Secondary structures

- Secondary structures are repeated local structural elements formed by consecutive amino acids with similar φ and ψ values.
- Stabilized by hydrogen bonds between backbone atoms but formation of a particular type of secondary structure is dictated by protein sequence.
- Formed in the early stages of protein folding following hydrophobic collapse.
- Formation of secondary structures allows the packing of polar backbone atoms in the hydrophobic core of protein structures.

α helix

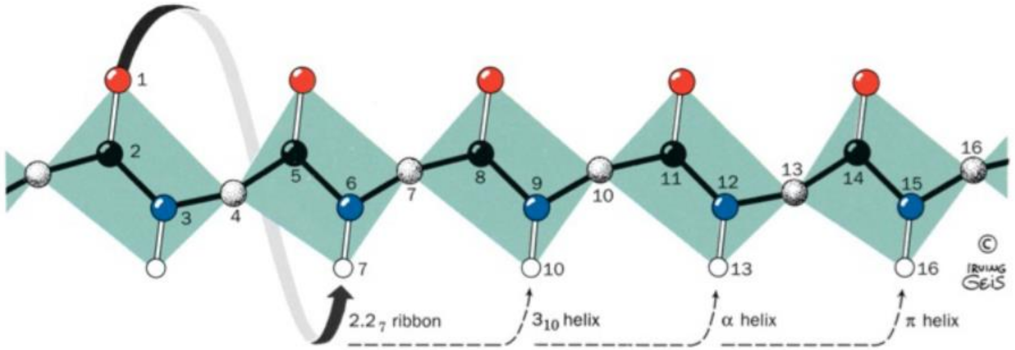
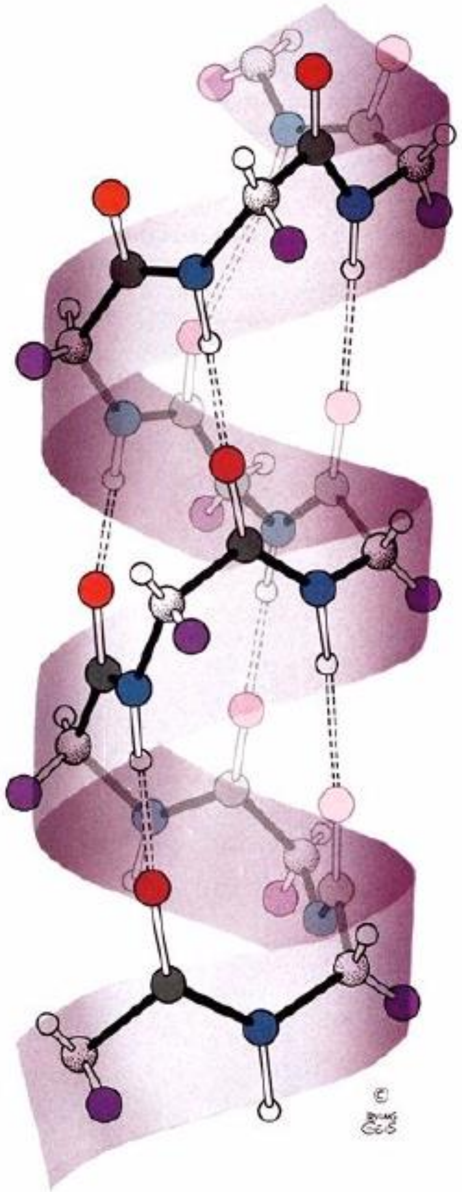
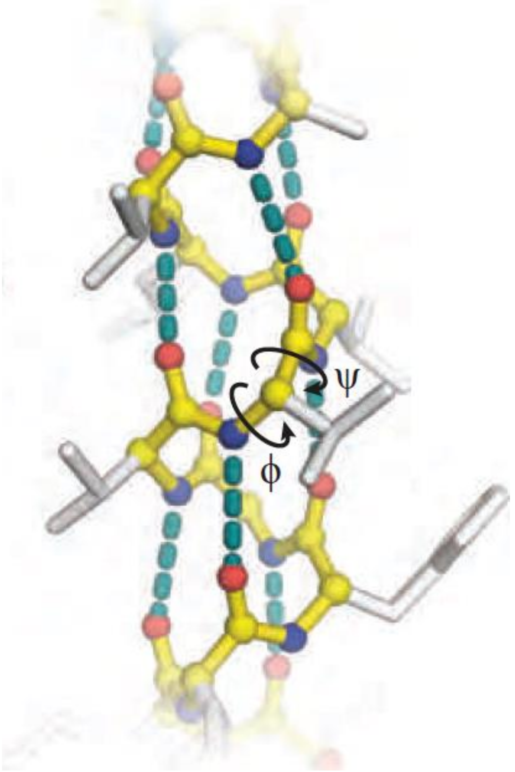


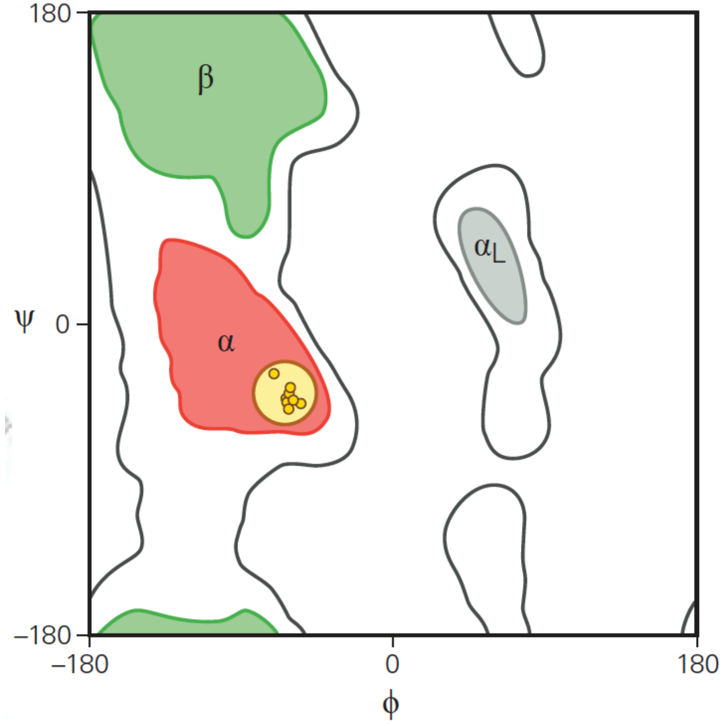
Figure 8-13
Illustration, Irving Geis. Image from the Irving Geis Collection, Howard Hughes Medical Institute. Reprinted with permission.



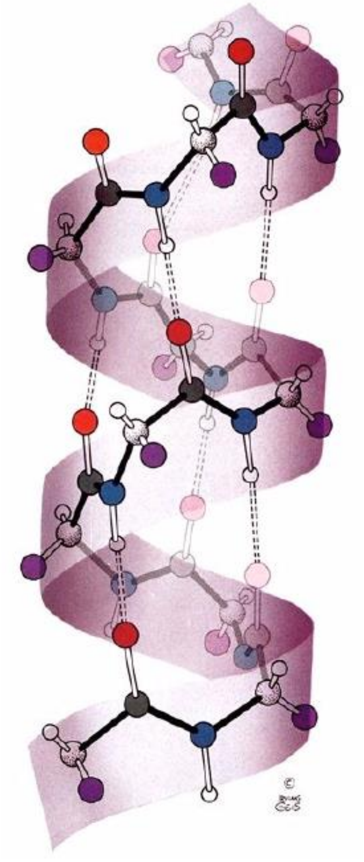
The right-handed α helix

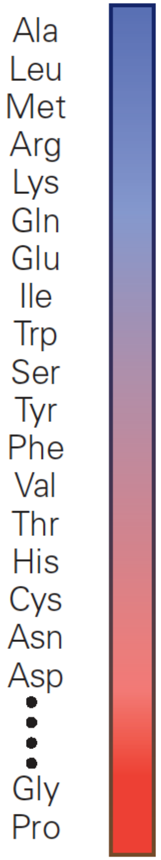
- Hydrogen bonds form between residue *n* and *n* + 3
- Φ and ψ are around -60° and -50°, respectively.
- 3.6 residues per turn; 5.4 Å between turns





Helix propensity of amino acids





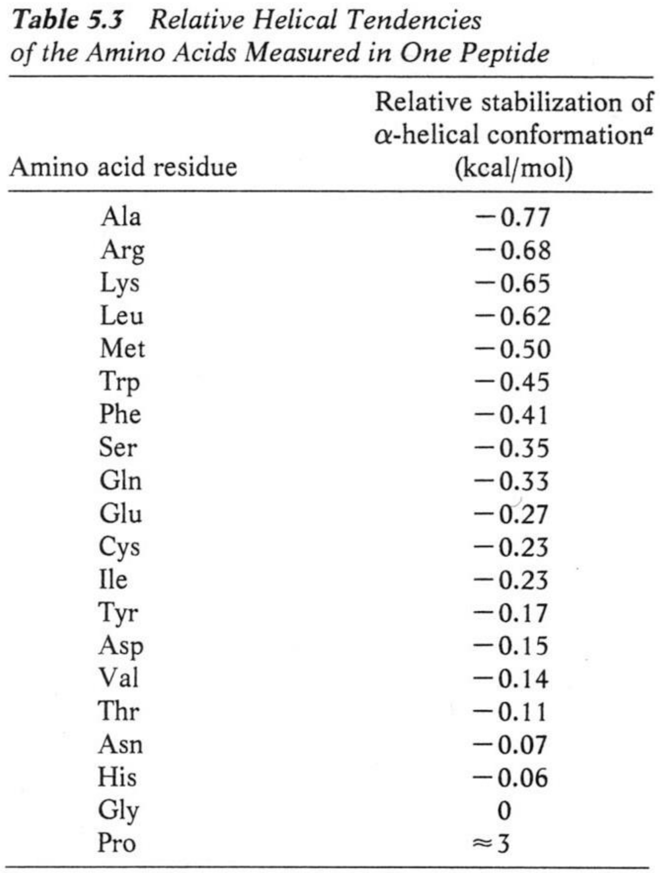
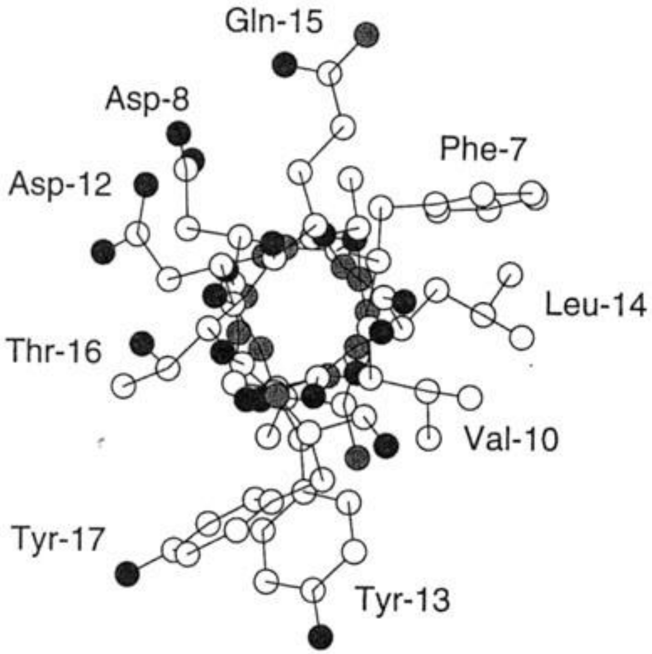


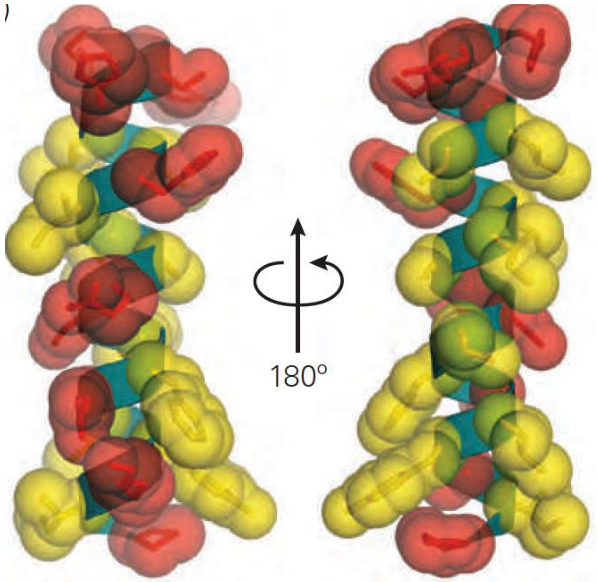
Table 5.3 Relative Helical Tendencies of the Amino Acids Measured in One Peptide

Amino acid residue	Relative stabilization of α-helical conformation[a] (kcal/mol)
Ala	−0.77
Arg	−0.68
Lys	−0.65
Leu	−0.62
Met	−0.50
Trp	−0.45
Phe	−0.41
Ser	−0.35
Gln	−0.33
Glu	−0.27
Cys	−0.23
Ile	−0.23
Tyr	−0.17
Asp	−0.15
Val	−0.14
Thr	−0.11
Asn	−0.07
His	−0.06
Gly	0
Pro	≈3

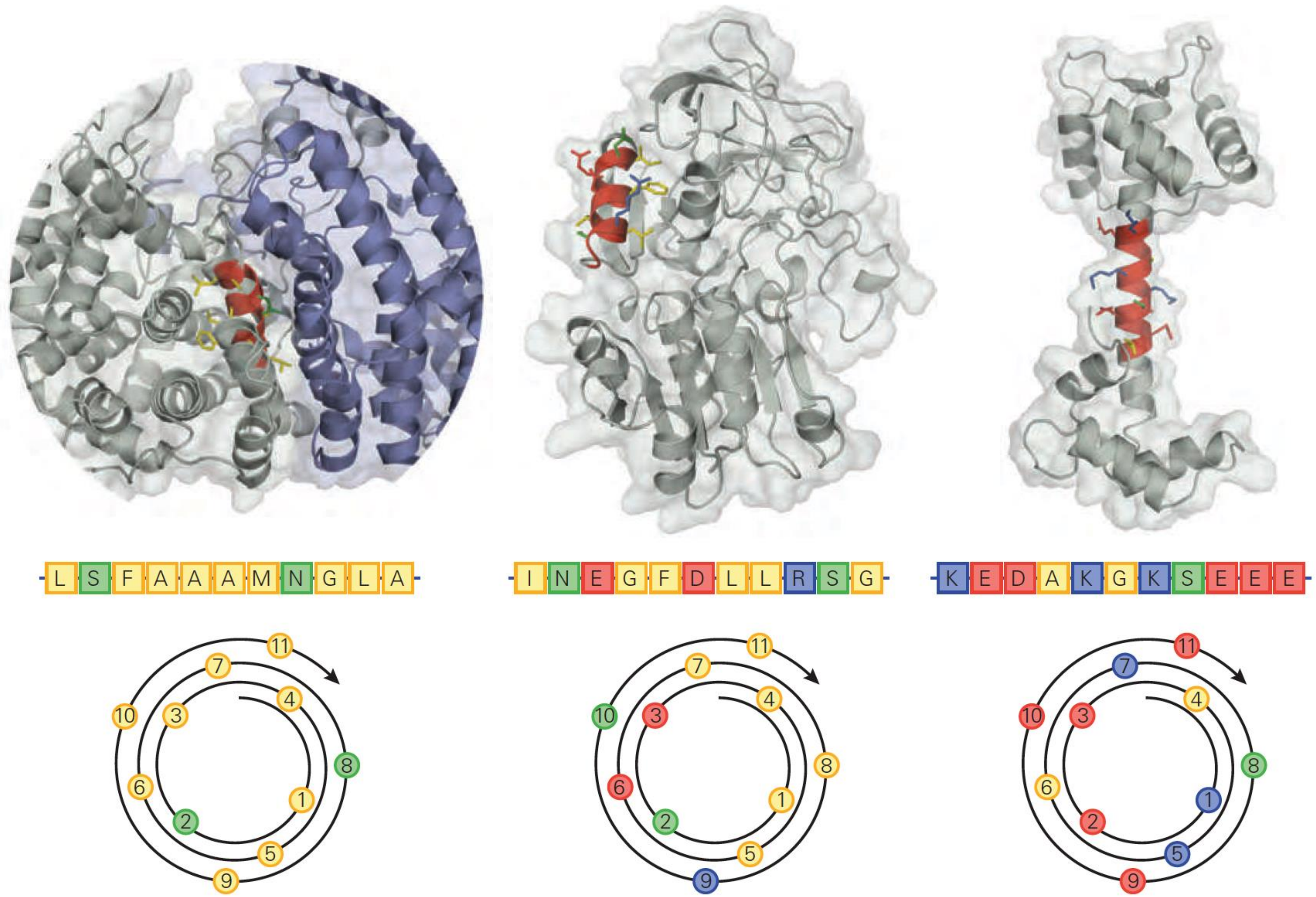
The helix wheel

- Amphipathic: having both hydrophilic and hydrophobic parts.



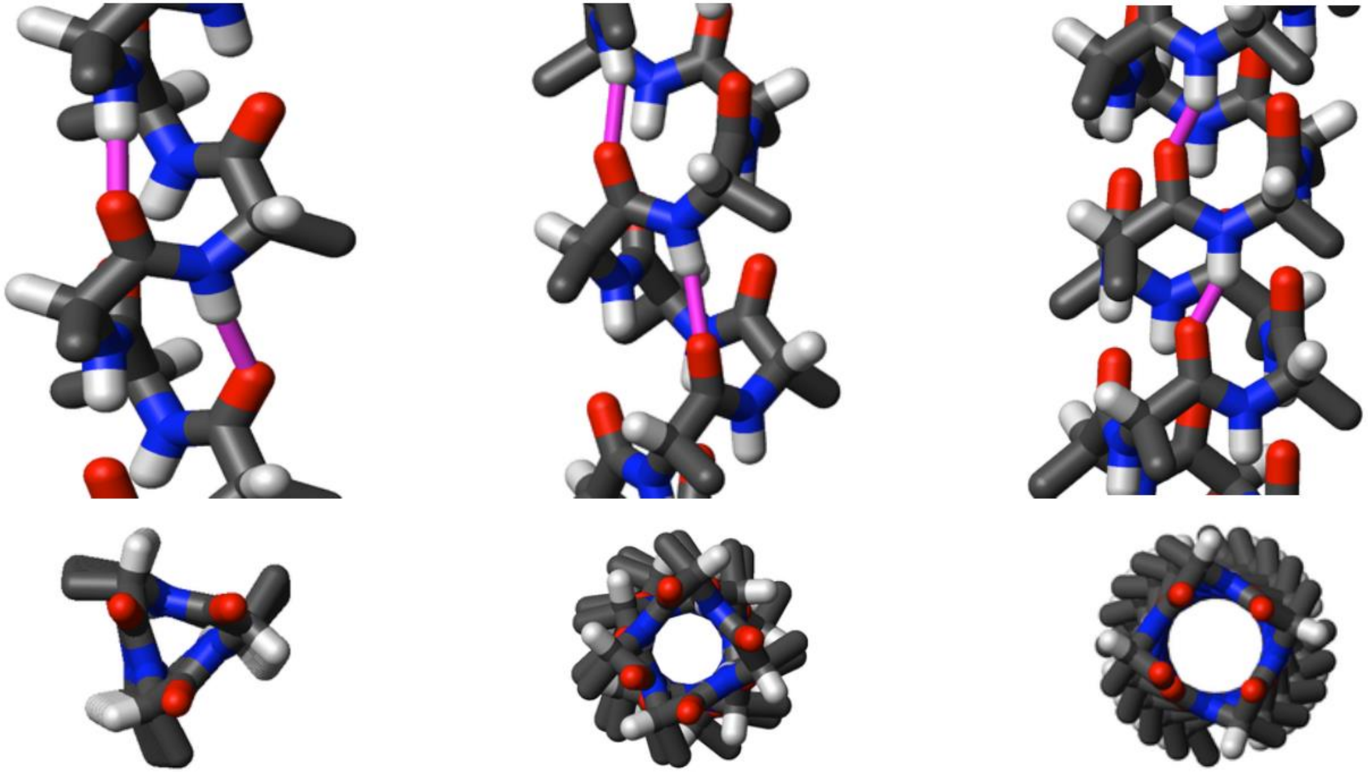


The helix wheel

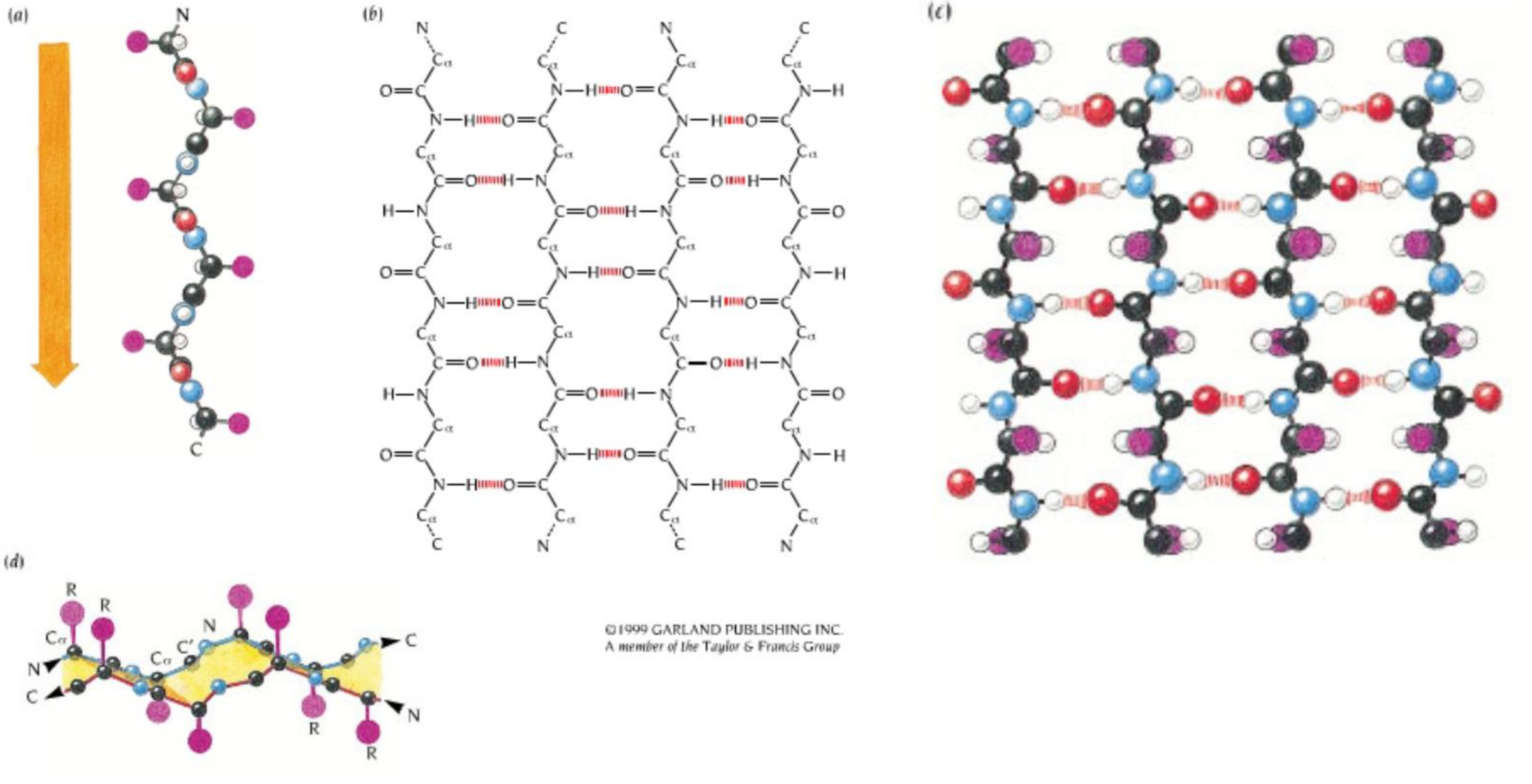


Three types of helices

- 3_{10} helix (φ: -49°, ψ: -26°, n: 3, d: 6.0Å)
- α-helix (φ: -57°, ψ: -47°, n: 3.6, d: 5.4Å): the most stable and common
- π-helix (φ: -57°, ψ: -70°, n: 4.4, d: 5.2Å)



Anti-parallel β sheet (φ: -139°, ψ: -135°)



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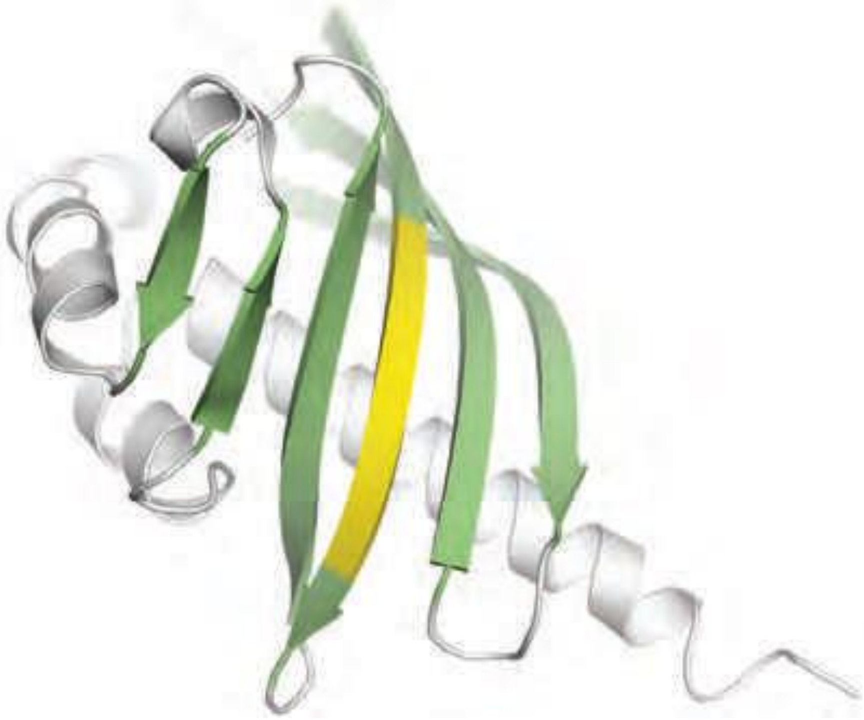
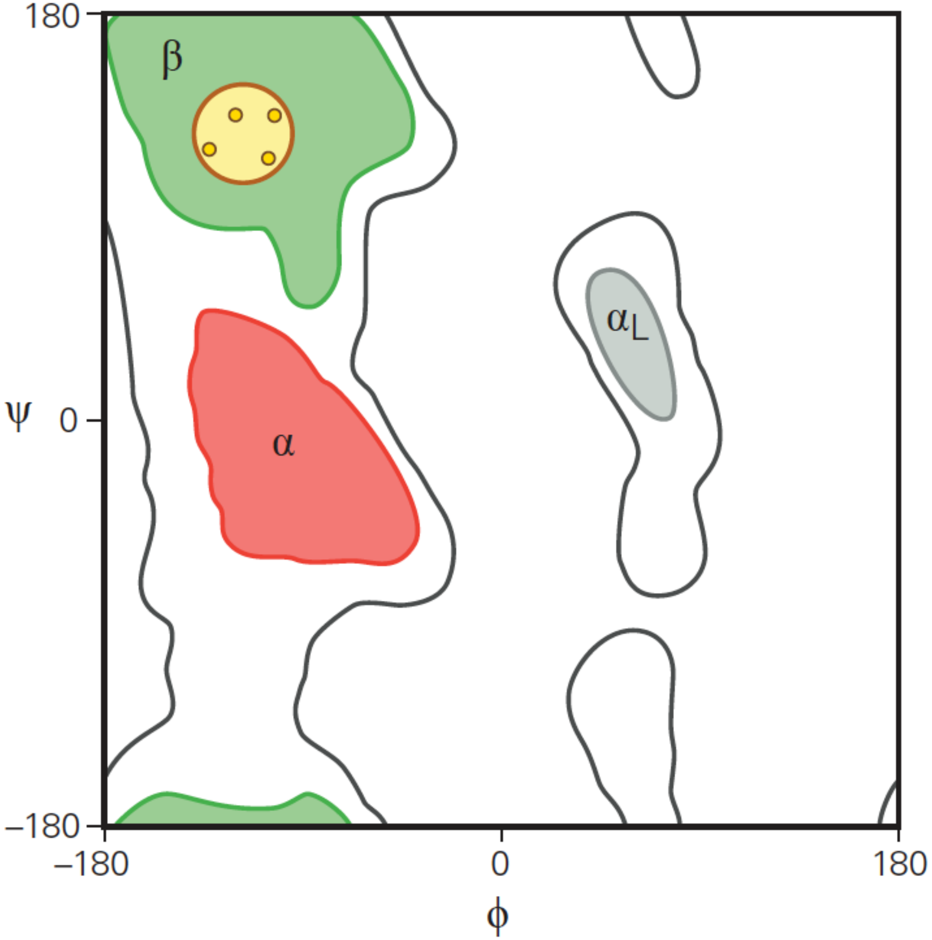
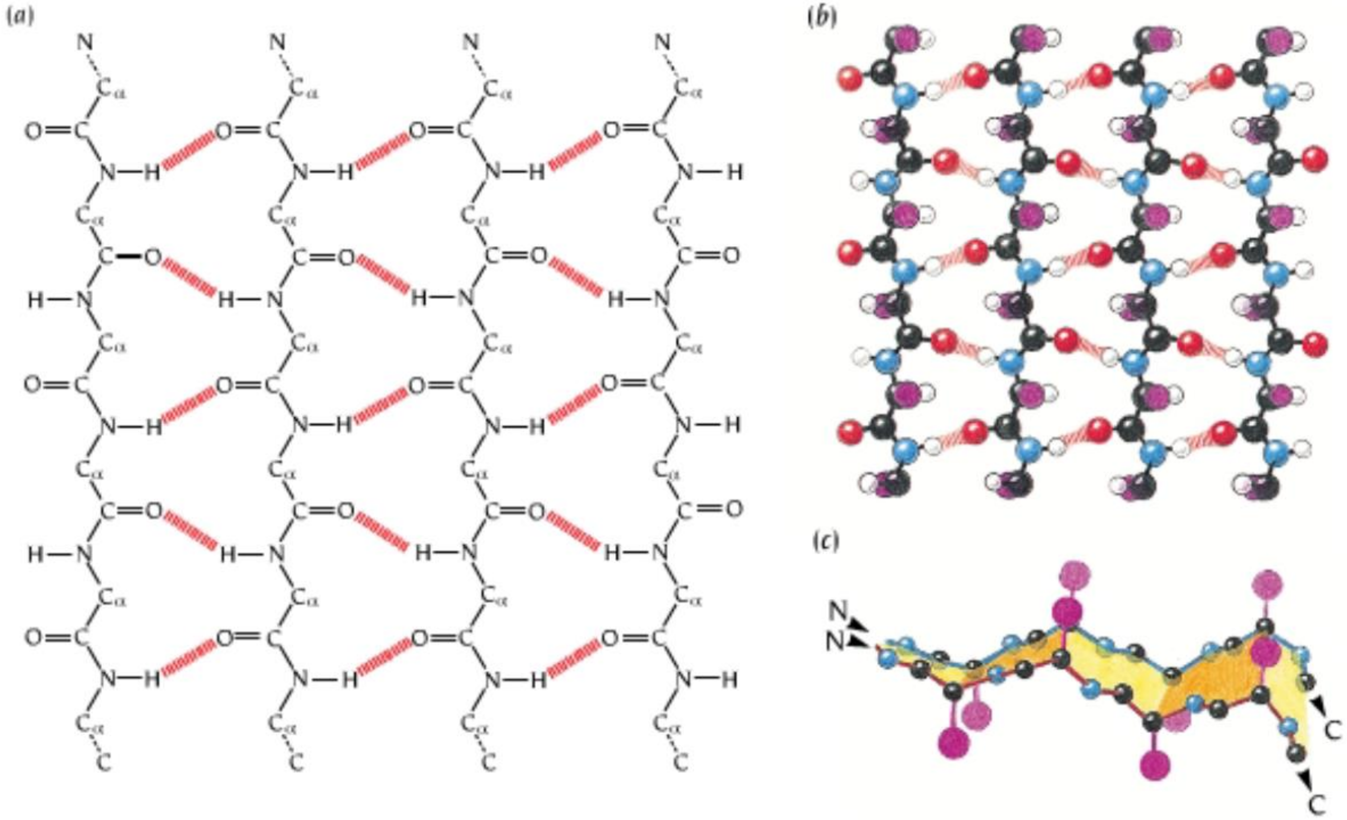
Anti-parallel β sheet (φ: -139°, ψ: -135°)

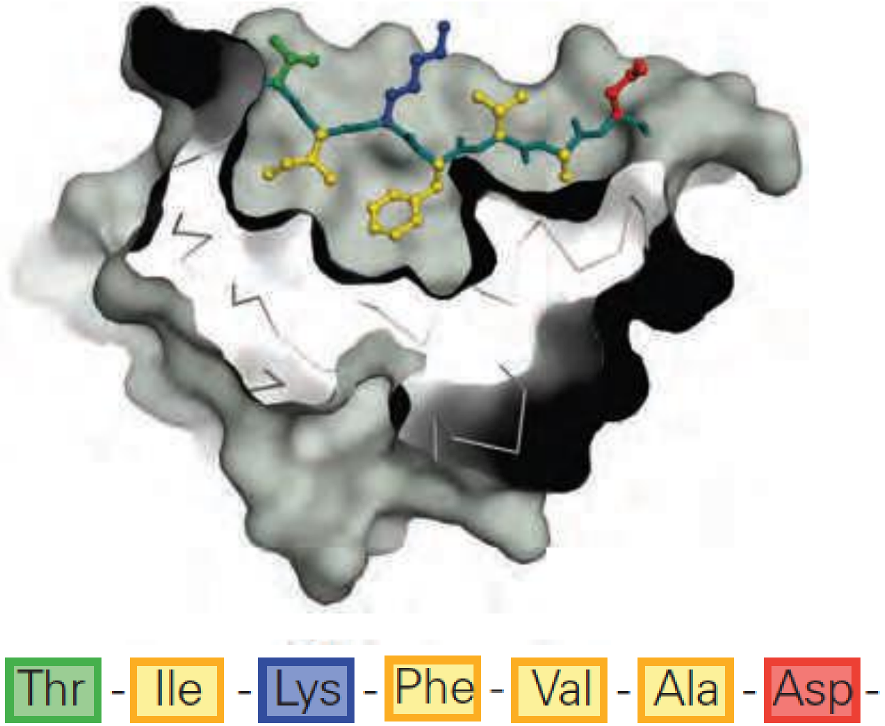




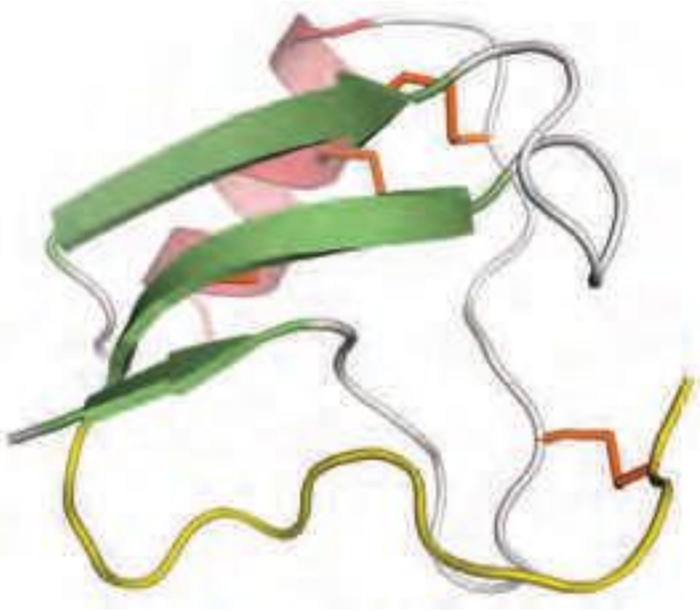
Parallel β sheet (φ: -119°, ψ: -113)

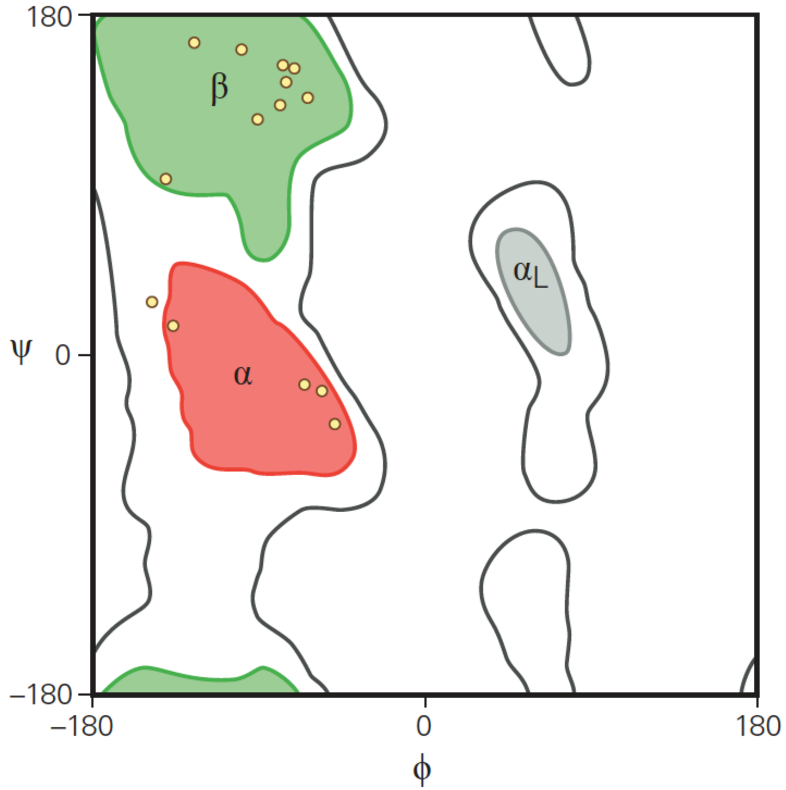


An amphipathic β sheet



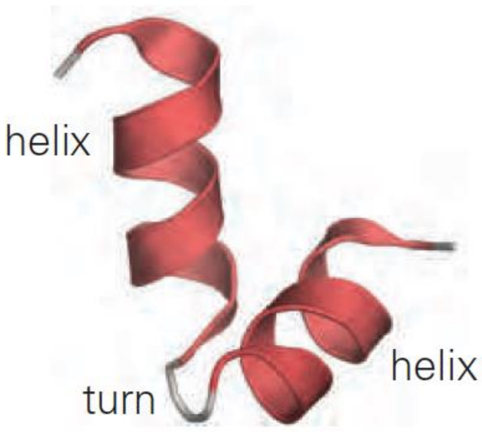
Loop



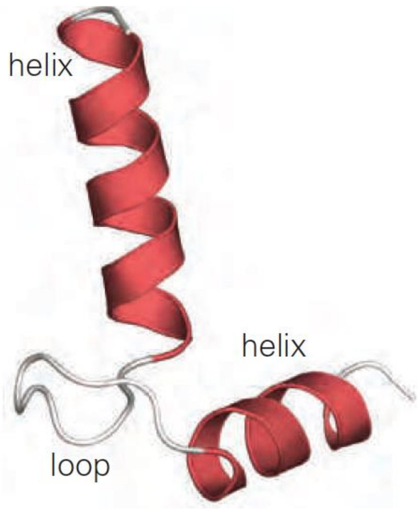


Structure motif

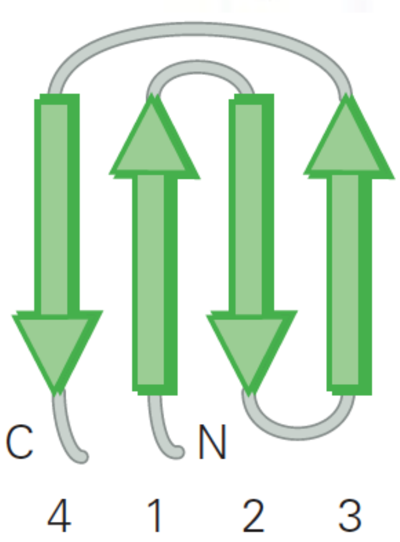
helix-turn-helix



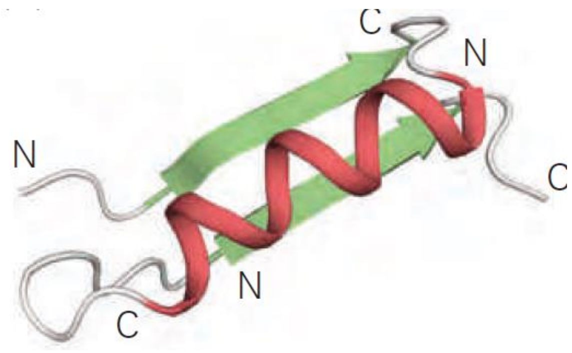
helix-loop-helix



Greek key motif

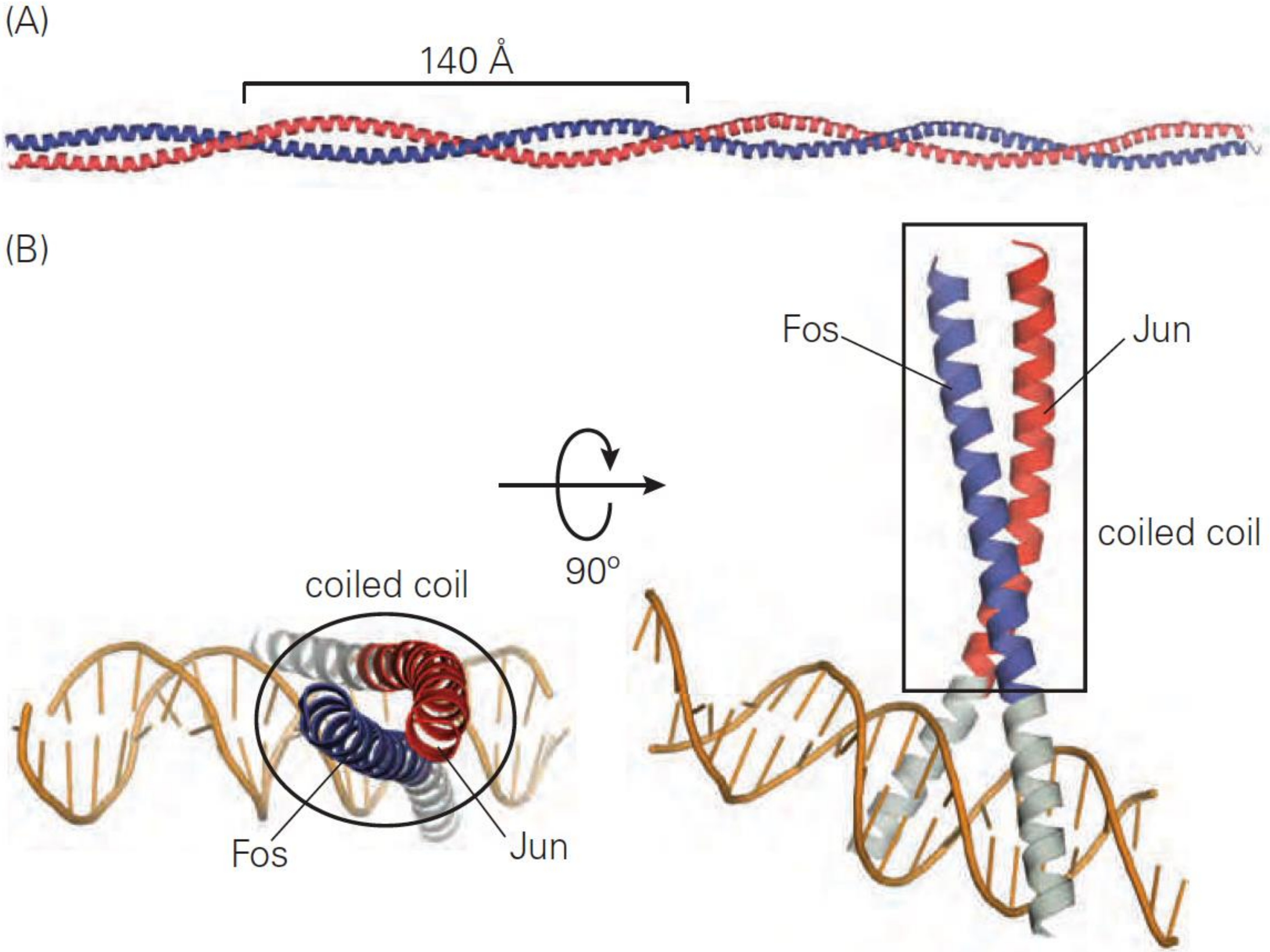


β-α-βmotif

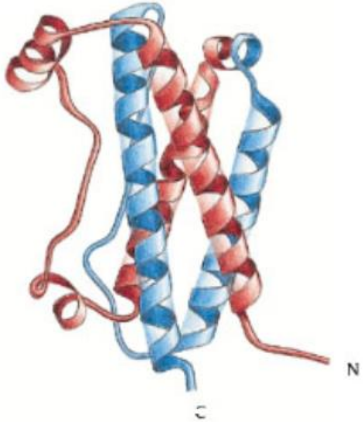


Structure motif

Coiled-coil

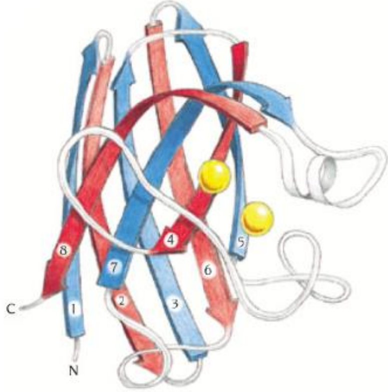


Protein domains



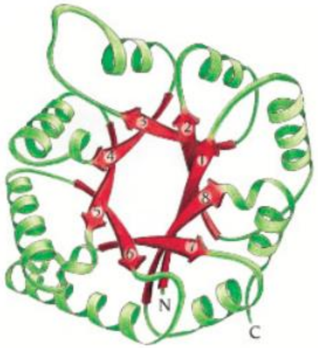
all-α domain

human growth hormone (3HHR)



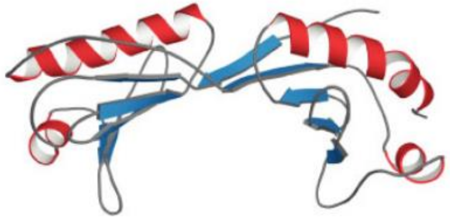
all-β domain

superoxide dismutase (2SOD)



α/β domain

triosephosphate isomerase (8TIM)



α+β domain

TATA-binding protein (1TBP)

small proteins

scorpion toxin (1B7D)

Where to find and visualize protein structures?

- Protein Data Bank: https://www.rcsb.org/
- Visualization software:
  - Chimera
  - VMD
  - PyMol