



## Section I: **Protein Structure**

- Proteins are linear chains of covalently linked amino acids
- Each amino acid has the same “backbone” structure, but with different chemical groups (sidechains) attached
- A chain of amino acids will spontaneously form a stable “secondary structure”; the two most common secondary structures are the alpha helix and beta sheet
- Regions of secondary structure will spontaneously fold into a specific “tertiary structure” that governs the protein’s function
- Folding to achieve a tertiary structure is due to the behavior of different chemical groups on amino acids in an aqueous environment
- The three dimensional structure of proteins is most often determined by x-ray diffraction or NMR analysis
- The structural coordinates for a protein are deposited as a “PDB file” in the Protein Data Bank.
- PDB files can be downloaded from the RCSB PDB website; they can be used with computer visualization software to visualize the 3D structure of a protein.