primary: sequence of AA’s; (recognize abbreviations, usually first 3 letters, see handout) 
covalent (peptide bond) 
Carboxyl (acid) (\(-C^0\)) and amino (\(-NH^+\)) groups (except those on side chains of asp, glu, his, lys, arg) appear only at ends of chain (N-terminal and C-terminal)

secondary: association by H-bonding of polar groups on backbone — does not involve side chains directly — results in major structure features, e.g., \(\alpha\)-helix

tertiary: folding of chain — noncovalent

- **nonpolar** side chains associate with selves in center of protein to avoid water
- **polar** side chains (-OH, -SH, -NH\(_2\), =O) H-bond with selves or on surface with water
- **charged** side chains \(-C^0\), \(-NH^+\) associate with selves (+ ↔ -) or water on surface
- **terminal** \(-C^0\), \(-NH^+\) same as charged side chains

example of mutation: Hb Wien: tyr → asp

quaternary: association of individual folded protein chains (subunits of multimeric protein) with each other and/or association of individual folded protein chains with nonprotein “cofactors”; involves noncovalent forces: hydrophobic bond, ionic bonds, polar/hydrogen bonds