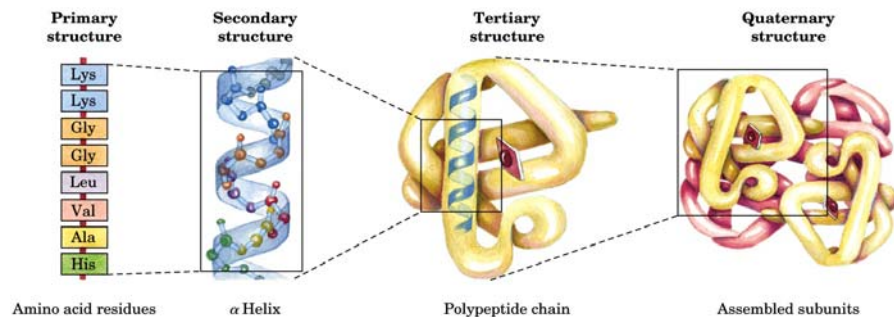


Tertiary structure: globular proteins

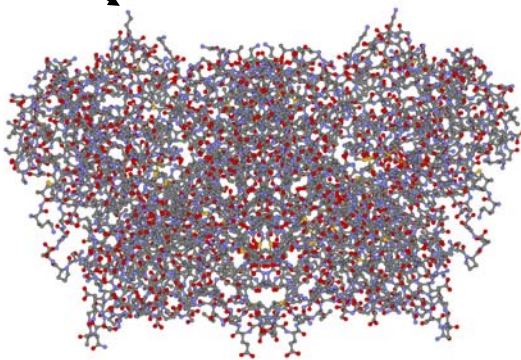


Tertiary structure: globular proteins

- 2° structural elements: α -helix, β -sheet, β -bend, random coil
- Motifs: simple combinations of a few 2° elements with a specific geometric arrangement
- Domains: a polypeptide chain or part of a polypeptide chain that can independently fold into a stable tertiary structure

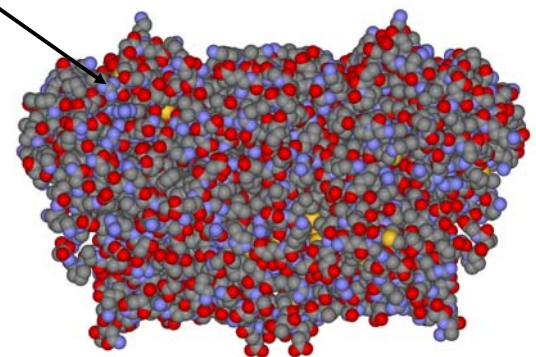
- Ways to represent protein structure:

- Ball and stick
- Space filling
- Ribbon trace
- C α trace
- schematic



- Ways to represent protein structure:

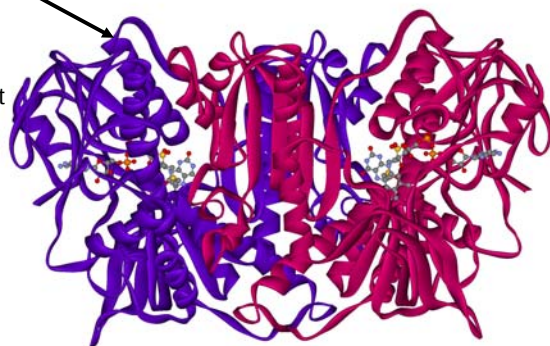
- Ball and stick
- Space filling
- Ribbon trace
- C α trace
- schematic



- Ways to represent protein structure:

- Ball and stick
- Space filling
- Ribbon trace
- C α trace
- schematic

Amino acid side chains not shown in this ribbon trace



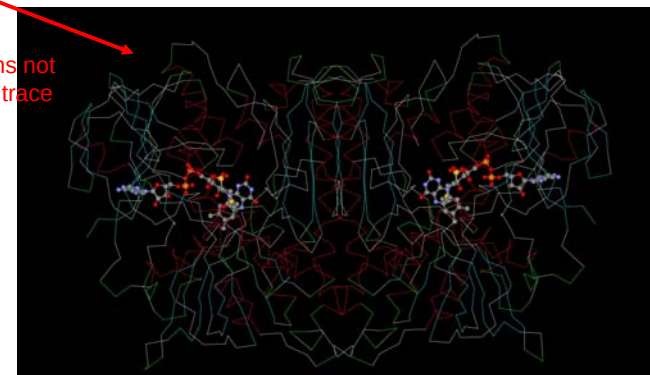
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5

- Ways to represent protein structure:

- Ball and stick
- Space filling
- Ribbon trace
- C α trace
- schematic

Amino acid side chains not shown in this c alpha trace



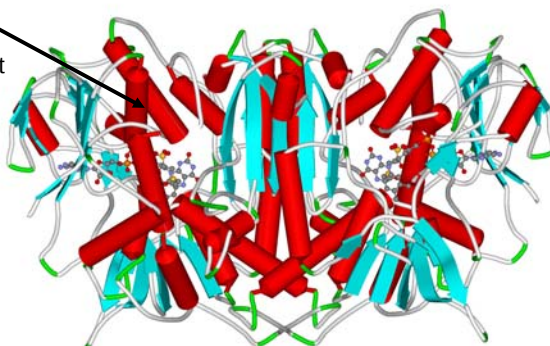
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6

- Ways to represent protein structure:

- Ball and stick
- Space filling
- Ribbon trace
- C α trace
- schematic

Amino acid side chains not shown in this schematic trace



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7

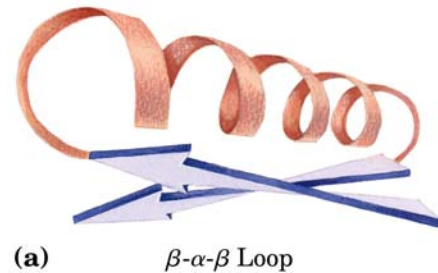
Representing α -helices and β -strands using ribbon diagrams



Figure adapted from Fred Cohen, University of California at San Francisco.

8

Representing α -helices and β -strands using ribbon diagrams

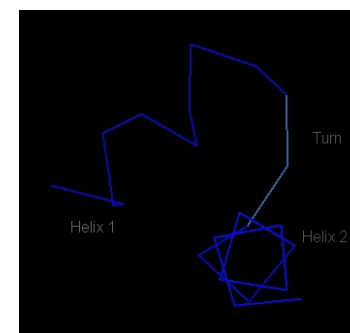


- Domains: a polypeptide chain or part of a polypeptide chain that can independently fold into a stable tertiary structure
 - α domain (α helix only)
 - β domain (β sheet only)
 - α/β domains (combination β – α – β motifs)
 - Some bends and/or random coils are always required to connect different 2° structural elements

Common structural motifs

- Helix-turn-helix
- Globin fold
- Four helix bundle
- α/β motifs:
 - Barrel
 - Saddle
 - Doubly-wound beta sheet

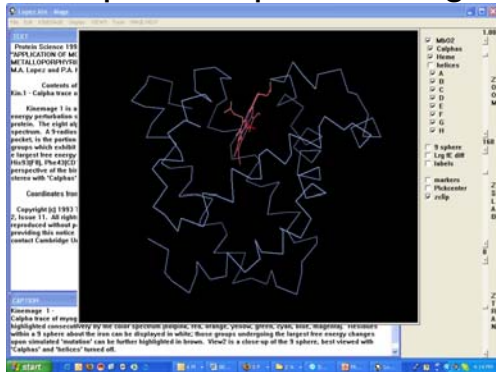
Helix-turn-helix



File5.kin

Globin fold: myoglobin

- “All” α -helix (>70%)
- 7-23 AA/helix
- Stabilized by hydrophobic effect
- Nonprotein “prosthetic group” (heme)



Lopez.kin

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Four helix bundle

- Hemerythrin: file4.kin
- Myohemerythrin, cytochrome B562: protour7.kin, kinemage



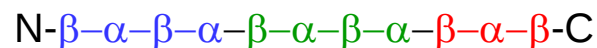
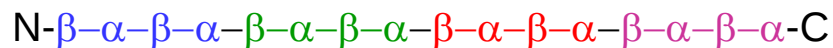
File4.kin



protour7.kin

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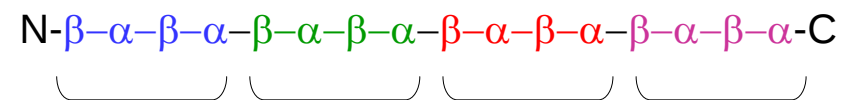
α/β motifs



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α/β barrel

- Core of 8 twisted $\parallel \beta$ strands arranged close together, like staves in a barrel
- α -helices connect β strands on outside of barrel
- Good example: triosephosphate isomerase (see protour7.kin kinemage 2, file9.kin)

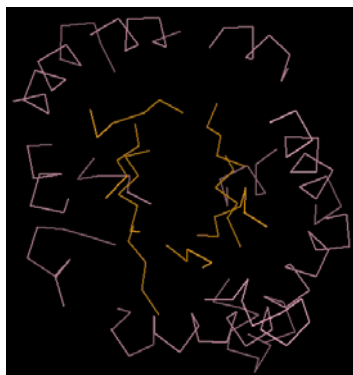


4 motifs $\rightarrow$ 1 domain

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α/β barrel

N- β - α - β - α - β - α - β - α - β - α - β - α - β - α -C



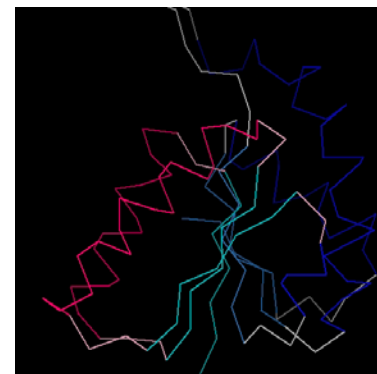
File9.kin



protour7.kin

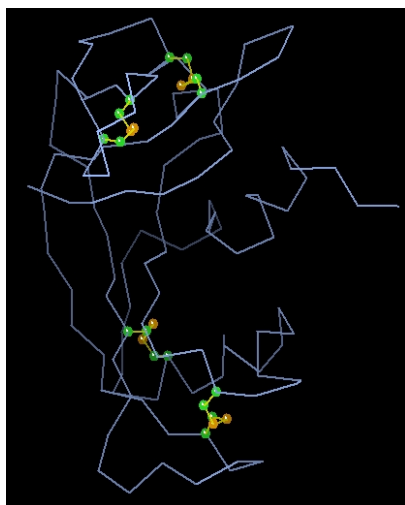
α/β saddle

N- β - α - β - α - β - α - β - α - β - α - β -C



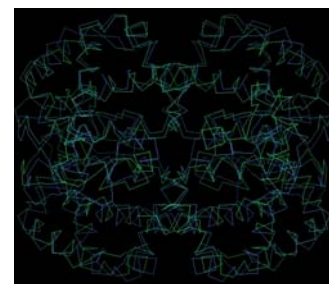
protour1.kin

Disulfide bonds example: ribonuclease A

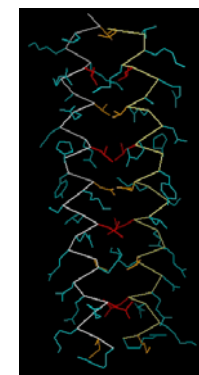


file16.kin

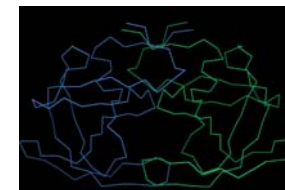
Protein quaternary structure



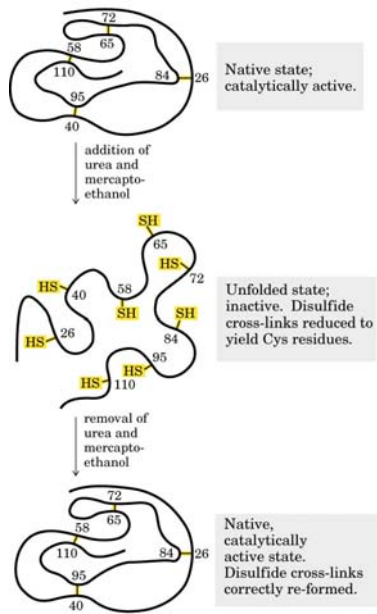
hemoglobin
file13.kin



Leucine zipper
file11.kin



HIV protease
file12.kin



Protein folding

- Stepwise
- Local 2° to higher structure
- Nucleate about motif
- Molecular chaperones
- Large protein complexes: spontaneous self assembly

