Consensus sequences, showing conserved sites, may be represented in different ways



### Differences between orthologous sequences suggest phylogenetic relationships



Tree calculated by comparing bacterial GroEL sequences

Different proteins have different sequence requirements and evolve at different rates



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Differences between paralogous sequences predict gene duplication events



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The connectivity of functional groups in the protein backbone directs its conformations



Pauling & Corey's studies of oligopeptides revealed structural requirements of proteins



#### Linus Pauling, 1901–1994

Unnumbered 4 p115a Lehninger Principles of Biochemistry, Fifth Edition © 2008 W. H. Freeman and Company



#### **Robert Corey, 1897–1971**

Unnumbered 4 p115b Lehninger Principles of Biochemistry, Fifth Edition © 2008 W. H. Freeman and Company Structural studies of peptides revealed a planar amide group with a short C-N bond



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Resonance explains the double-bond character of the C-N amide bond



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The protein backbone (main chain) is a connected series of peptide planes



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## Although fixed along the amide bond, the backbone may rotate about the other bonds



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Looking down the C<sub> $\alpha$ </sub>-X bond, the value of  $\phi$  or  $\psi$  increases as the rear group rotates CW



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Some values of  $\phi$  and  $\psi$  correspond to overlap of atoms (steric clashes)

Ex: Backbone-backbone clash  $0^{\circ}$ , 180°



Ex: Backbone-side chain clash  $120^{\circ}$ ,  $180^{\circ}$ 



The Ramachandran plot depicts favorable, allowed, and disallowed backbone angles





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# Pauling, Corey, and Herman Branson predicted the major secondary structures

They considered:

- Planarity of peptide bond
- Measured bond lengths and angles within the peptide plane
- Allowed  $\phi$  and  $\psi$  dihedral angles
- Favorable hydrogen-bonding arrangements of backbone groups



### The $\alpha$ -helix forms within a continuous strech of the polypeptide chain



The  $\alpha$ -helix is a right-handed helix



#### α-Helices have a dipole moment, due to unbonded and aligned N-H and C=O groups



