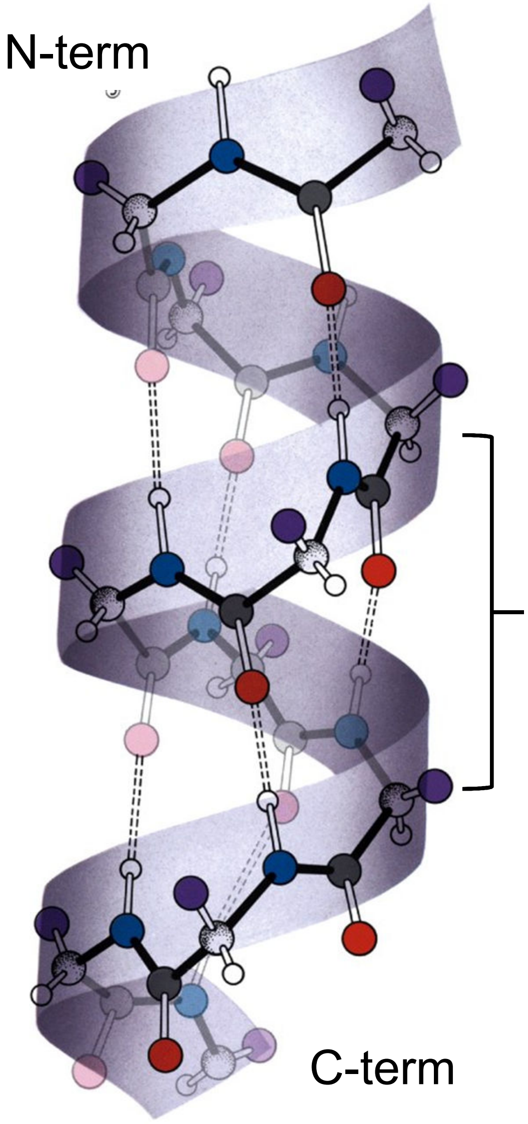
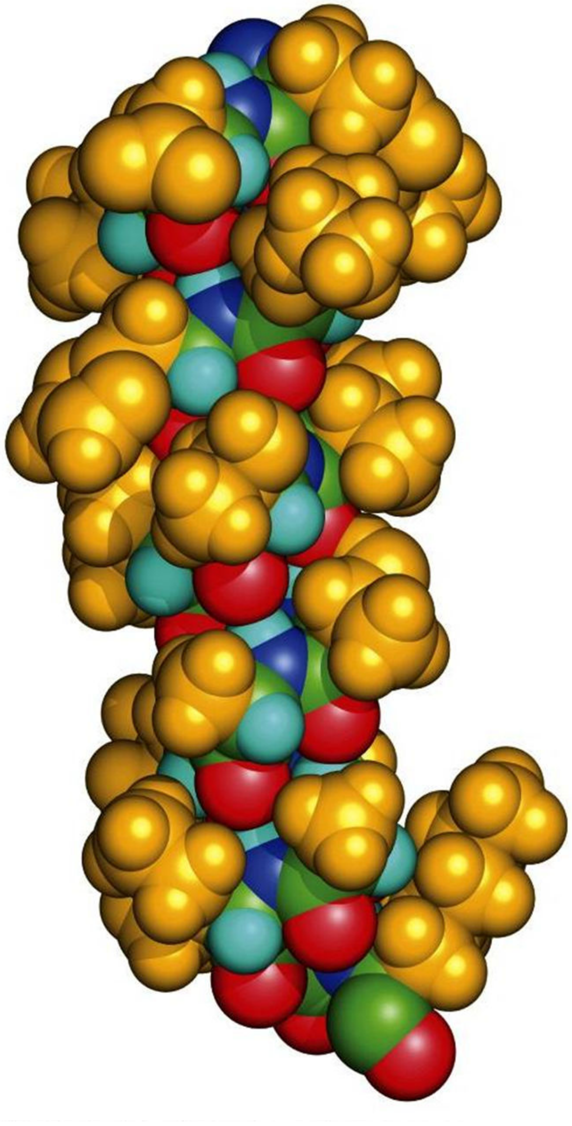
The α-helix forms within a continuous strech of the polypeptide chain

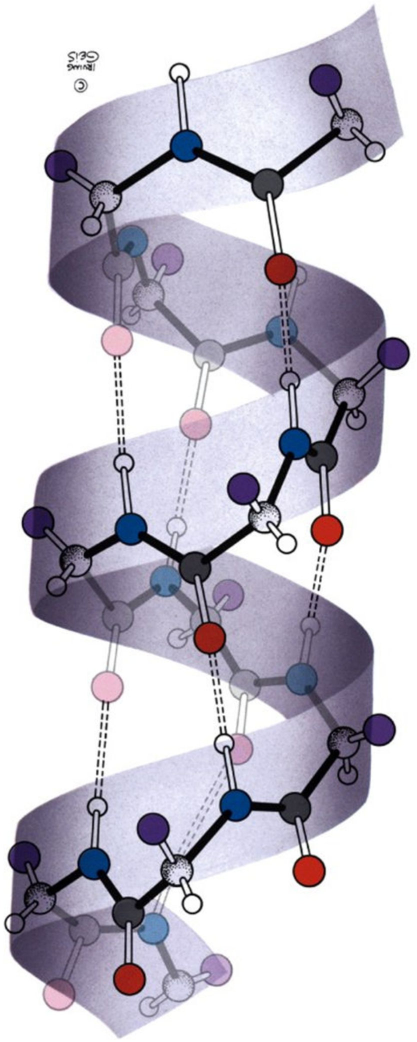


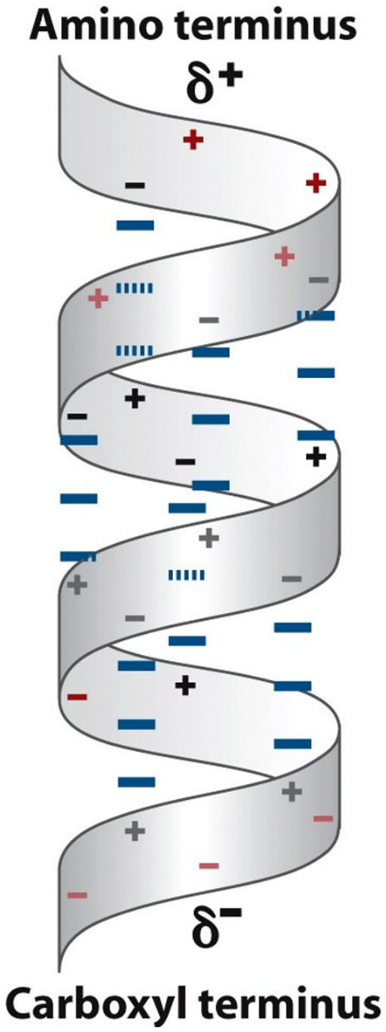
prototypical
$\phi = -57^\circ$
$\psi = -47^\circ$

5.4 Å rise,
3.6 aa/turn
∴ 1.5 Å/aa



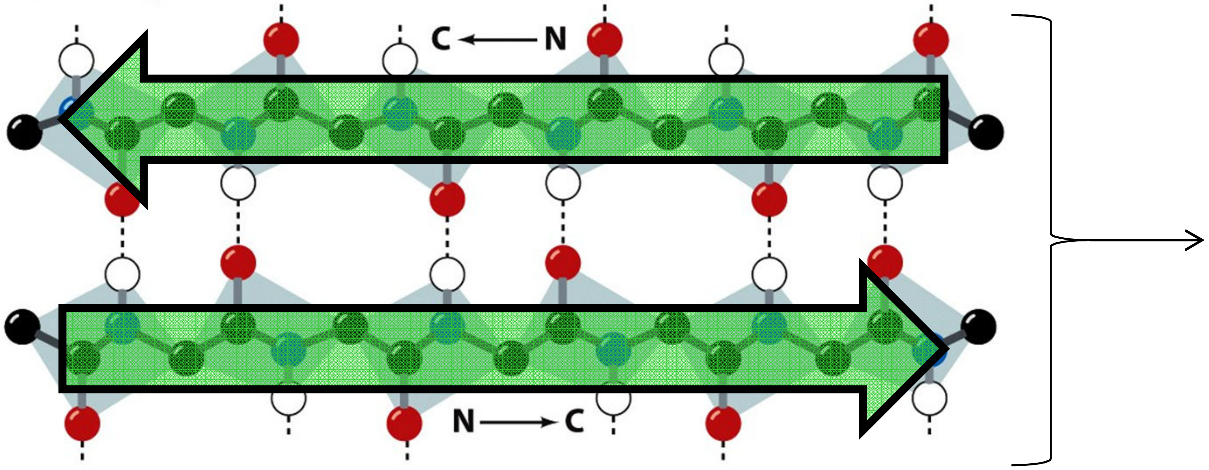
α-Helices have a dipole moment, due to unbonded and aligned N-H and C=O groups

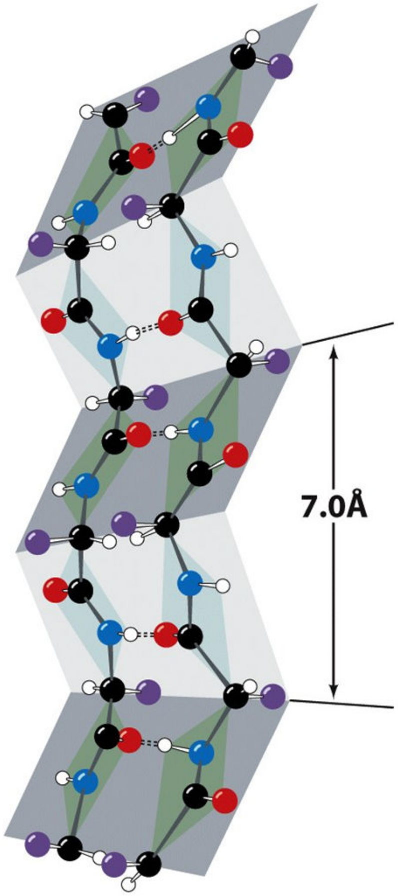




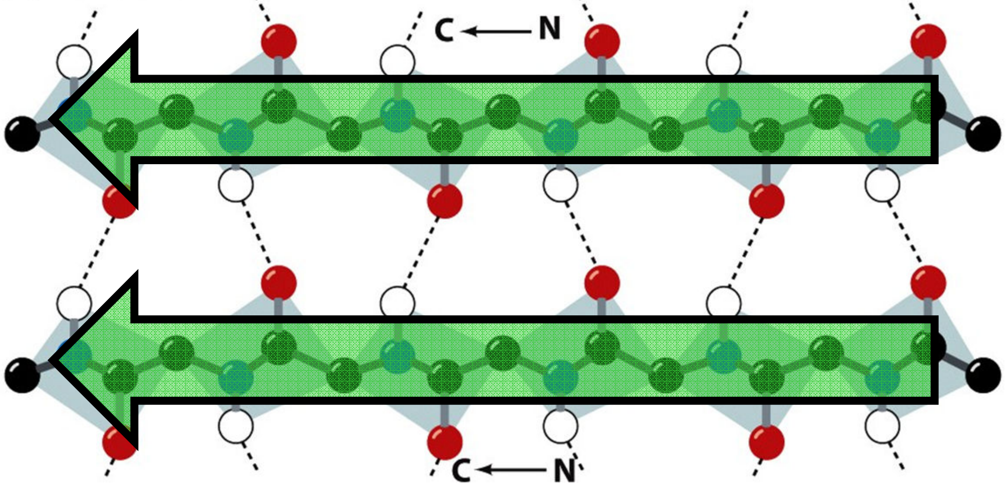
β-Sheets contain extended (β-strand) segments from separate regions of a protein

***(a)* Antiparallel** prototypical ϕ = -139°, ψ = +135°





***(b)* Parallel** prototypical ϕ = -119°, ψ = +113°



(6.5Å repeat length in parallel sheet)

Antiparallel β-sheets may be formed by closer regions of sequence than parallel

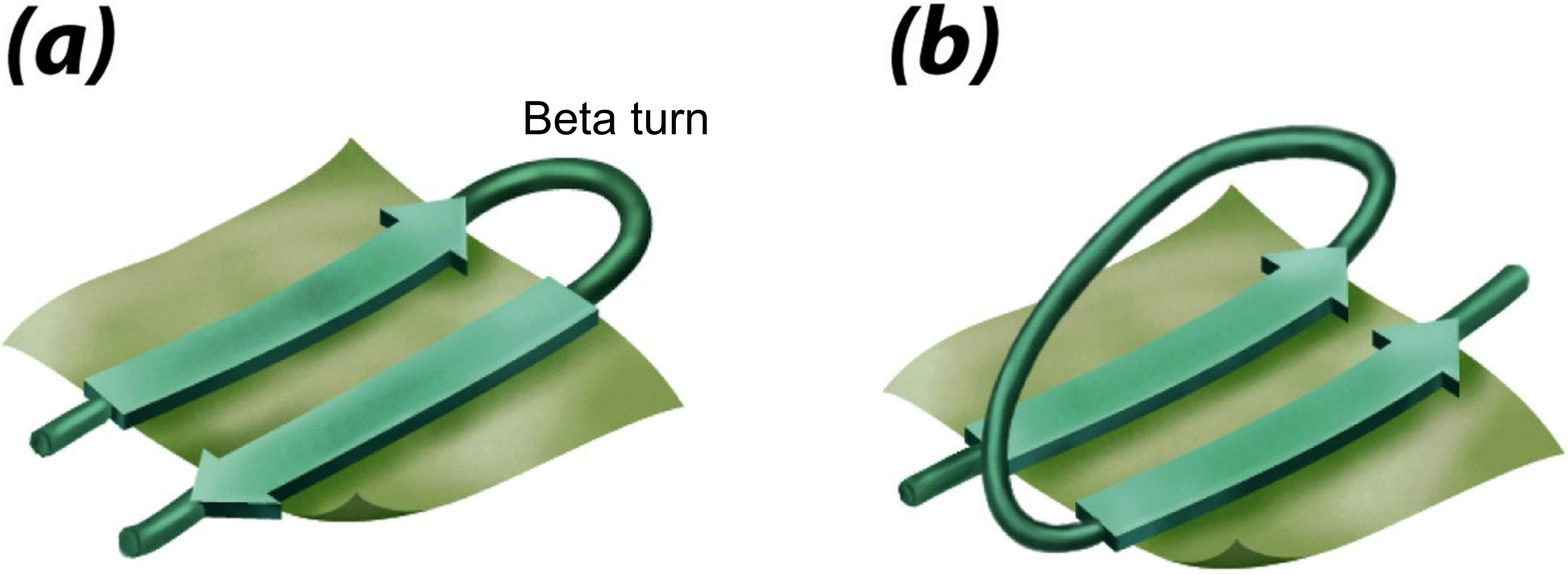


Figure 6-13

The stability of helices and sheets depends on their sequence of amino acids

- Intrinsic propensity of an amino acid to adopt a helical or extended (strand) conformation

The stability of helices and sheets depends on their sequence of amino acids

- Intrinsi helical or extend

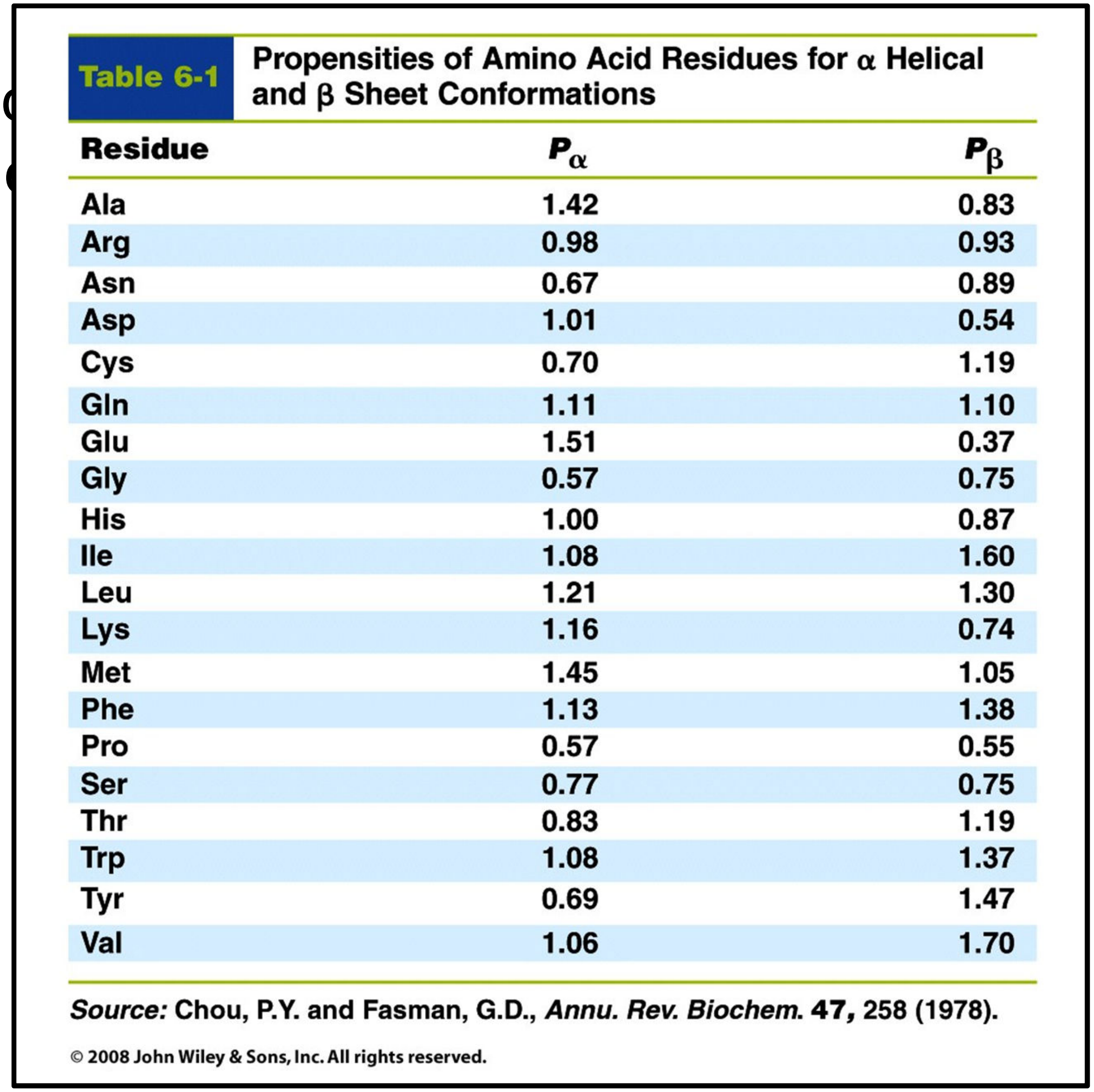


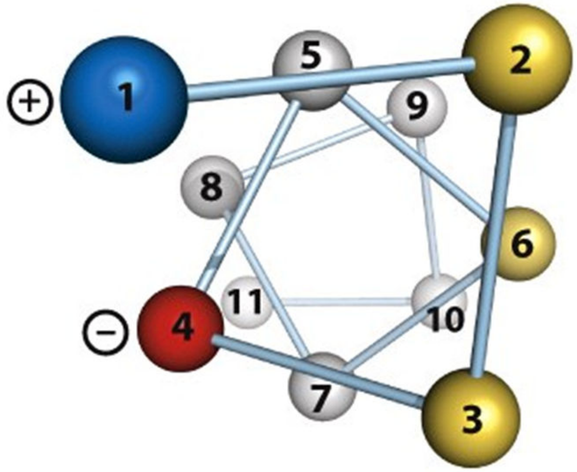
Table 6-1 Propensities of Amino Acid Residues for α Helical and β Sheet Conformations

Residue	P_α	P_β
Ala	1.42	0.83
Arg	0.98	0.93
Asn	0.67	0.89
Asp	1.01	0.54
Cys	0.70	1.19
Gln	1.11	1.10
Glu	1.51	0.37
Gly	0.57	0.75
His	1.00	0.87
Ile	1.08	1.60
Leu	1.21	1.30
Lys	1.16	0.74
Met	1.45	1.05
Phe	1.13	1.38
Pro	0.57	0.55
Ser	0.77	0.75
Thr	0.83	1.19
Trp	1.08	1.37
Tyr	0.69	1.47
Val	1.06	1.70

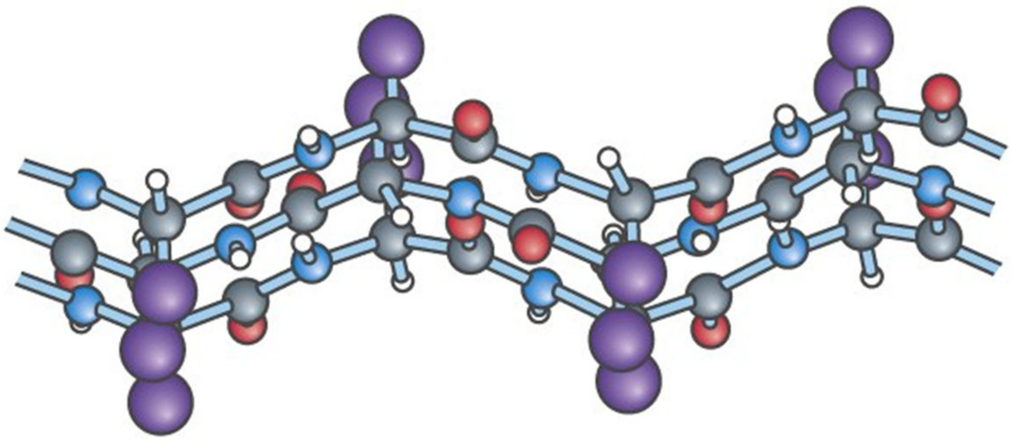
Source: Chou, P.Y. and Fasman, G.D., *Annu. Rev. Biochem.* **47,** 258 (1978).

The stability of helices and sheets depends on their sequence of amino acids

- Intrinsic propensity of an amino acid to adopt a helical or extended (strand) conformation
- Interactions between adjacent R-groups
  - Ionic attraction or repulsion
  - Steric hindrance of adjacent bulky groups

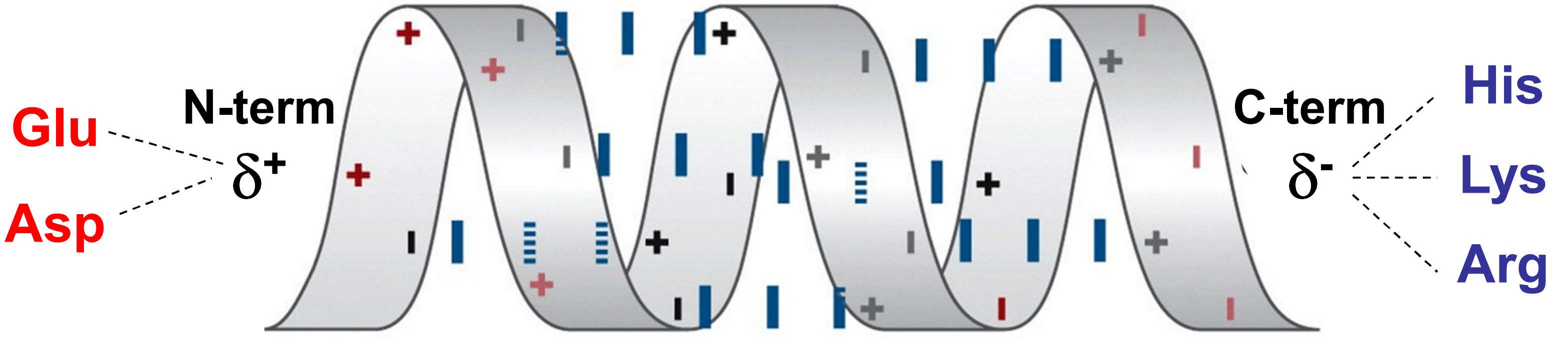


Helix wheel

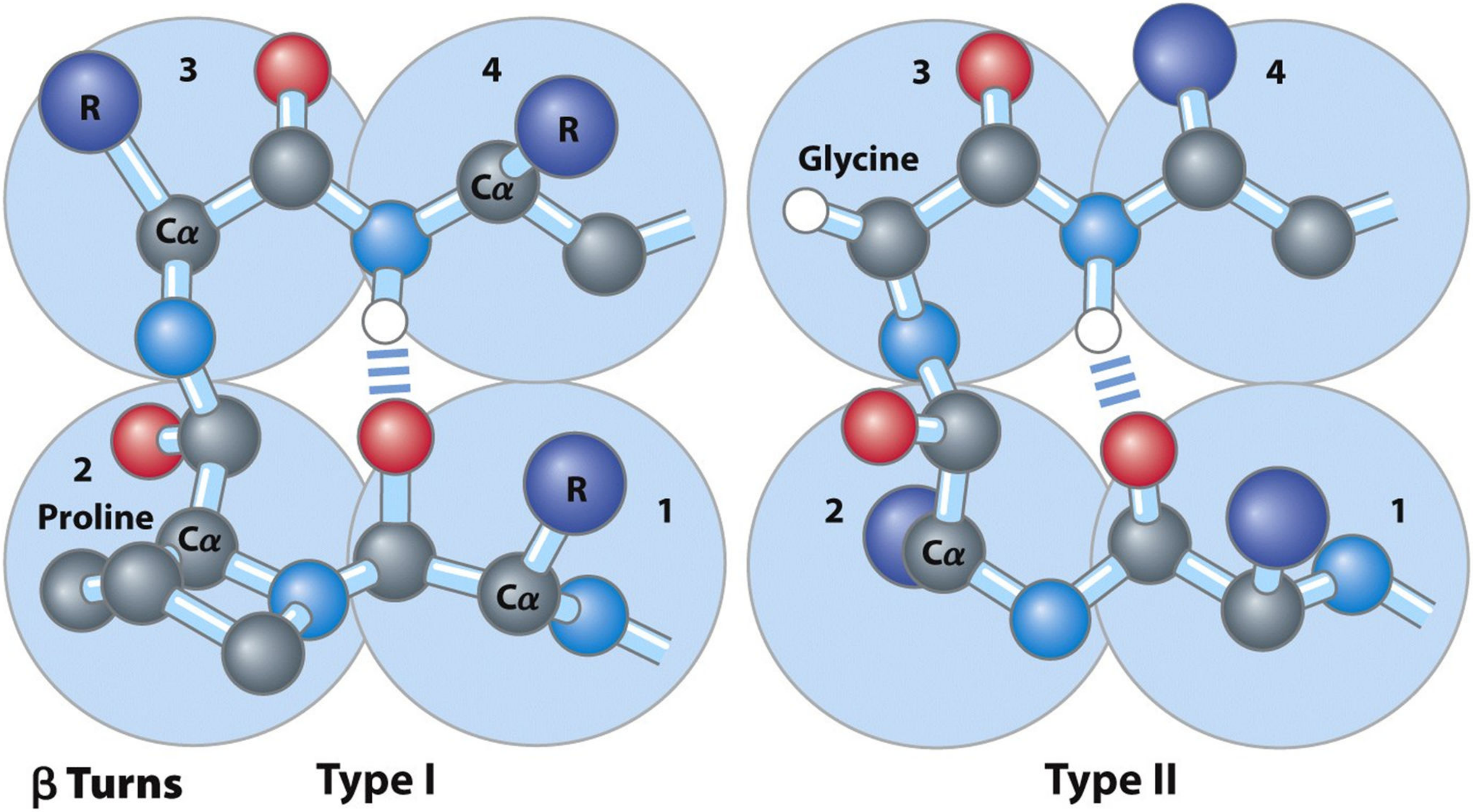


The stability of helices and sheets depends on their sequence of amino acids

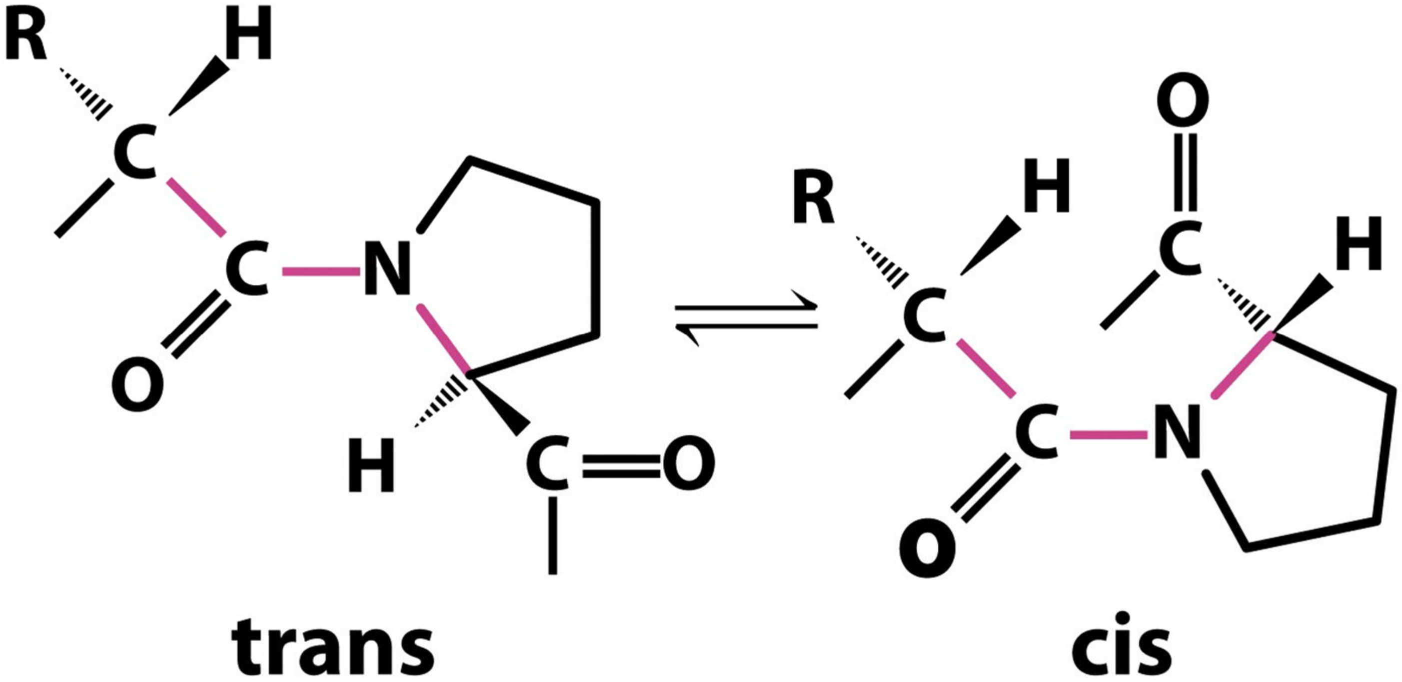
- Intrinsic propensity of an amino acid to adopt a helical or extended (strand) conformation
- Interactions between adjacent R-groups
  - Ionic attraction or repulsion
  - Steric hindrance of adjacent bulky groups
- Occurrence of proline and glycine
- Interactions between ends of helix and aa R-groups

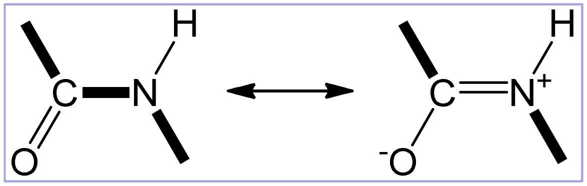


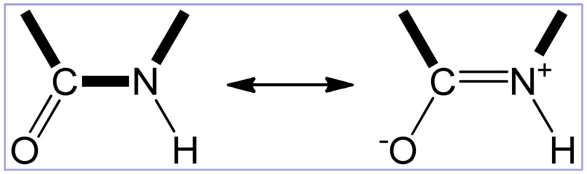
Turns are important secondary structures that change the direction of the chain



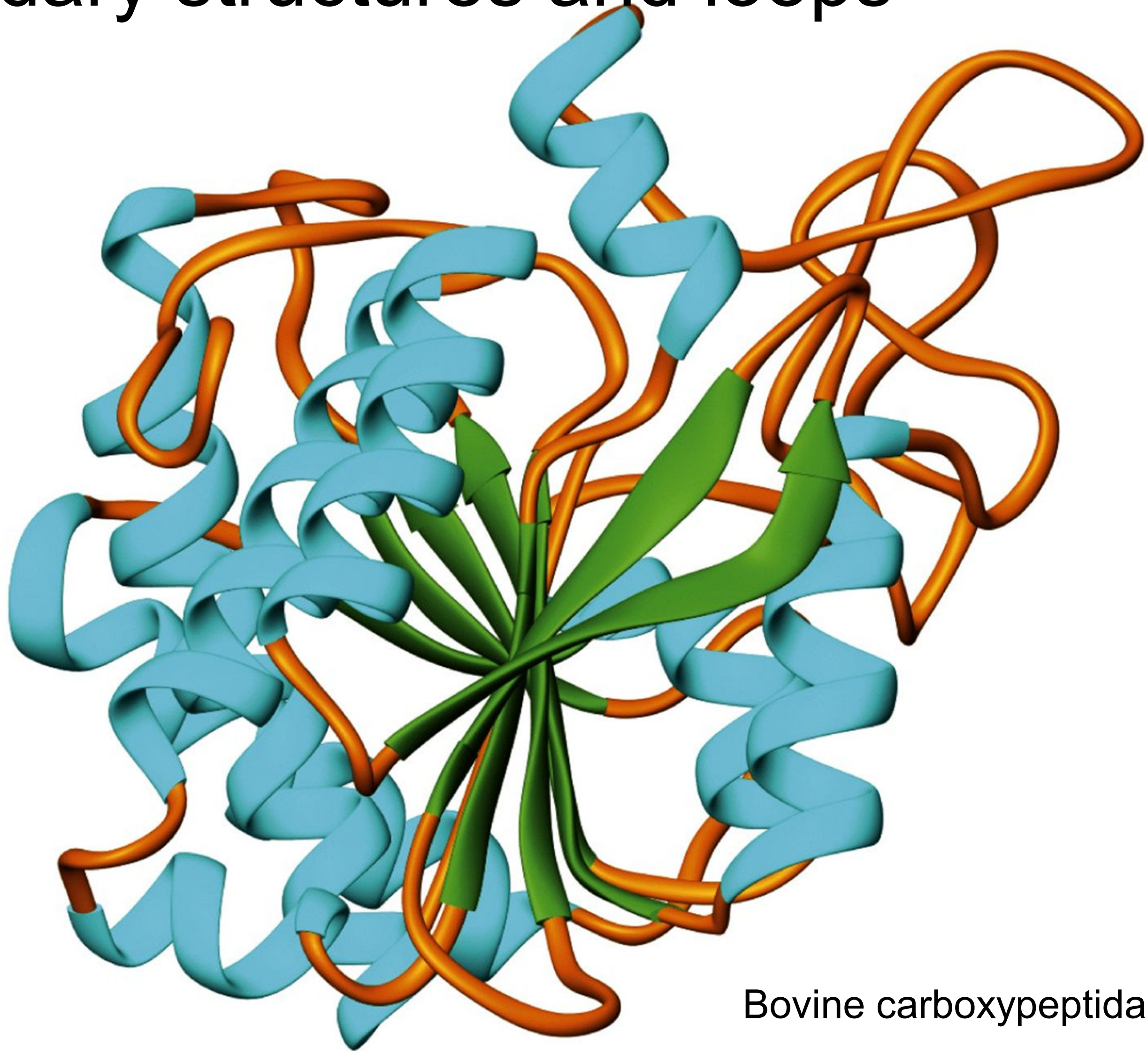
Backbones are usually *trans* at the peptide bond, but *cis*-Pro is found in some β-turns





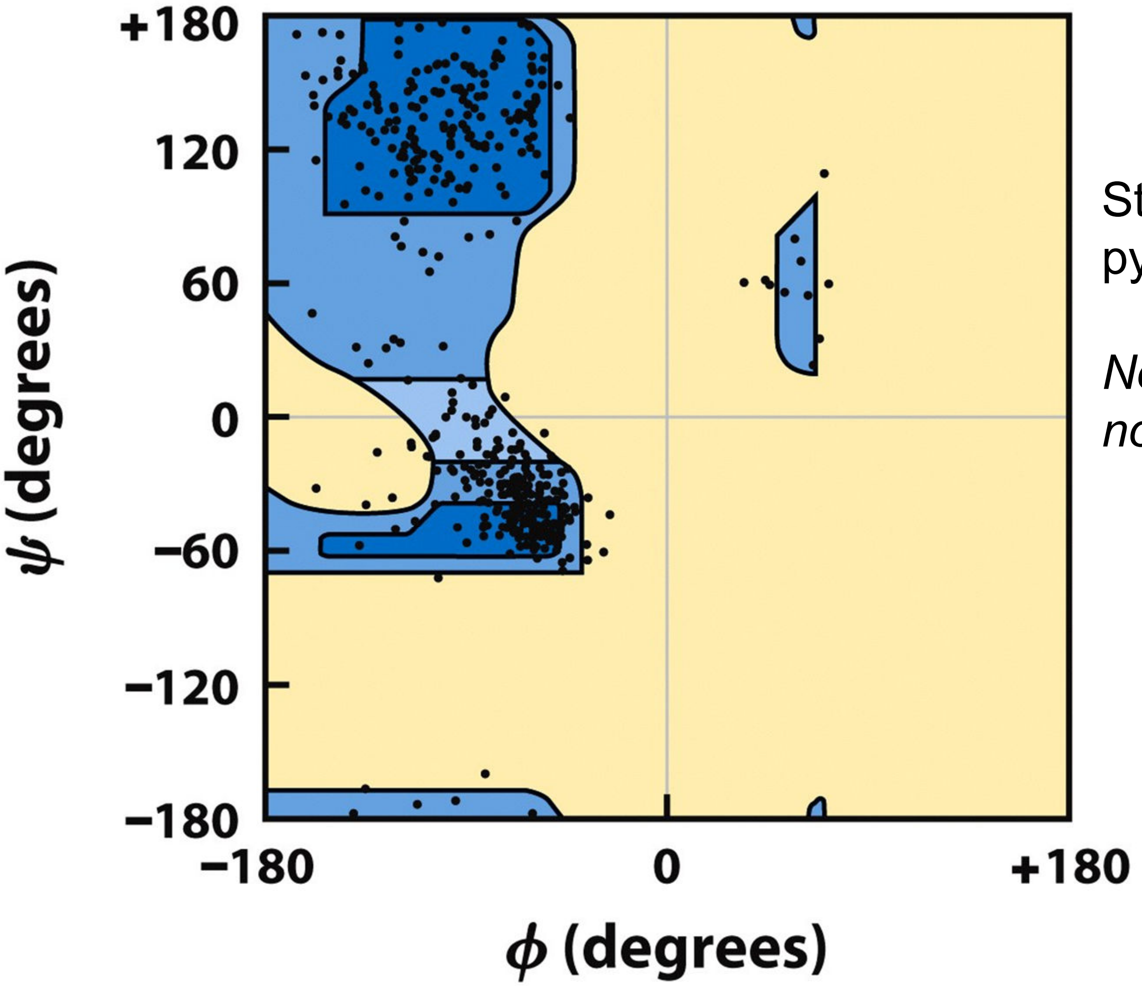


Tertiary structure combines regular secondary structures and loops



Bovine carboxypeptidase A

Most dihedral angles of a protein's tertiary structure are "allowed"



Structure:
pyruvate kinase

Note: glycine not shown

Figure 4-8b
Lehninger Principles of Biochemistry, Fifth Edition

Fibrous proteins are dominated by secondary (and quaternary) structure

Silk fibroin forms stacked,
antiparallel β-sheets

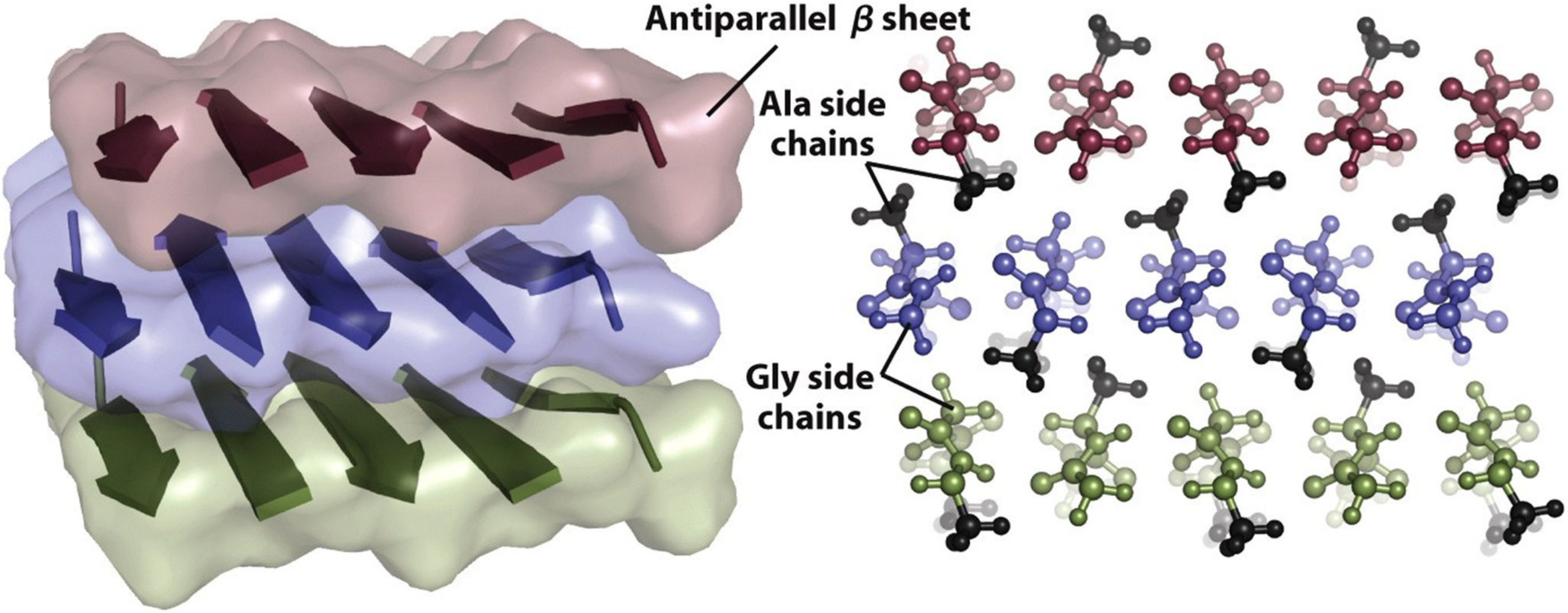
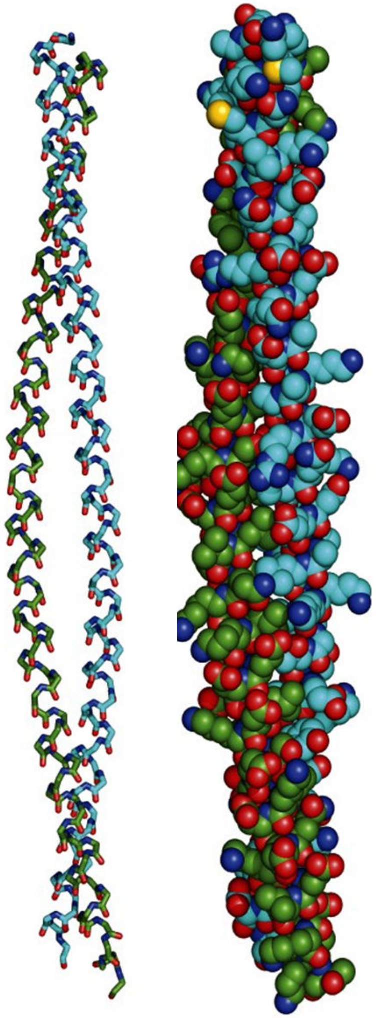


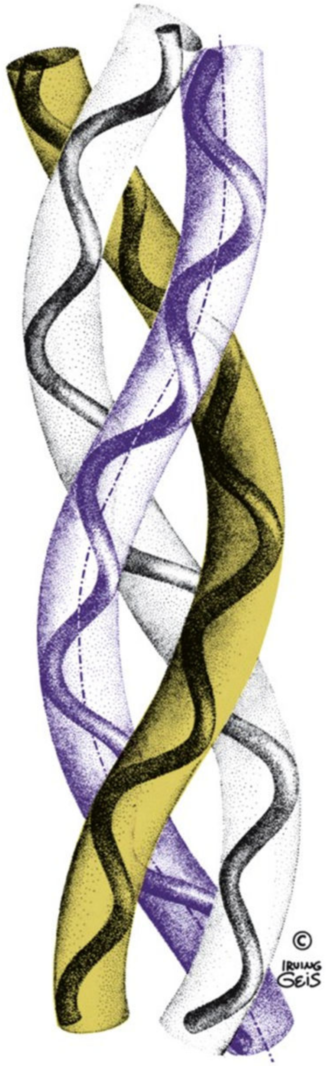
Figure 4-13a
Lehninger Principles of Biochemistry, Fifth Edition

Fibrous proteins are dominated by secondary (and quaternary) structure

α-Keratin forms
an α-helical
coiled-coil



Collagen
forms a
triple-helix



Illustration, Irving Geis. Image from the Irving G
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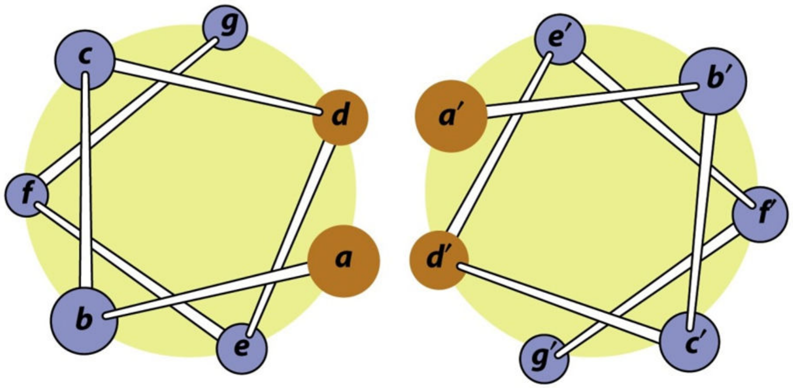
Figure 6-15b

Regular spacing of hydrophobic aa’s in α-keratin promotes quaternary interactions



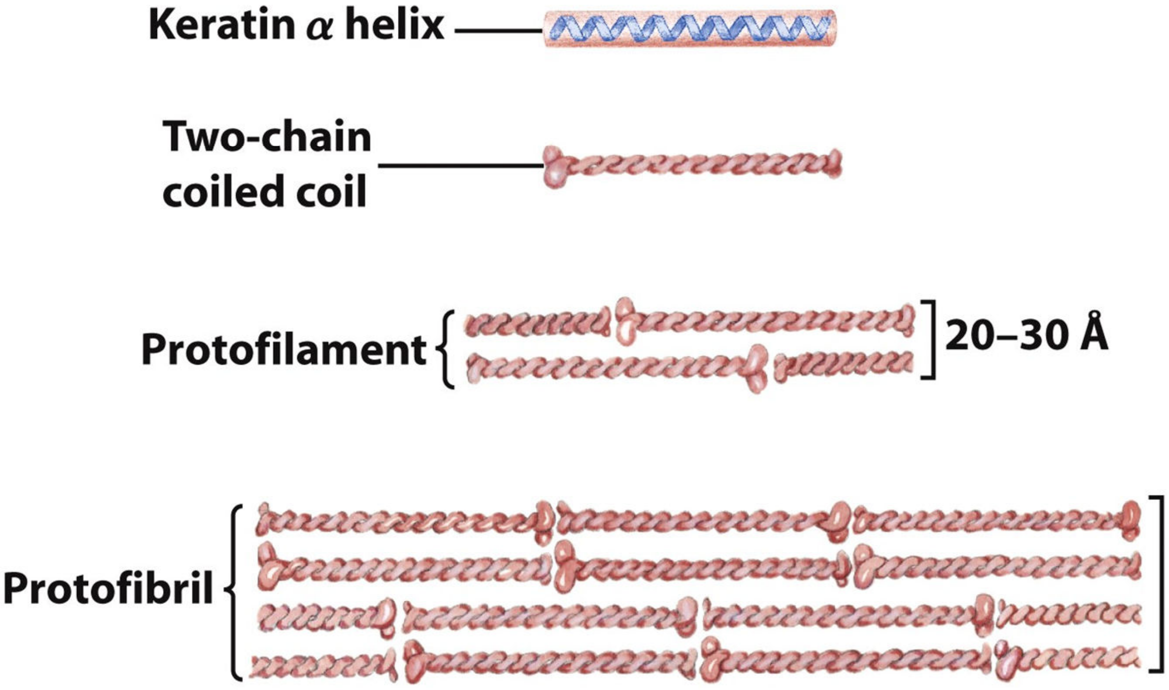
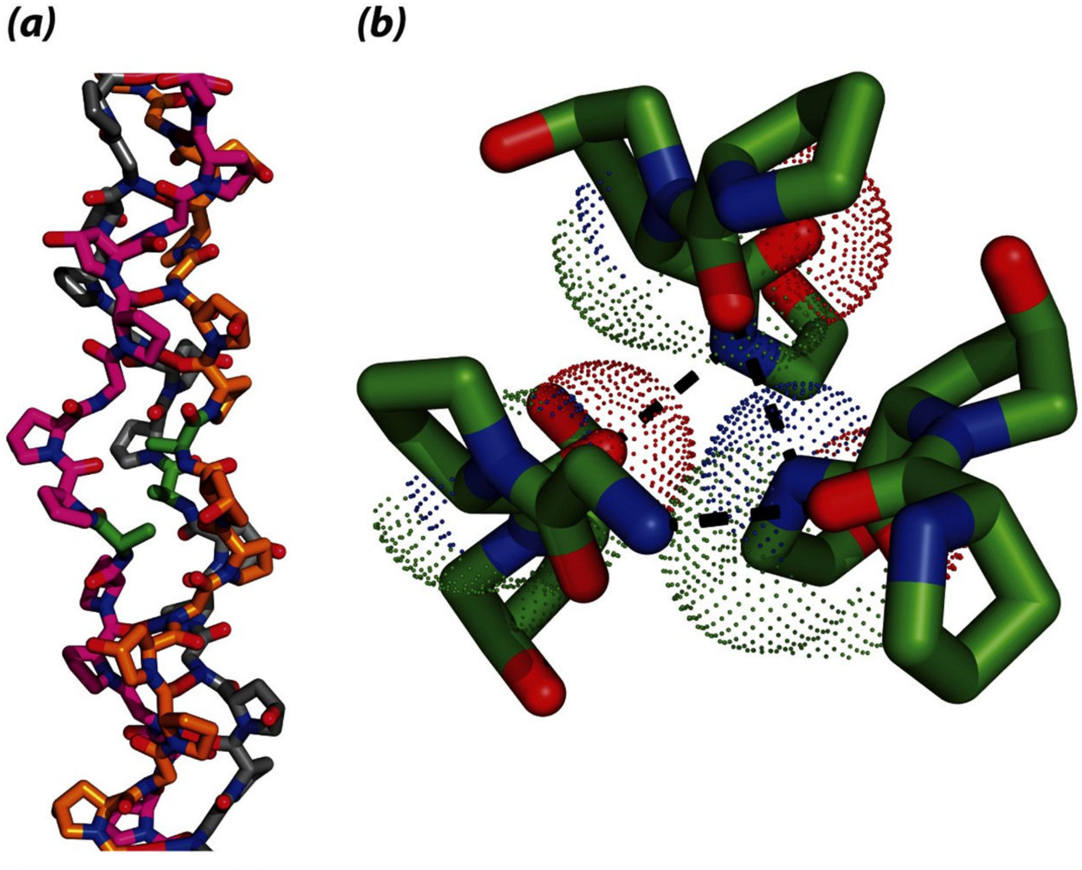
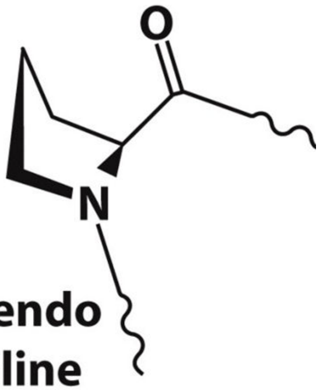


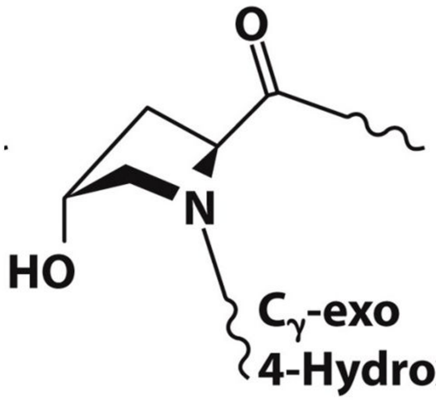
Figure 4-10a

Gly-X-Y motif and hydroxylated aa’s of collagen allow for tight coiling and packing





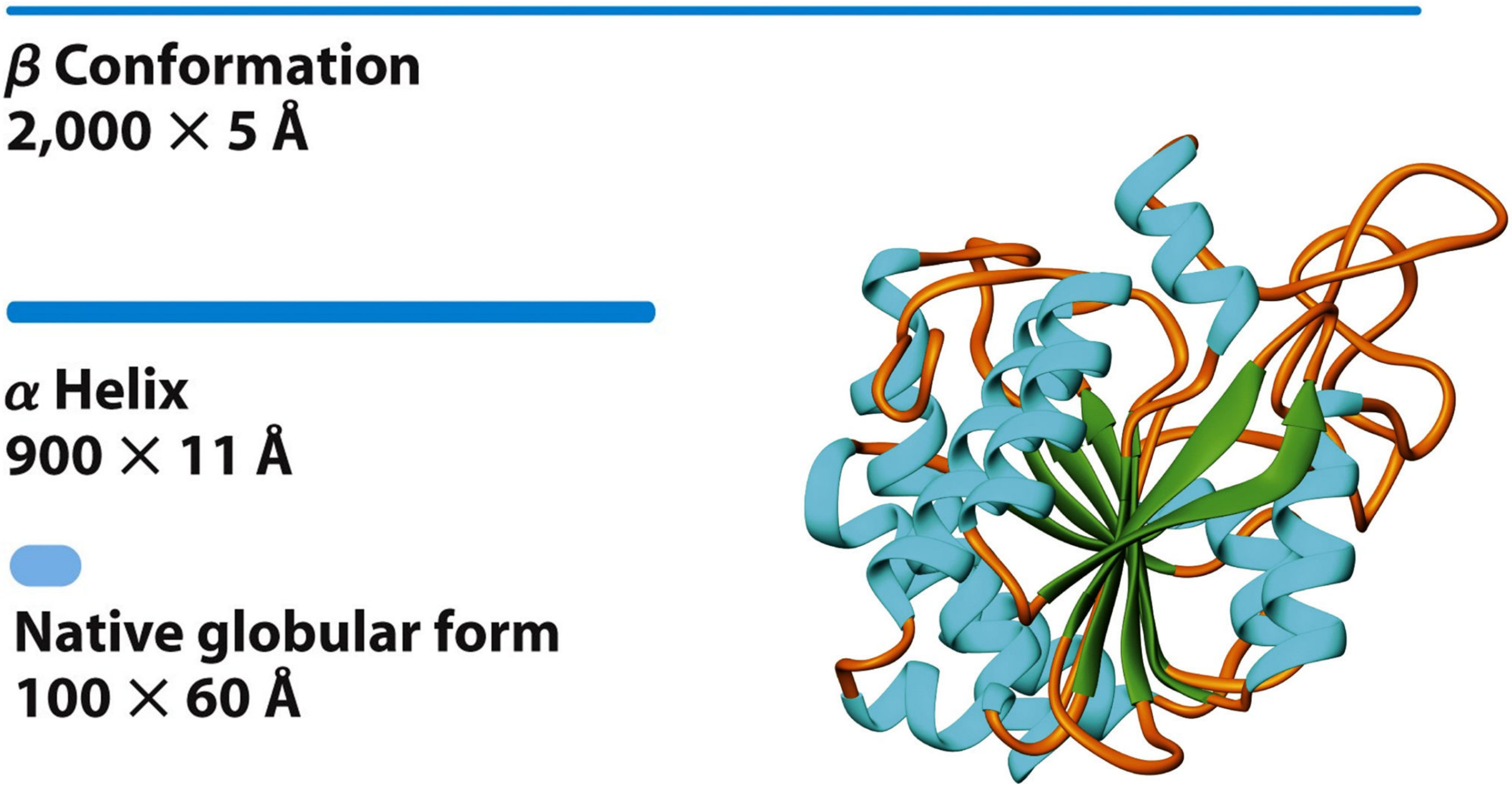
C_γ-endo Proline



C_γ-exo 4-Hydroxyproline

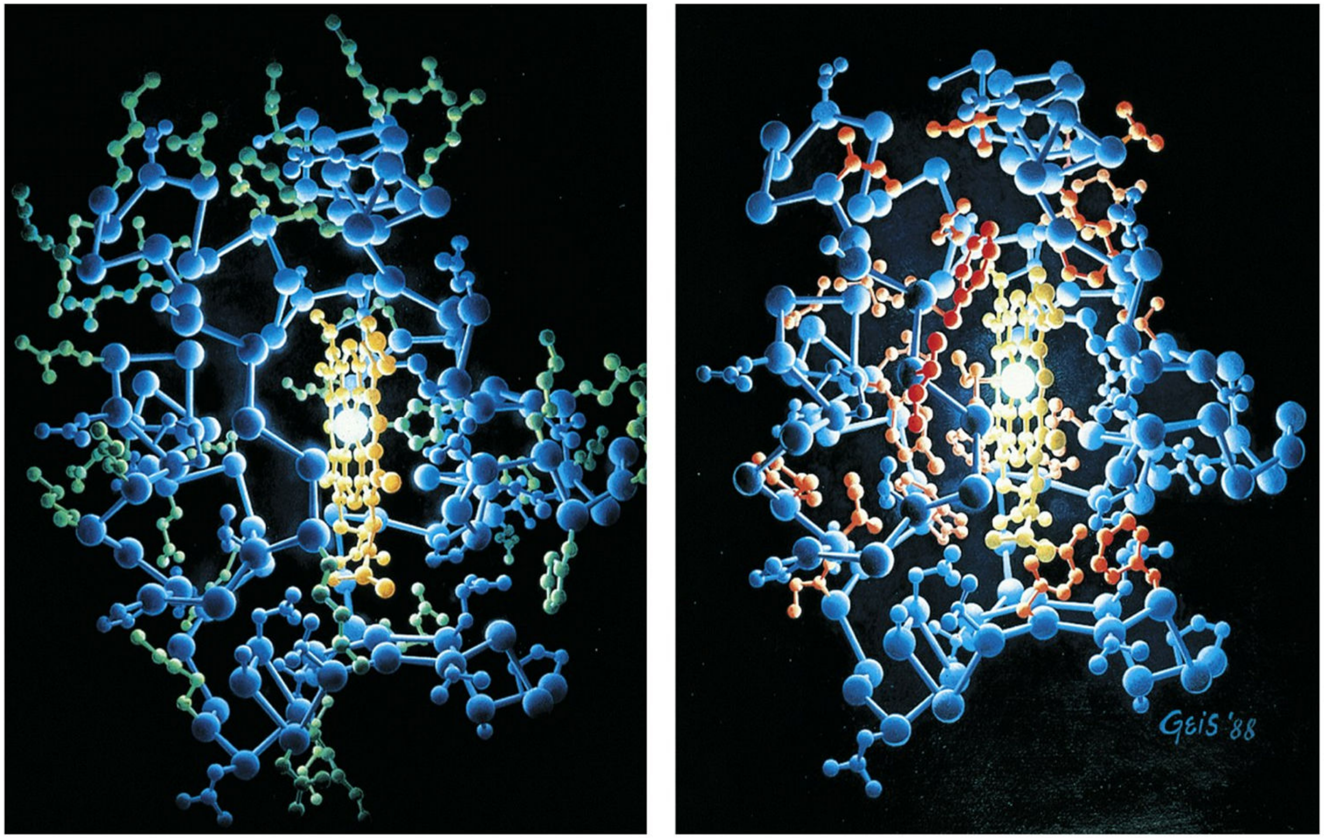
Figure 6-18

Globular proteins are compact and often combine multiple secondary structures



Globular proteins have hydrophobic groups inside and hydrophilic groups on the surface

aa side chains: green=hydrophilic; orange=hydrophobic



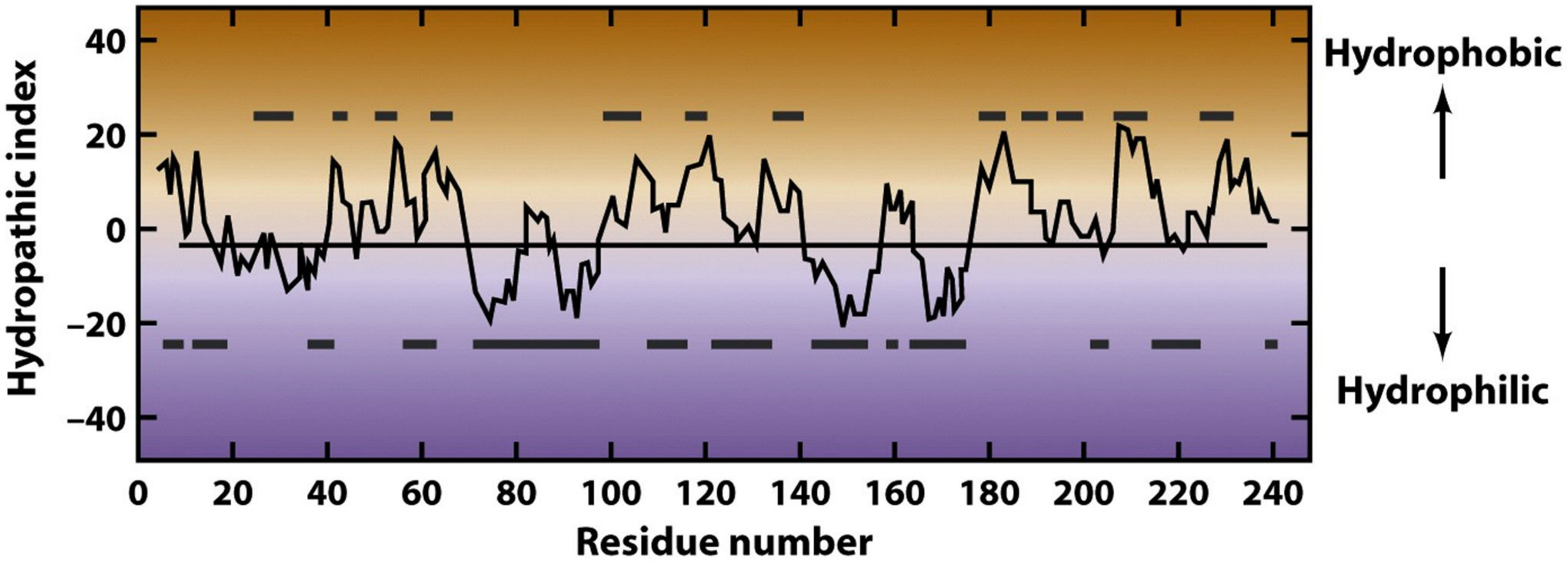
Horse heart cytochrome C

Table 6-3 **Hydropathy Scale for Amino Acid Side Chains**

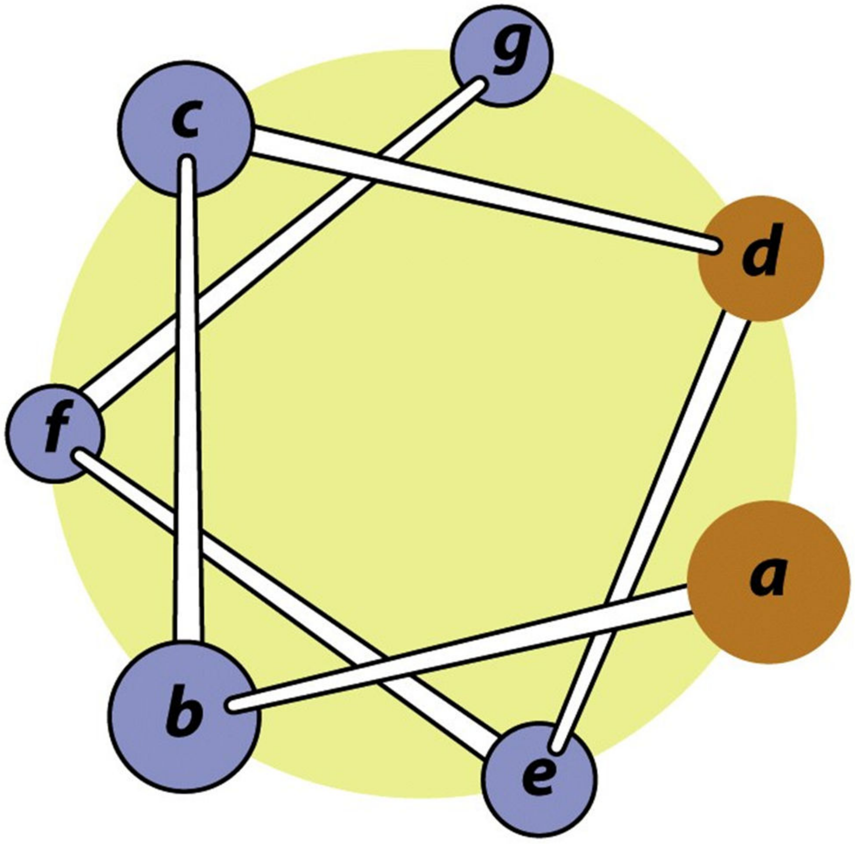
Side Chain	Hydropathy
Ile	4.5
Val	4.2
Leu	3.8
Phe	2.8
Cys	2.5
Met	1.9
Ala	1.8
Gly	−0.4
Thr	−0.7
Ser	−0.8
Trp	−0.9
Tyr	−1.3
Pro	−1.6
His	−3.2
Glu	−3.5
Gln	−3.5
Asp	−3.5
Asn	−3.5
Lys	−3.9
Arg	−4.5

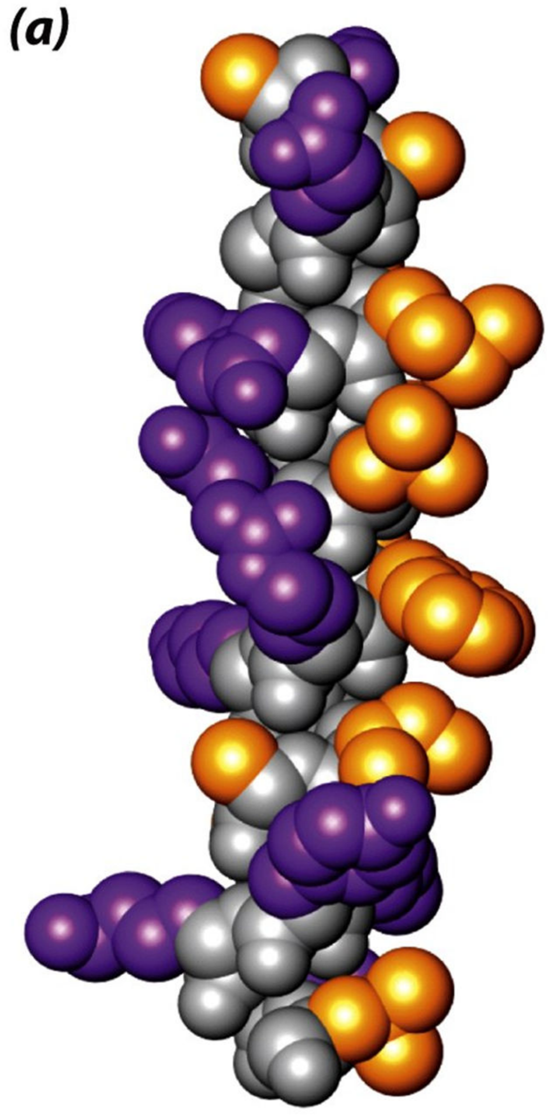
Source: Kyte, J. and Doolittle, R.F., *J. Mol. Biol.* **157,** 110 (1982).

Hydropathic index can be plotted for a protein, to predict internal & external zones

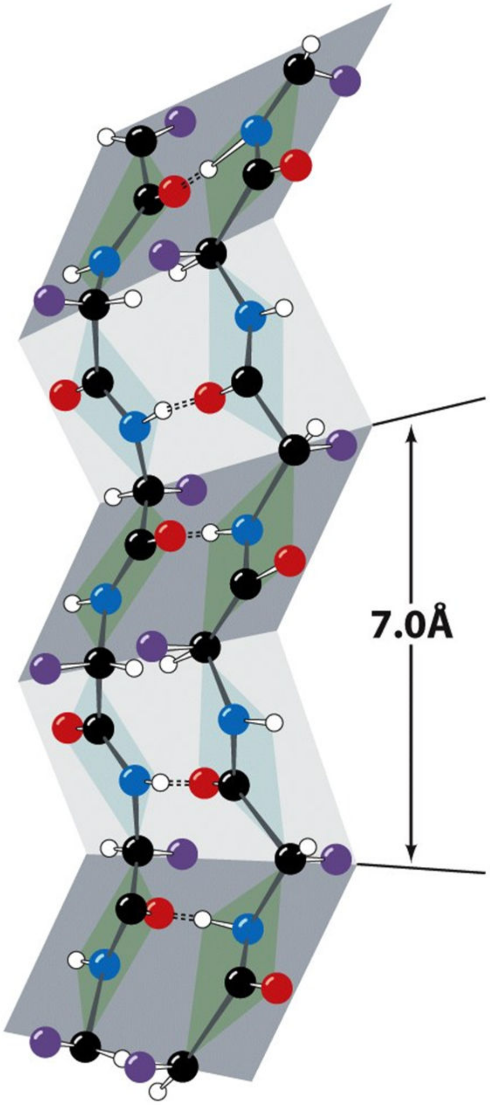


Particular arrangements of polar and apolar residues can form amphipathic helices

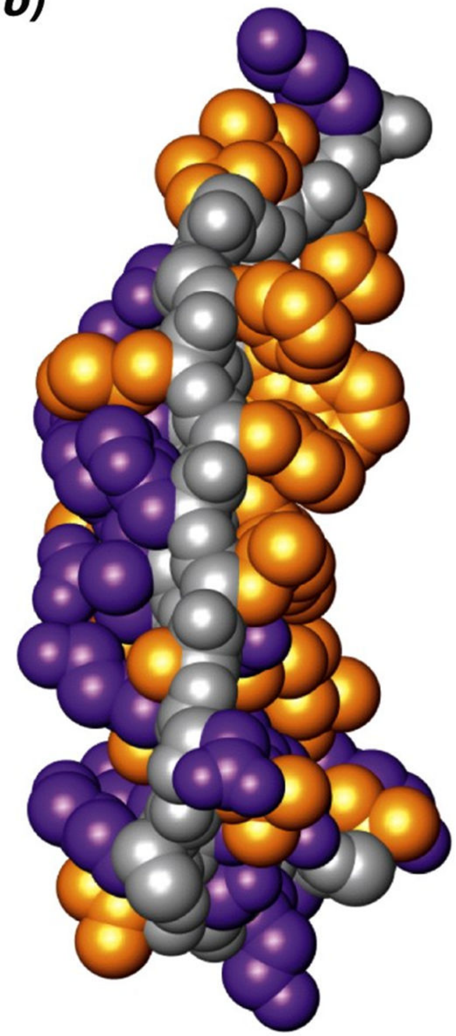




An alternating sequence of polar and apolar residues can form an amphipathic sheet



(b)



Some tertiary structures contain common patterns, or motifs, of secondary structures (= supersecondary structures)

βαβ

β-hairpins

αα
(coiled-coil)

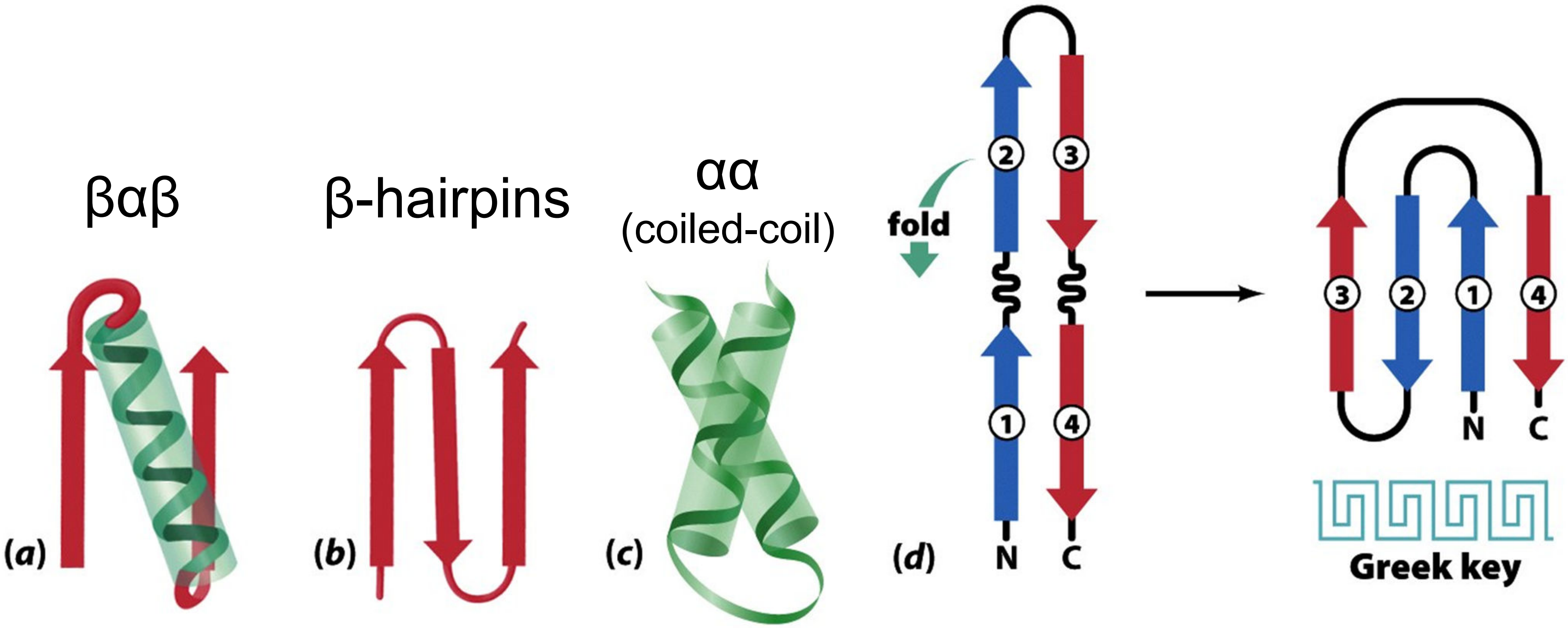
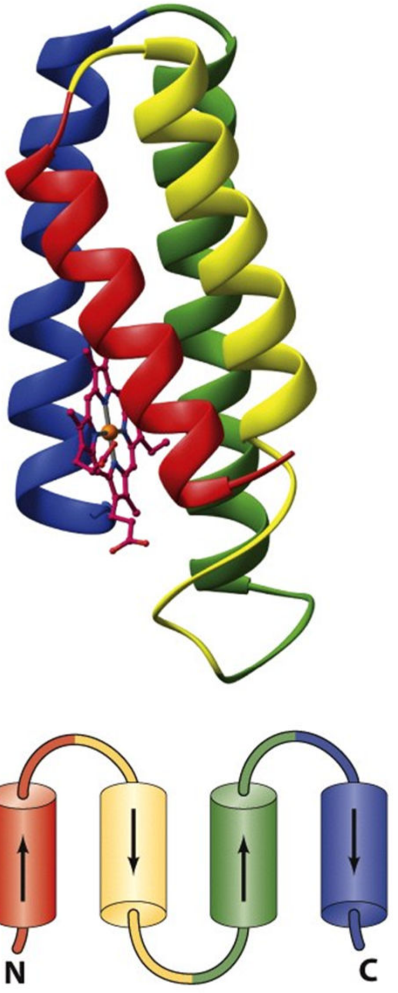


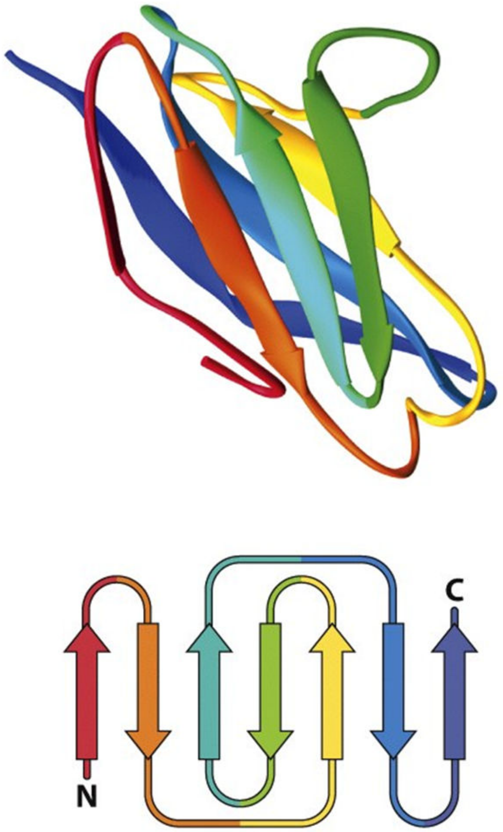
Figure 6-28

Proteins folds can be grouped by predominant secondary structure(s)

α



β



α/β