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

(a) 

\[ \text{[AG]-x(4)-G-K-[ST].} \]

(b) 

\[ \text{D-\{-W\}-[DNS]-\{-ILVFWY\}-[DENSTG]-[DNQGHRK]-\{GP\}-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW].} \]
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.
Differences between paralogous sequences predict gene duplication events

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

Amide groups love to form H-bonds.

R-group direction disfavors certain conformations due to steric clashes.
Pauling & Corey’s studies of oligopeptides revealed structural requirements of proteins
Structural studies of peptides revealed a planar amide group with a short C-N bond.
Resonance explains the double-bond character of the C-N amide bond.
The protein backbone (main chain) is a connected series of peptide planes.
Although fixed along the amide bond, the backbone may rotate about the other bonds.

Dihedral angle: the angle between two planes.
Looking down the $C_\alpha$-X bond, the value of $\phi$ or $\psi$ increases as the rear group rotates CW.
Some values of $\phi$ and $\psi$ correspond to overlap of atoms (steric clashes)

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

Ex: Backbone-side chain clash
$120^\circ, 180^\circ$
The Ramachandran plot depicts favorable, allowed, and disallowed backbone angles.
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 α-helix forms within a continuous stretch of the polypeptide chain

- 5.4 Å rise,
- 3.6 aa/turn
- \( \therefore 1.5 \text{ Å/aa} \)

N-term

C-term

prototypical
\( \phi = -57^\circ \)
\( \psi = -47^\circ \)
The α-helix is a right-handed helix
α-Helices have a dipole moment, due to unbonded and aligned N-H and C=O groups