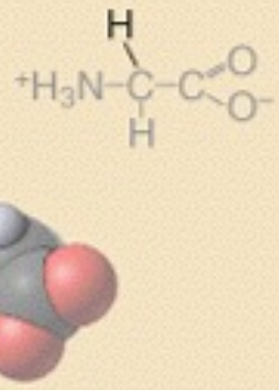
Protein Structure

Primary structure (sequence)
Secondary structure (“building blocks”)
Tertiary structure (“packing”)
Quaternary structure (“assemblies”)

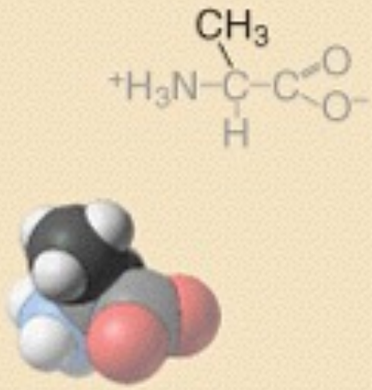
The 20 Natural Amino Acids

UNCHARGED

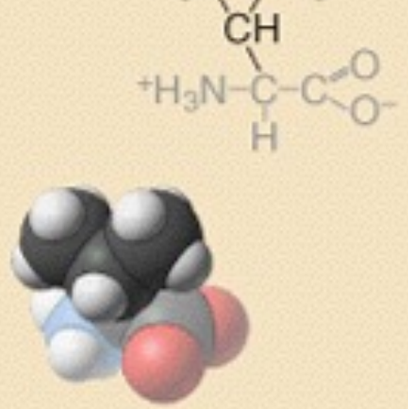
Glycine
Gly
G



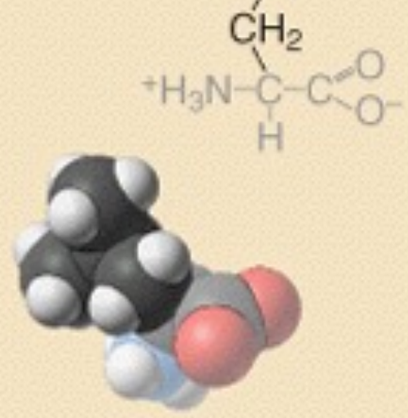
Alanine
Ala
A



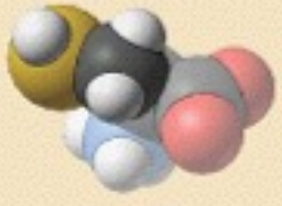
Valine
Val
V



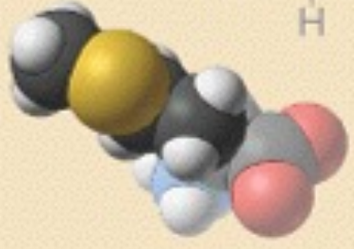
Leucine
Leu
L



Cysteine
Cys
C

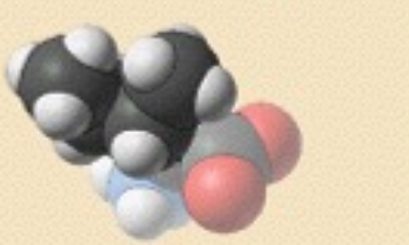


Methionine
Met
M



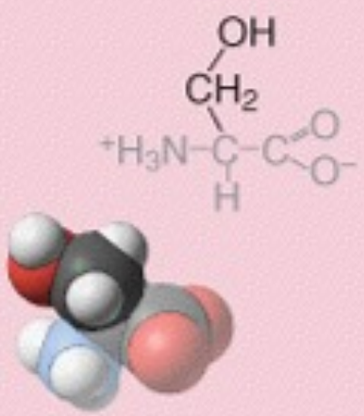
Proline
Pro
P

Isoleucine
Ile
I



POLAR UNCHARGED

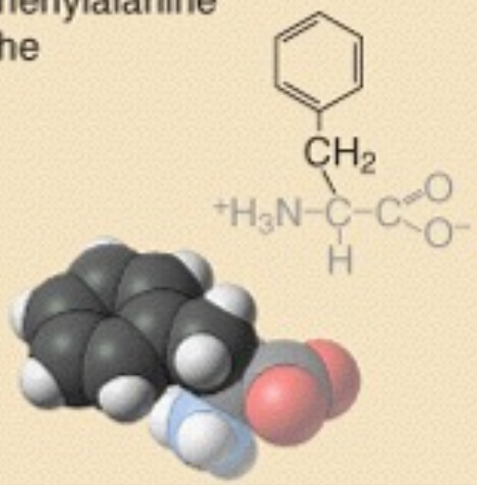
Serine
Ser
S



Threonine
Thr
T

Tyrosine
Tyr
Y

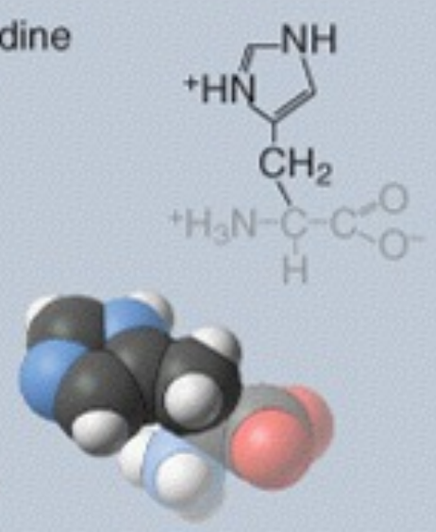
Phenylalanine
Phe
F



Asparagine
Asn
N

Glutamine
Gln
Q

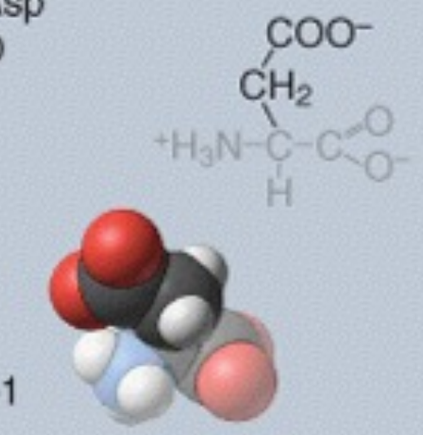
Histidine
His
H



Tryptophan
Trp
W

CHARGED

Aspartic acid
Asp
D

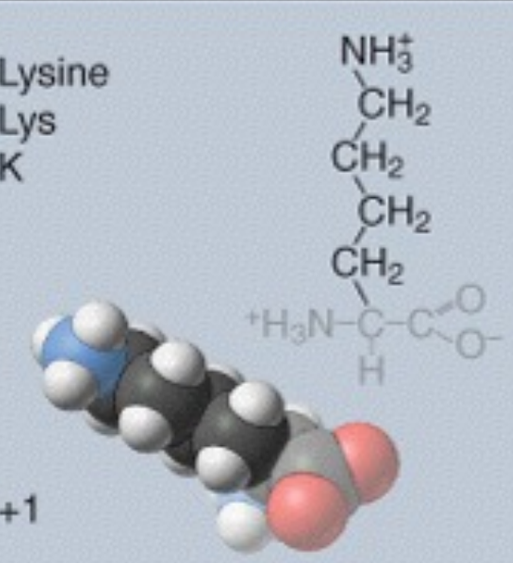


–1

Glutamic acid
Glu
E

–1

Lysine
Lys
K



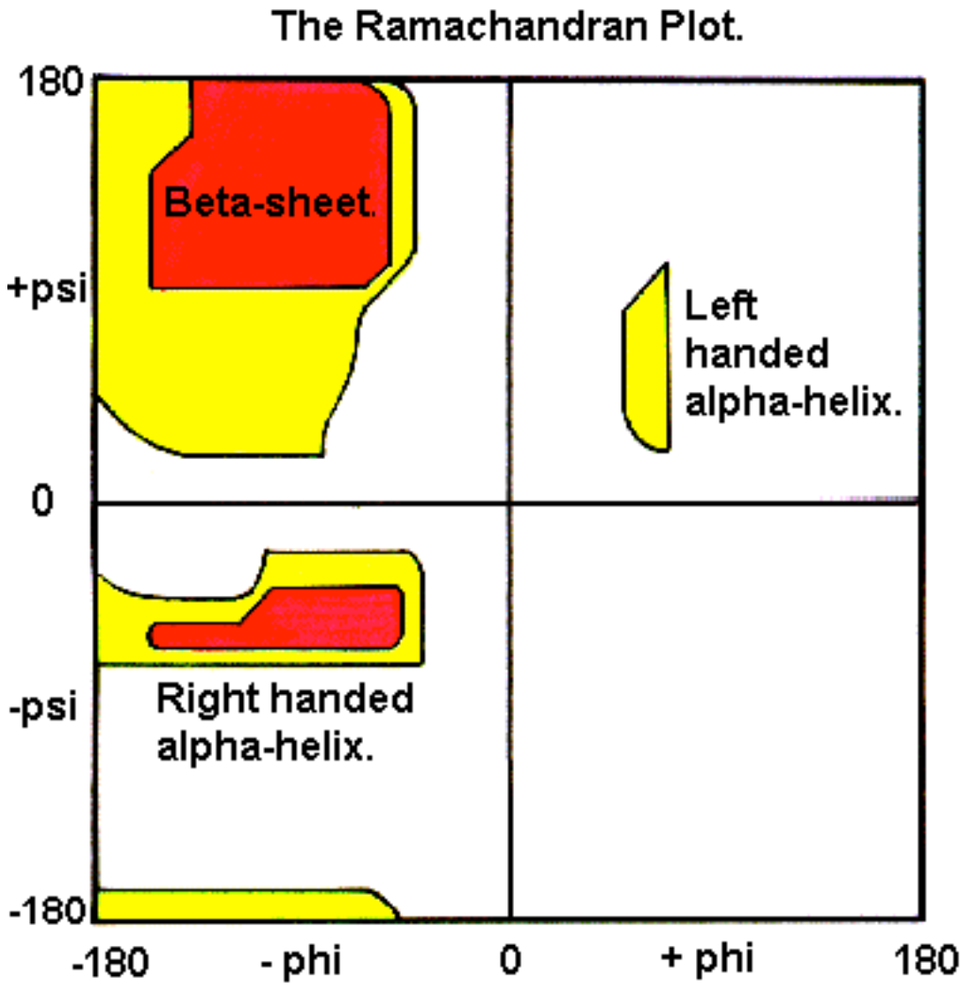
+1

Arginine
Arg
R

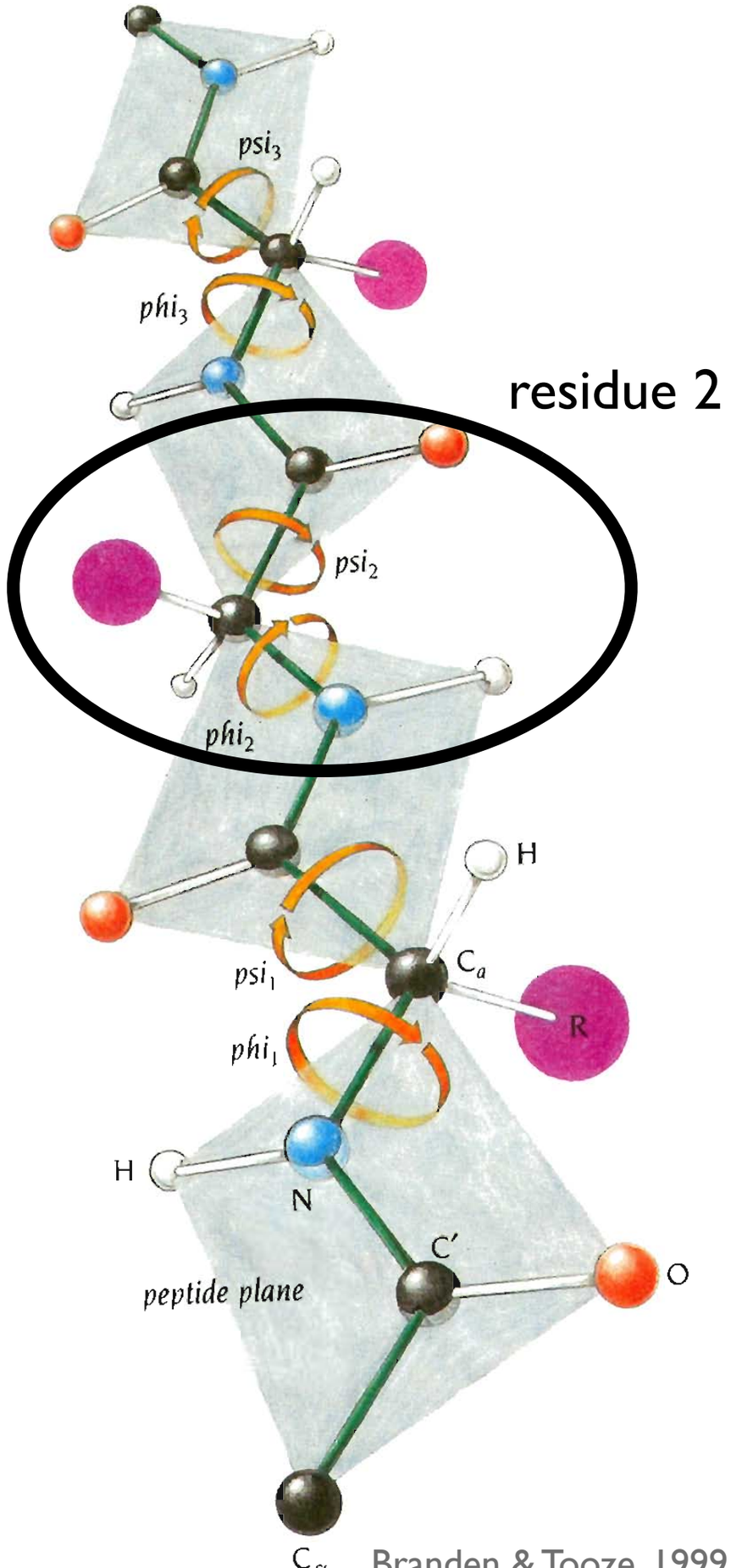
+1

Polypeptide conformation

- backbone dihedrals Φ, ψ, and ω
- "allowed" regions

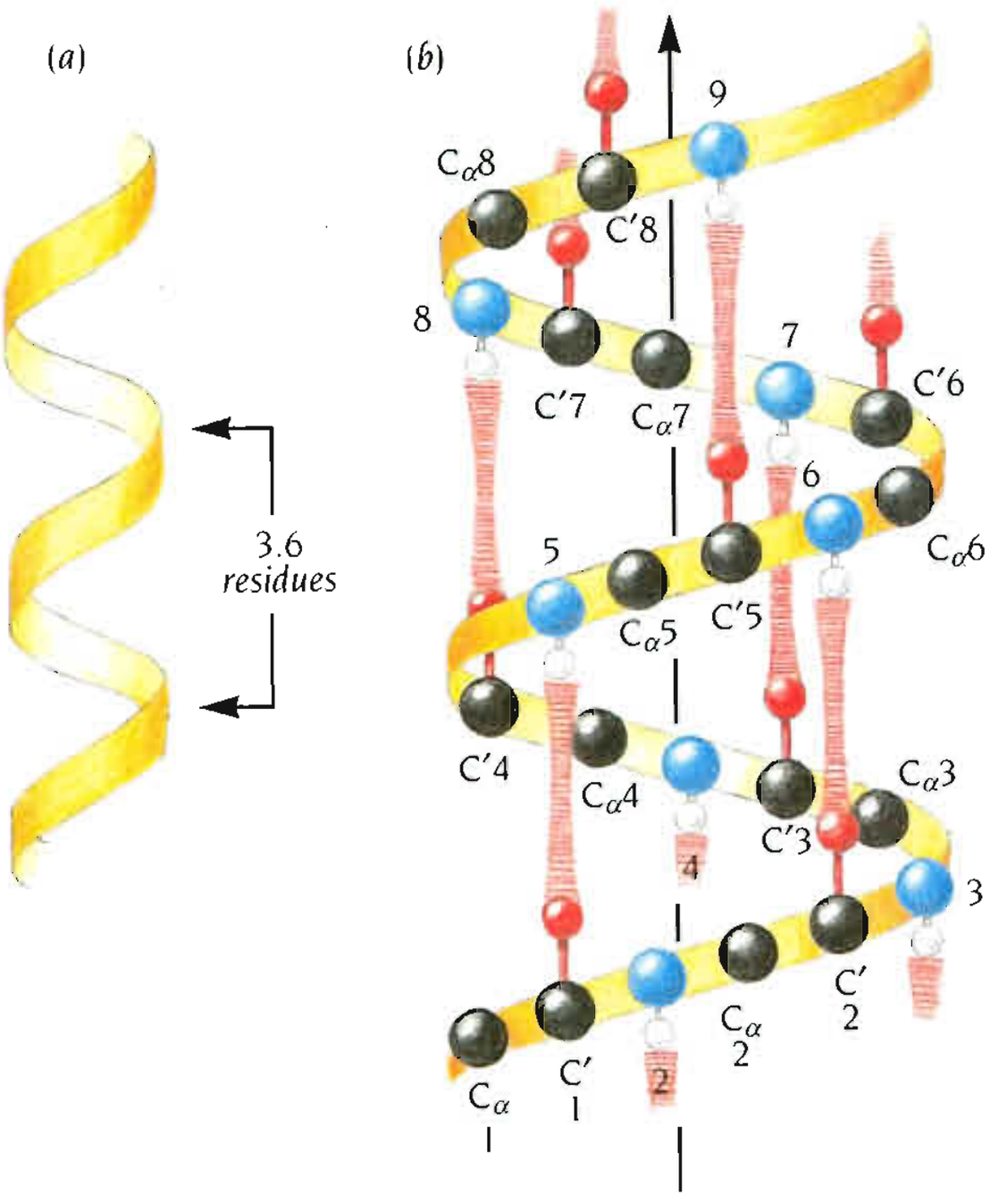


http://swissmodel.expasy.org/course/text/chapter1.htm



Branden & Tooze, 1999

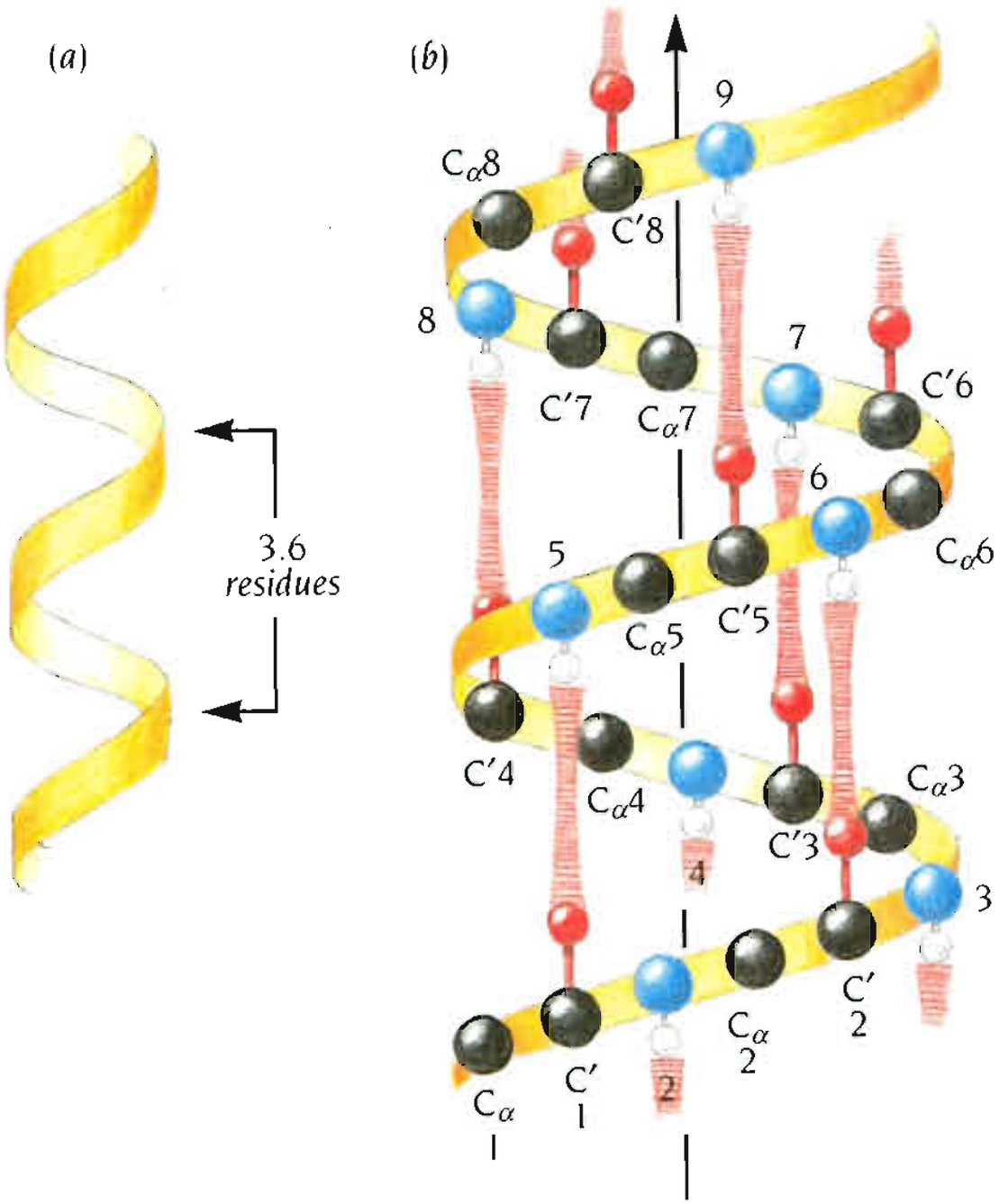
α-helix

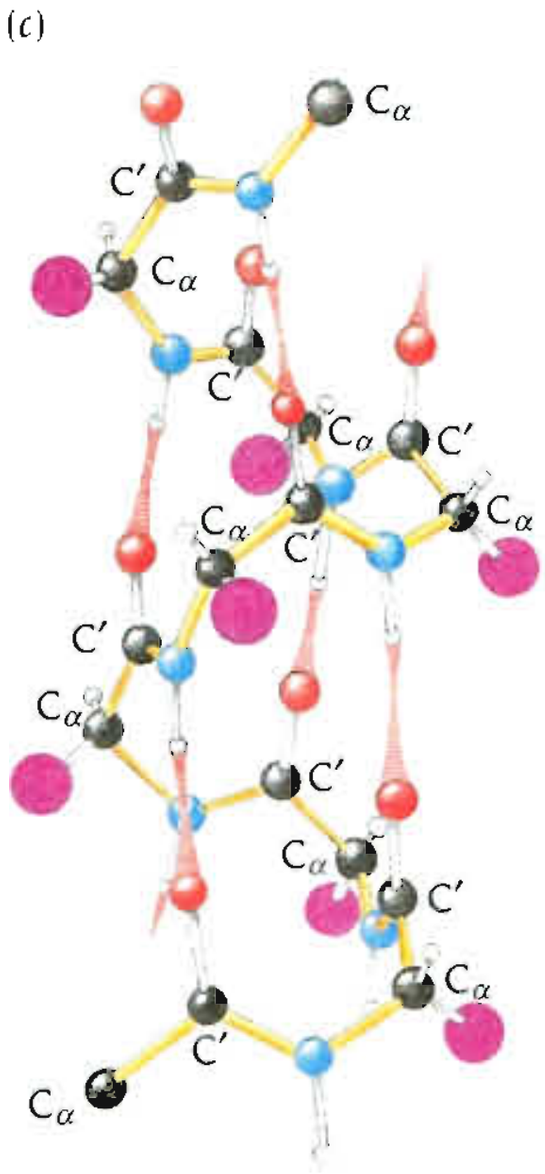


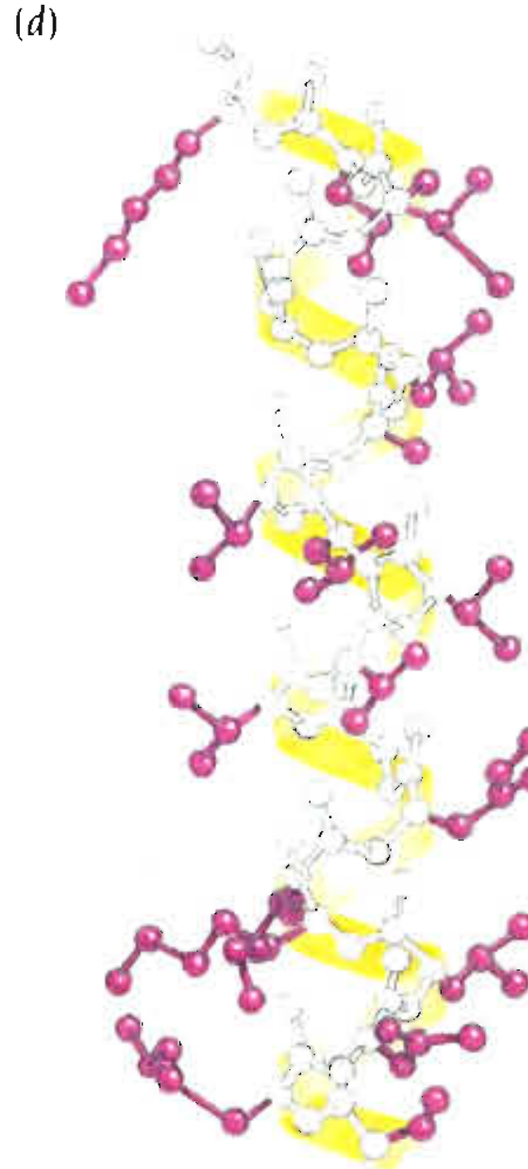
hydrogen bonds: *i* ··· *i*+4

Branden & Tooze, 1999

α-helix





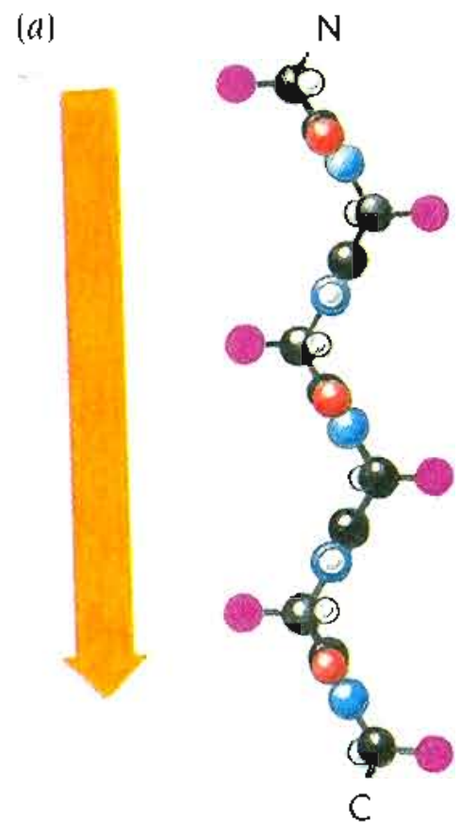


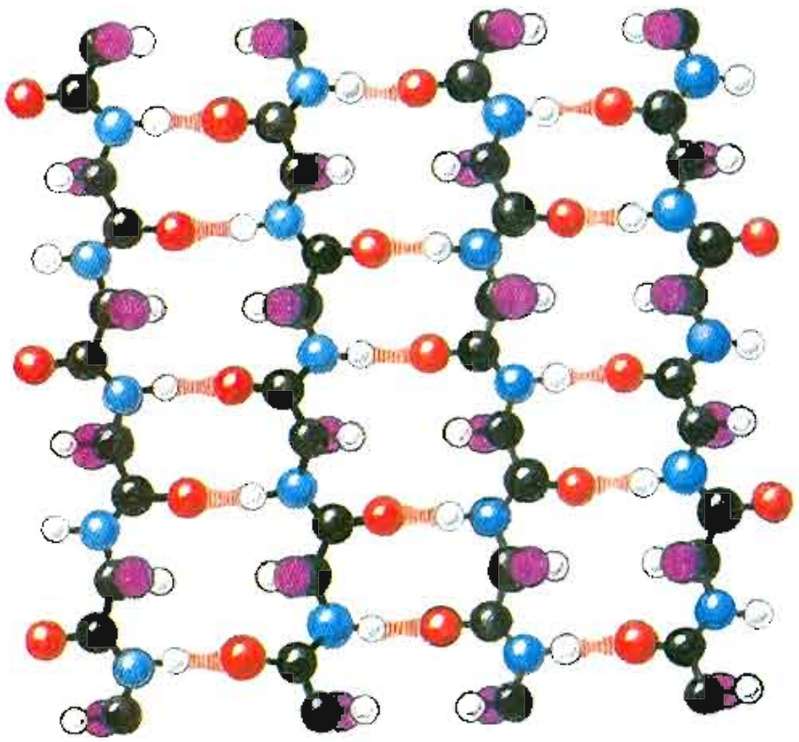
hydrogen bonds: ***i*** ••• ***i*+4**

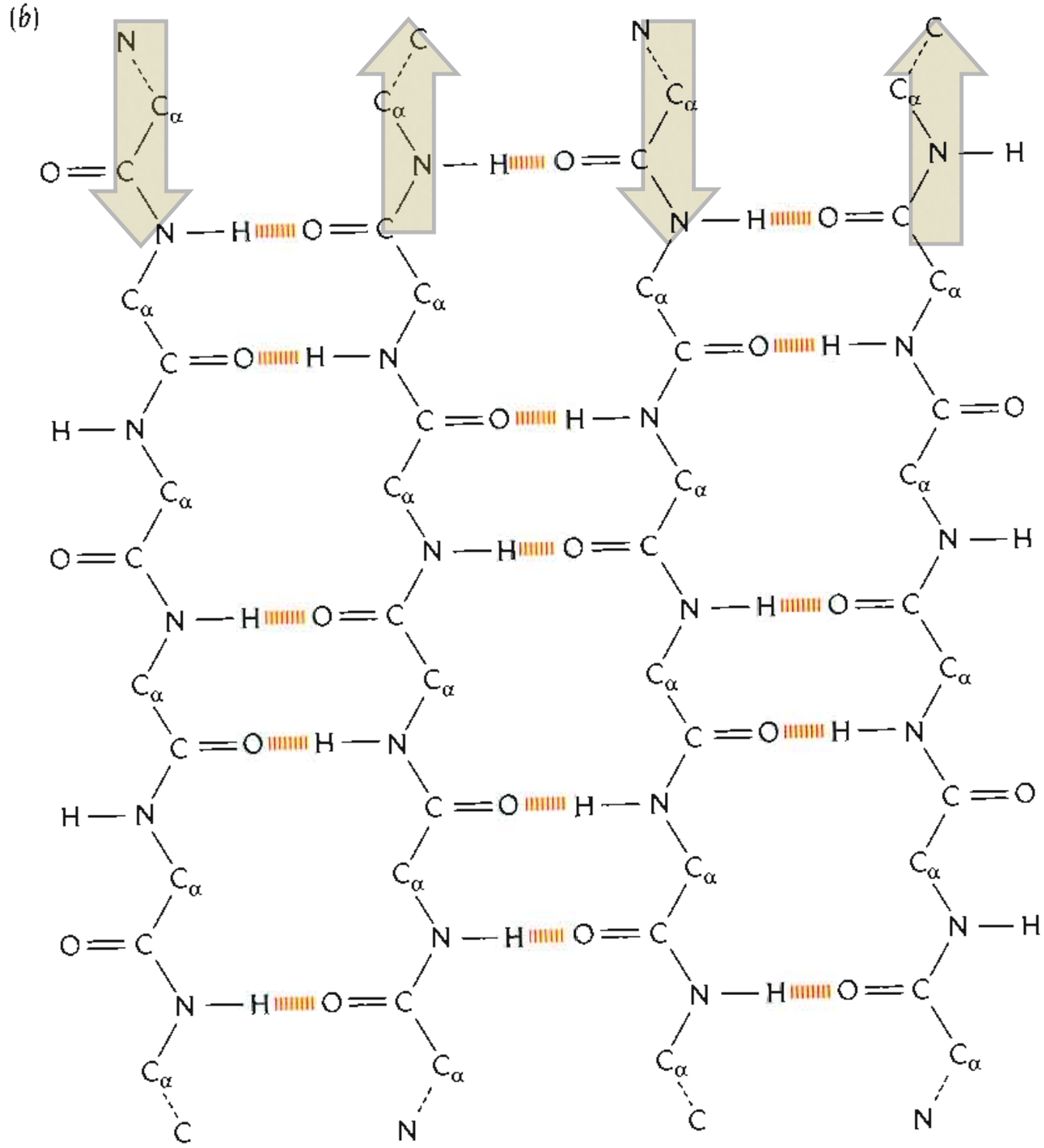
Branden & Tooze, 1999

β-sheets

anti-
parallel



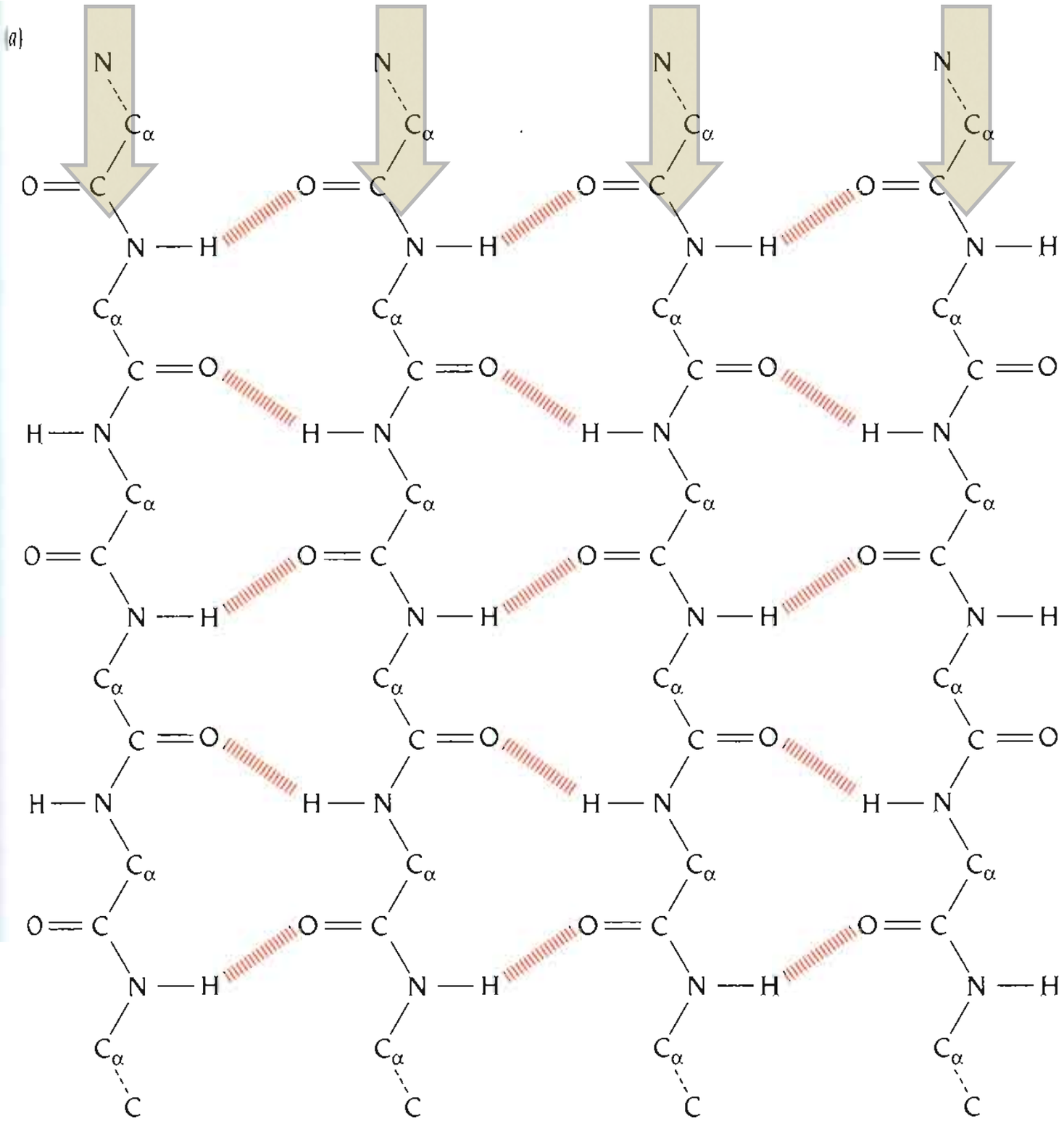


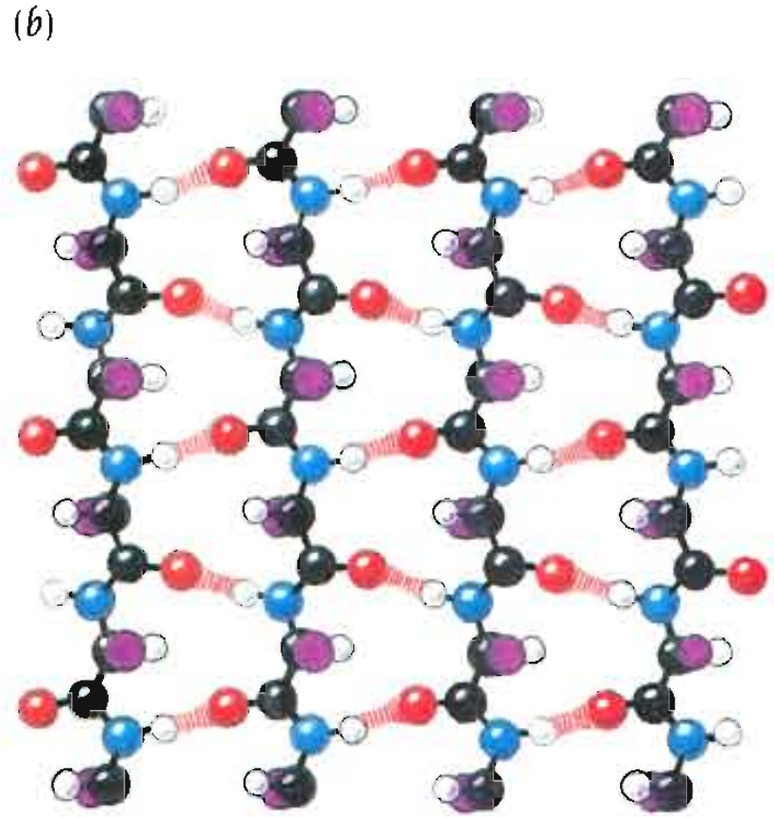


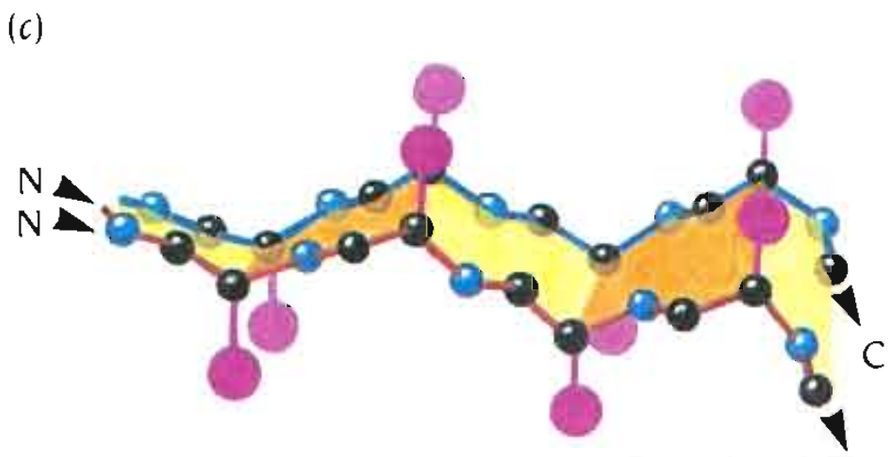
Branden & Tooze, 1999

β-sheets

parallel

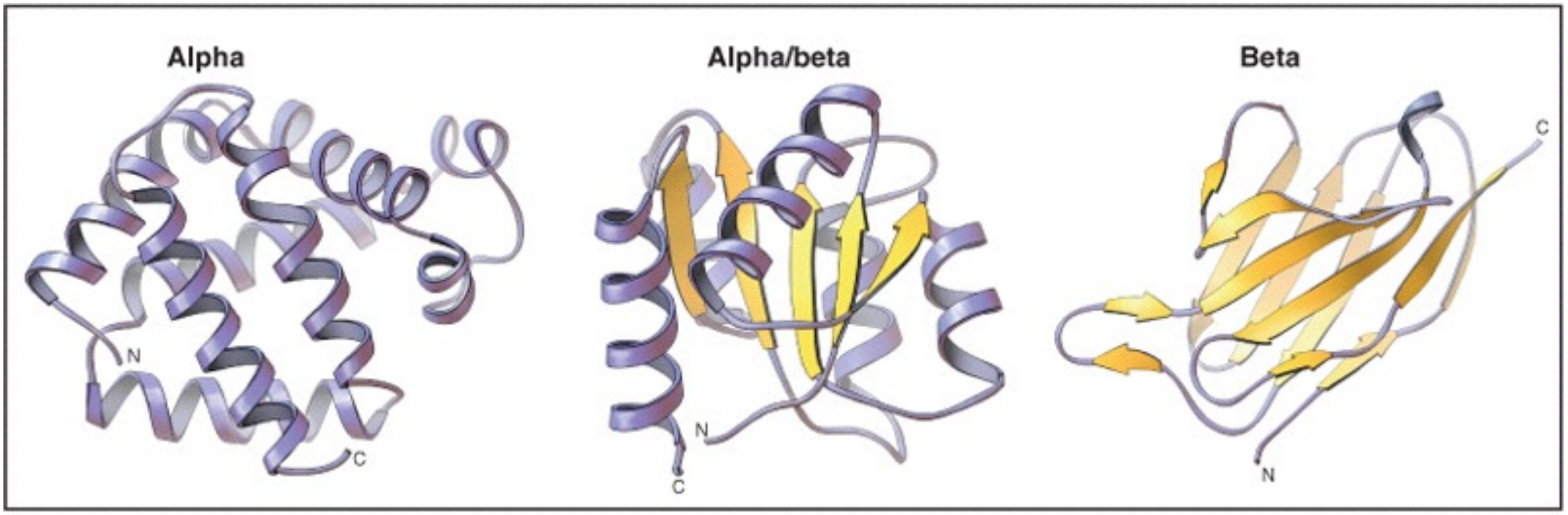






Branden & Tooze, 1999

Tertiary structure



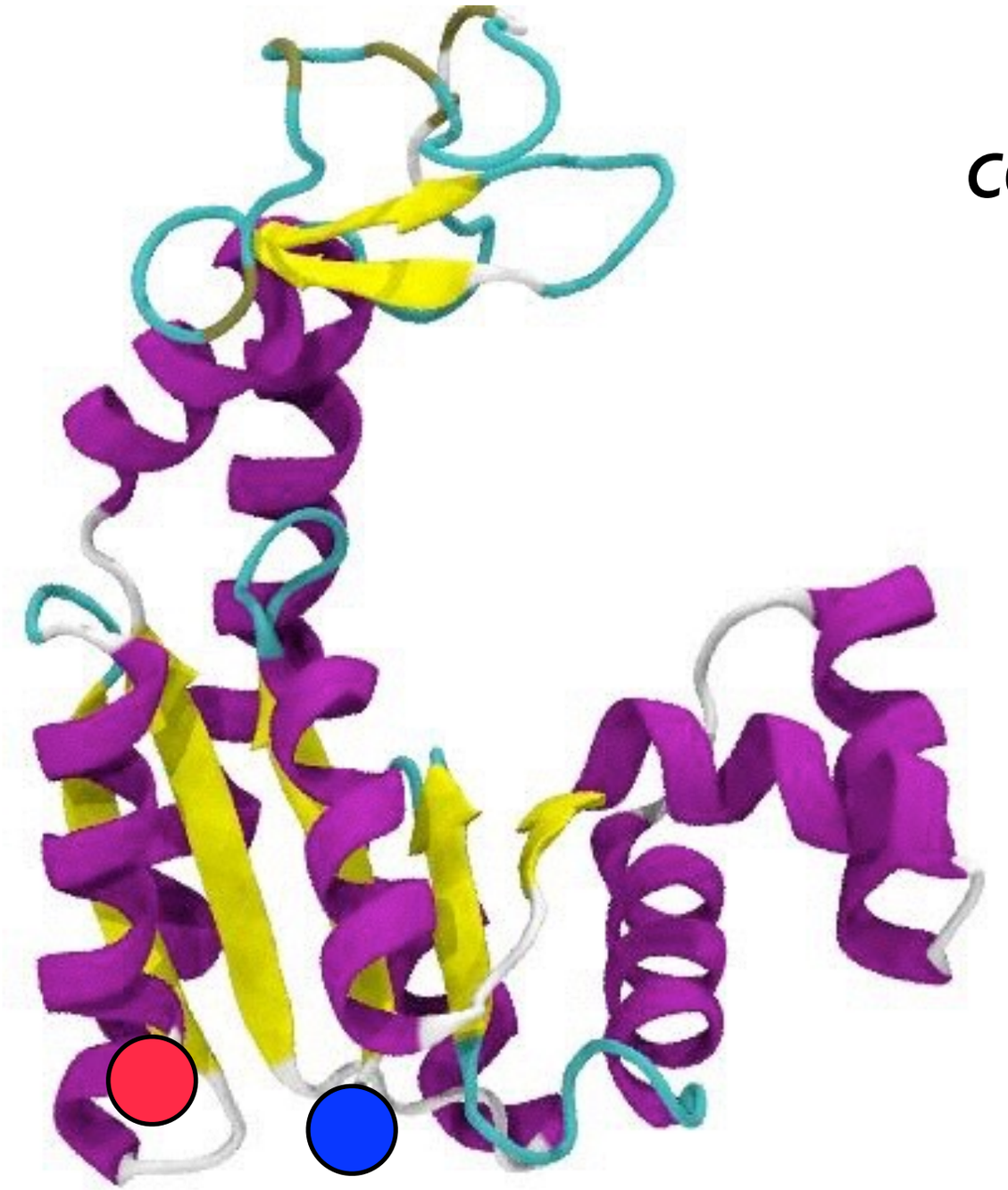
Visualizing proteins with VMD

- https://becksteinlab.physics.asu.edu/pages/courses/2016/PHY542/practicals/vmd/index.html
- **https://goo.gl/nGTVXB**
- load *adk_open.pdb*
- settings:
  - `Display/Orthographic`
  - `Display/Rendermode`:GLSL
  - `Graphics/Color`:Display:Background:White

Visualizing proteins with VMD

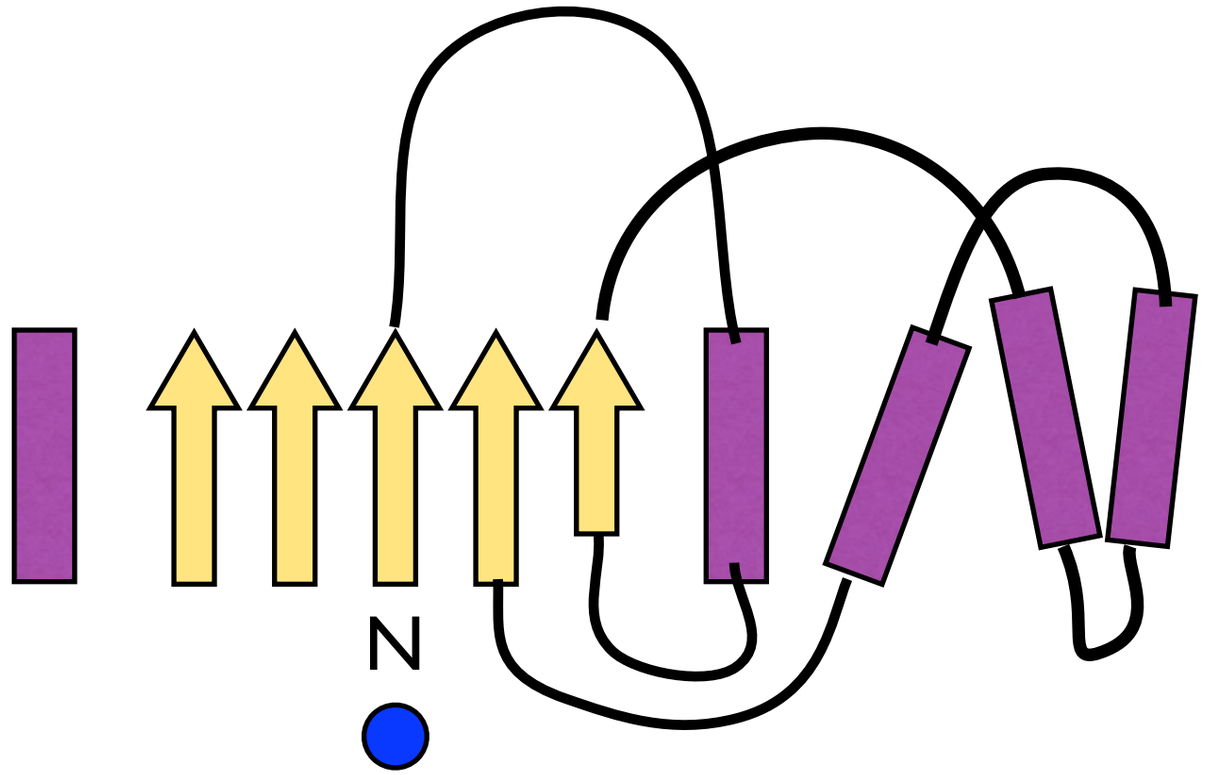
- `Graphics/Representations`
  - Selected Atoms: *protein*
  - Drawing method: *New Cartoon*
  - Coloring Method: *Secondary Structure*
- `mouse:`
  - Left: rotate X/Y,
  - Right/Command: rotate Z
- `Mouse/Rotate (r), Translate (t), Scale (s)` modes

AdK secondary structure

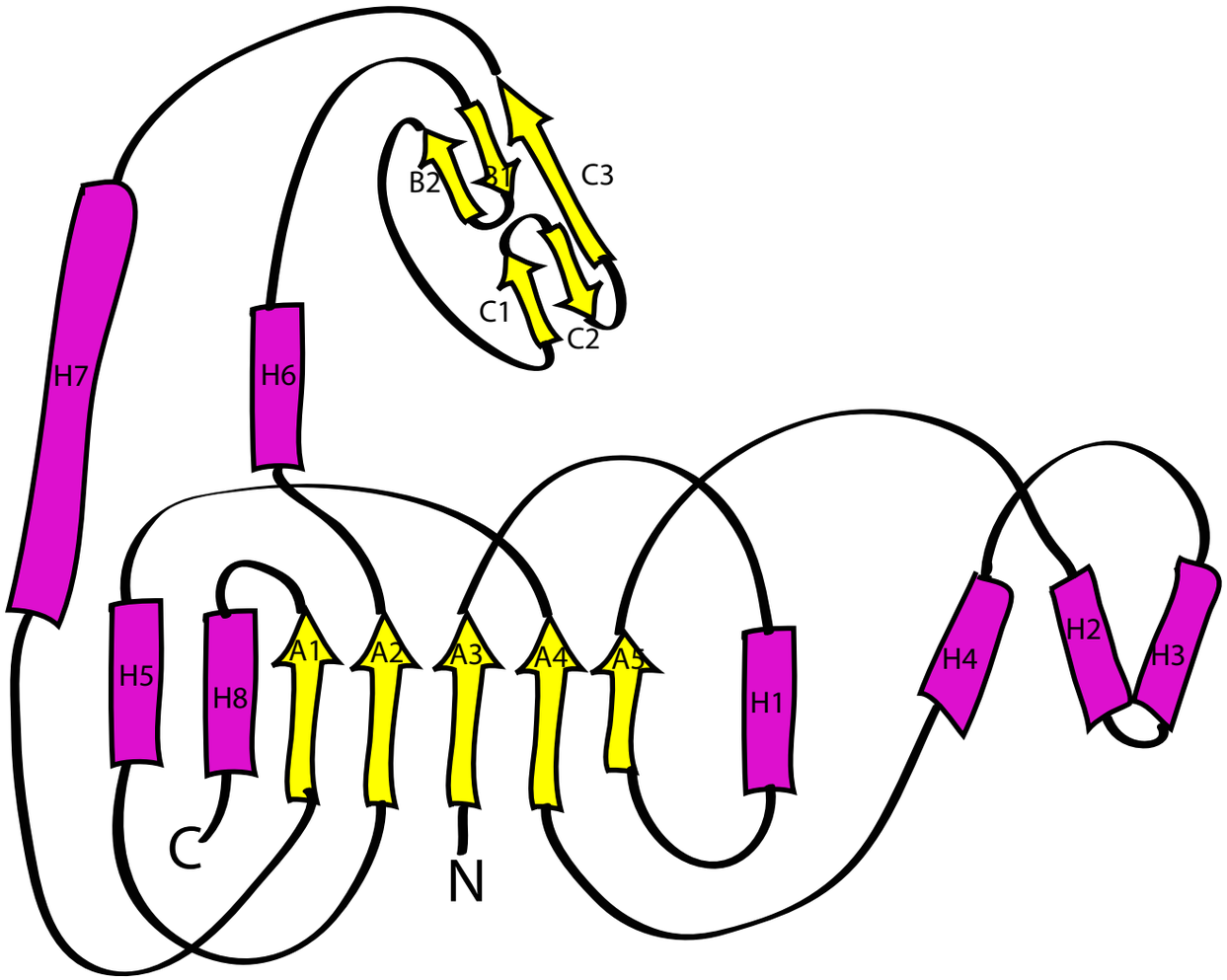


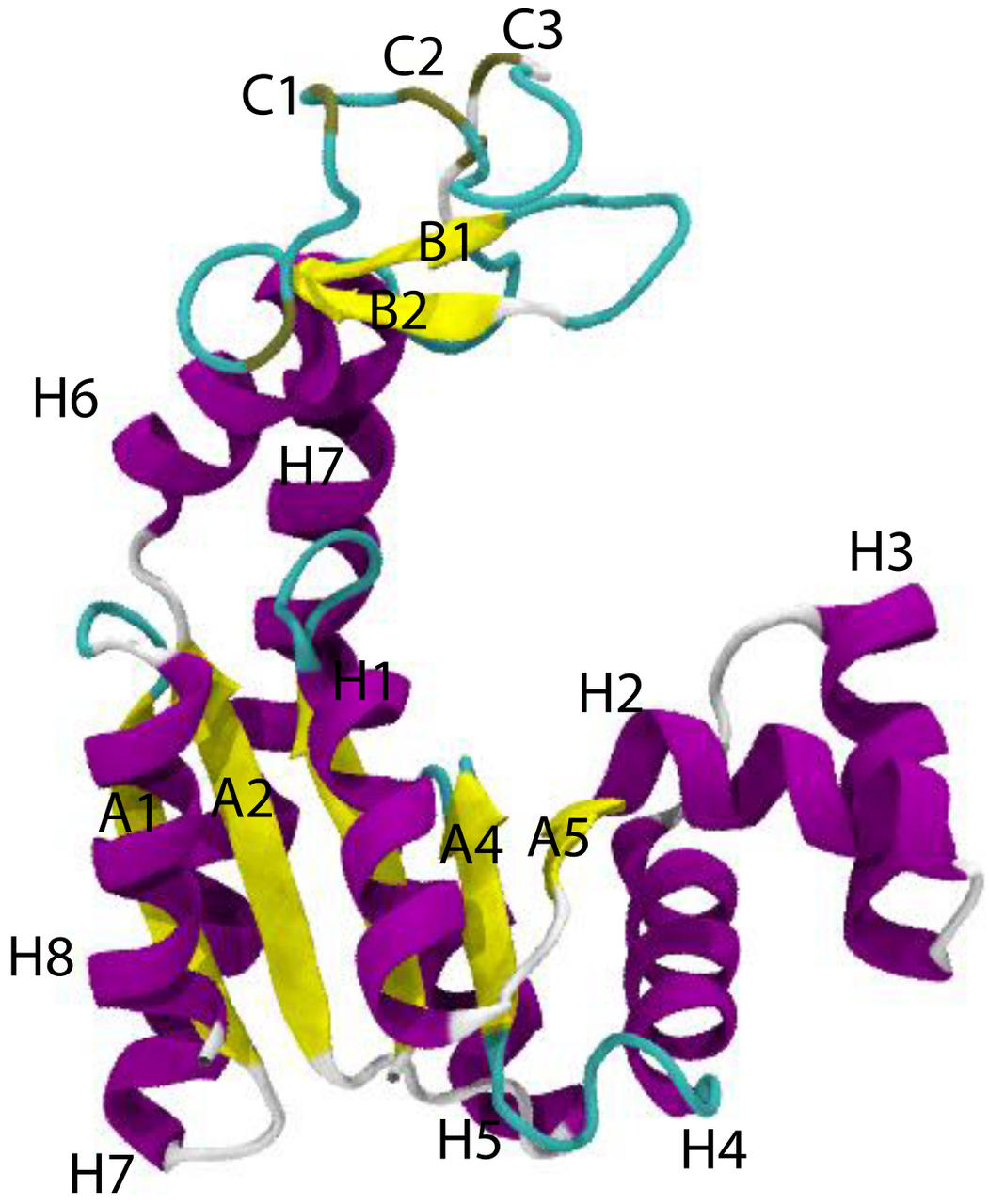
C-terminus N-terminus

complete the topology diagram

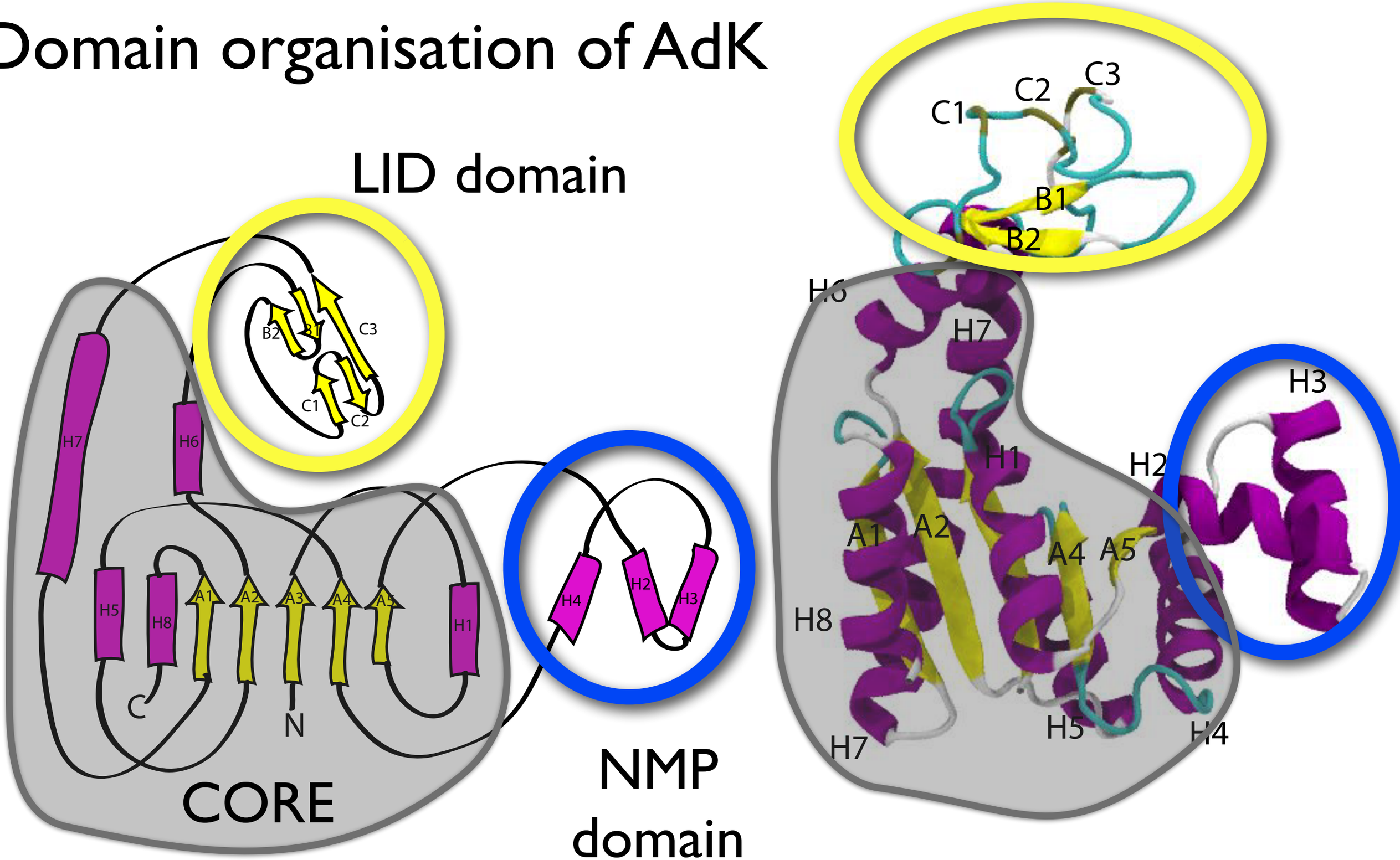


Topology of AdK





Domain organisation of AdK



Closed vs Open AdK

- load *adk_closed.pdb*
- select *protein*, color
- superimpose *protein backbone*:

  `Extensions/Analysis/RMSD Tool`: *protein*:
  Minimize RMSD by rigid body rotation

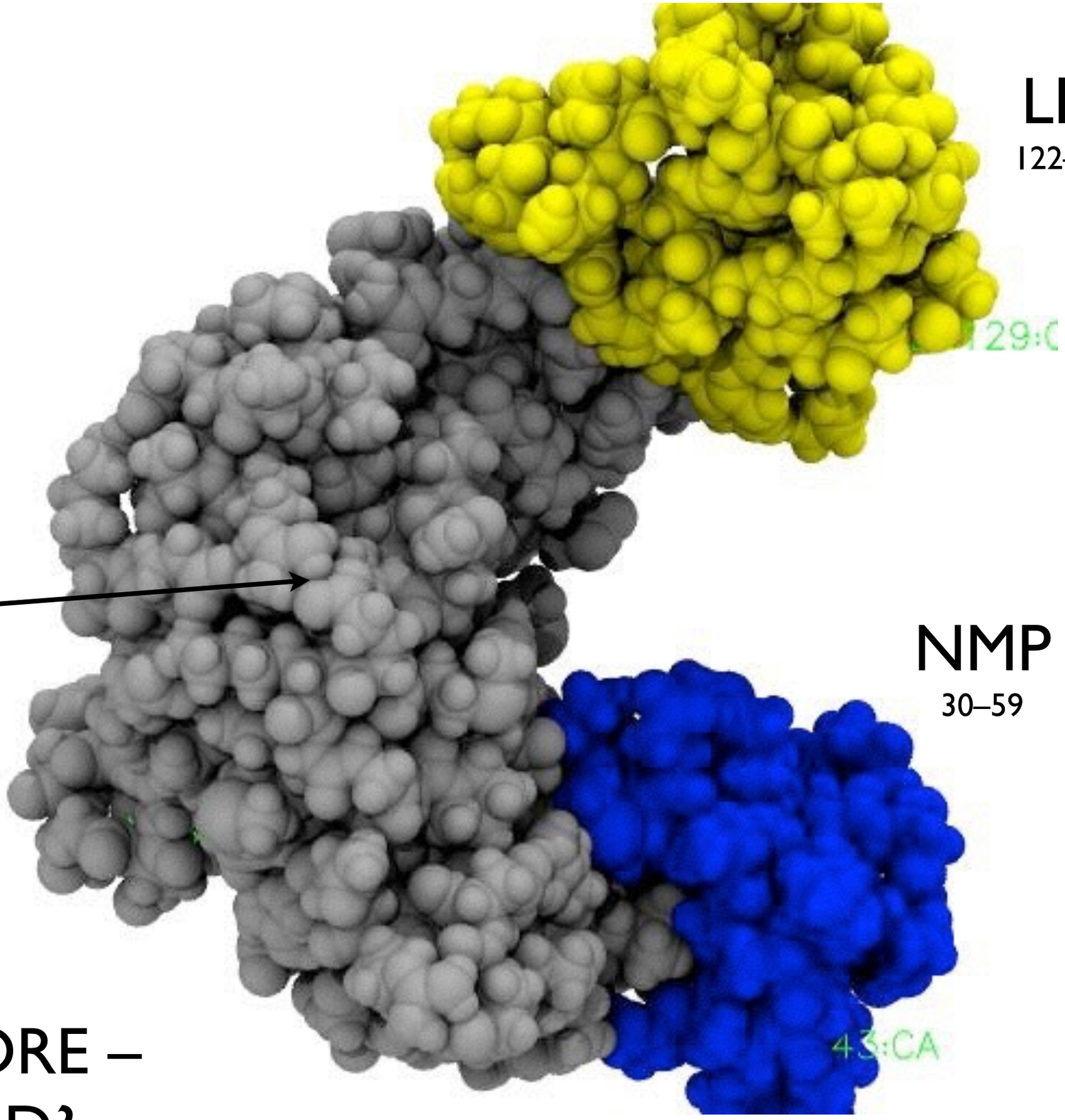
$$\mathrm{RMSD}(a,b) = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(\mathbf{x}_{a,i} - \mathbf{x}_{b,i})^2}$$

- identify regions ("domains") that move (resid ranges)
- use `Extensions/Analysis/Sequence Viewer`
- color regions differently

LID
122–159

CORE
1–29, 60–121,
160–214

NMP
30–59



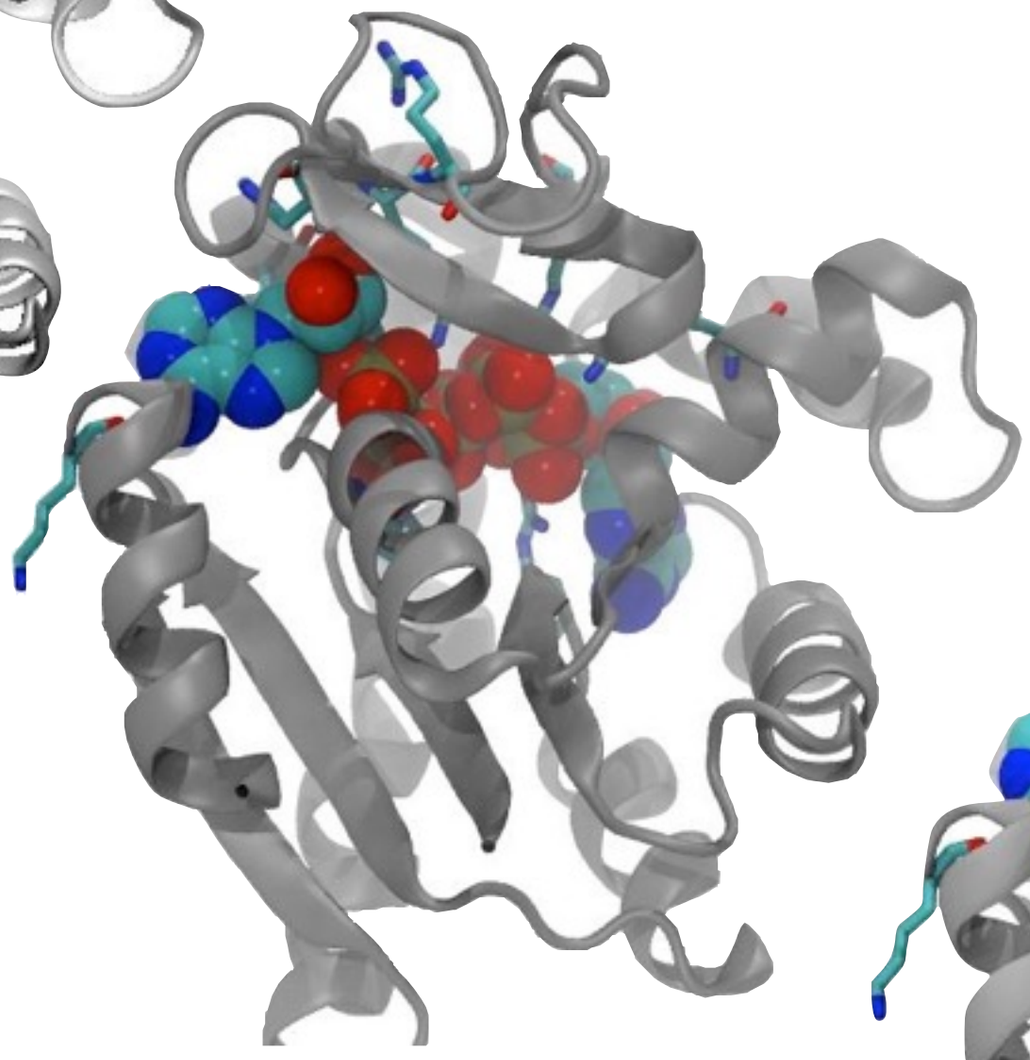
align on CORE –
final RMSD?

Rendering

- Display → Display Settings:
  - Shadows On, Amb Occl On
  - Cue Mode: Linear, Cue start: 1.75, Cue end: 3.0
- File → Render
  - *snapshot* (fast, good with GLSL)
  - *tachyon (internal)* (can do AO etc)
    - change materials for AO
  - convert tga to jpg or png (open, Save As or ‘convert’)

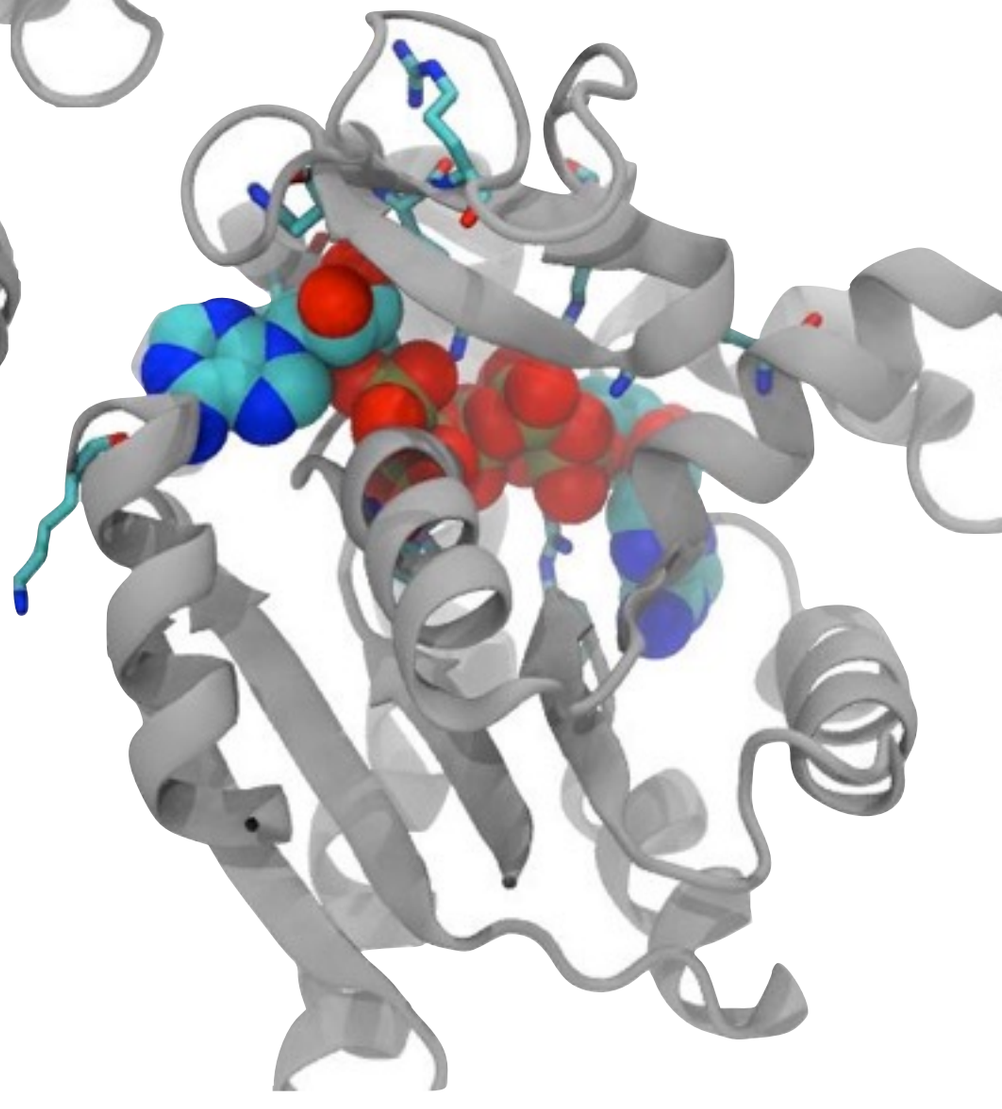
Rendering in VMD

snapshot
(GLSL)



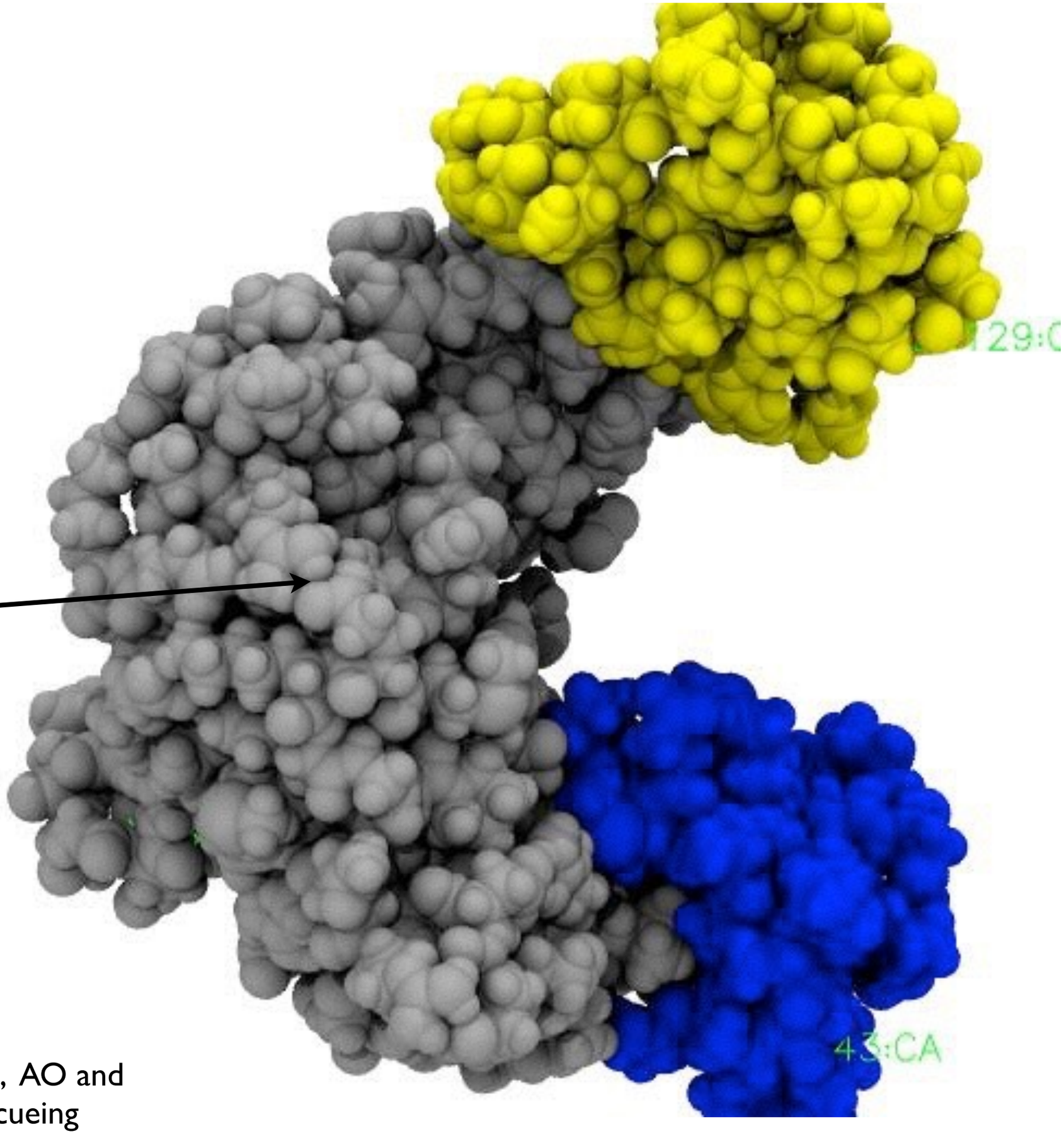
tachyon
(AO, normal materials)

tachyon
(AO, AO materials)



AO = ambient occlusion lighting

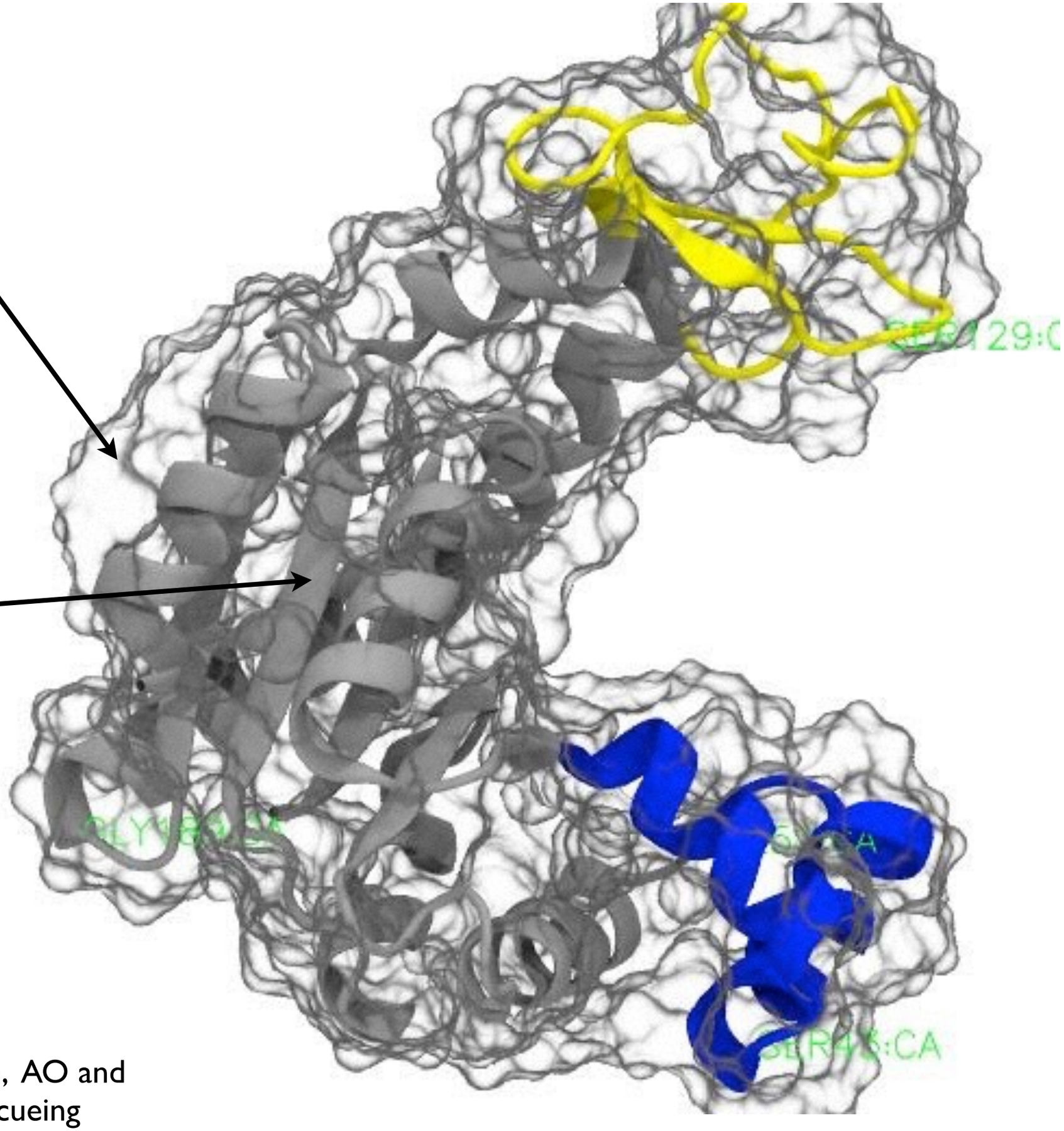
VDW, silver,
AOchalky



Rendered with Tachyon, AO and shadows, no depth cueing

Surf, silver, GlassBubble

New Cartoon, silver, AOchalky



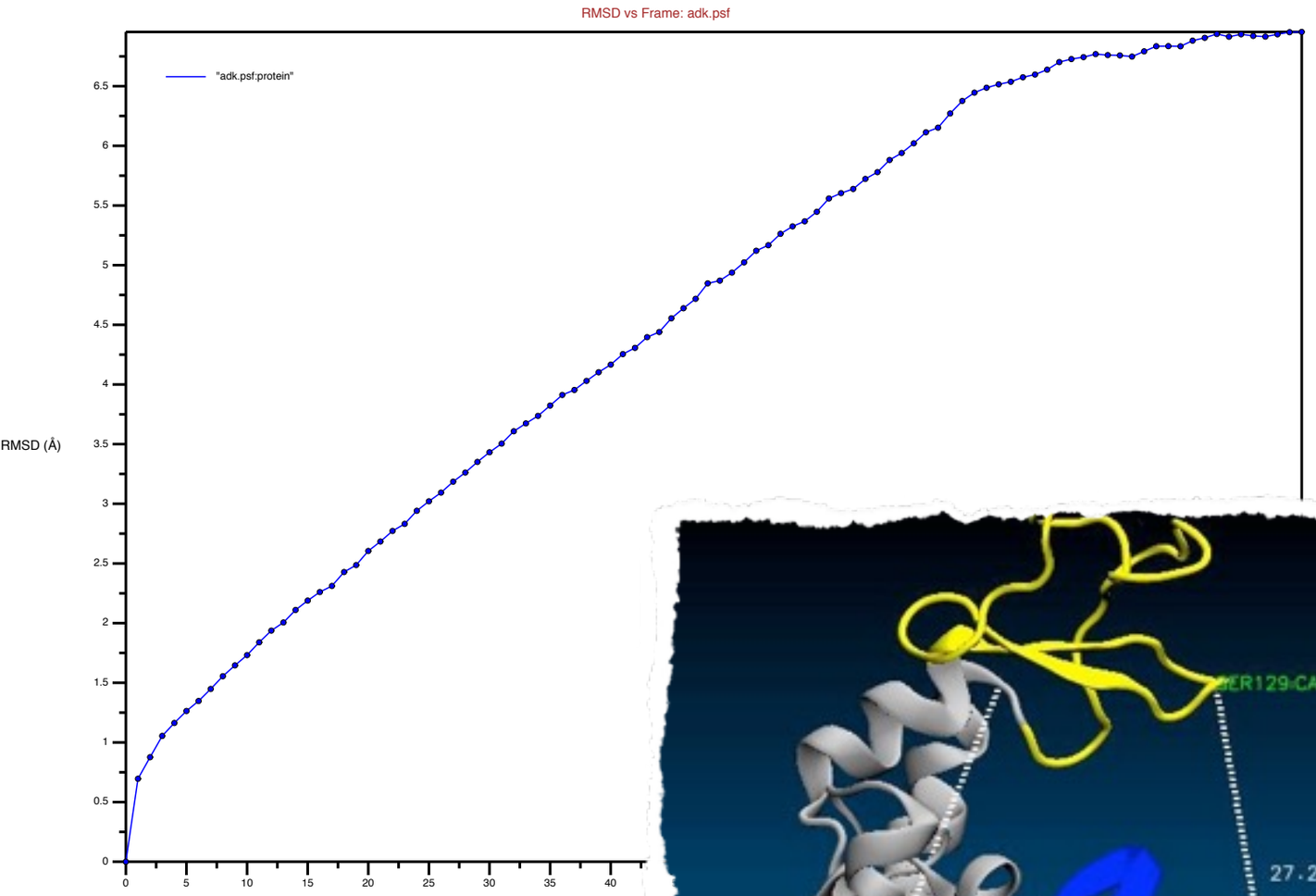
Rendered with Tachyon, AO and shadows, no depth cueing

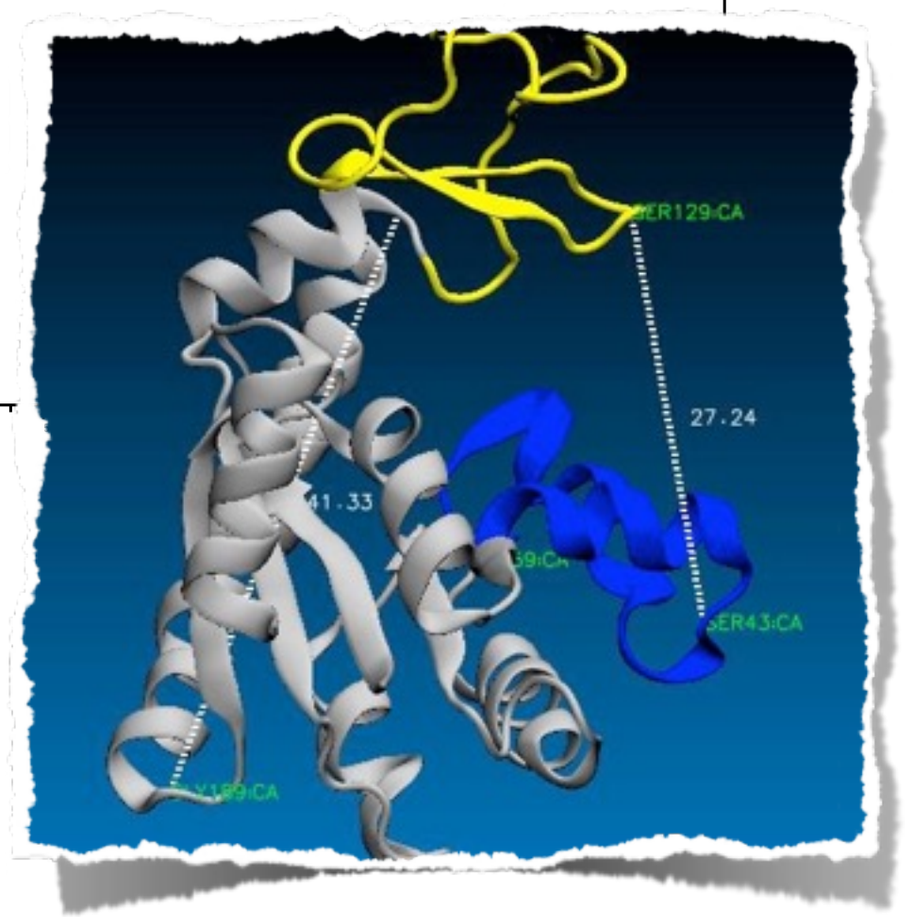
Visualizing dynamics

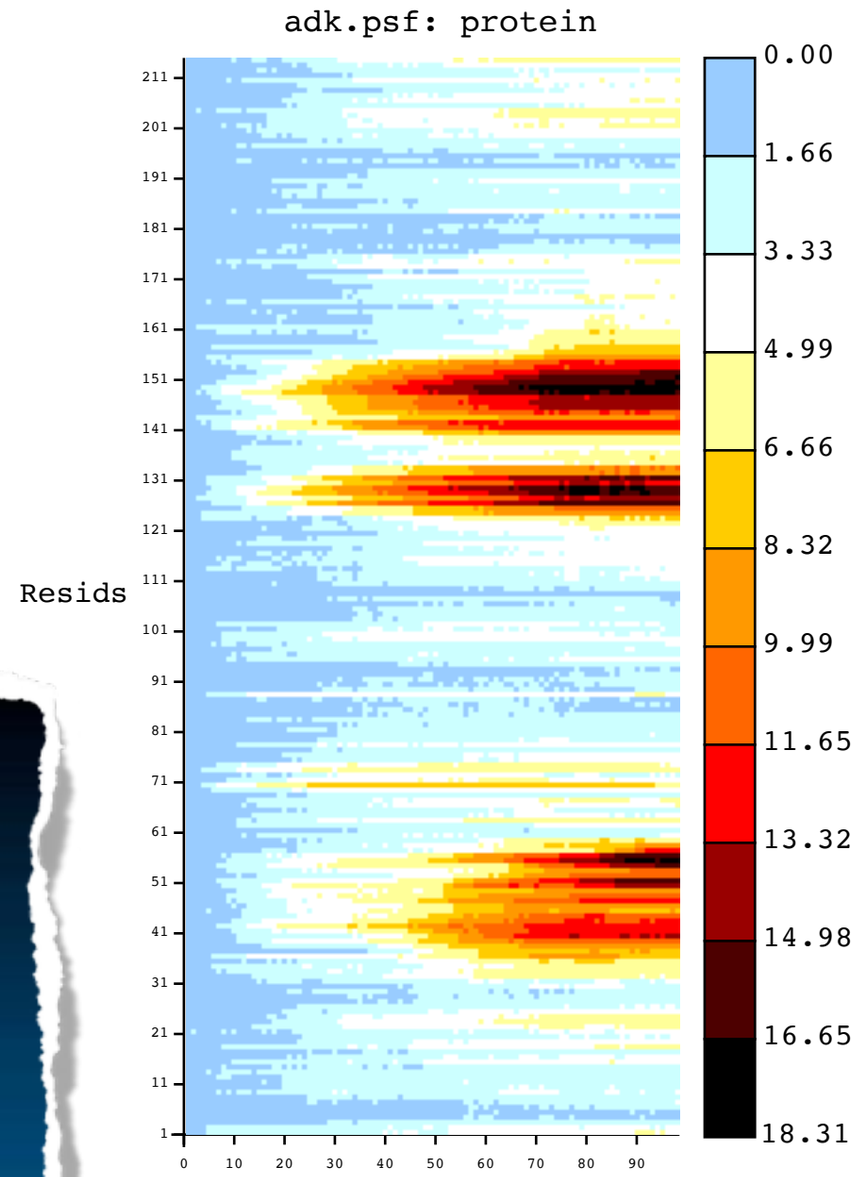
- load *adk.psf*, then load *adk_dims.dcd* into same molecule
- color domains, use New Cartoon
- play (set loop to "rock")
- interactive distances: Mouse/Label/Bonds (2)
  - click residue in LID and in NMP
  - Graphics/Labels:Bonds – graph

DIMS trajectory analysis

RMSD Trajectory Tool



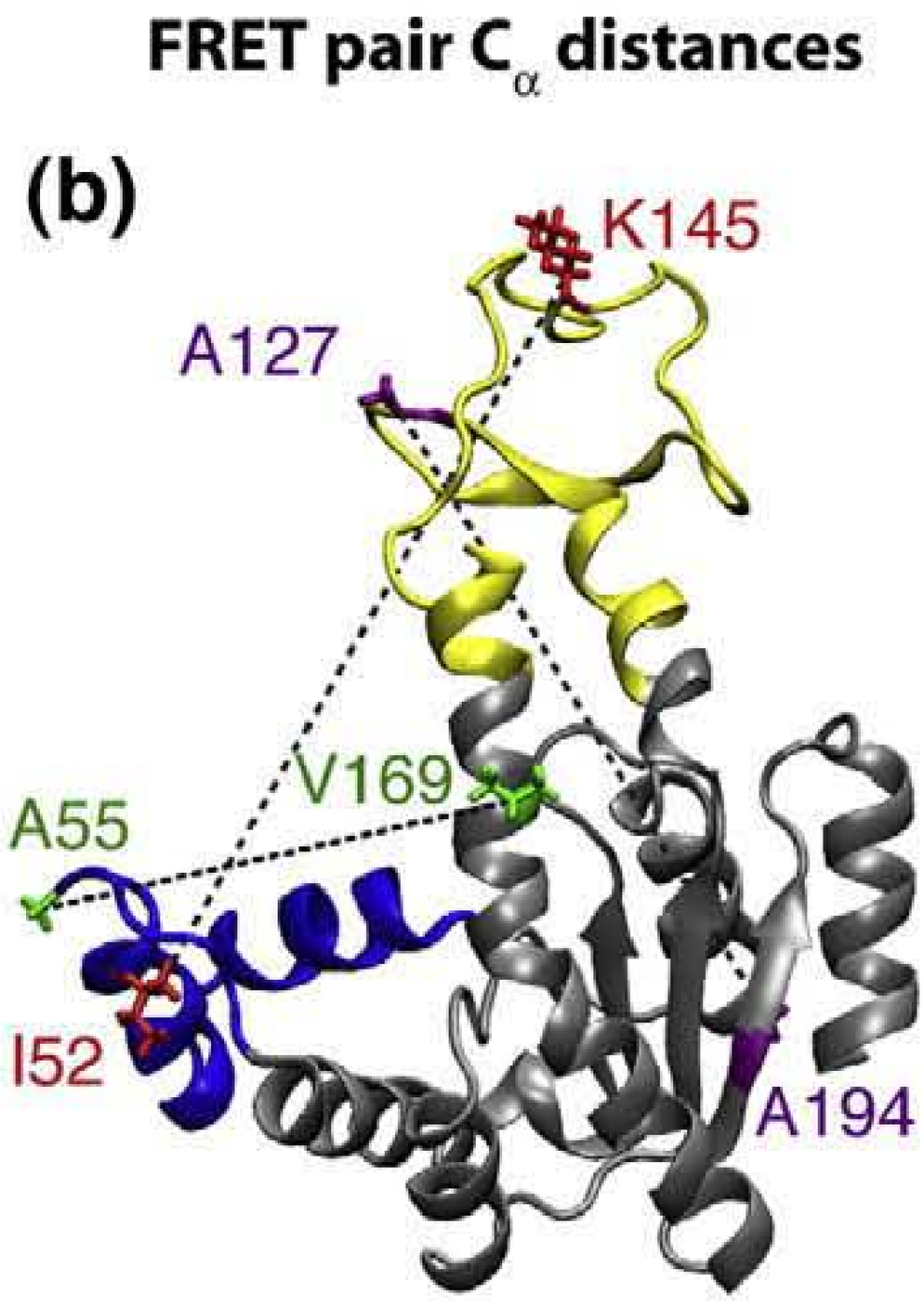




RMSDVisualizer

(VMD 1.9.1)

Analysing FRET distances



I52 – K145

A55 – V169

A127 – A194

Selections: 1AKE

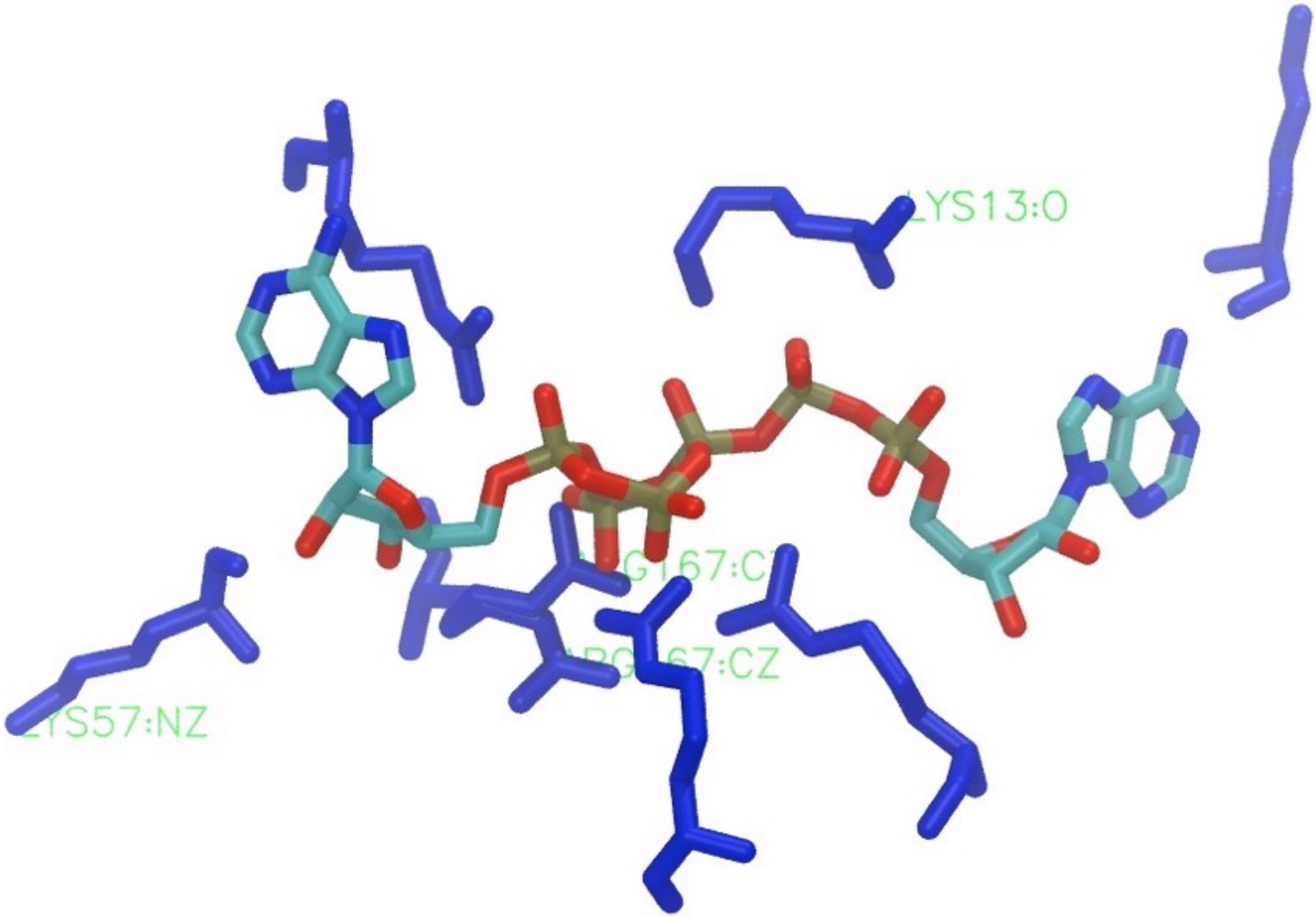
- download 1AKE from PDB
- show protein chain A (`protein and chain A`)
- show ligand Ap5 (`resname AP5`)
- show charged residues near ligand
  (`(protein and charged and chain A) and within 3 of (resname AP5)`)
- try `same residue as (...)`

Which side-chains make contact? (residues?)
What have they got in common?

Selections: 1AKE

K13
(K57)
R88
R123
R156
R167
K200

basic
(positively
charged)



~/.vmdrc

- copy `/Applications/Science/VMD 1.9.app/Contents/vmd/.vmdrc` to ~
- add

```
axes location off
color Display Background white
display projection orthographic
display rendermode GLSL
display shadow on
display ambientocclusion on
display height 4.0
```