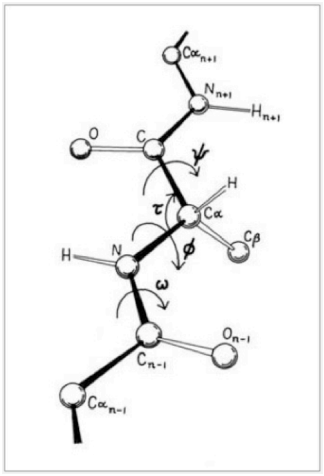
BCH 258 lecture notes Fri. Aug 28, 2009



Graphics: restrictions on mainchain conformation, continued:
- Mage: ala_dipept_geom_dotball5.1.kin
- Mage: idealpolyala12.kin, appendstuff2.kin
- Ramachandran plot regions

Handouts:
Amino-Acids diagram
Homework: Worksheet 3: Handedness & Amino Acid Roles
Kinemage file – c1Basics-2-5-QKiNG.kin

Amino Acid Roles: introduce homework...
- occurrence vs secondary structure

Geometry of polypeptide backbone: in class...
ala_dipep_geom_dotball5.1.kin, revisited,
now lead in to idealpolyala12.kin and secondary structure
- rotatable-bond Ala dipeptide (~like c1Basics)
- Rama regions - show β better than 180,180
- general data contours - show helix good; go off edge; 0,0 dire
- Gly data, contours - show Cβ clash in $L3_{10}$, Lβ; not in β

Polypeptide: amino acids condense to residues, forming peptide bond
- peptide bond (C--N) and C--O are partial double bonds, so planar & shorter
- entire Cα---Cα peptide unit is planar and trans

Sidechains have χ_1, χ_2 , etc. dihedrals (χ_4 max, for Lys & Arg)
- for bonds between tetrahedral carbons, staggered >> eclipsed
- overall, a few well-defined sidechain conformations are good: rotamers
- [only 2 good (4 more OK) for Leu;
  - 13 for Met with 3 χ angles and no branches]

RNA has one χ from ribose to base, but the ribose has limited flexibility and there are 7 degrees of freedom along the backbone between the attachment of one base to the attachment of the next.
suitefitroc_...kin