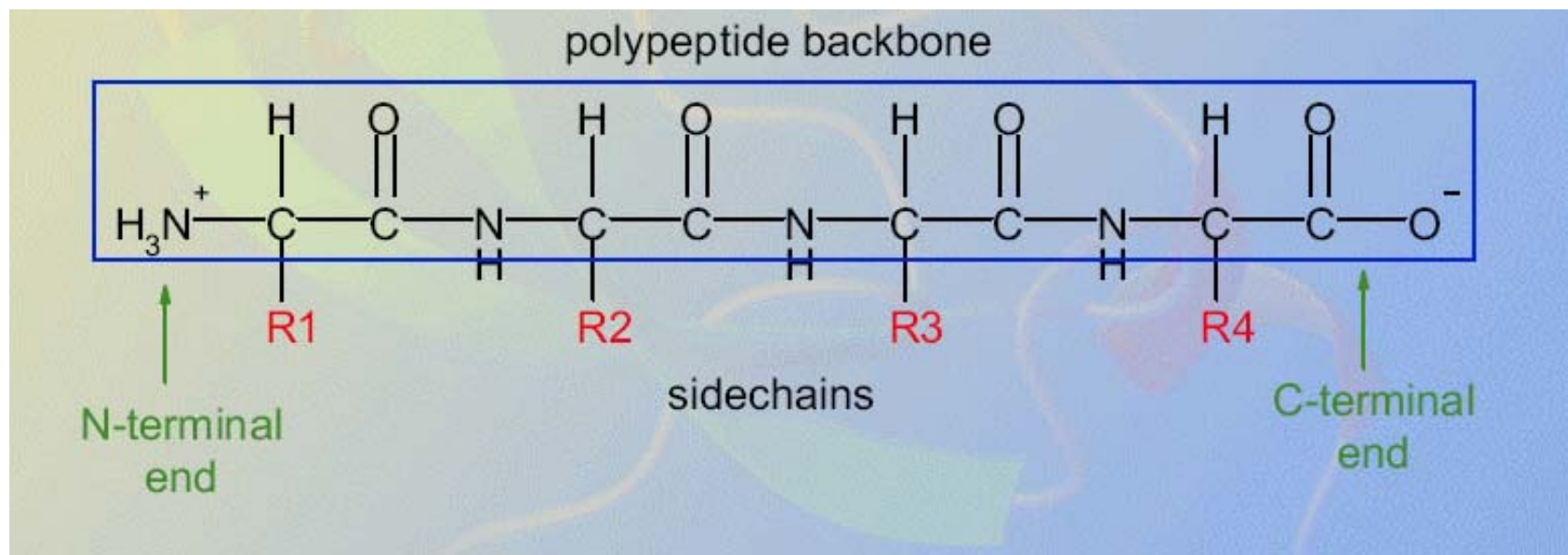




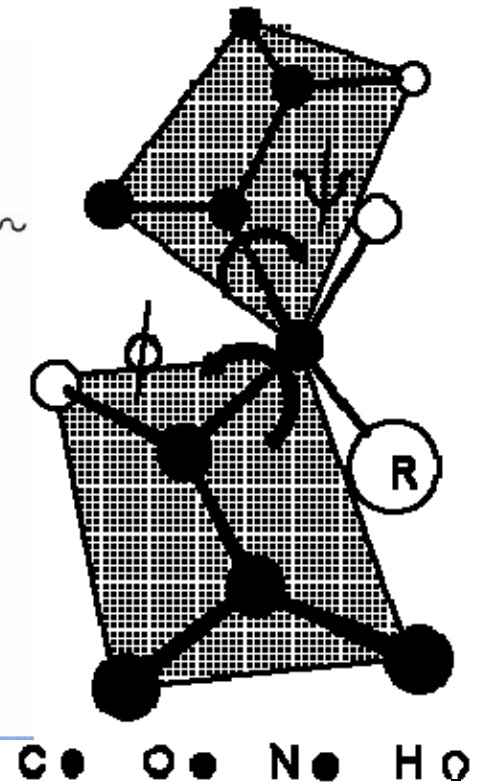
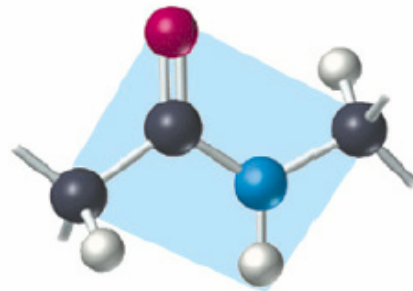
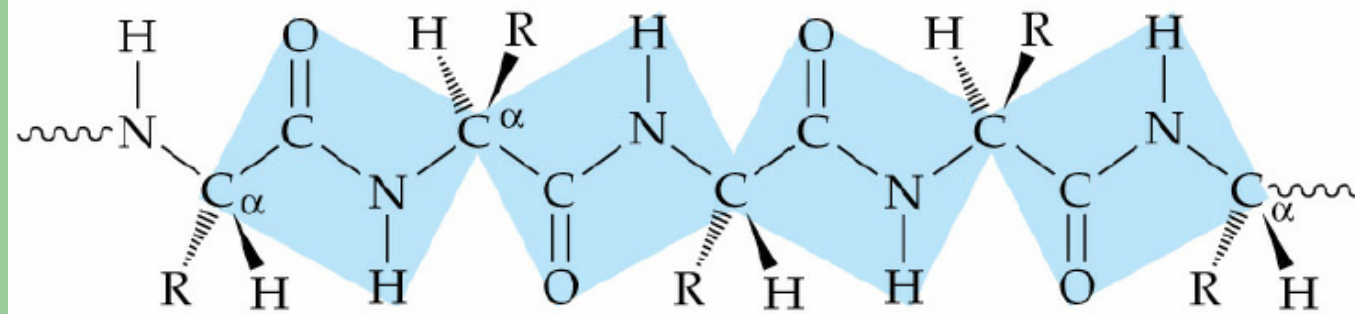
# Primary sequence



- The order of amino acids in a protein is genetically determined
- Contains all the information to assume its correct 3-D structure



# Peptides





# Primary structure

- The oxygen and hydrogen of the CO-NH group are in the trans position as consequence of the stabilization resonance
- $\alpha$ -carbon atoms are the only ones that may rotate freely
- -NH- group does not protonate
- Polypeptidic chain may be presented by a series of rigid planes separated by HCR- groups



# Protein Folding

- Balance between Chain entropy and Solvent Entropy
- Non-covalent interactions
  - Steric restraints: bulky side chains
  - Hydrogen bonding
  - Interchain electrostatic interactions
  - Hydrophobic interactions
  - Disulfide bonds



# Secondary Structure

- Spatial structure the polypeptide chain assumes exclusively along the axis
- Native conformation
  - Minimal free energy
- Main structures:
  - helix
  - $\beta$ -structures



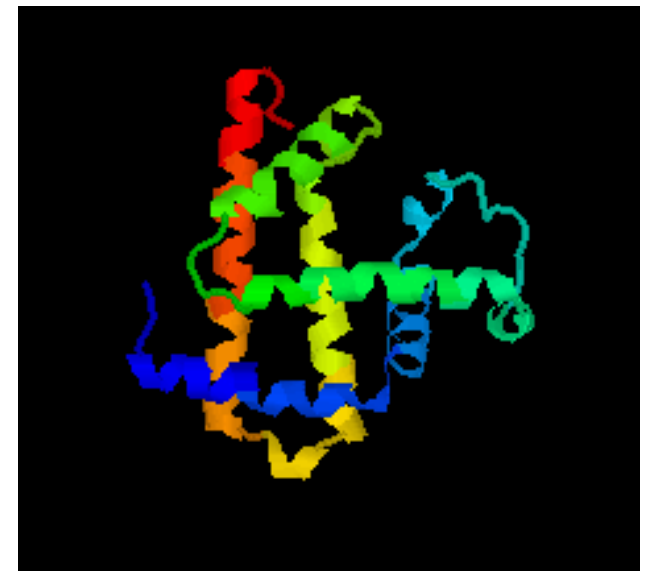
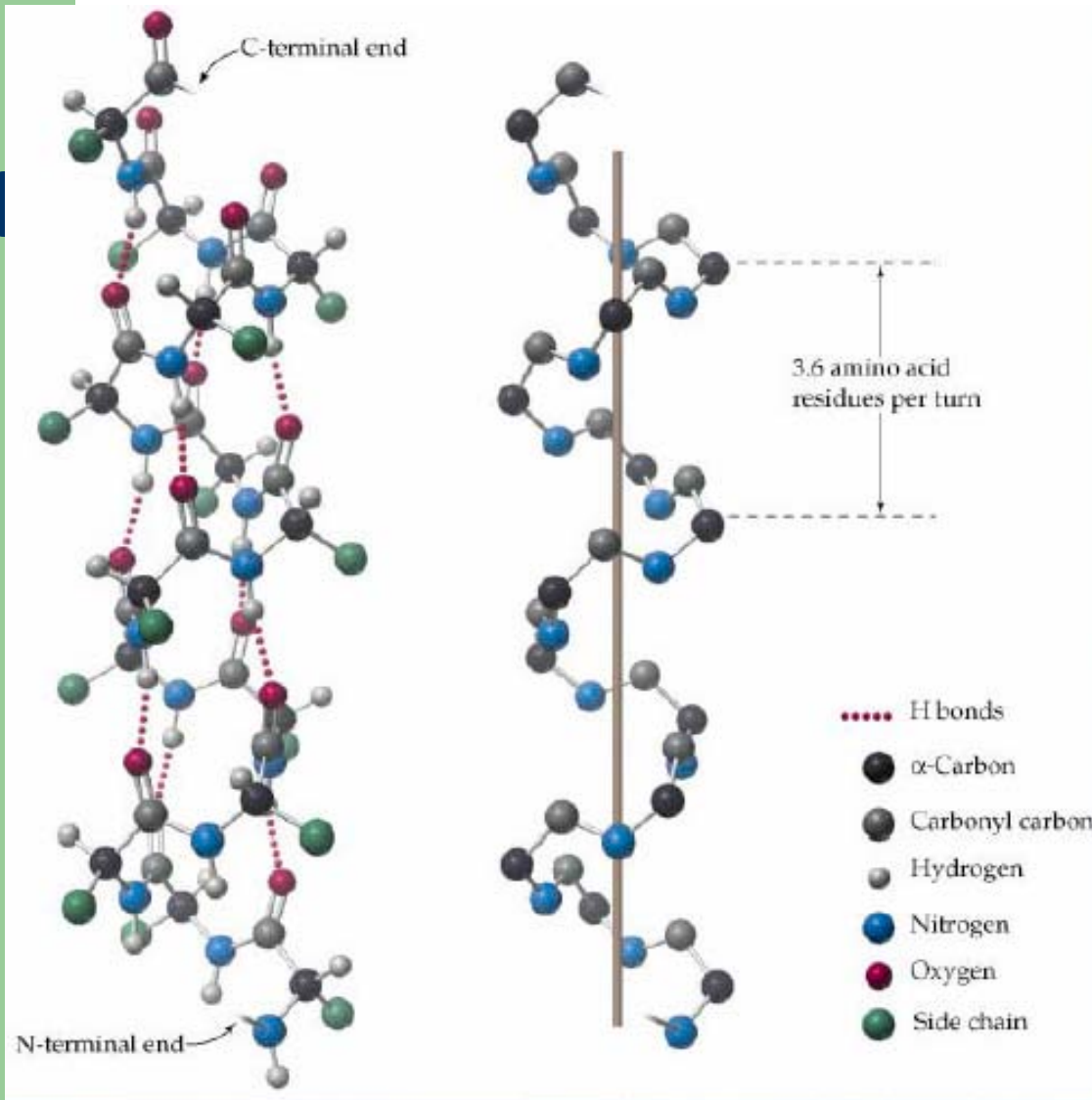
# Secondary Structure

- Adds new properties to a protein such as flexibility, strength



# $\alpha$ -helix

- Each peptide bond is engaged in formation of H-bonds
- Very compact structure
  - High density that restricts interaction with other molecules
- Proteins
  - Rigid, long, narrow rod
  - 5-80% content
- High stability
- Proline
  - not compatible; interrupts, bending of the chain

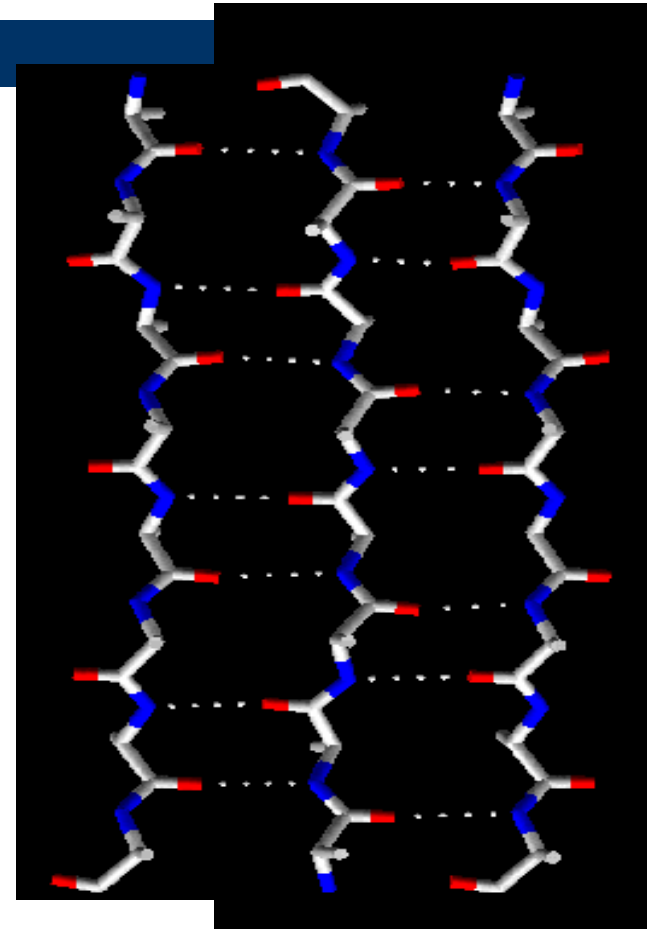






# $\beta$ -structure

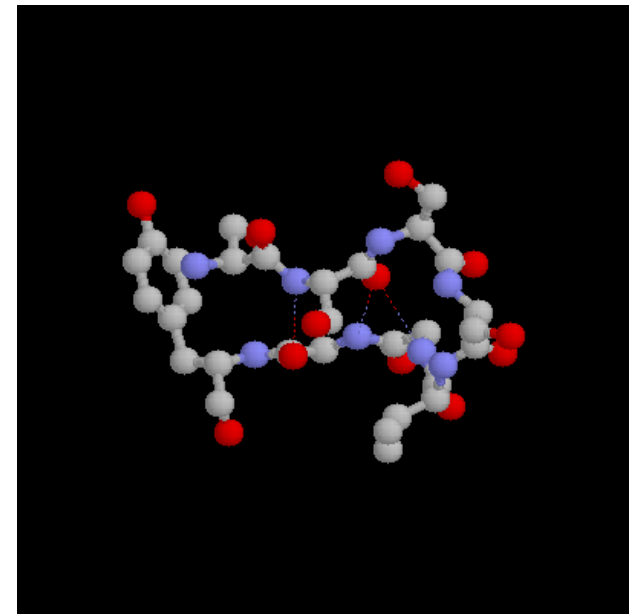
- Pleated sheets
- Interchain H-bonds
  - All peptide bonds participate
- Parallel or antiparallel
- R-groups
  - Anti-parallel: sides with either all hydrophilic or hydrophobic chains
  - Parallel: more uniformly hydrophobic, rarely exposed to solvent
- More stable than  $\alpha$ -helix
- Anti-parallel: associate in barrels
  - Core is very hydrophobic





## $\beta$ -bends

- A chain folds back on itself to form an antiparallel  $\beta$ -sheet
- Important to protein structure
  - Direct chains of proteins to allow proper interactions
- Protein folding
- 20-45% of total structure of all proteins
- proline and glycine are prevalent

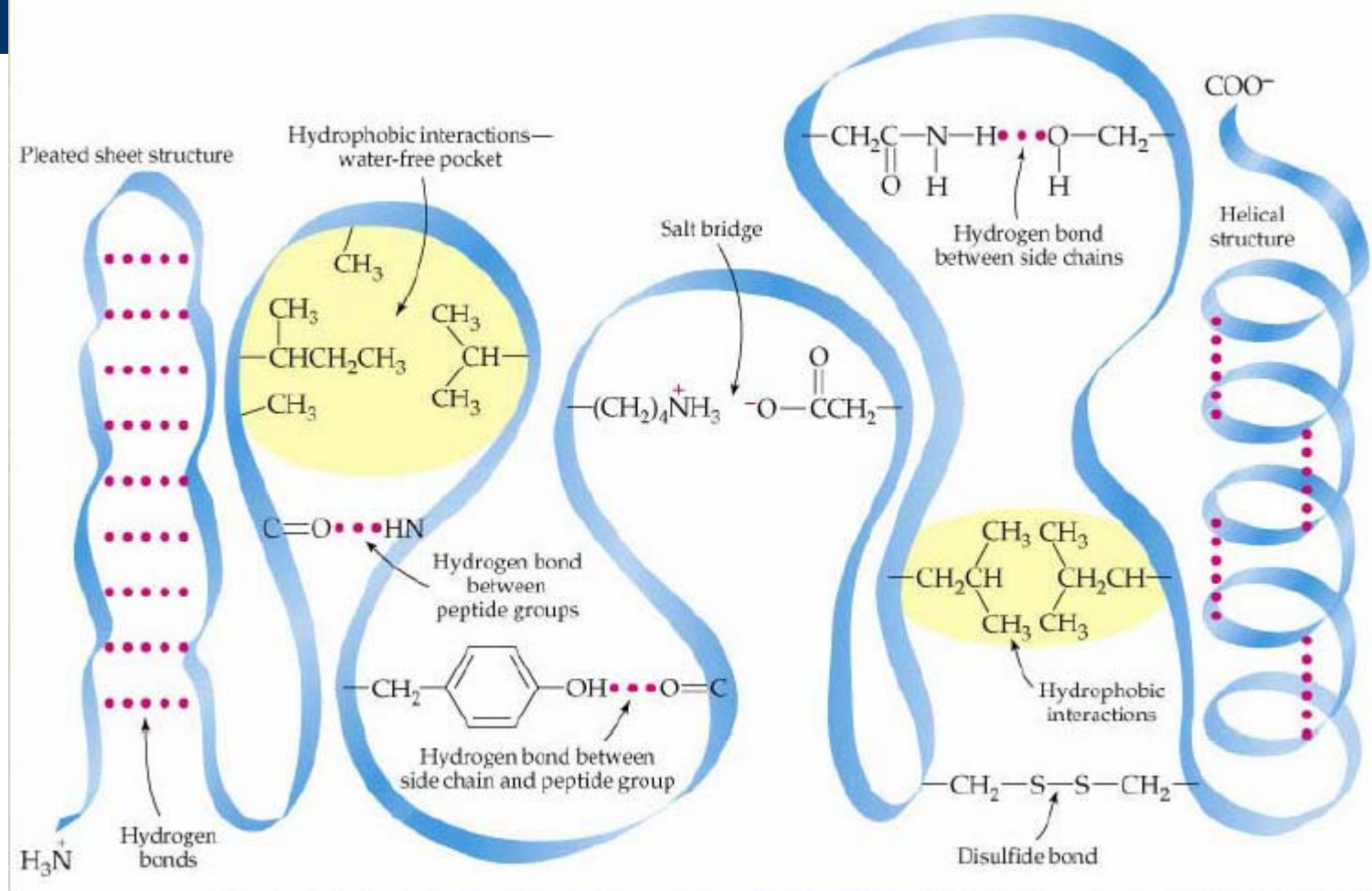




# Tertiary structure

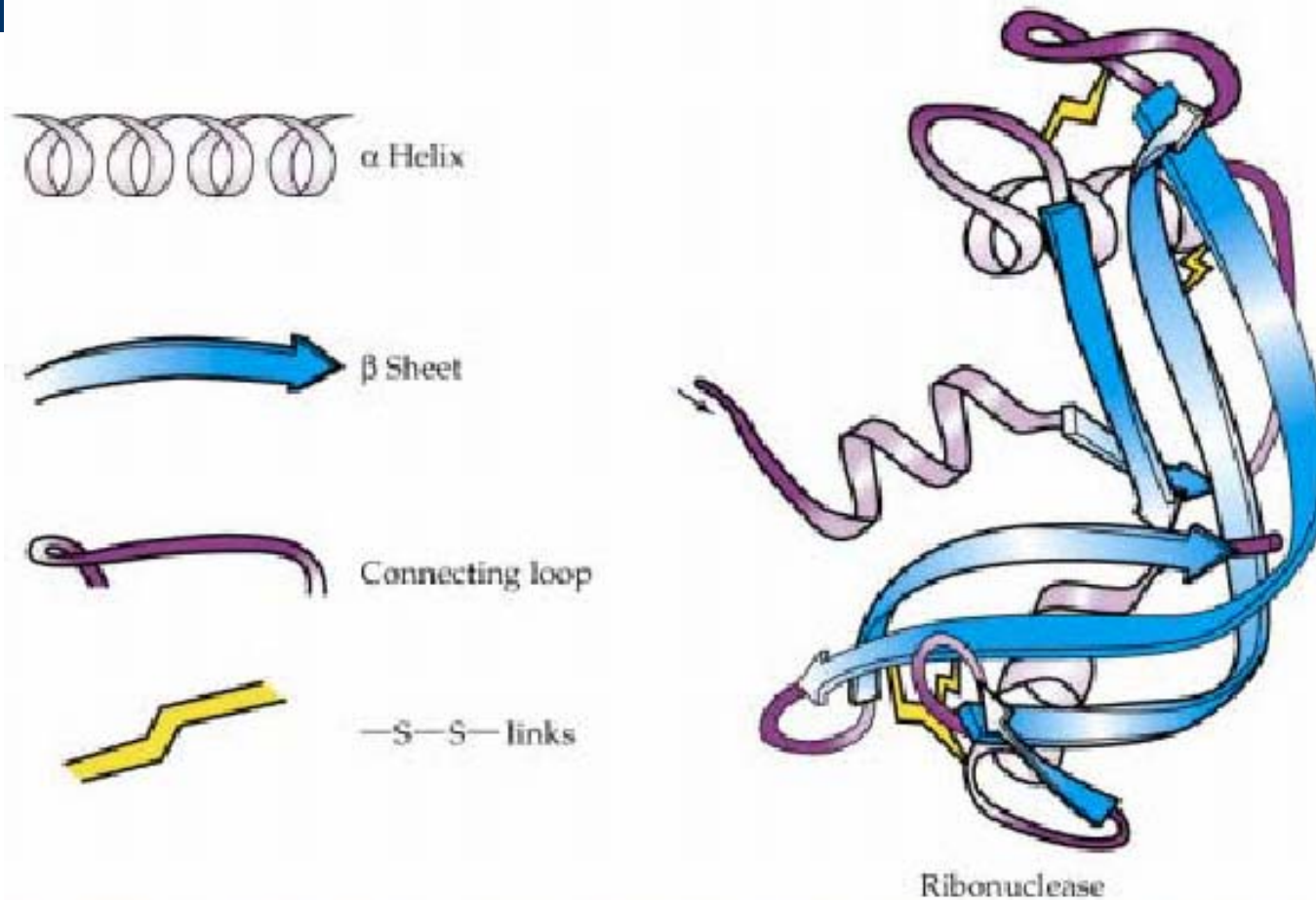
- 3-D organization of a polypeptide chain
- Relative compact structures
- Folding
  - Remove hydrophobic groups
  - Interior devoid of water molecules or charged groups
  - Except for specific functionality

# Shape-Determining Interactions in Proteins





# Ribonuclease





# Quaternary structure

- Non-covalent association of protein units
- Examples:
  - Soy globulins
  - Actomyosin: Myosin and actin (muscle protein)
  - Hemoglobin



# Example

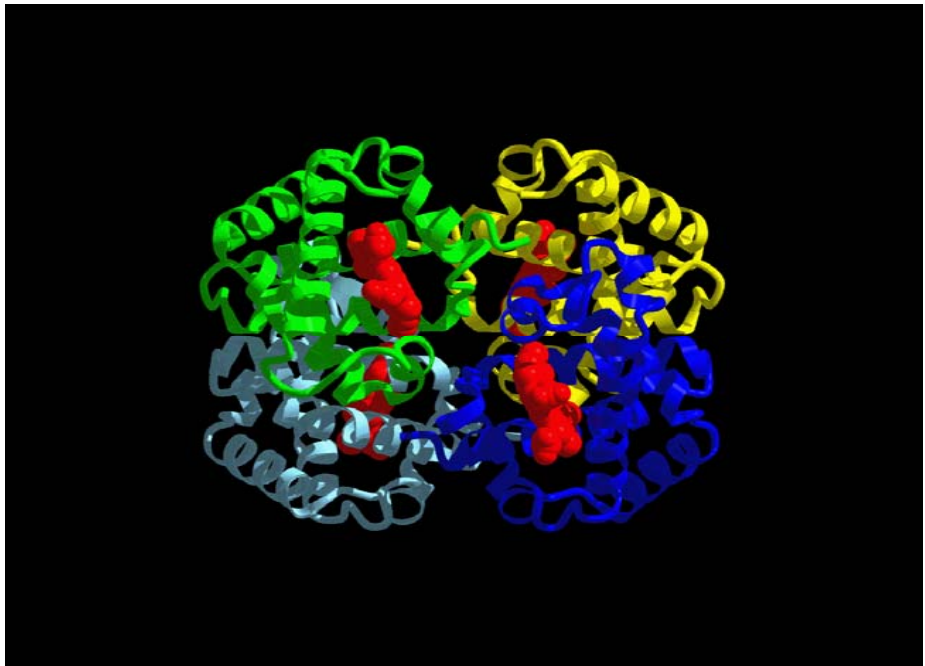
F1-ATPase



$\alpha$  - subunit

$\beta$  - subunit (catalytic)

$\gamma$  - subunit



Hemoglobin