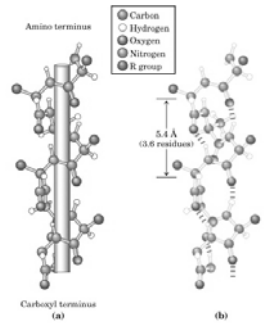
Primary Structure Determines Secondary Structure

Dipeptide model- not all conformations are possible

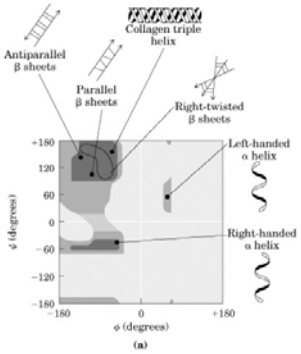
α-Helix
Pitch: rise/residue

Fig. 6-4 (a and b) Lehninger POB 3rd Ed.



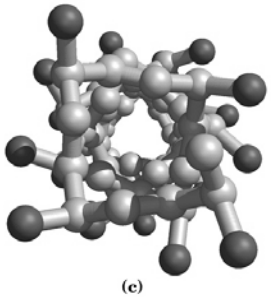
Ramachandran Plot

Fig. 6-3 Lehninger POB 3rd Ed.



α-Helix
Location of R Groups

Fig. 6-4 (c) Lehninger POB 3rd Ed.



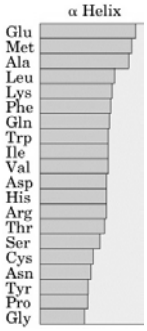
Primary Structure Determines Secondary Structure

Secondary (2°)- local 3-D shape

- α-helix
- ß-sheet
- collagen triple helix

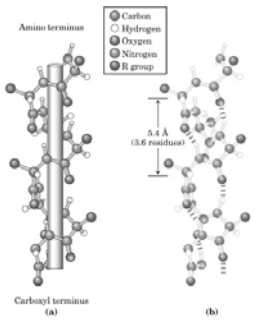
Not all Amino Acids Can be Present in an α-Helix

Fig. 6-10 (left) Lehninger POB 3rd Ed.



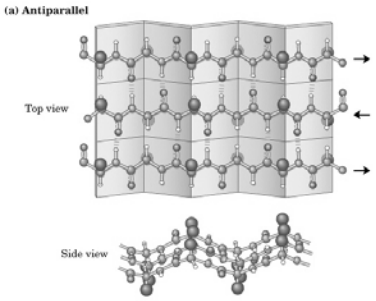
The Force Responsible For the α-Helix is the h-bond, Parallel to Axis

Fig. 6-4 (a and b) Lehninger POB 3rd Ed.



The ß-Sheet
R Groups Alternate Above/Below Plane

Fig. 6-7 (a) Lehninger POB 3rd Ed.

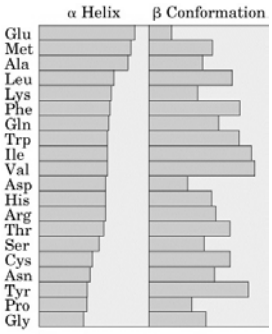


Charged Amino Acids are Often Localized on Ends of Helical Segment

- On amino terminus, negative charges stabilize and positive charges destabilize
- Carboxyl terminus opposite
- Due to dipole of peptide bond

"All" Amino Acids Can be Present in a ß-Sheet

Fig. 6-10 Lehninger POB 3rd Ed.

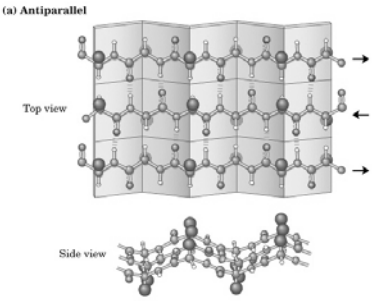


The ß-Sheet is a More Extended Conformation

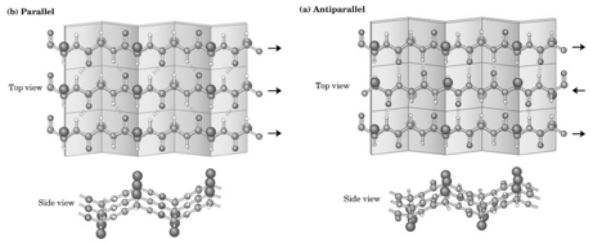
- No dimensions because extension is variable
- Wool extended; heat, shrinks because in a less extended ß-sheet

The Force Responsible For the ß-Sheet is the h-bond, Perpendicular to Axis

Fig. 6-7 Lehninger POB 3rd Ed.



The ß-Sheet Can be Parallel or Antiparallel



Forces Involved in 2° Structure

Weak (non-covalent)
- hydrogen bonds
- electrostatic interactions
- metal ion coordination
- hydrophobic effect

The ß-Sheet is Usually Short

Average is 8 amino acid residues
Many more are possible

Collagen Triple Helix

Kinky
Pro-X-Gly or Hyp-X-Gly
Pro makes kinks
X varies
Why Gly?