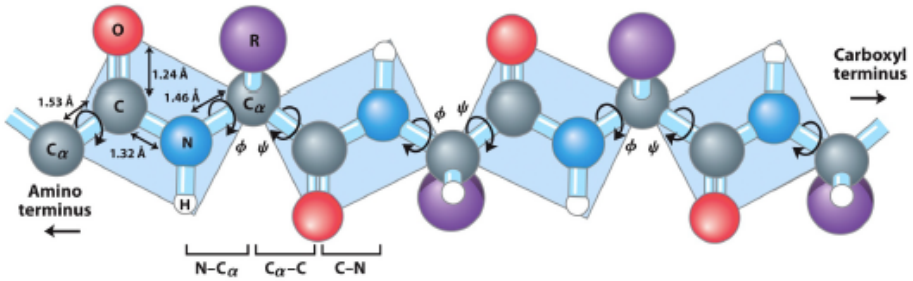
- Resonance structure, partial sharing of 2 pairs of electrons between carbonyl O and amide N
- Resonance causes the peptide bonds to be:
    - Less reactive
    - Exhibit a dipole (partial negative at carbonyl oxygen, partial positive at amide nitrogen)
    - Rigid and planar
    - Rotation about the peptide bond is not permitted, rotation around the alpha carbon is permitted



Secondary Structure

- Local spatial arrangement of the polypeptide backbone
- Alpha Helix
    - Stabilized by H bonds between C=O and N-H groups 4 amino acid residues apart
    - Polypeptide backbone winds tightly around a longitudinal axis
    - Right handed (thumb up) helix with 3.6 residues per turn
    - R groups stick out
    - Sequence affects alpha helix stability
        - Interactions between R groups can stabilize or destabilize a helix
            - Glutamic acid R groups will repel each other
            - Bulky amino acids won't fit close together in the chain (steric hindrance)
            - Proline breaks the helix because rotation around the alpha carbon is impossible
            - Glycine is a helix breaker because its tiny R groups gives too much flexibility
            - Small hydrophobic residues such as Alanine and Leucine are strong helix formers
- Beta Pleated Sheet
    - Stabilized by H bonds between adjacent segments
    - Several beta strands that run alongside each other
    - Stabilized by H bonds between C=O and N-H groups from an adjacent segment that may be nearby or distant
    - Parallel: run in same direction, bent H bonds, weaker
    - Antiparallel: run in opposite direction, linear H bonds, stronger
    - B turns = when strands change direction, stabilized by H bond
- Random Coil
    - Irregular arrangement of the polypeptide chain

Tertiary Structure

- Overall spatial arrangement of atoms in a protein
- Stabilized by numerous, longer range, weak interactions between amino acid side chains
    - Hydrophobic interactions, polar interactions, covalent disulfide bonds, ionic bonds