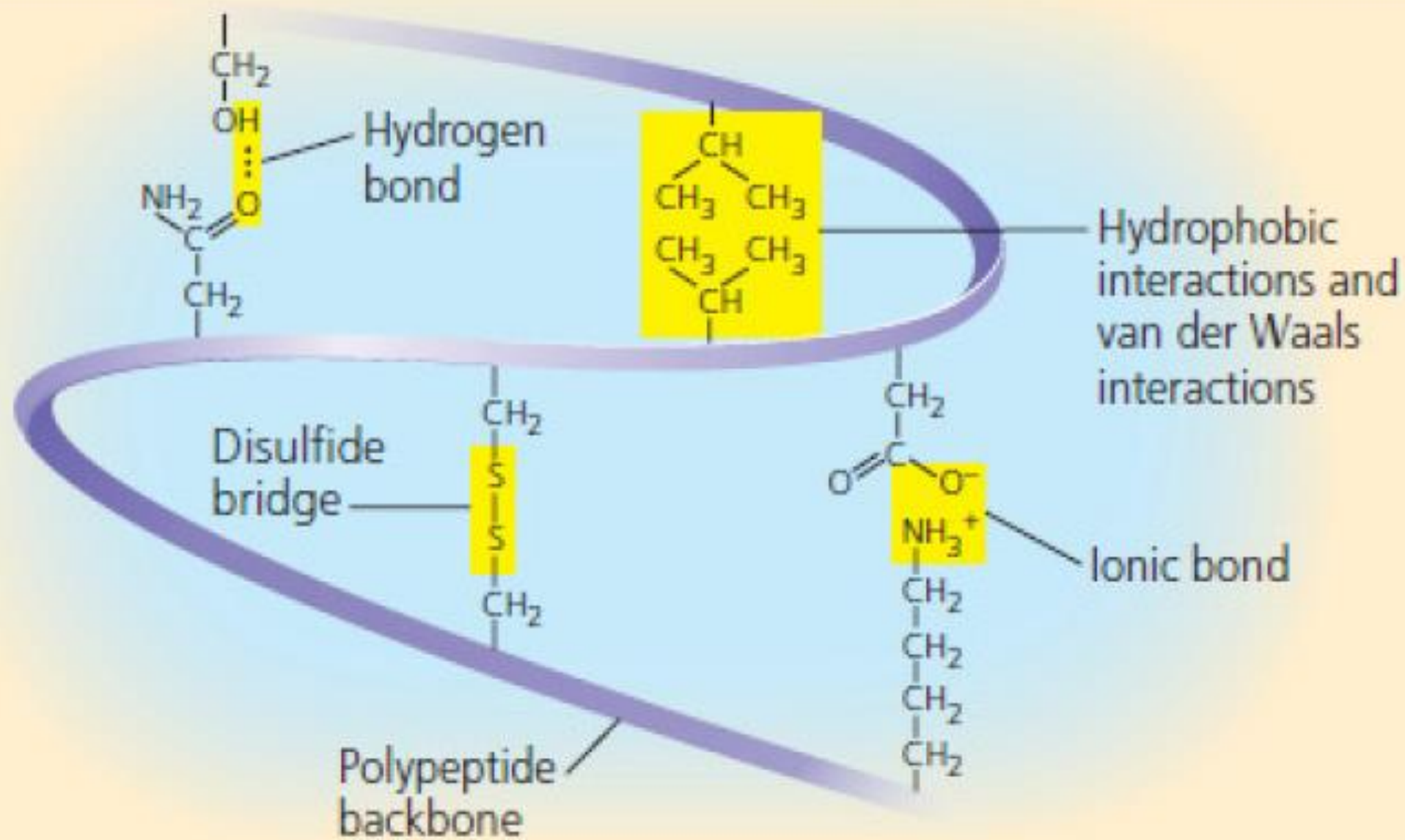
β strand, shown as a flat arrow pointing toward the carboxyl end

Hydrogen bond

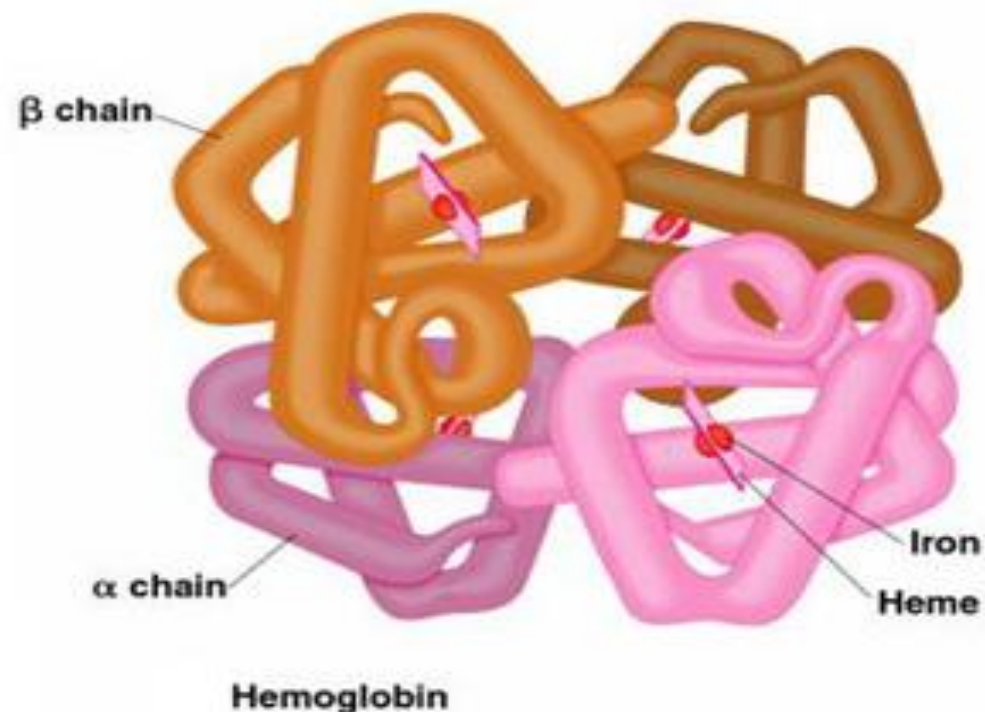
Tertiary Structure

- non-linear
- 3 dimensional
- global but restricted to the amino acid polymer
- formed and stabilized by hydrogen bonding, covalent (e.g. disulfide) bonding, hydrophobic packing toward core and hydrophilic exposure to solvent
- A globular amino acid polymer folded and compacted is somewhat functional (catalytic) and energetically favorable → interaction!





Quaternary Structure



- non-linear
- 3 dimensional
- global, and across distinct amino acid polymers
- formed by hydrogen bonding, covalent bonding, hydrophobic packing and hydrophilic exposure
- favorable, functional structures occur frequently and have been categorized

References

- C. Branden, J. Tooze. "Introduction to Protein Structure." Garland Science Publishing, 1999.
- . Komili. "Section 8: Protein Structure." Biophysics 101: Computational Biology and Genomics, November 12, 2002.
- D.L. Nelson, A.L. Lehninger, M.M. Cox. "Principles of Biochemistry, Third Edition." Worth Publishing, May 2002.