F1190: Proteiny

doc. Mgr. Karel Kubíček, Ph.D.

Proteiny

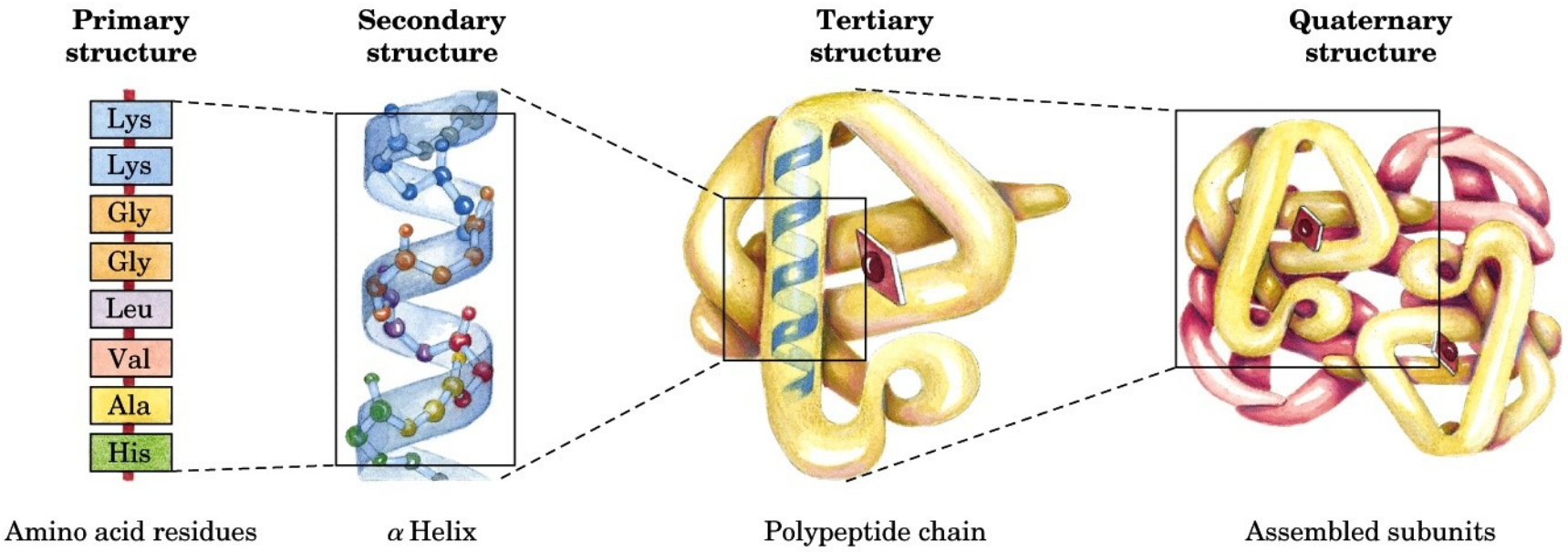
I] **Doporučená literatura**

1) Whitford, D.: Proteins – Structure and Function, John Wiley & Sons, Ltd. 2005
2) Cotterill, R.: Biophysics: An Introduction, John Wiley & Sons, Ltd. 2002
3) Voet, D, and Voetová, J.G.: Biochemie, Victoria Publishing
4) Murray, R.K., Granner, D. K., Mayes, P., A., Rodwell, V., W.: Harper's Illustrated Biochemistry, Lange Medical Books, 2003
5) Schuenemann, V.: Biophysik: Eine Einfuehrung, Springer, 2005
6) Garrett, R.H., Grisham, C.M.: Biochemistry, 2nd ed., 1999

II] **Aminokyseliny**

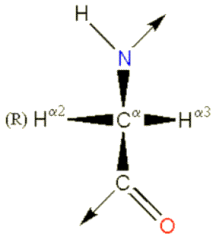
1) Tvoří monomerní jednotky peptidů a proteinů
2) 20 L-α-aminokyselin
3) Všechny aminokyseliny složeny ze tří částí – **NH2-** (amino) skupina, **-COOH** (karboxylová) skupina, **-C_α-R** (alfa uhlík s postranním řetězcem)
4) Esenciální a neesenciální kyseliny – organismus si je umí syntetizovat nebo je potřeba je přijímat v potravě
5) Označujeme třípísmennými nebo jednopísmennými zkratkami (zápis Val-Thr-Ile-Pro nebo VTIP – u jednopísmenného zápisu bez pomlčky)

Levels of Protein Structure

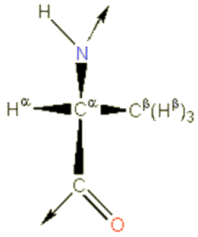


6) Aminokyseliny s alifatickým postranním řetězcem

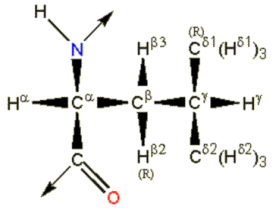
Glycine
(Gly)



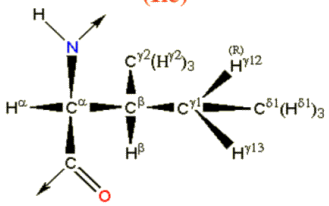
L-Alanine
(Ala)



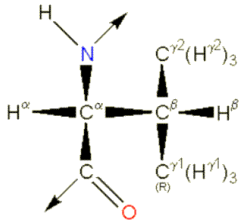
L-Leucine
(Leu)



L-Isoleucine
(Ile)

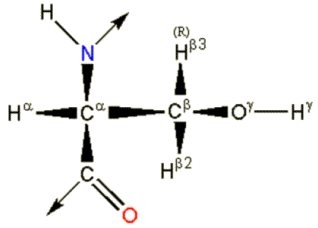


L-Valine
(Val)

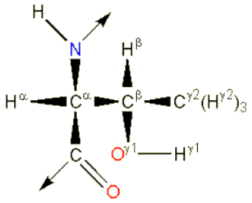


7) Aminokyseliny s hydroxylovou (OH) skupinou

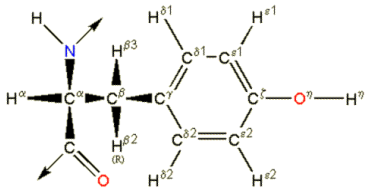
L-Serine (Ser)



L-Threonine (Thr)

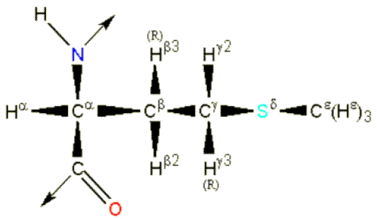


L-Tyrosine (Tyr)

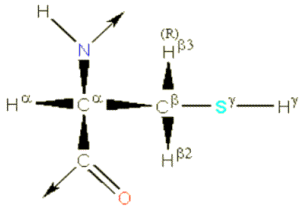


8) Aminokyseliny s atomem síry

Methionine (Met)

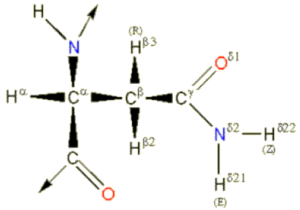


L-Cysteine (Cys)

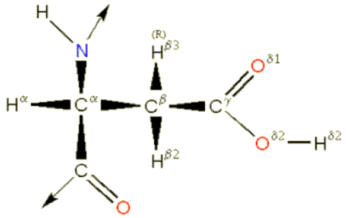


9) Aminokyseliny s acidickými skupinami nebo jejich amidy

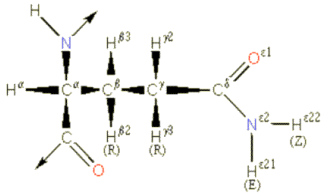
L-Aspargine
(Asn)



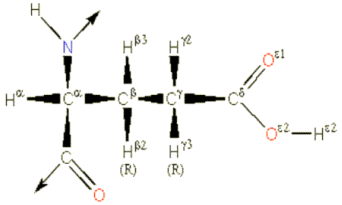
L-Aspartic Acid
(Asp)



L-Glutamine
(Gln)

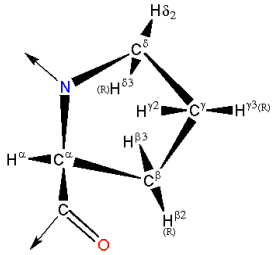


L-Glutamic Acid
(Glu)



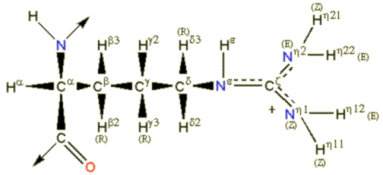
10) Imino kyselina

L-Proline
(Pro)

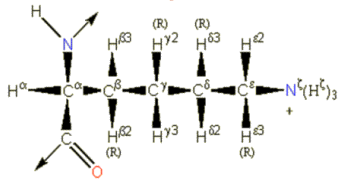


11) Aminokyseliny s basickými skupinami

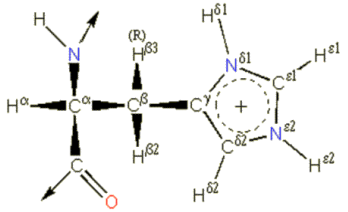
L-Arginine (Arg)



L-Lysine (Lys)

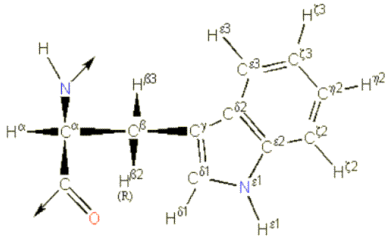


L-Histidine (His)

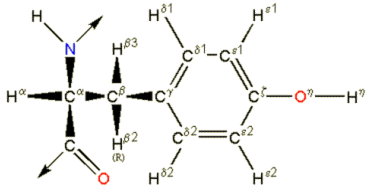


12) Aminokyseliny s aromatickými kruhy

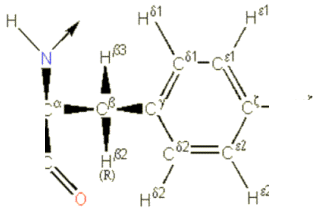
L-Tryptophan (Trp)



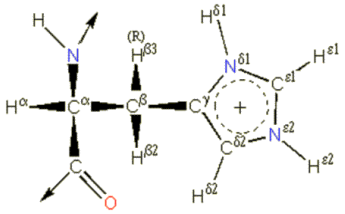
L-Tyrosine (Tyr)



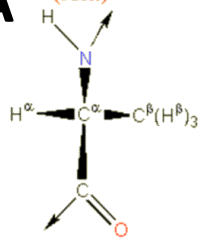
L-Phenylalanine (Phe)



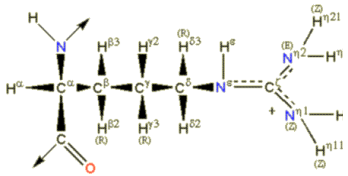
L-Histidine (His)



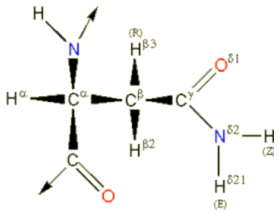
A **L-Alanine (Ala)**



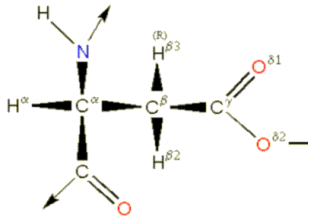
R **L-Arginine (Arg)**



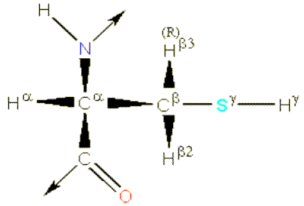
N **L-Aspargine (Asn)**



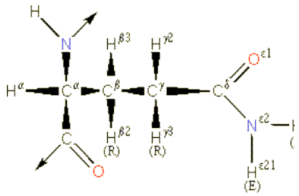
D **L-Aspartic Acid (Asp)**



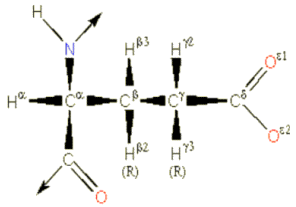
C **L-Cysteine (Cys)**



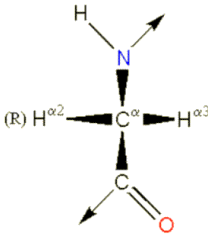
Q **L-Glutamine (Gln)**



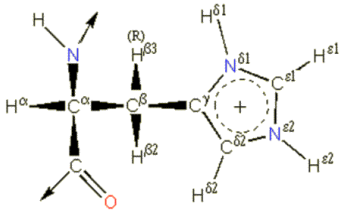
E **L-Glutamic Acid (Glu)**



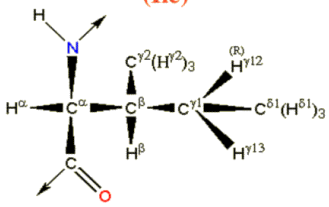
G **Glycine (Gly)**



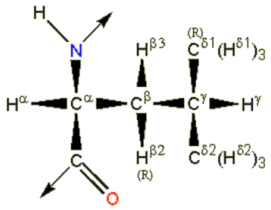
H **L-Histidine (His)**



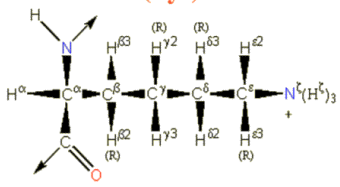
I **L-Isoleucine (Ile)**



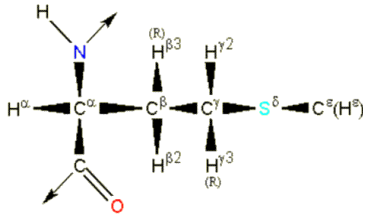
L **L-Leucine (Leu)**



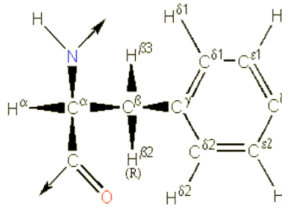
K **L-Lysine (Lys)**



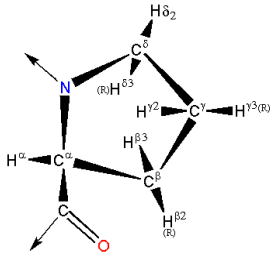
M **Methionine (Met)**



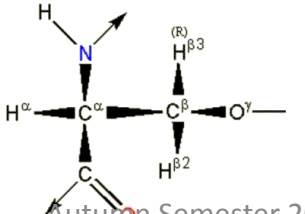
F **L-Phenylalanine (Phe)**



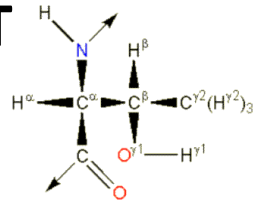
P **L-Proline (Pro)**



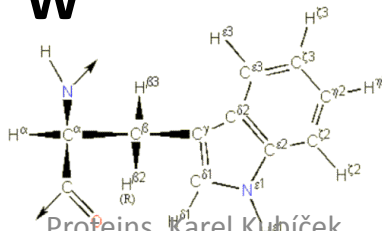
S **L-Serine (Ser)**



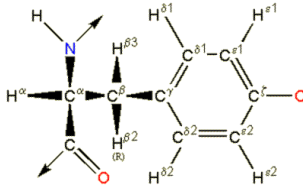
T **L-Threonine (Thr)**



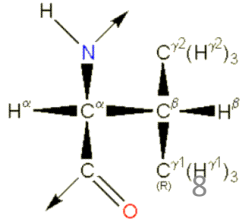
W **L-Tryptophan (Trp)**



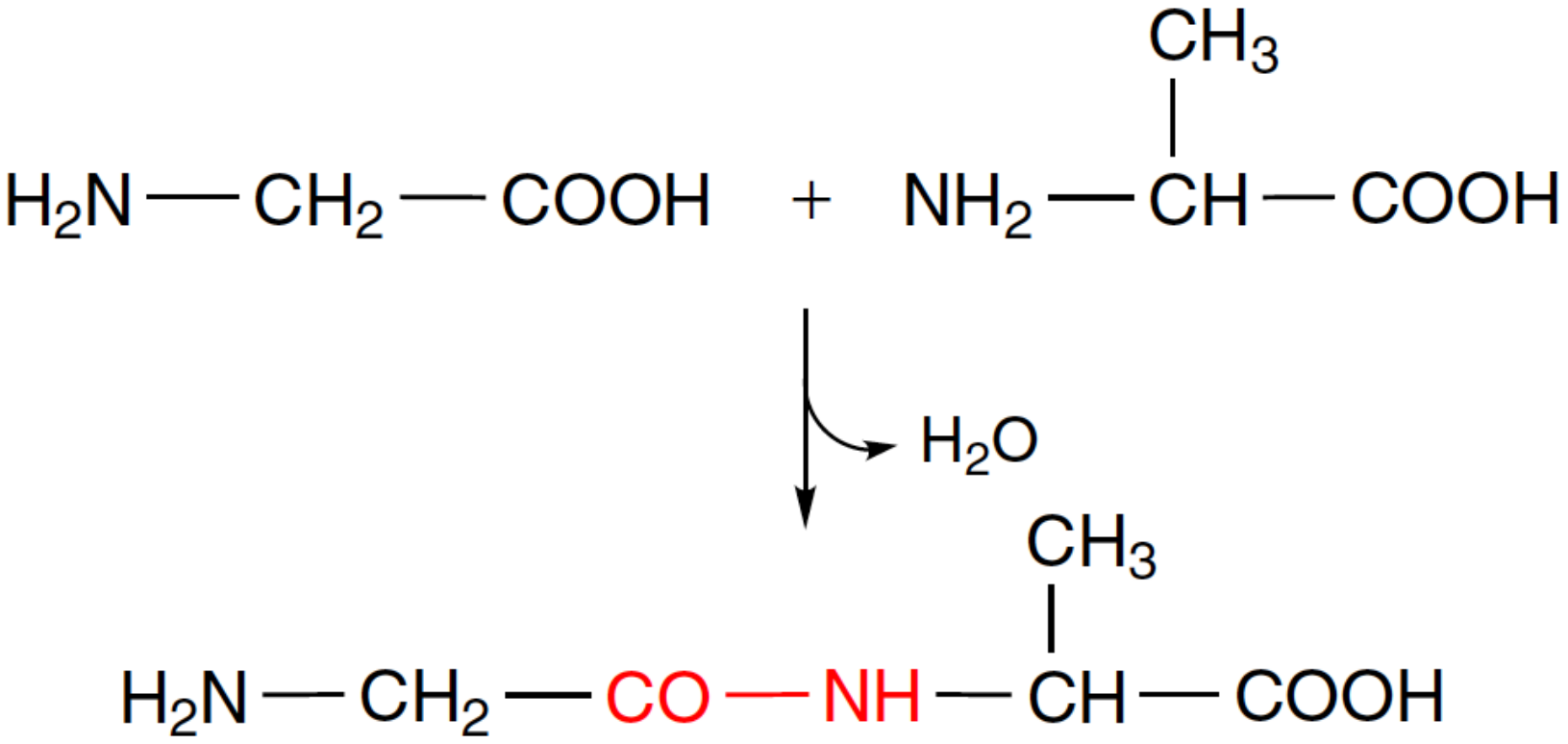
Y **L-Tyrosine (Tyr)**



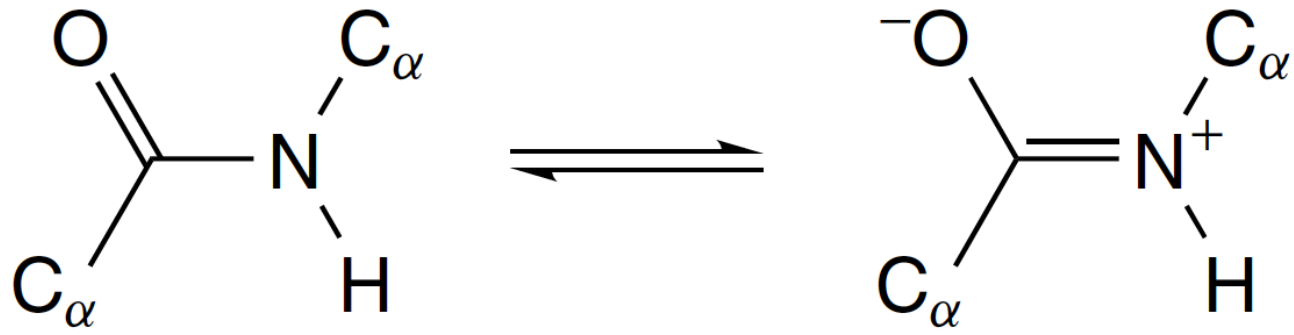
V **L-Valine (Val)**

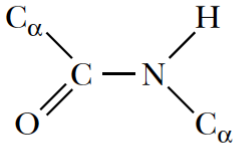


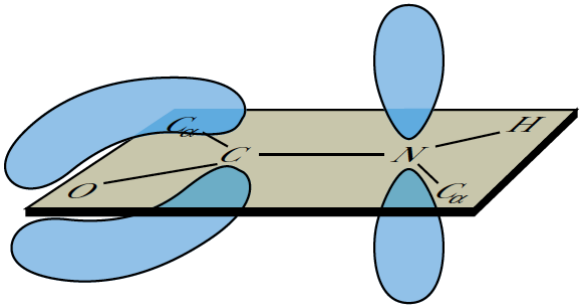
III] Peptidy, proteiny – vznik polymerů polymerizační reakcí

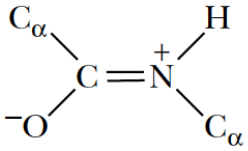


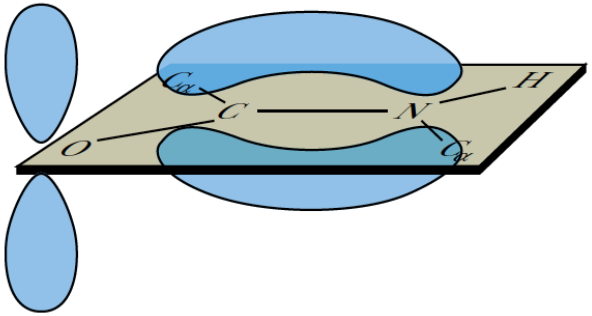
IV] Peptidová vazba – pseudo dvojitá vazba => amidová rovina

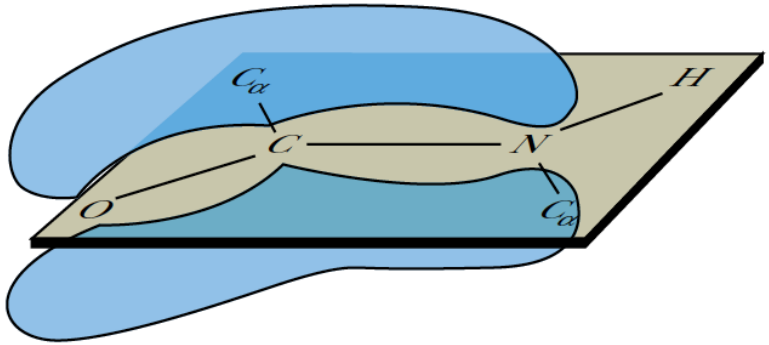




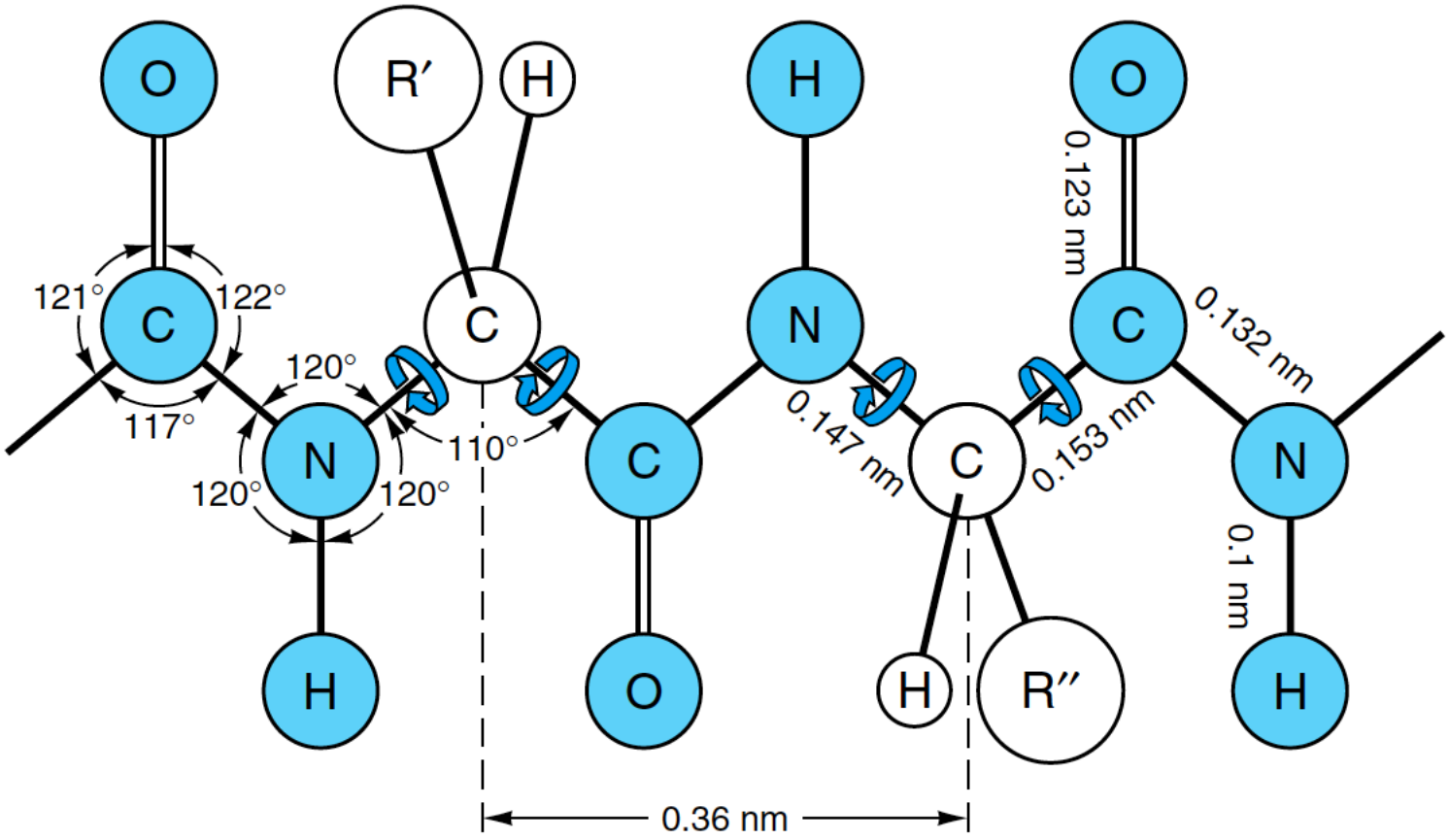








V] Proteinová páteř, primární struktura, číslování od **N**-konce (terminu) směrem k **C**-konci



Informace o 3D (proteinové) struktuře jsou zapsány v kartézských souřadnicích
Nejrozšířenější formát PDB (ProteinDataBank, www.pdb.org)

```
ATOM    128  N   HIS O  18     20.321   6.124  17.761  1.00 11.40
ATOM    129  CA  HIS O  18     21.097   5.169  18.563  1.00 13.62
ATOM    130  C   HIS O  18     22.581   5.413  18.454  1.00 17.00
ATOM    131  O   HIS O  18     23.031   5.592  17.321  1.00 15.45
ATOM    132  CB  HIS O  18     20.883   3.747  18.034  1.00 16.68
ATOM    133  CG  HIS O  18     19.557   3.103  18.437  1.00 11.72
ATOM    134  ND1 HIS O  18     19.252   2.806  19.725  1.00 11.66
ATOM    135  CD2 HIS O  18     18.479   2.751  17.657  1.00 16.32
ATOM    136  CE1 HIS O  18     18.021   2.238  19.730  1.00 14.91
ATOM    137  NE2 HIS O  18     17.552   2.185  18.473  1.00 17.58

HETATM 1633  NC  HEM O 104     15.182   3.191  16.831  1.00 21.22
HETATM 1634  C1C HEM O 104     15.433   3.334  15.488  1.00 17.49
HETATM 1635  C2C HEM O 104     15.046   4.605  15.145  1.00 31.21
HETATM 1636  C3C HEM O 104     14.623   5.242  16.323  1.00 14.38
HETATM 1637  C4C HEM O 104     14.661   4.346  17.360  1.00 14.50
HETATM 1638  CMC HEM O 104     15.299   5.349  13.850  1.00 15.54
HETATM 1639  CAC HEM O 104     14.314   6.707  16.409  1.00 31.67
HETATM 1640  CBC HEM O 104     13.170   7.262  15.615  1.00 10.23

HETATM 1609 FE   HEM O 104     15.801   1.483  17.954  1.00  9.37
```

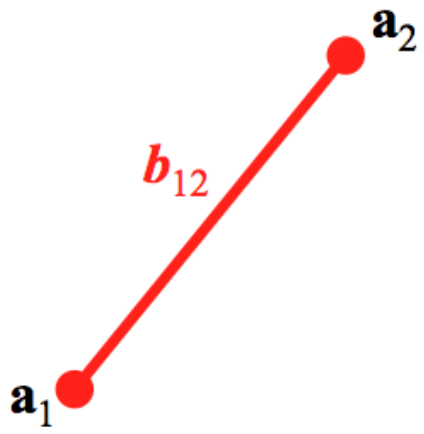
ftp://ftp.wwpdb.org/pub/pdb/doc/format_descriptions/Format_v33_A4.pdf

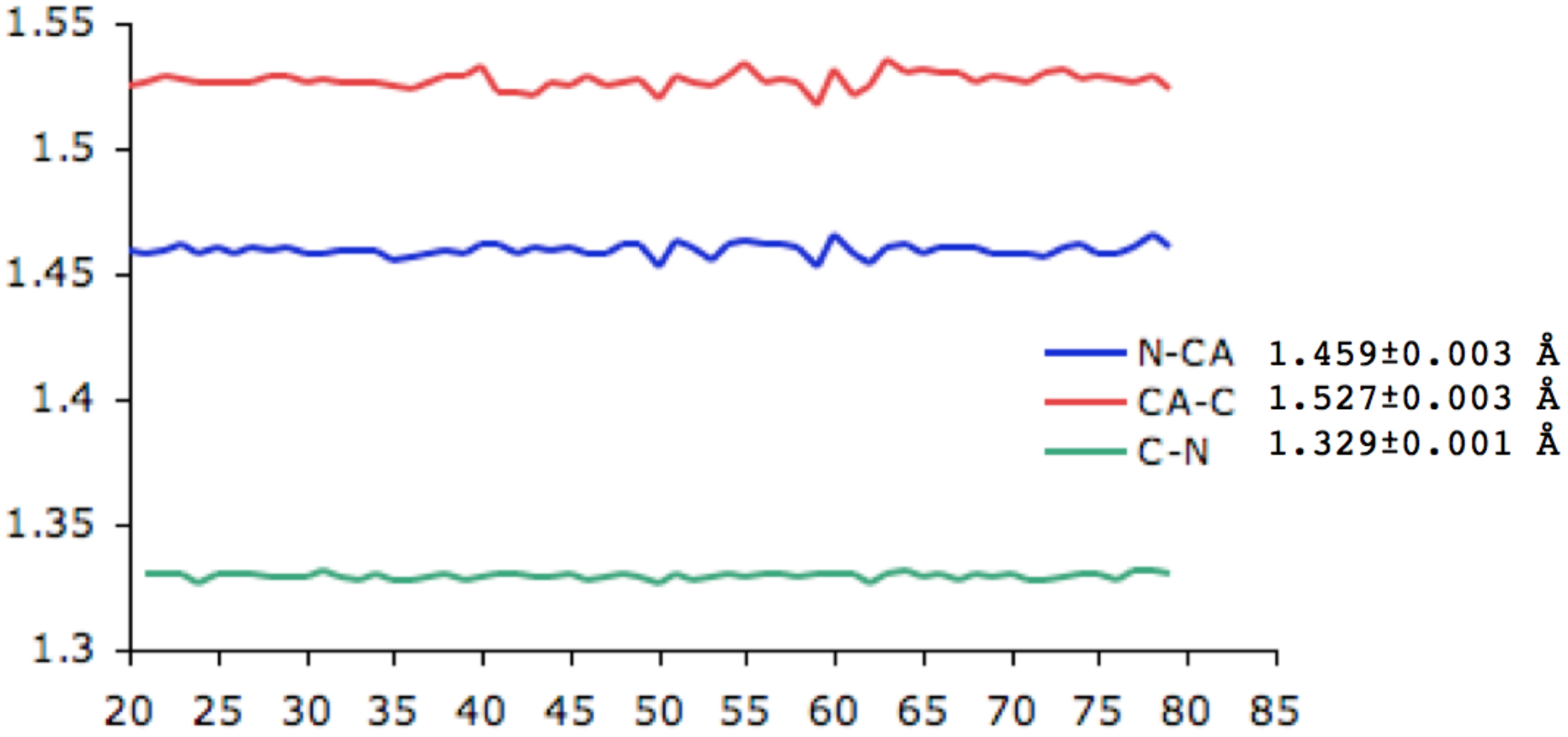
Atomic coordinates

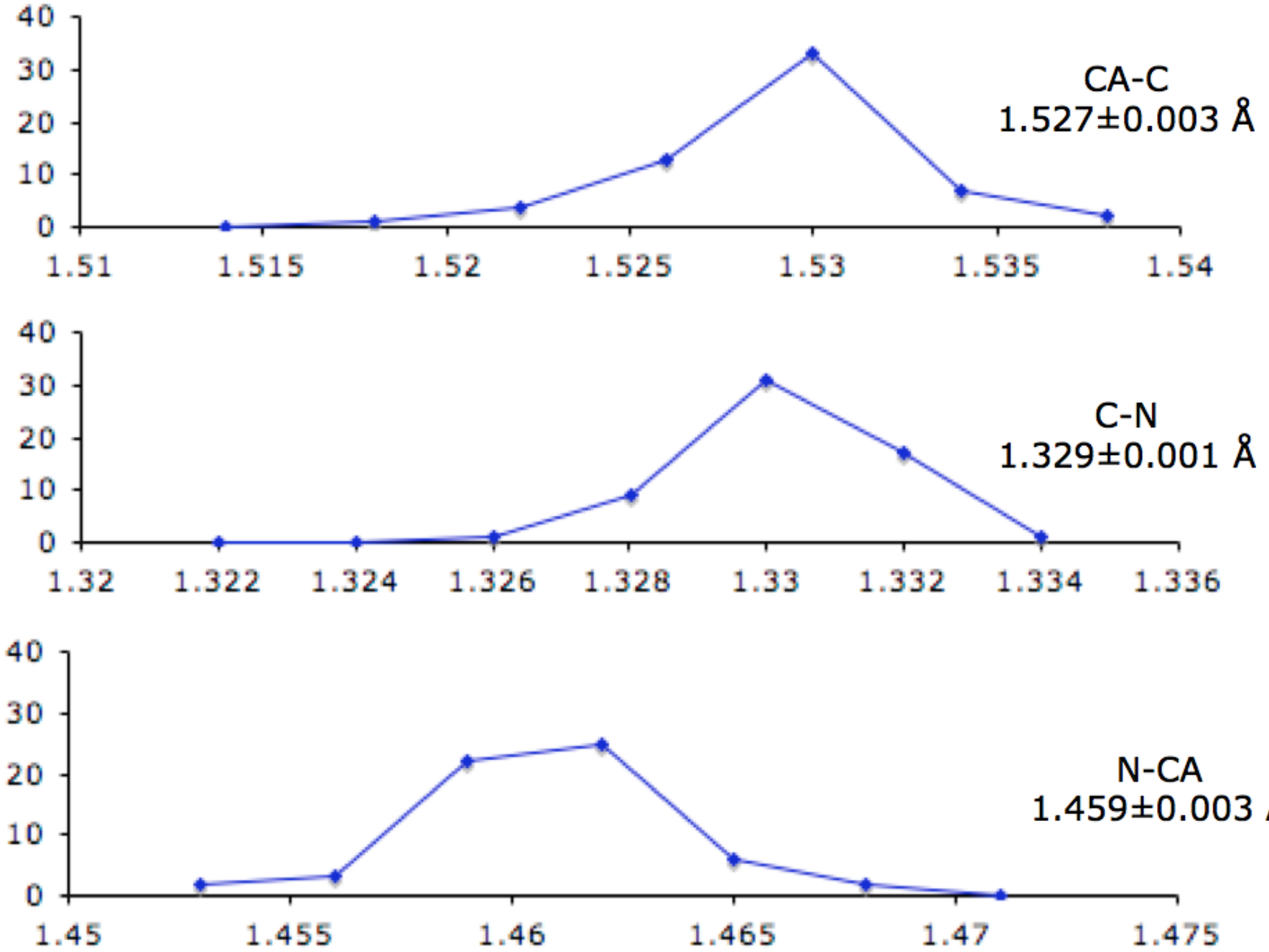
$$\mathbf{a}_1 = (a_{1x},\ a_{1y},\ a_{1z}) \qquad \mathbf{a}_2 = (a_{2x},\ a_{2y},\ a_{2z})$$

Bond length

$$b_{12} = ((a_{2x}-a_{1x})^2+(a_{2y}-a_{1y})^2+(a_{2z}-a_{1z})^2)^{1/2}$$




1.55
1.5
1.45
1.4
1.35
1.3
20 25 30 35 40 45 50 55 60 65 70 75 80 85
N-CA 1.459±0.003 Å
CA-C 1.527±0.003 Å
C-N 1.329±0.001 Å


40
30
20
10
0
1.51
1.515
1.52
1.525
1.53
1.535
1.54
CA-C
1.527±0.003 Å
40
30
20
10
0
1.32
1.322
1.324
1.326
1.328
1.33
1.332
1.334
1.336
C-N
1.329±0.001 Å
40
30
20
10
0
1.45
1.455
1.46
1.465
1.47
1.475
N-CA
1.459±0.003 Å

Atomic coordinates

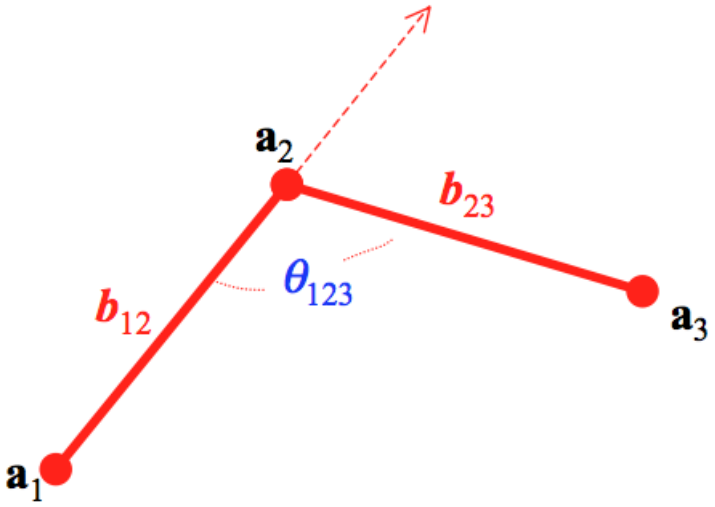
$$\mathbf{a}_1 = (a_{1x},\ a_{1y},\ a_{1z}) \qquad \mathbf{a}_2 = (a_{2x},\ a_{2y},\ a_{2z}) \qquad \mathbf{a}_3 = (a_{3x},\ a_{3y},\ a_{3z})$$

Bond vectors

$$\mathbf{b}_{12} = (a_{2x}-a_{1x},\ a_{2y}-a_{1y},\ a_{2z}-a_{1z}) \qquad \mathbf{b}_{23} = (a_{3x}-a_{2x},\ a_{3y}-a_{2y},\ a_{3z}-a_{2z})$$

Scalar product

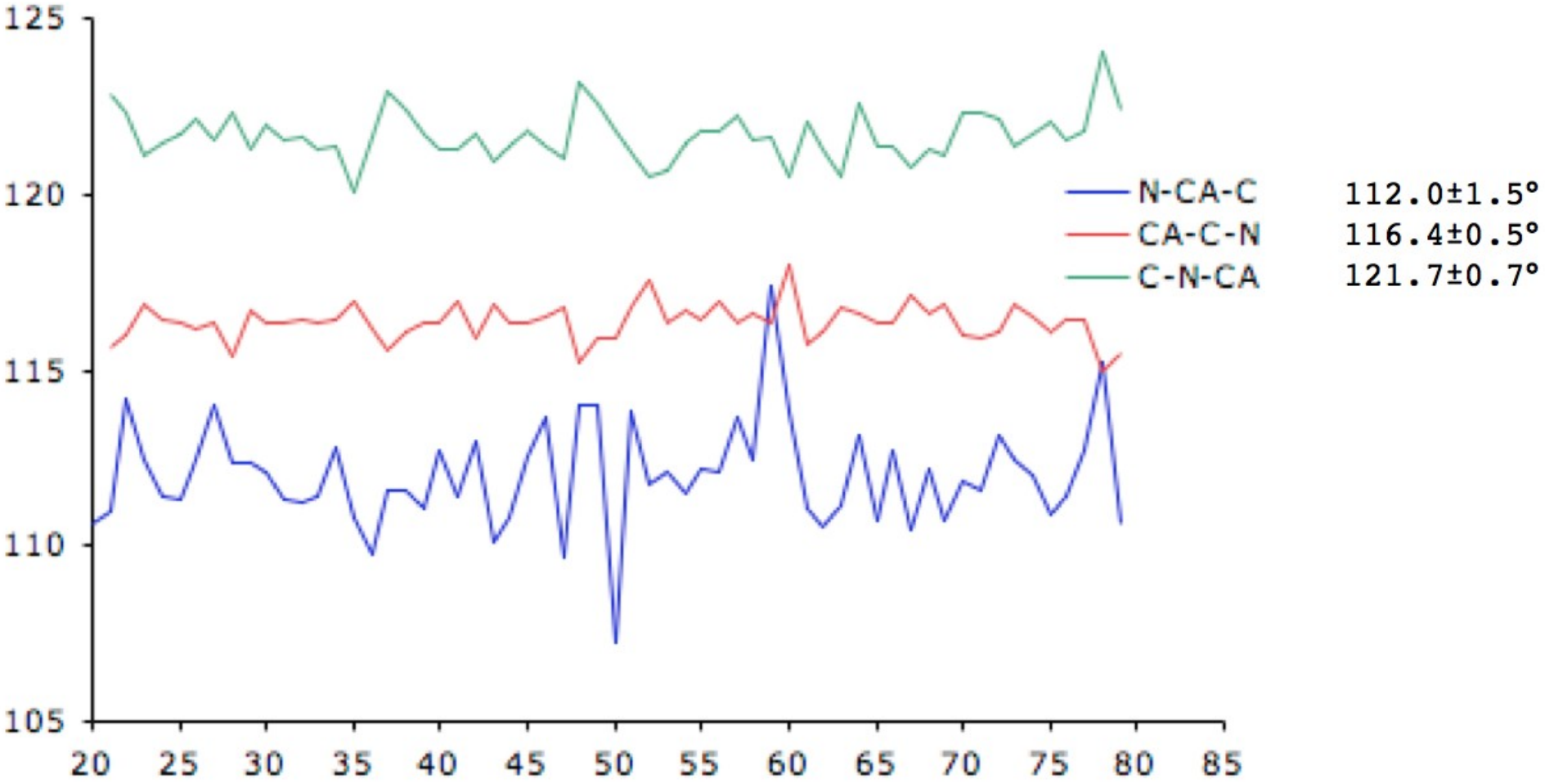
$$\mathbf{b}_{12}\cdot\mathbf{b}_{23} = (a_{2x}-a_{1x})(a_{3x}-a_{2x})+(a_{2y}-a_{1y})(a_{3y}-a_{2y})+(a_{2z}-a_{1z})(a_{3z}-a_{2z})$$



$$\mathbf{b}_{12}\cdot\mathbf{b}_{23} = b_{12}b_{23}\cos(\pi-\theta_{123})$$

$$\cos\theta_{123} = -\mathbf{b}_{12}\cdot\mathbf{b}_{23}/(b_{12}b_{23})$$

$$\cos(\pi-\theta_{123}) = \cos\pi\cos\theta_{123} + \sin\pi\sin\theta_{123} = -\cos\theta_{123}$$

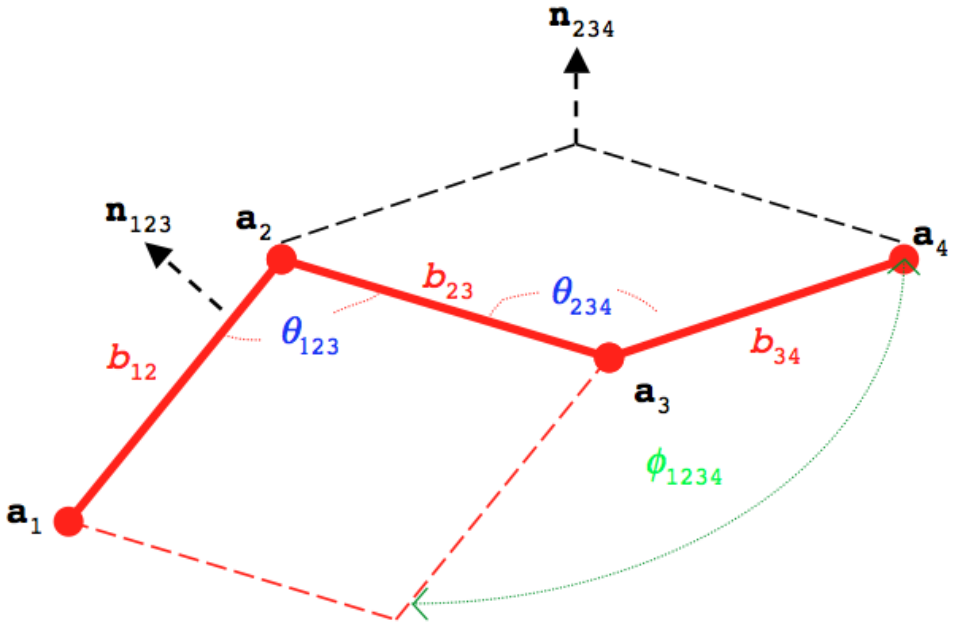

125
120
115
110
105
20
25
30
35
40
45
50
55
60
65
70
75
80
85
N-CA-C
CA-C-N
C-N-CA
112.0±1.5°
116.4±0.5°
121.7±0.7°

Atomic coordinates

$\mathbf{a}_1 = (a_{1x}, a_{1y}, a_{1z})$ $\mathbf{a}_2 = (a_{2x}, a_{2y}, a_{2z})$ $\mathbf{a}_3 = (a_{3x}, a_{3y}, a_{3z})$ $\mathbf{a}_3 = (a_{4x}, a_{4y}, a_{4z})$

Bond vectors

$\mathbf{b}_{12}=(a_{2x}-a_{1x}, a_{2y}-a_{1y}, a_{2z}-a_{1z})$ $\mathbf{b}_{23}=(a_{3x}-a_{2x}, a_{3y}-a_{2y}, a_{3z}-a_{2z})$ $\mathbf{b}_{34}=(a_{4x}-a_{3x}, a_{4y}-a_{3y}, a_{4z}-a_{3z})$



$\mathbf{n}_{123} = \mathbf{b}_{12} \times \mathbf{b}_{23}$

$\mathbf{n}_{234} = \mathbf{b}_{23} \times \mathbf{b}_{34}$

$\mathbf{n}_{123} \cdot \mathbf{n}_{234} = \cos\phi_{1234}$

$(\mathbf{n}_{123} \times \mathbf{n}_{234}) \cdot \mathbf{b}_{23} > 0 \Rightarrow \phi_{1234} > 0$

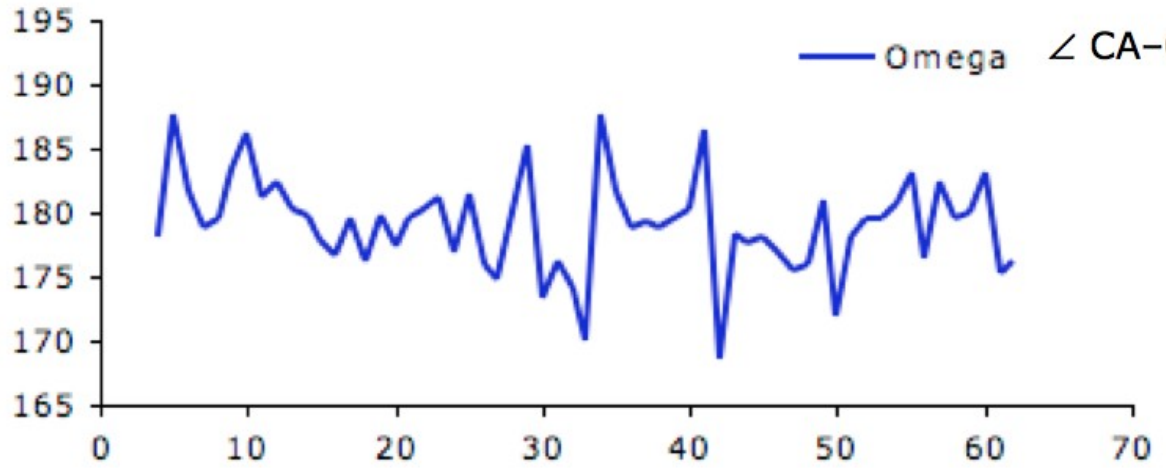
$(\mathbf{n}_{123} \times \mathbf{n}_{234}) \cdot \mathbf{b}_{23} < 0 \Rightarrow \phi_{1234} < 0$

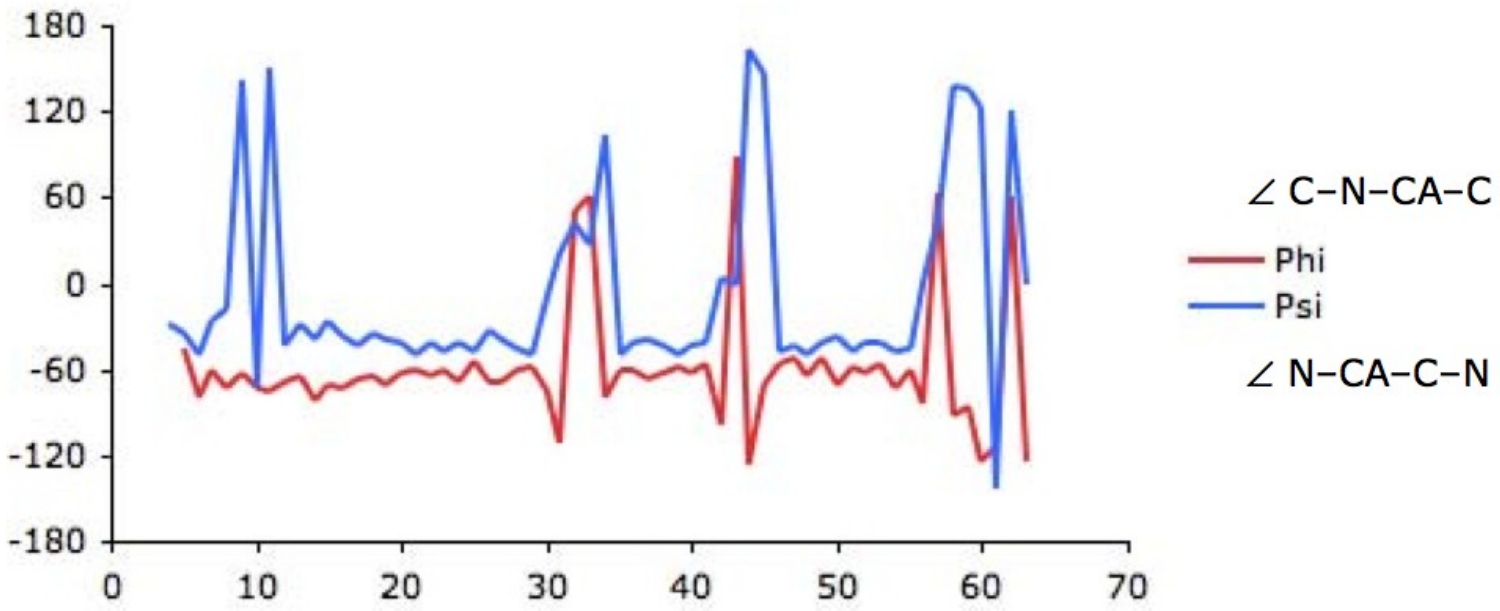
$$\mathbf{v}_1 \times \mathbf{v}_2 = \begin{vmatrix} i & j & k \\ v_{1x} & v_{1y} & v_{1z} \\ v_{2x} & v_{2y} & v_{2z} \end{vmatrix}$$

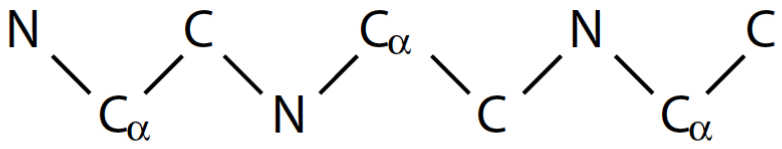
$$= \left(v_{1y}v_{2z} - v_{2y}v_{1z}\right) i + \left(v_{1z}v_{2x} - v_{2z}v_{1x}\right) j + \left(v_{1x}v_{2y} - v_{2x}v_{1y}\right) k$$

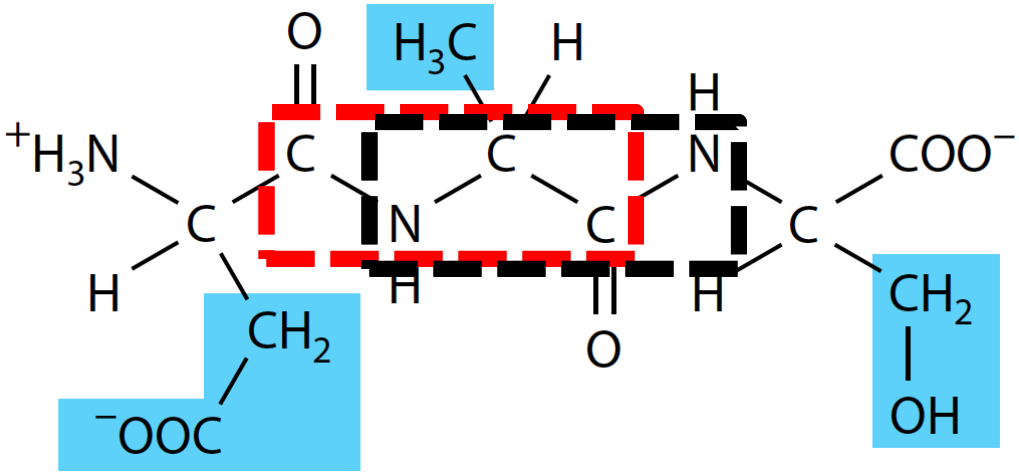
$$= \left[\left(v_{1y}v_{2z} - v_{2y}v_{1z}\right), \left(v_{1z}v_{2x} - v_{2z}v_{1x}\right), \left(v_{1x}v_{2y} - v_{2x}v_{1y}\right)\right]$$

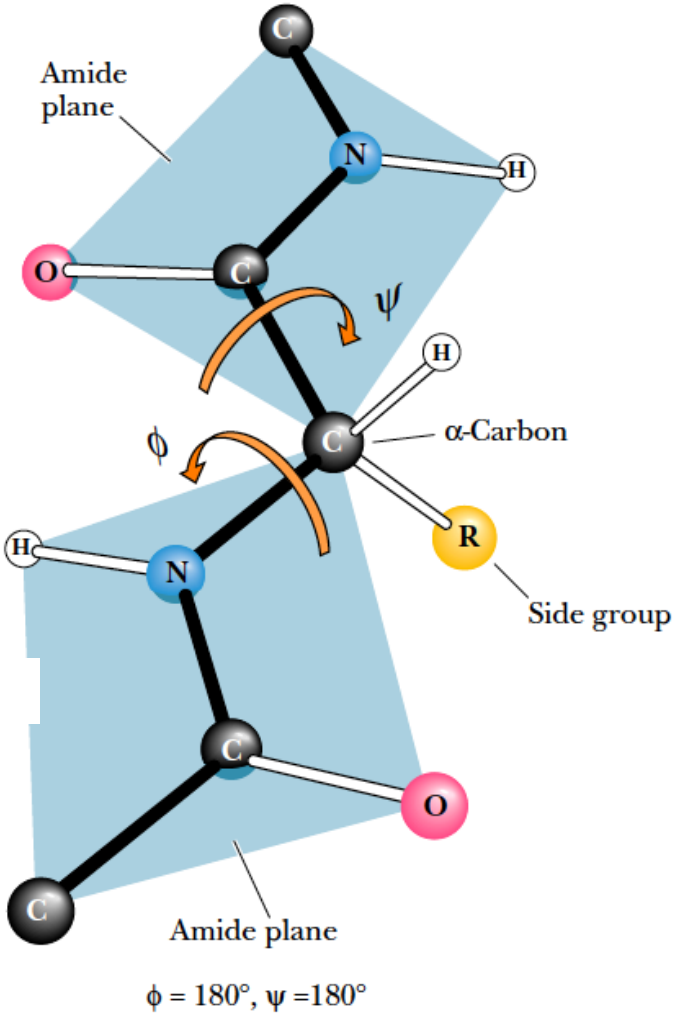
$$= \left(c_1, c_2, c_3\right)$$


195
190
185
180
175
170
165
0
10
20
30
40
50
60
70
Omega
∠ CA–C–N–CA


180
120
60
0
-60
-120
-180
0
10
20
30
40
50
60
70
∠ C–N–CA–C
Phi
Psi
∠ N–CA–C–N







ϕ – **CO, N, C_α, CO** (CO někdy značeno C')

ψ – **N, C_α, CO, N**

Structural parameters for protein secondary structures

Structural element	ϕ	ψ	*n*	*d*	*p*
α-helix	-57	-47	3.6	1.5	5.5
3_{10}-helix	-49	-26	3.0	2.0	6.0
β-helix	-57	-70	4.4	1.1	5.0
Polyproline II helix	-79	+149	3.0	3.1	9.4
Parallel β-strand	-119	+113	2.0	3.2	6.4
Antiparallel β-strand	-139	+135	2.0	3.4	6.8

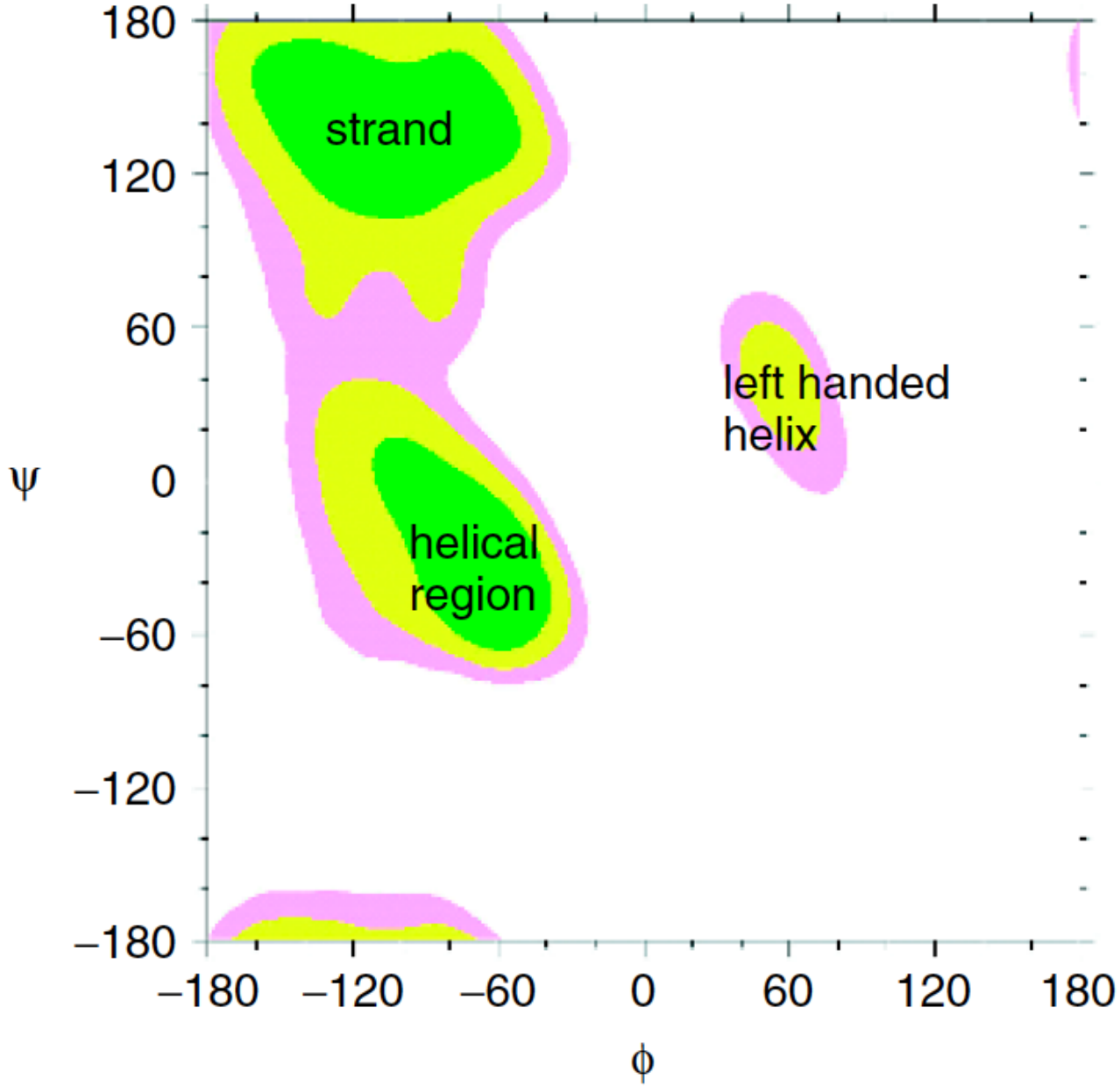
ϕ and ψ are the conformational angles of the mainchain, with ω ~180°(trans conformation)

n = number of residues per turn

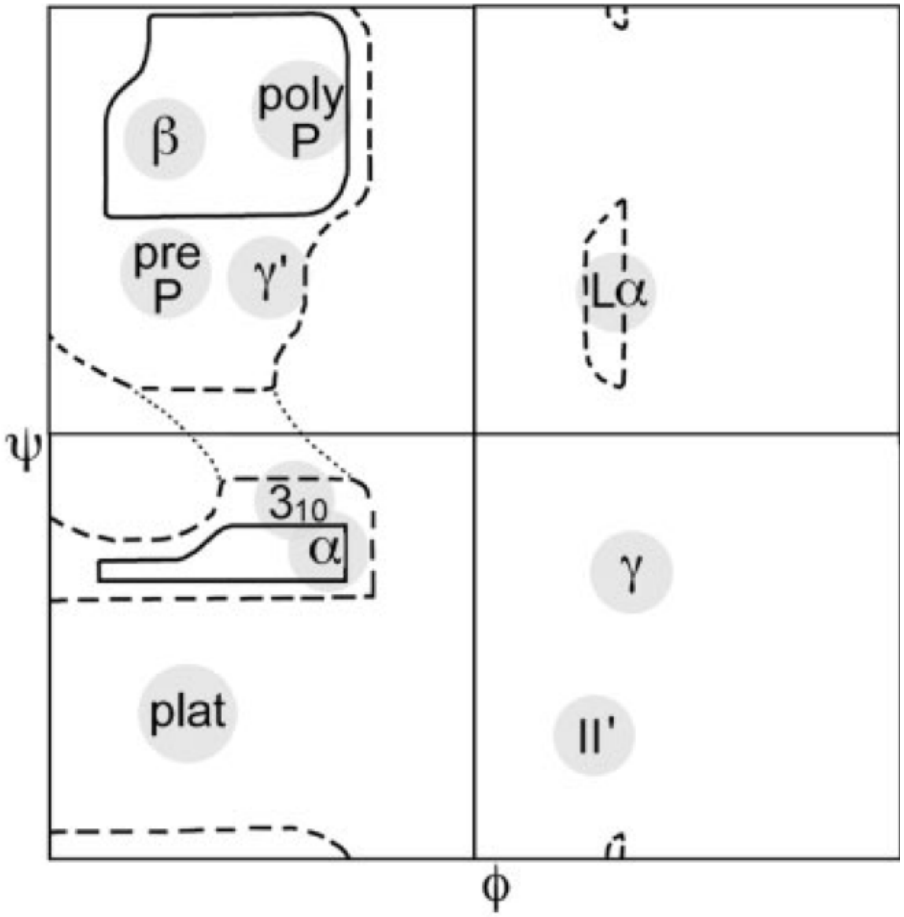
d = displacement between successive residues along the helix/strand axis

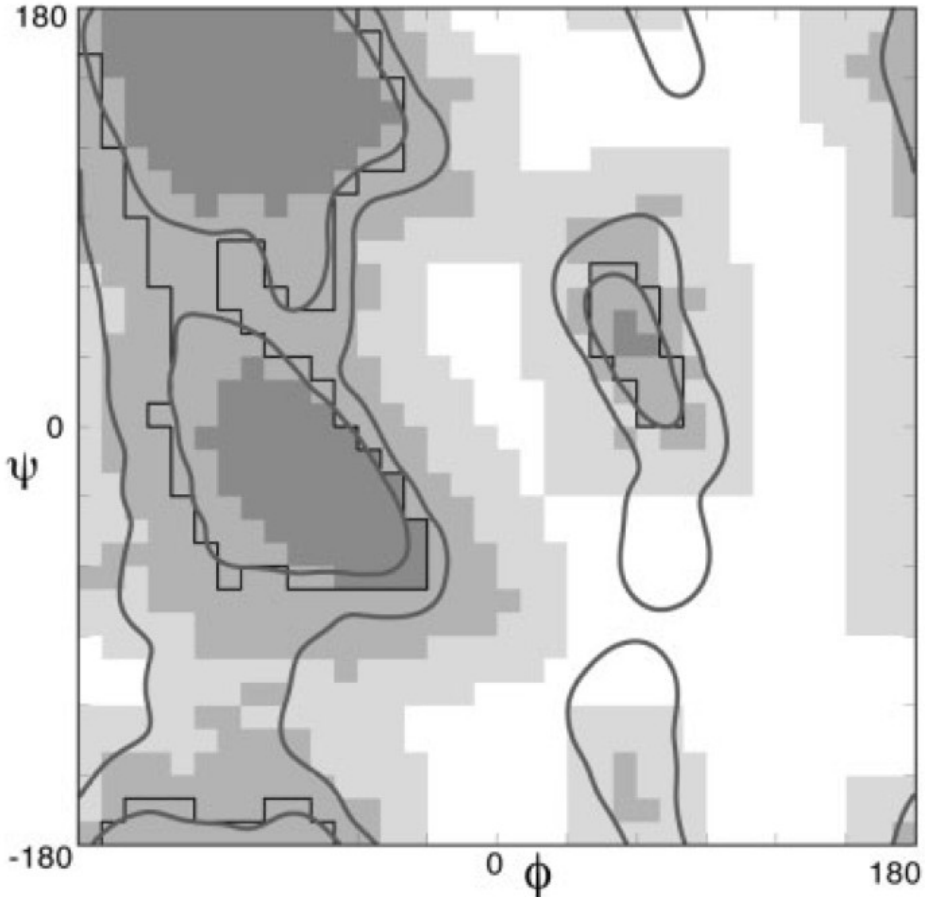
p = the pitch of helix/strand, the distance along the helix/strand axis of a complete sec. struct. element. Note that *p*=*n* x *d* (equation is exact, error is in rounding of *n* and *d*)

VI] Ramachandranův diagram



Ramachandranův diagram – komplet





https://proteopedia.org/wiki/index.php/Tutorial:Ramachandran_principle_and_phi_psi_angles

Tutorial:Ramachandran principle and phi psi angles

The Ramachandran Principle
Phi (ϕ) and Psi (ψ) Angles in Proteins

The Ramachandran Principle says that alpha helices, beta strands, and turns are the most likely conformations for a polypeptide chain to adopt, because most other conformations are impossible due to steric collisions between atoms.

This interactive tutorial is also available as an Animated Slideshow or YouTube Video, and there is a Quiz.

At right is a fragment of a polypeptide chain. In the center is a single complete alanine residue. Check **Alanine** to identify its atoms[1]. The other atoms are fragments of adjacent amino acids[2]. *Drag with your mouse to rotate the model.*

The Alanine is covalently bonded to other amino acids through **peptide bonds**. Check **Peptide Bonds** to locate them.

The double bonds between main chain (backbone) C and O delocalize, making the peptide bonds also have partial double bonds (*half-dotted bonds*). This prevents the peptide bond from rotating.

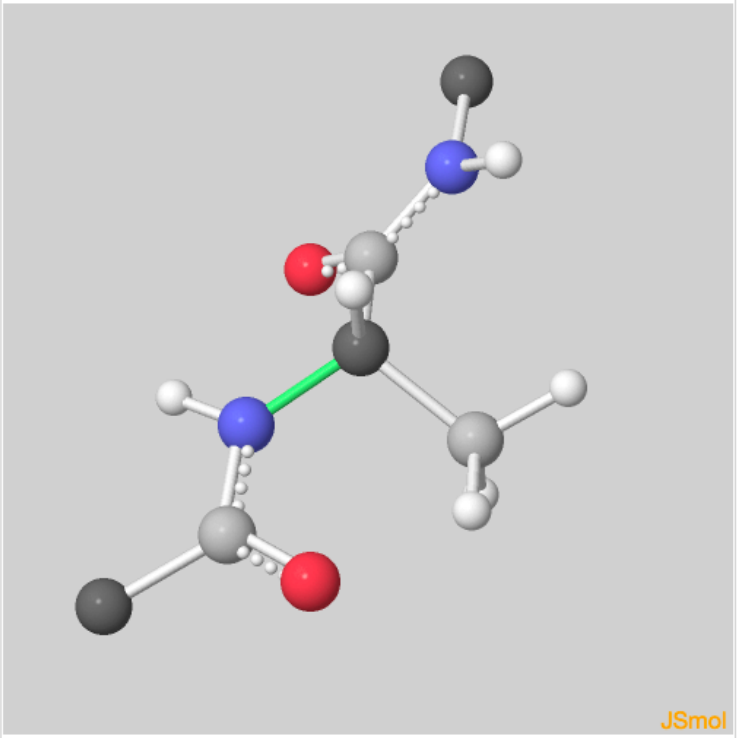
Each peptide bond holds six atoms in a plane. Check **Planes** to see them.

The **alpha carbon (Cα)** in the center of each amino acid is held in the main chain by two rotatable bonds. The dihedral (torsion) angles of these bonds are called[3] **Phi** and **Psi** (in Greek letters, ϕ and ψ). *Use the radio buttons (top of right panel) to identify the rotatable main-chain bonds, and click the -20° and +20° buttons to see them rotate.*

Click the **Reset** button.

The balls shown are much smaller than the atoms they represent. Check **van der Waals** to see the real sizes of the atoms[4]. In fact, most **Phi** and **Psi** angle combinations are impossible because two atoms cannot occupy the same space.

Check **Show Clashes** to see where non-bonded atoms are overlapping, and thus in physically impossible positions. (This model simulation allows two atoms to overlap, unlike real atoms.)



Cα C H N O

Phi ϕ Psi ψ
165° 165°
-20° +20°

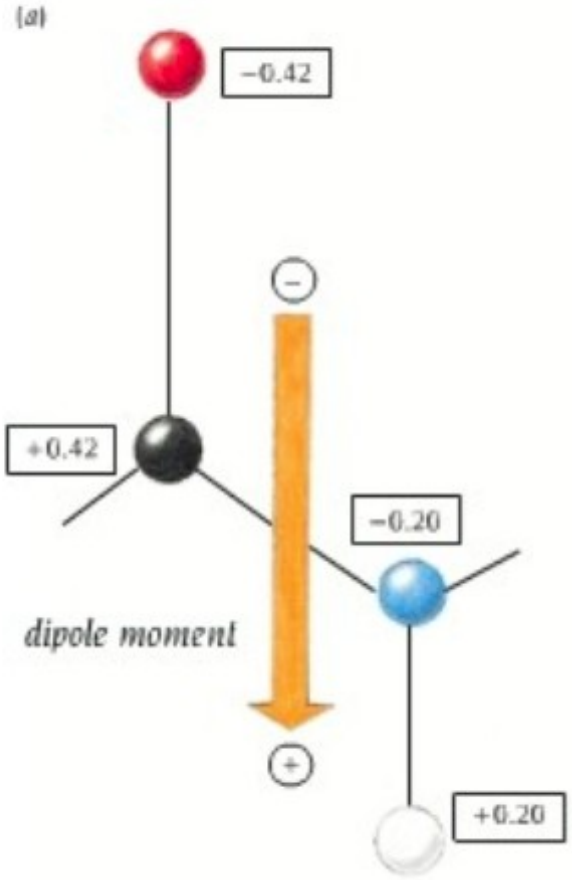
Alanine
Peptide Bonds
Planes

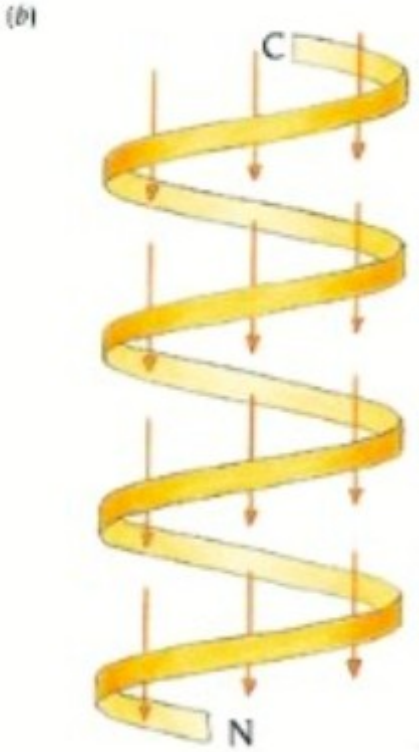
van der Waals[4]
Show Clashes

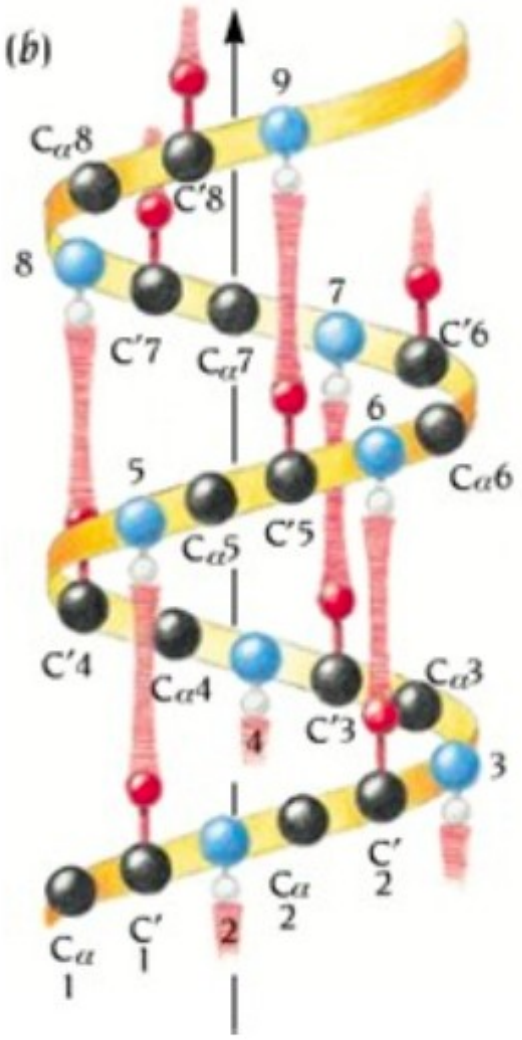
Reset

Figure 7.1. Sir John Kendrew with the model of insulin, one of the first protein structures to be determined by X-ray crystallography. Components of the actual model are just visible through the forest of vertical support rods.

The α helix has a dipole moment





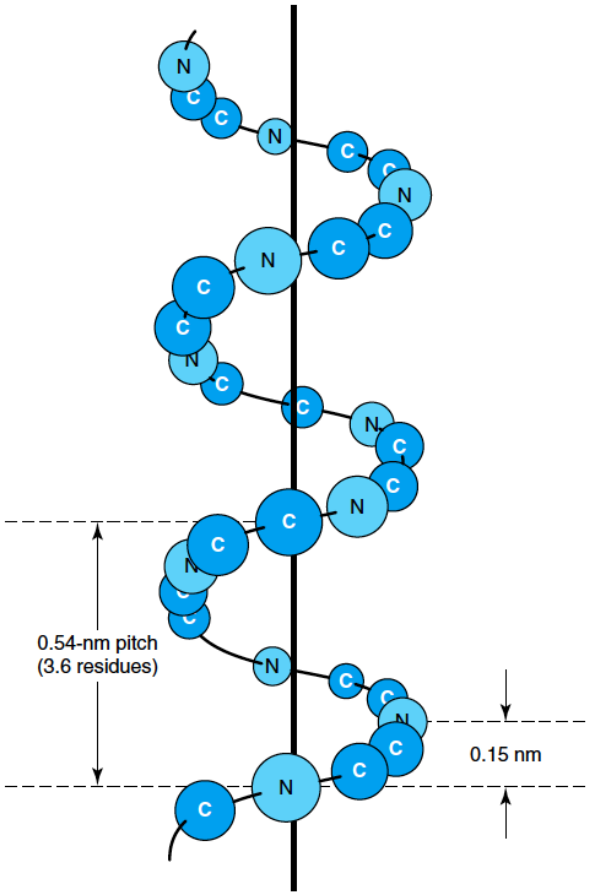


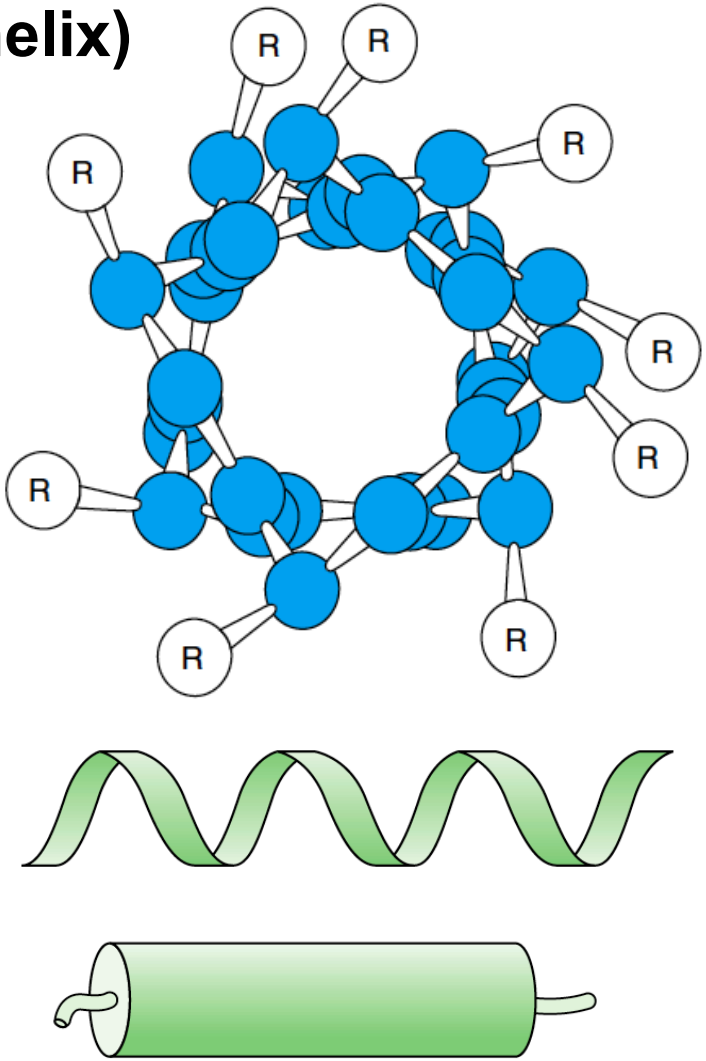
VII] Sekundární struktura

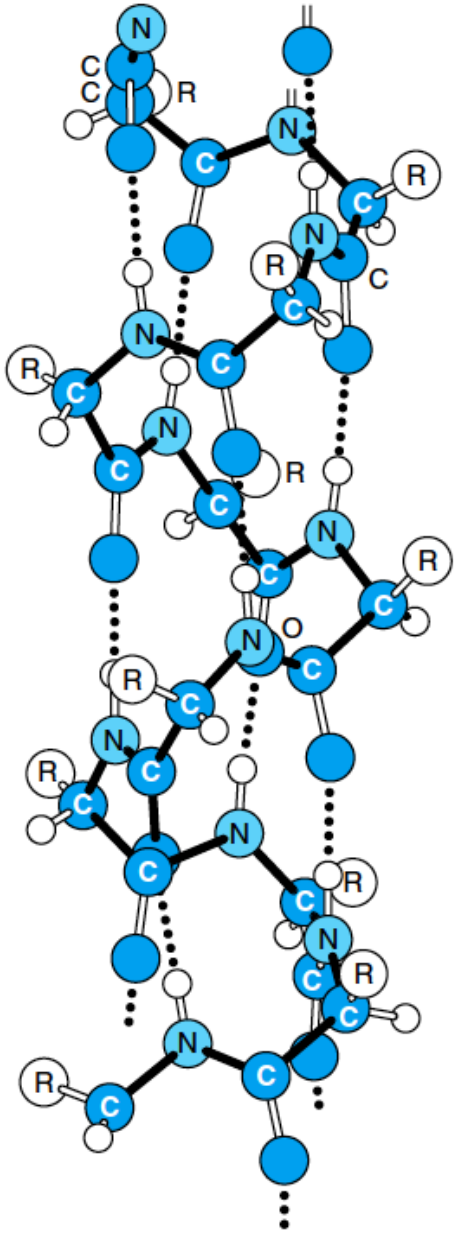
1) α-šroubovice (α-helix)

2) β-skládaný list (β-sheet)

3) Ohyb, smyčka (loop/turn)







3_{10}helix, α helix, π helix

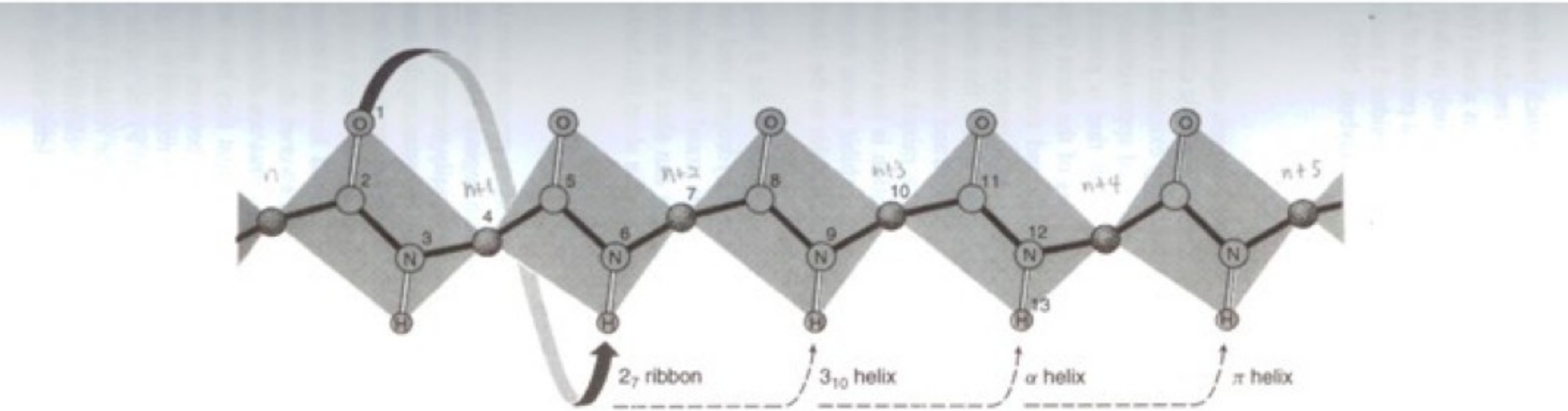
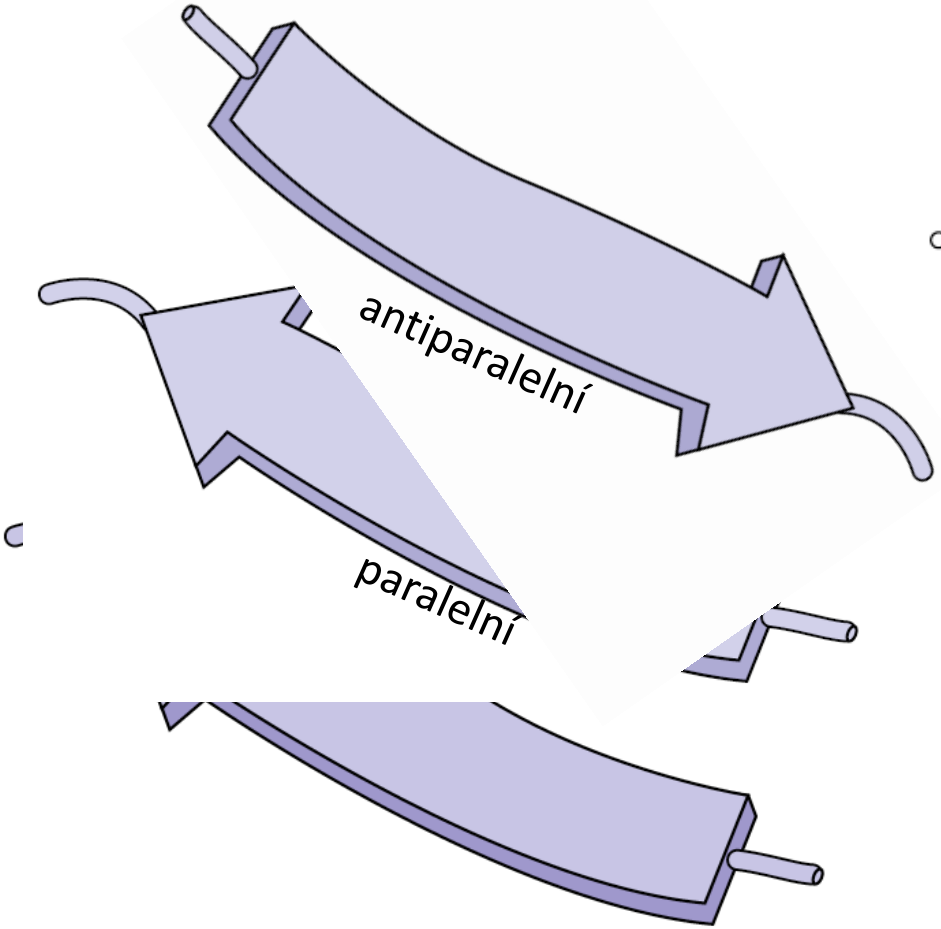


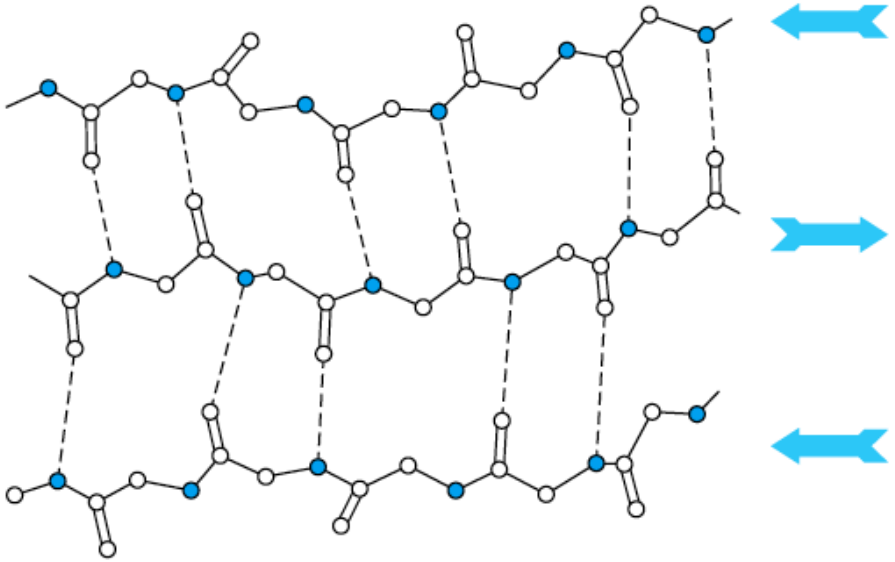
Figure 2.8. The hydrogen bonding patterns of different helical secondary structures. The peptide backbone is shown in an extended conformation, with an arrow denoting the hydrogen bonding pairings that would occur in each type of helix. The common α helix, depicted in Figure 2.7, forms hydrogen bonds between the carbonyl oxygen of each residue and the amide proton of the residue 4 residues ahead in the helix. The 3_{10} helix forms hydrogen bonds between the carbonyl oxygen of each residue and the amide proton of the residue 3 residues ahead, forming a more narrow and elongated helix. The π helix forms hydrogen bonds between the carbonyl oxygen of each residue and the amide proton of the residue five residues ahead, forming a wider helix. The 2_7 ribbon is not a regular secondary structure, but is shown here to demonstrate all possible hydrogen bond pairings. *From R. E. Dickerson and I. Geis. The Structure and Action of Proteins. New York: Harper & Row, 1969. Used with permission from Geis Archives.*

VII] Sekundární struktura

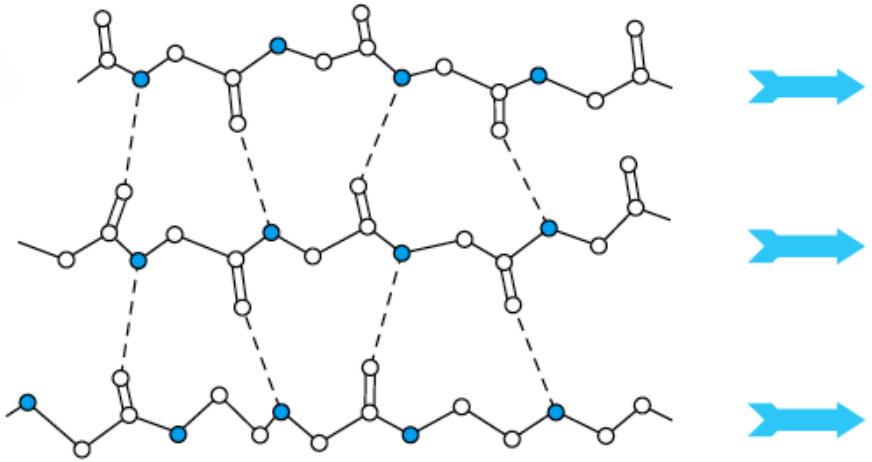
1) α-šroubovice (α-helix)
2) **β-skládaný list (β-sheet)**
3) Ohyb, smyčka (turn)



antiparalelní uspořádání



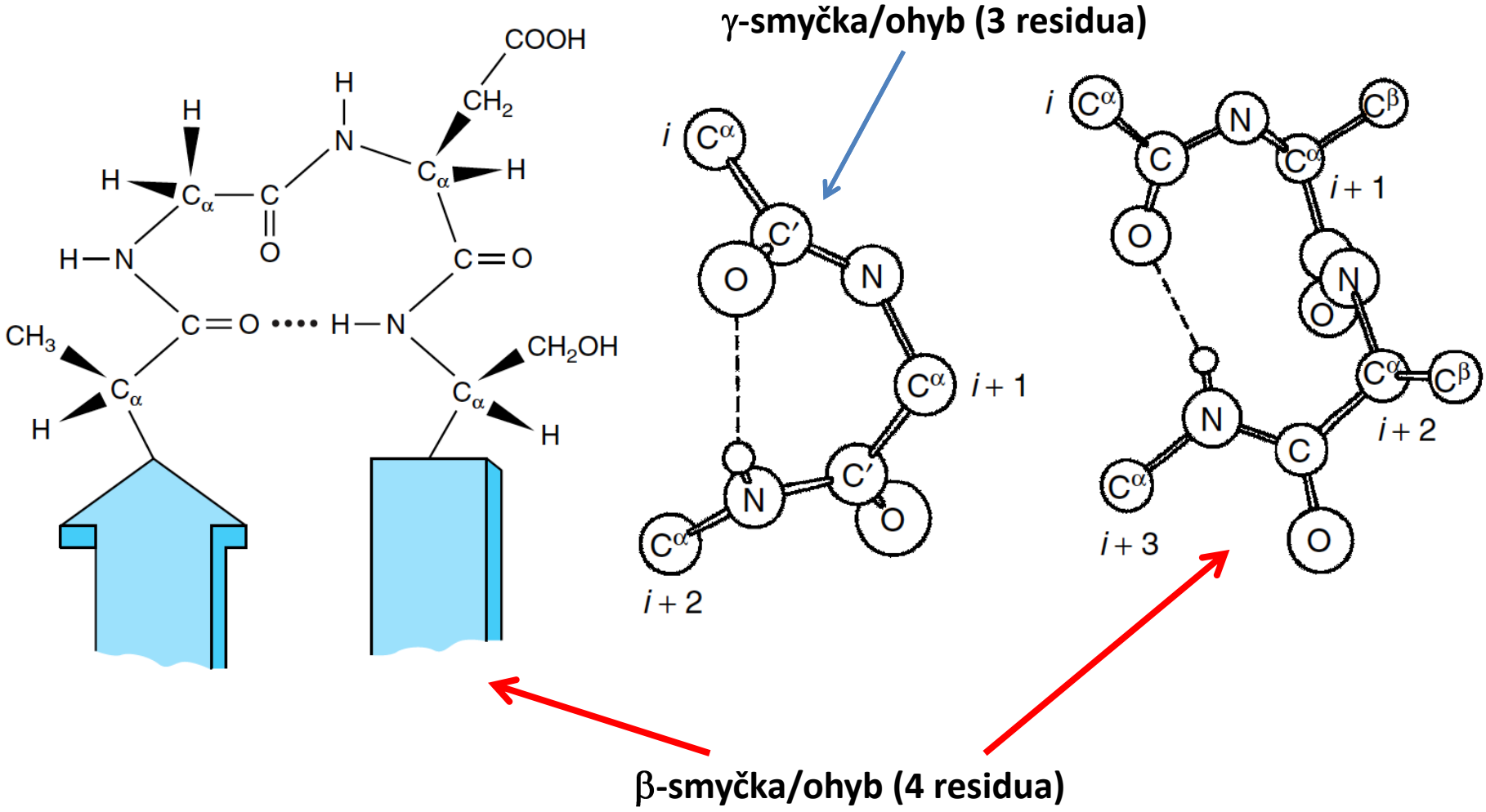
paralelní uspořádání



VII] Sekundární struktura

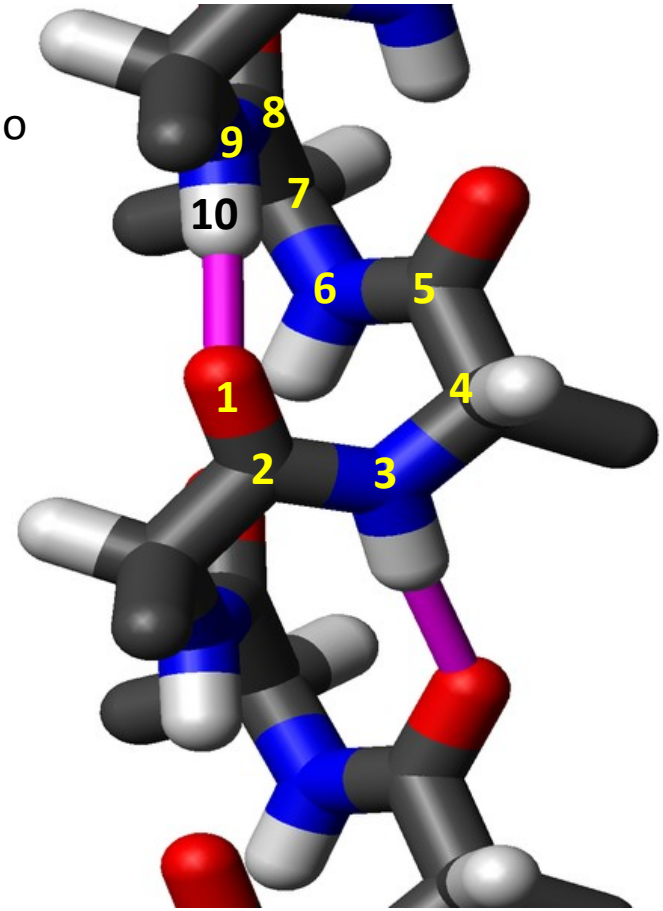
1) α-šroubovice (α-helix)
2) β-skládaný list (β-sheet)

3) Ohyb, smyčka (loop/turn)



Ostatní motivy sekundární struktury :

1. polyprolinová šroubovice I & II – levotočivá, 3.3 nebo 3 (PPI, PPII, v uvedeném pořadí) aminokyseliny/otočku
2. šroubovice 3_{10} (srovnej s 3.6_{13})– pravotočivá, 3 aminokyseliny/otáčku, 10 atomů vytváří kruh uzavřený vodíkovou vazbou, např. poly-Ala
3. π-šroubovice – pravotočivá, 4.1 aminokyseliny/otáčku
4. β-šroubovice – vzniká uspořádáním β-skládaných listů do pravo- i levotočivé šroubovice.



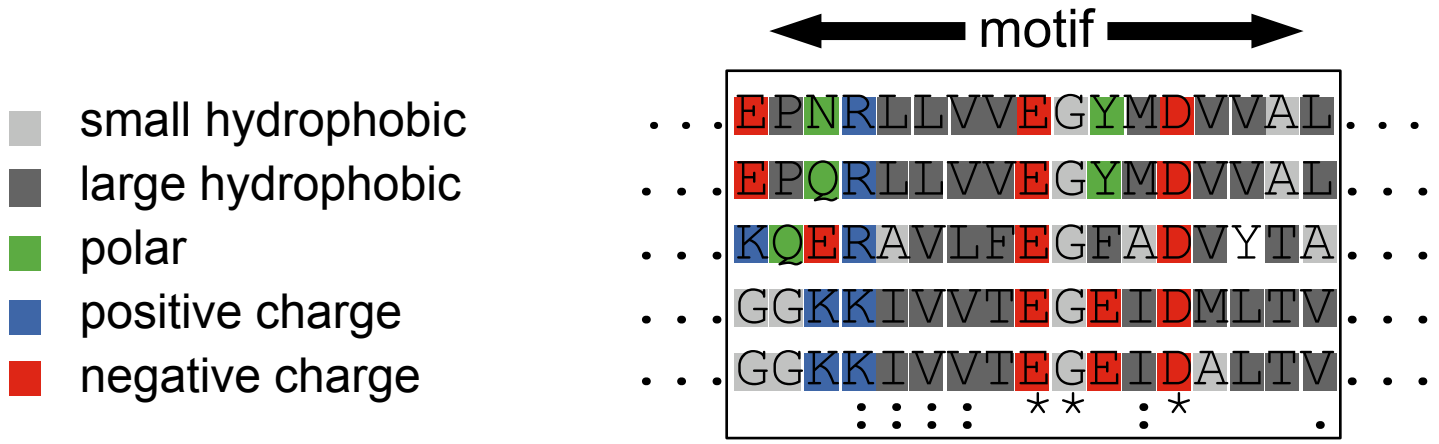
Primary sequence reveals important clues about a protein

One sequence keeps silent about its three-dimensional structure
Two aligned sequences whisper
But tables of many aligned sequences shout out loud

Primary sequence reveals important clues about a protein

• Evolution conserves amino acids that are important to protein structure and function across species. Sequence comparison of multiple “homologs” of a particular protein reveals highly conserved regions that are important for function.

• Clusters of conserved residues are called “motifs” -- motifs carry out a particular function or form a particular structure that is important for the conserved protein.

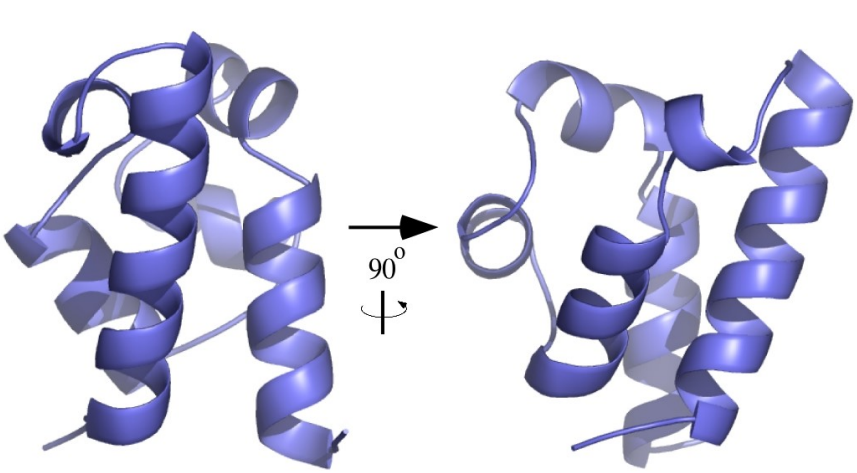


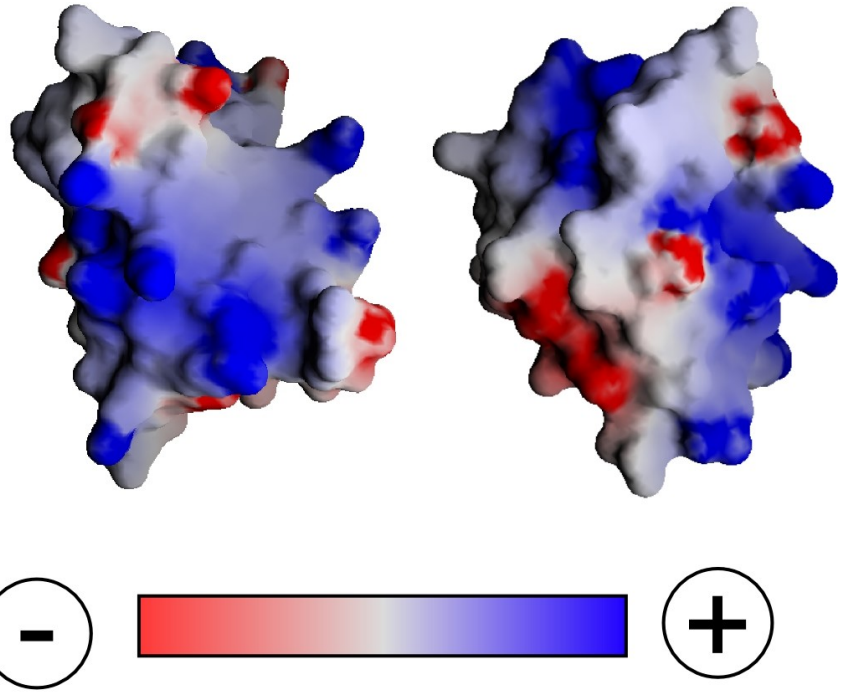
Some motifs in protein sequences

Structure of function identified	Motif
Nucleotide-binding site	**G*G**G**
N-glycosylation site	**N*S** or **N*T**
Nuclear protein transit sequence	**KKKRKV**
Factor IX proteinase cleavage site	**IEGR**
Serine proteinase active site	**GDSGG**
Acid proteinase active site	**FDTGS**
Fibronectin cell adhesion sequence	**RGDS**
Copper binding site	**H***H…H** or **H****H…H**

* = any single amino acid (AA)
*** = several AAs
… = any number of AAs

Charged and polar R-groups tend to map to protein surfaces





Protein folding

The **Levinthal paradox** states that if an averaged sized protein would sample all possible conformations before finding the one with the lowest energy, the whole **process would take billions of years**.

Proteins **typically** fold within **0.1 and 1000 seconds**, therefore the protein folding process must be directed some way through a specific folding pathway.

Protein folding

Anfinsen's Classic Experiment: The "Protein Folding Problem" asks a very simple question:

"How does the primary structure of a protein determine its 2⁻ and 3⁻ structure?".

We have known for many decades that proteins fold into their correct 3-D structures inside the cell. But correct folding during synthesis on the ribosome or later with assistance from unknown cellular factors could explain the *in vivo* results.

In the 1960's, Anfinsen and his coworkers performed a series of seminal experiments *in vitro* that answered a key part of the problem. The original work led Anfinsen to propose his "Thermodynamic Hypothesis", which states that the native conformation of a protein is adopted spontaneously. In other words, there is sufficient information contained in the protein sequence to guarantee correct folding from any of a large number of unfolded states. A schematic diagram of Anfinsen's experiment is shown below in two parts:

Proceedings of the

NATIONAL ACADEMY OF SCIENCES

Volume 47 · Number 9 · September 15, 1961

THE KINETICS OF FORMATION OF NATIVE RIBONUCLEASE DURING OXIDATION OF THE REDUCED POLYPEPTIDE CHAIN

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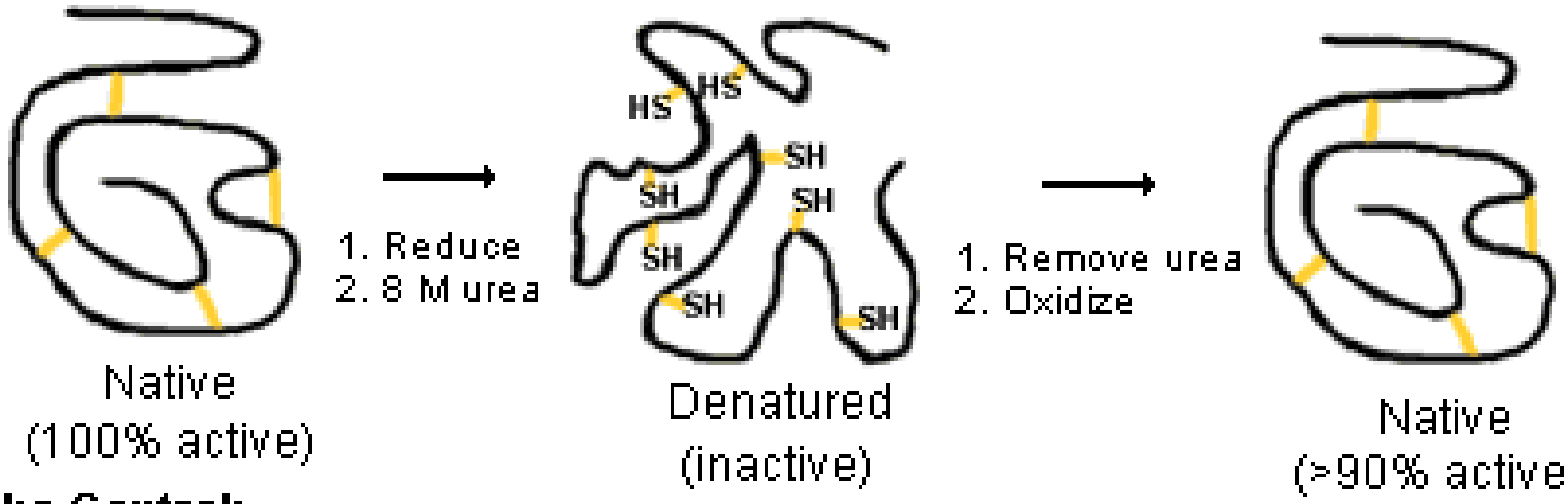
LABORATORY OF CELLULAR PHYSIOLOGY AND METABOLISM, NATIONAL HEART INSTITUTE, NATIONAL INSTITUTES OF HEALTH

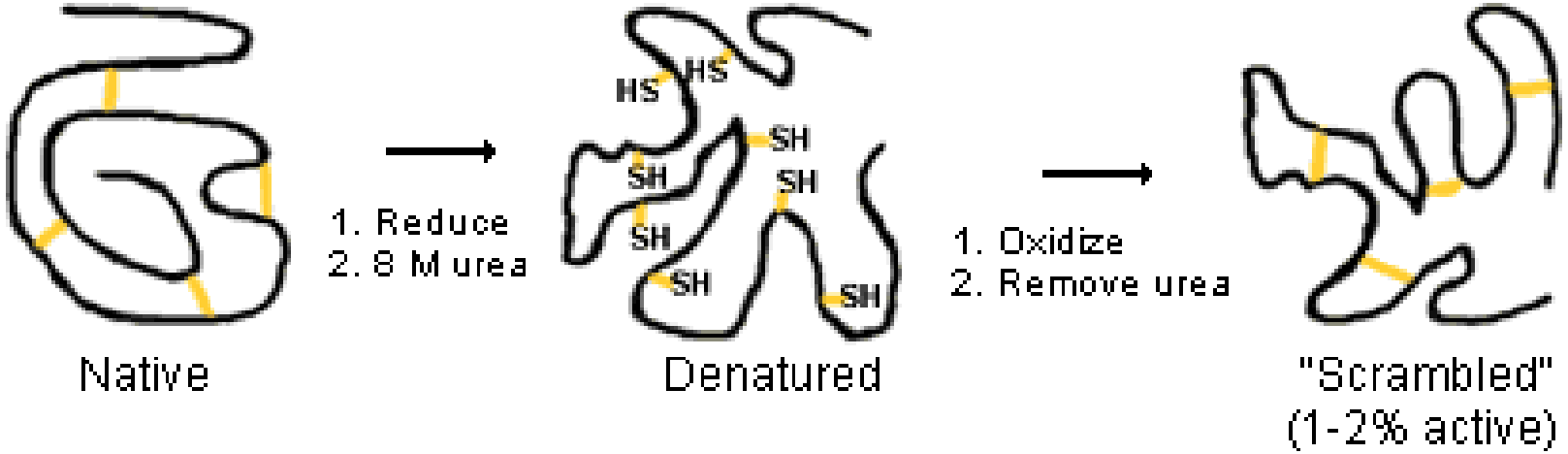
Communicated by John T. Edsall, July 31, 1961

Bovine pancreatic ribonuclease is completely reduced by treatment with mercaptoethanol in 8 *M* urea to yield a randomly coiled polypeptide chain containing eight cysteine residues.[1–3] Under optimal conditions of polypeptide concentration and pH, essentially complete reformation of the disulfide bonds of the native enzyme occurs in the presence of molecular oxygen.[2, 3] From chemical and physical studies of the reformed enzyme, it may be concluded that the information for the correct pairing of half-cystine residues in disulfide linkage, and for the assumption of the native secondary and tertiary structures, is contained in the amino acid sequence itself.

The Observation:



The Control:



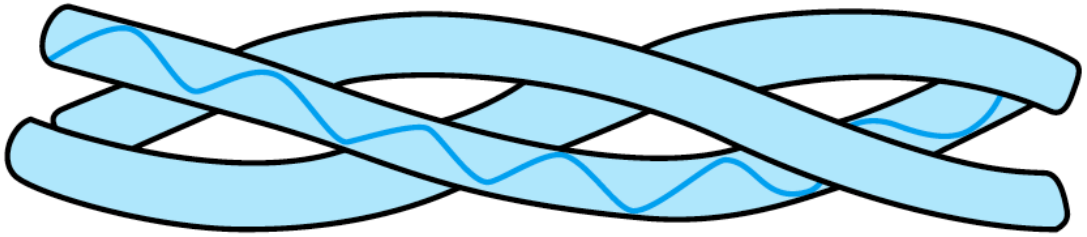
VII] Terciární struktura proteinů

1) Kolagen

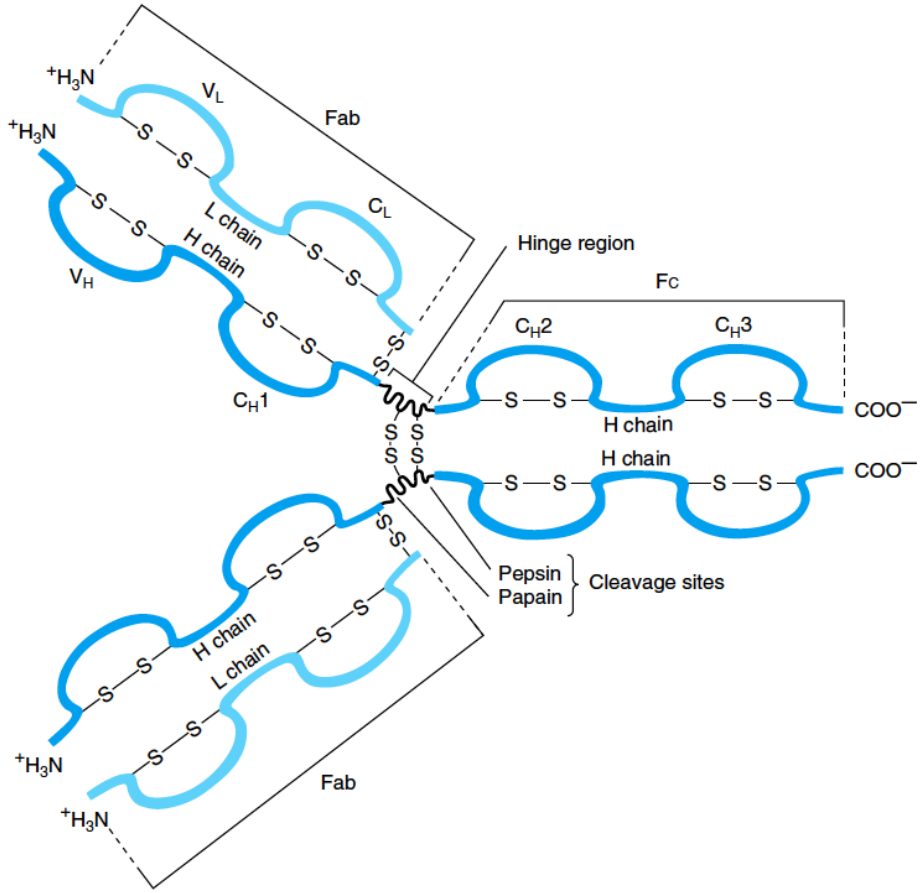
Primární struktura: – Gly – X – Y – Gly – X – Y – Gly – X – Y –

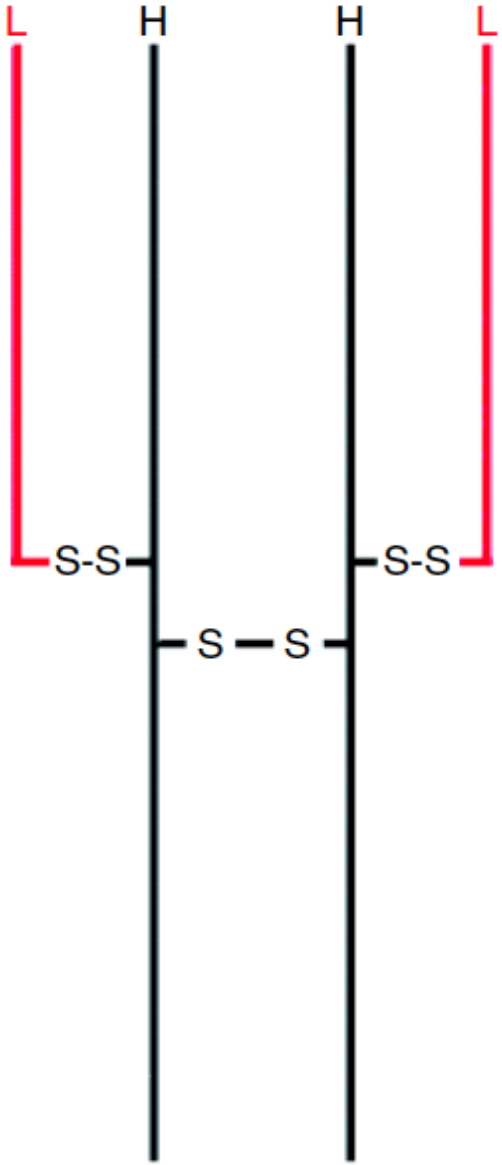
Sekundární struktura:

Terciární struktura:



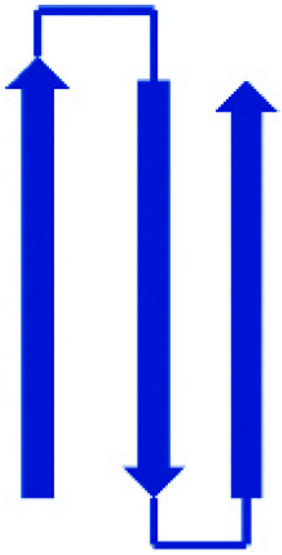
2) Disulfidický můstek: 2-SH (z cysteinu)-> -S-S-



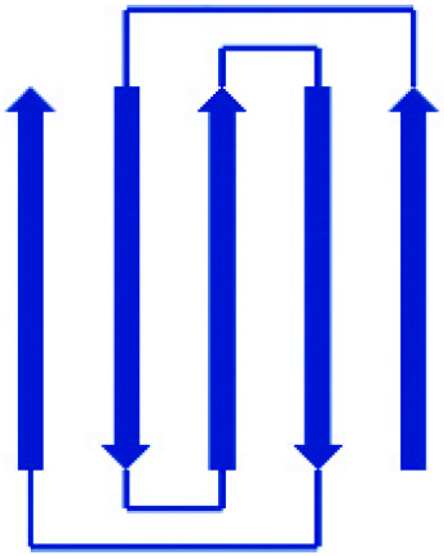


Disulfidické můstky v imunoglobulinu G

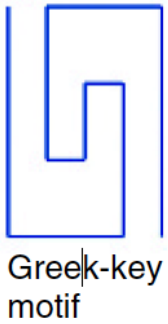
3) Strukturní motivy v proteinech

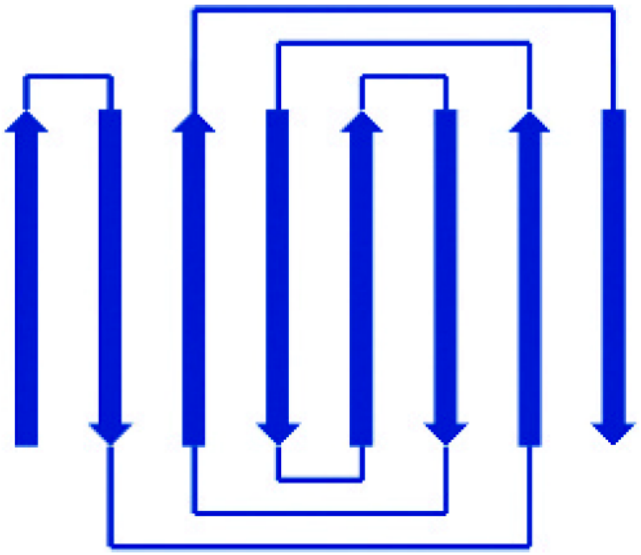


β-meandr



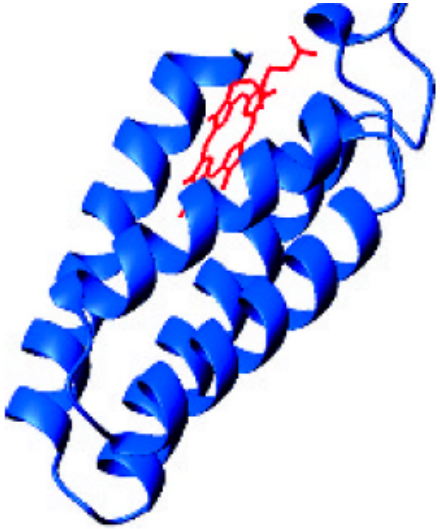
Řecký klíč



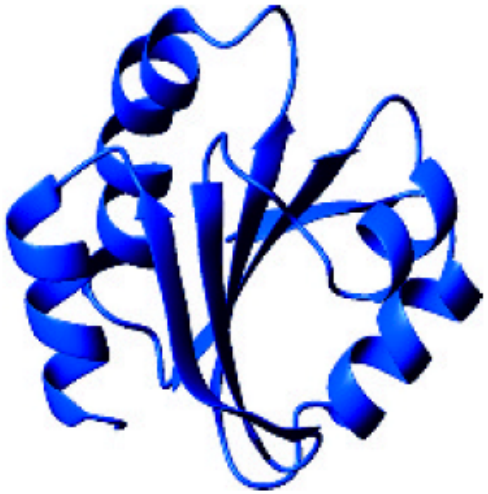


Swiss/Jelly roll

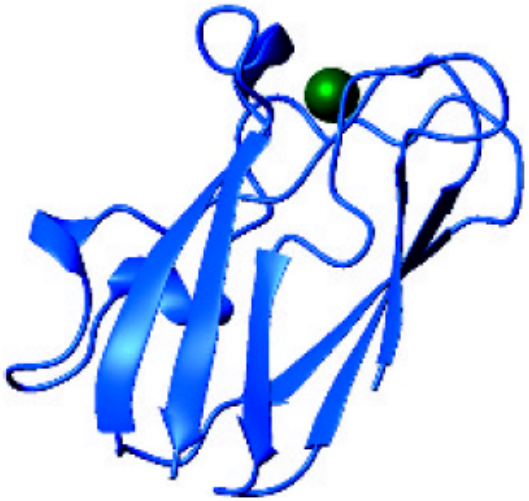
λ repressor



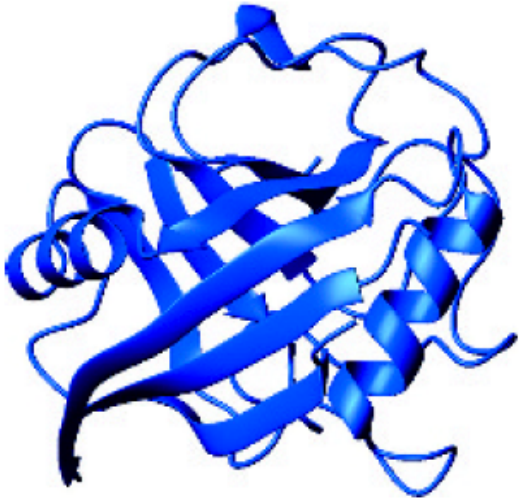
Cytochrome b_{562}



Thioredoxin



Plastocyanin

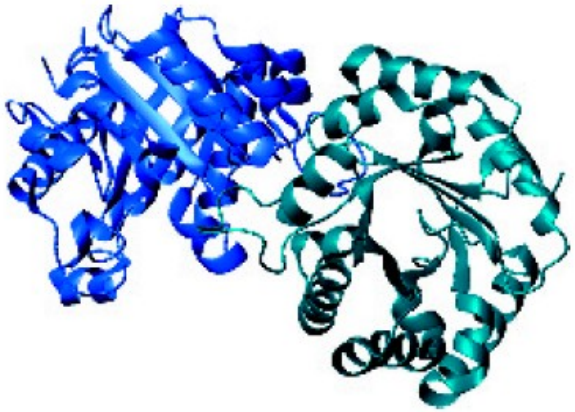


cis-trans proline isomerase

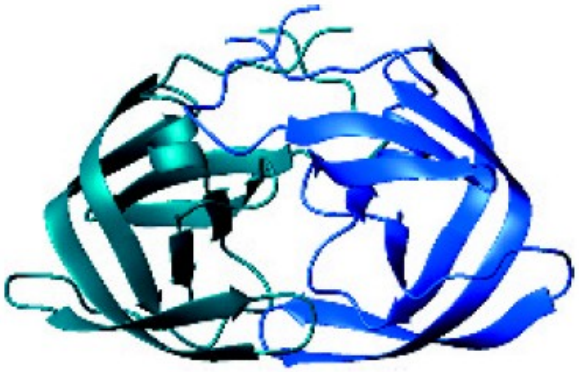
γ-crystallin

VIII] Kvartérní struktura proteinů

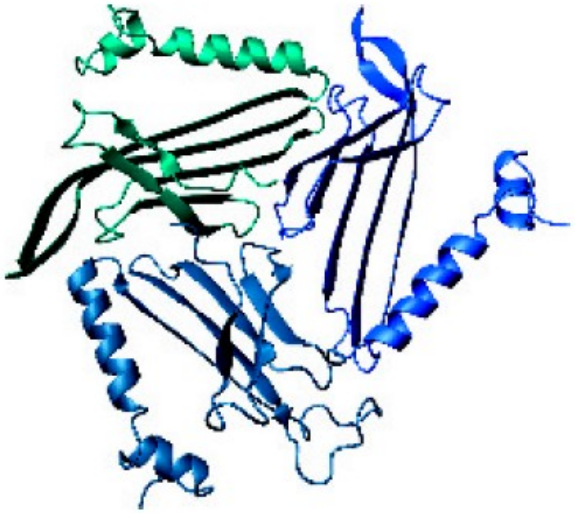
1) **Multimery**
2) **Homo-/hetero-mery**



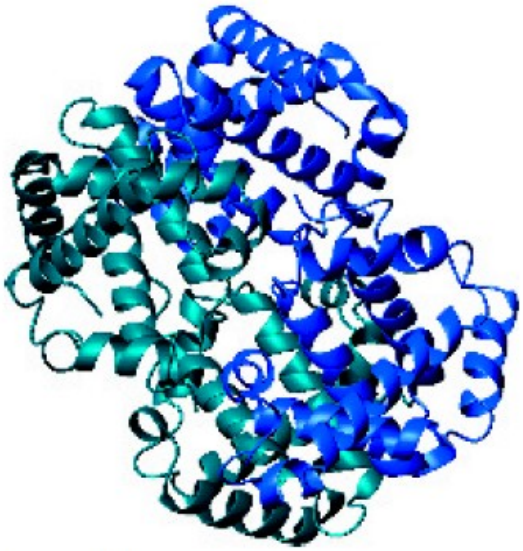
Triose phosphate isomerase (TIM)



HIV protease



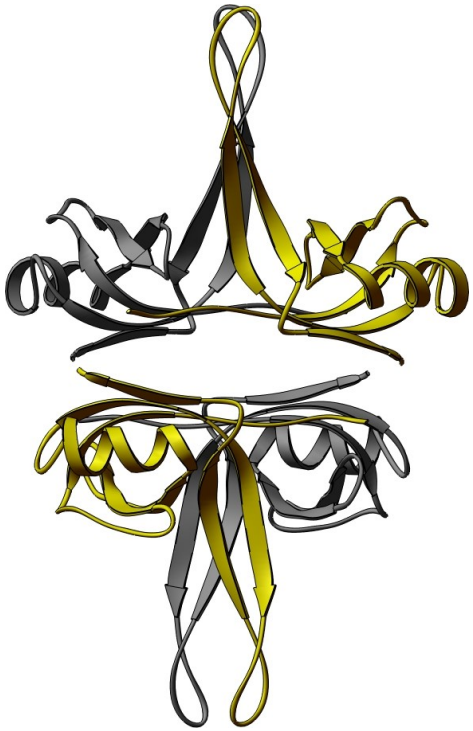
MS2 viral capsid protein



Haemoglobin

Examples of other quaternary structures

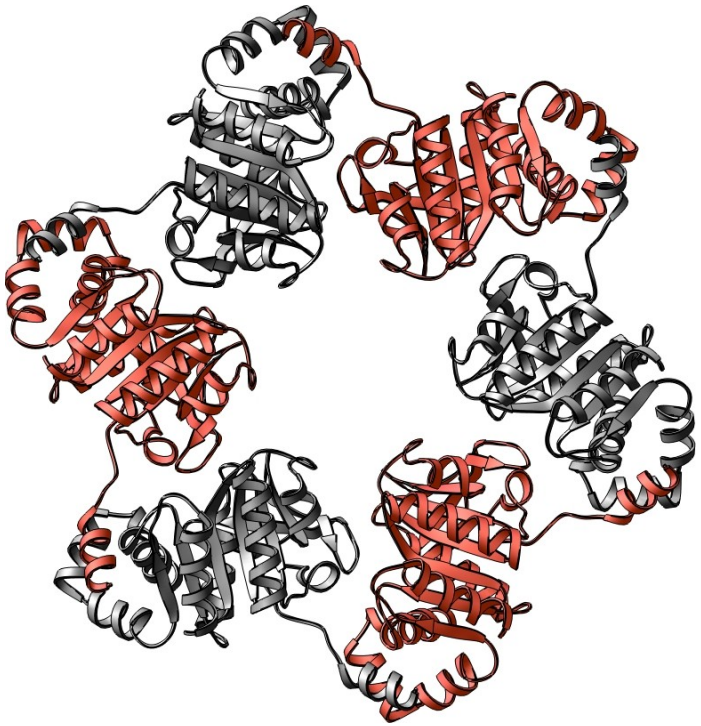
Tetramer



SSB

Allows coordinated DNA binding

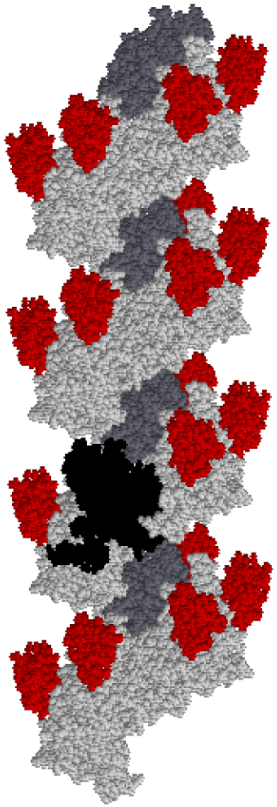
Hexamer



DNA helicase

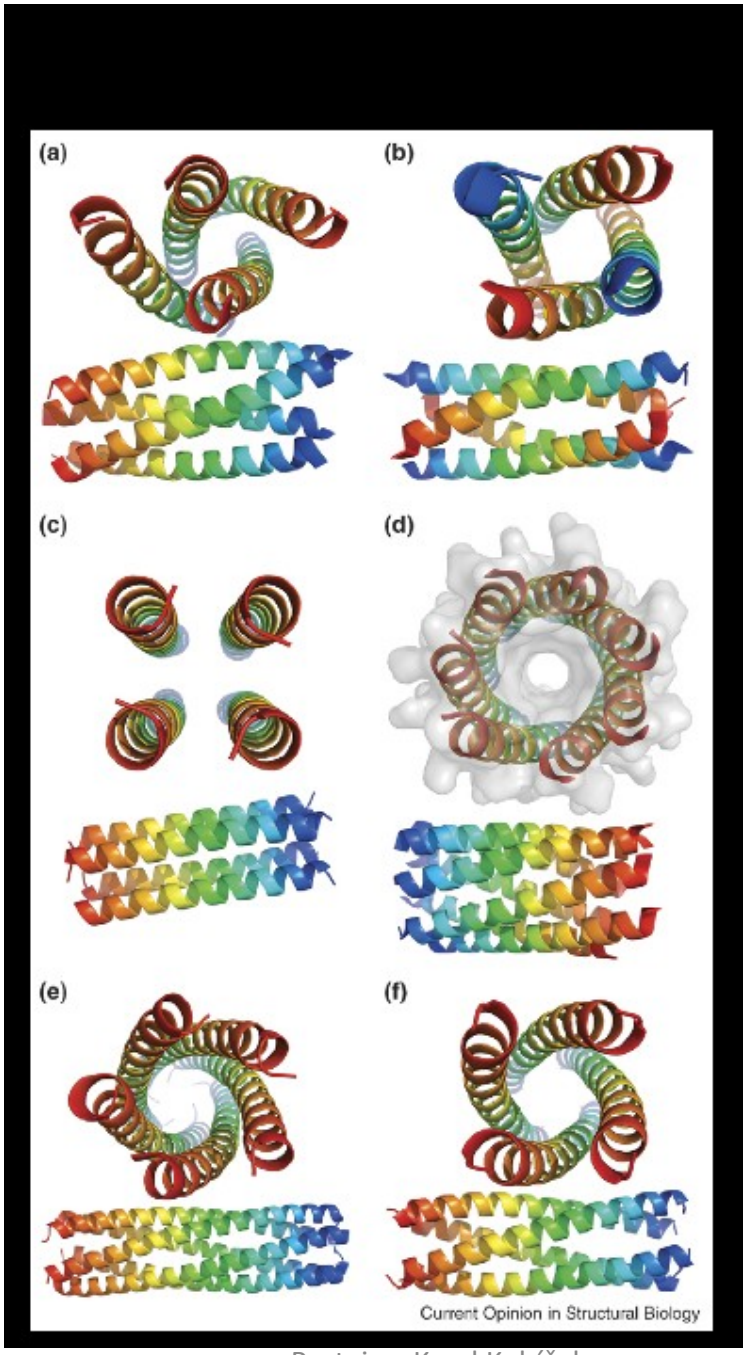
Allows coordinated DNA binding and ATP hydrolysis

Filament



Recombinase

Allows complete coverage of an extended molecule



Grigoryan and Keating, 2008

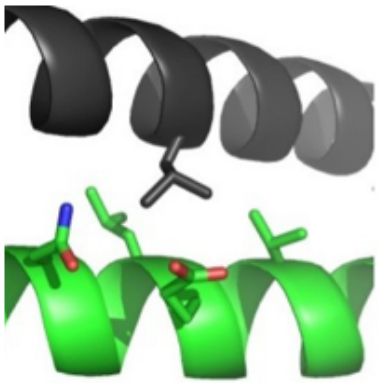
Coiled coils

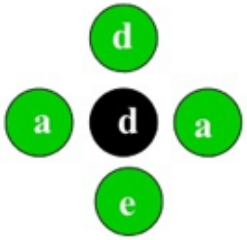
- bundle of α-helices
- usually 2,3,4 helices
- parallel or antiparallel
- oligomers: homo- or hetero-

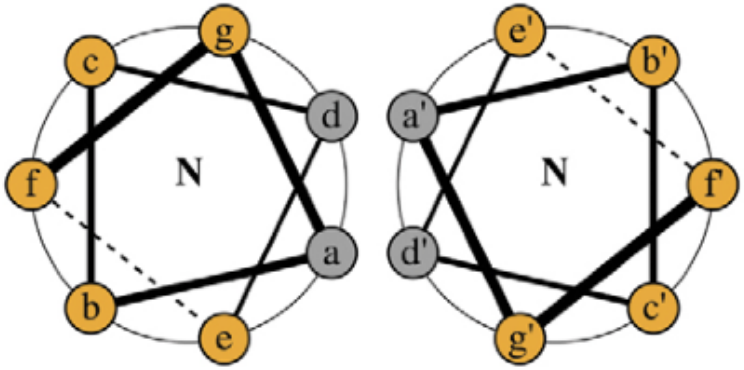
- 3.5 amino acids / turn
- 7 amino acid register
- inner residues - **hydrophobic**
- outer residues - **hydrophilic**

- **knobs-into-holes**:
  a residue from one helix (**knob**) packs into a space surrounded by **4** side-chains of the facing helix (**hole**)

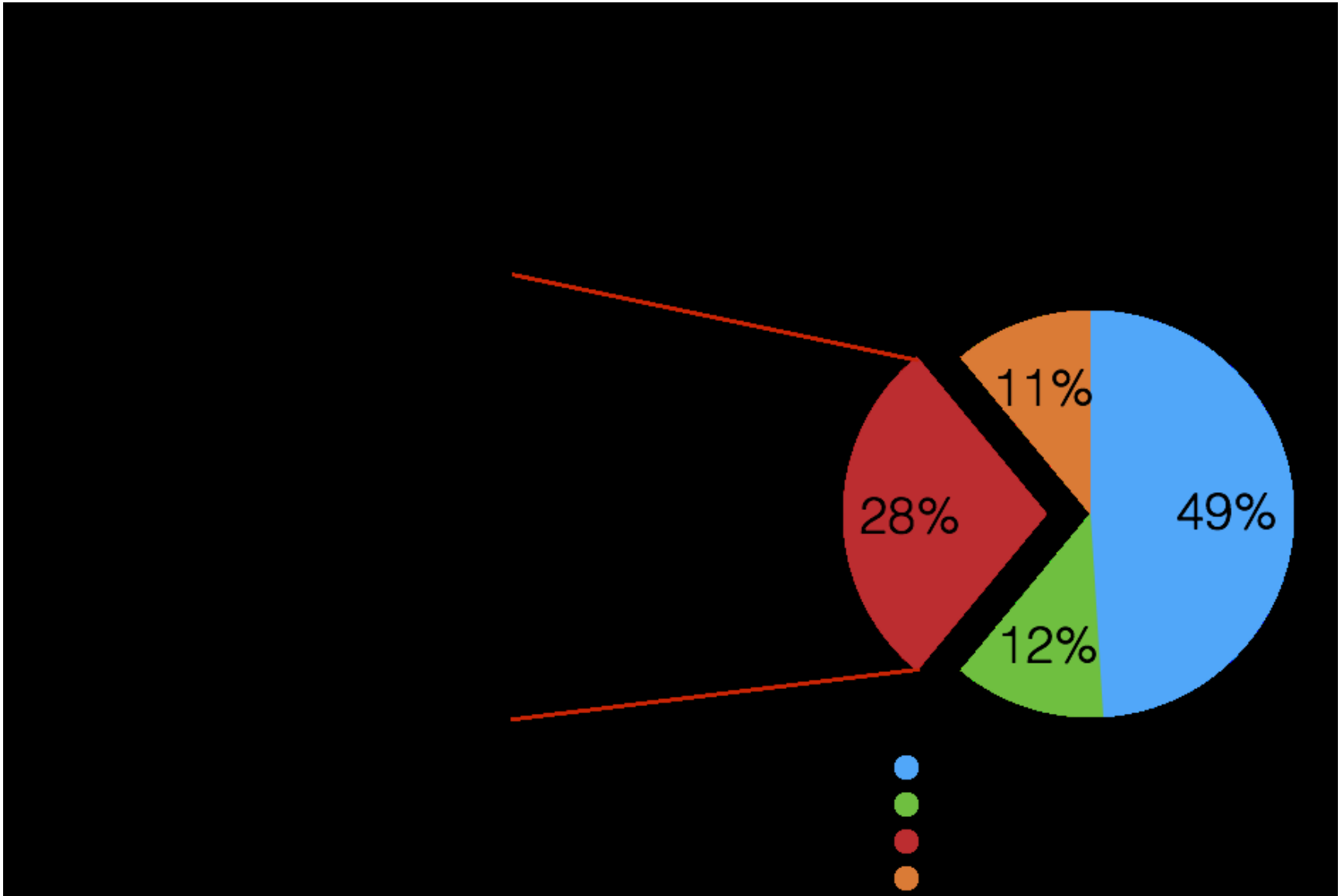
[abcdefg]n



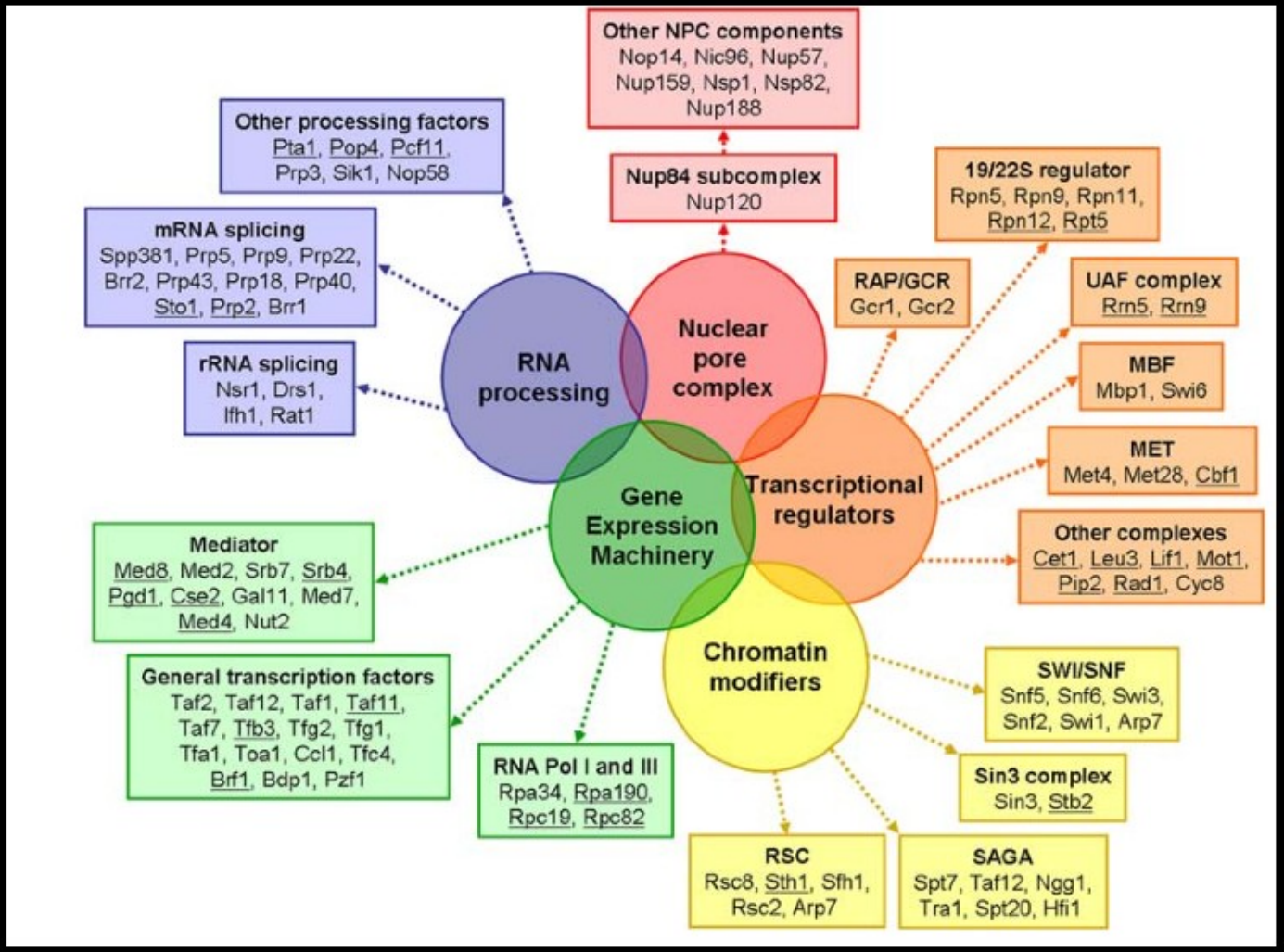




Lupas, A.N., and Gruber, M. (2005).
The Structure of α-Helical Coiled Coils.



Barbara, et al 2007
Coiled coil structures and transcription: an analysis of the S. cerevisiae coilome.



Barbara, et al 2007
Coiled coil structures and transcription: an analysis of the S. cerevisiae coilome.

Useful software

- **COILS** (prediction of coiled coil regions)
  http://embnet.vital-it.ch/software/COILS_form.html
- **MARCOIL** (prediction of coiled coil regions)
  http://bcf.isb-sib.ch/webmarcoil/webmarcoilINFOC1.html
- **MULTICOIL** (prediction of coiled coil regions, oligomeric state)
- **LOGICOIL** (oligomeric state probabilities)
  http://coiledcoils.chm.bris.ac.uk/LOGICOIL/
- **DrawCoil 1.0** (heptade diagrams)
  http://www.grigoryanlab.org/drawcoil/
- **CCBuilder** (building CC from the sequence)
  http://coiledcoils.chm.bris.ac.uk/app/cc_builder/
- **SOCKET** (locate knobs-into-holes packing between alpha-helices in PDB structures)
  http://coiledcoils.chm.bris.ac.uk/socket/index.html
- **CCCP** (Coiled-coil Crick Parameterization)
  http://www.grigoryanlab.org/cccp/

Confidence in structural features of proteins determined by X-ray crystallography

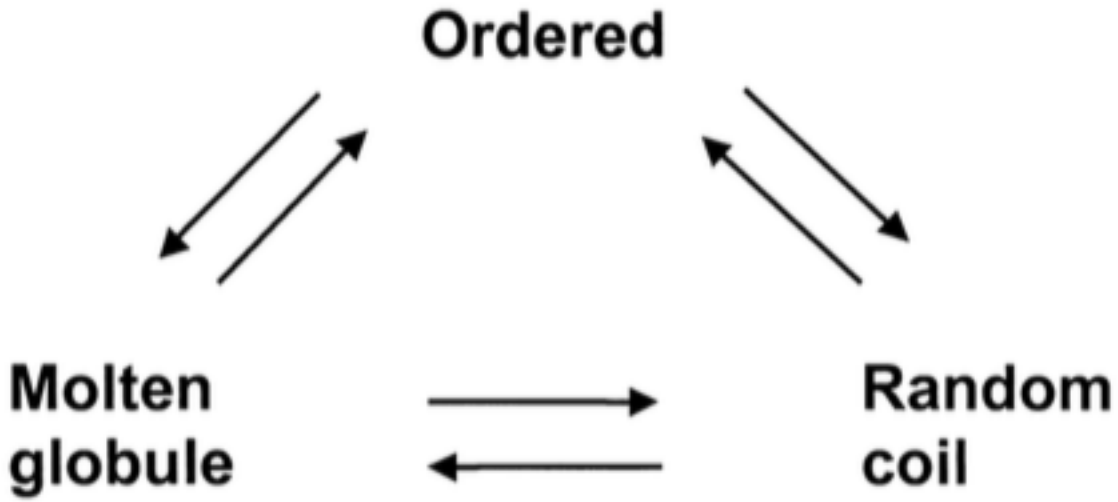
(estimates are very rough and strongly depend on the quality of the data)

Structural feature			Resolution		
	5 Å	3 Å	2.5 Å	2 Å	1.5 Å
Chain tracing	-	Fair	Good	Good	Good
Secondary structure	Helices fair	Fair	Good	Good	Good
Sidechain conformations	-	-	Fair	Good	Good
Orientation of peptide planes	-	-	Fair	Good	Good
Protein hydrogen atoms visible	-	-	-	-	Good

XII] Metody pro určování třídimenzionální struktury (bio)molekul na atomární úrovni

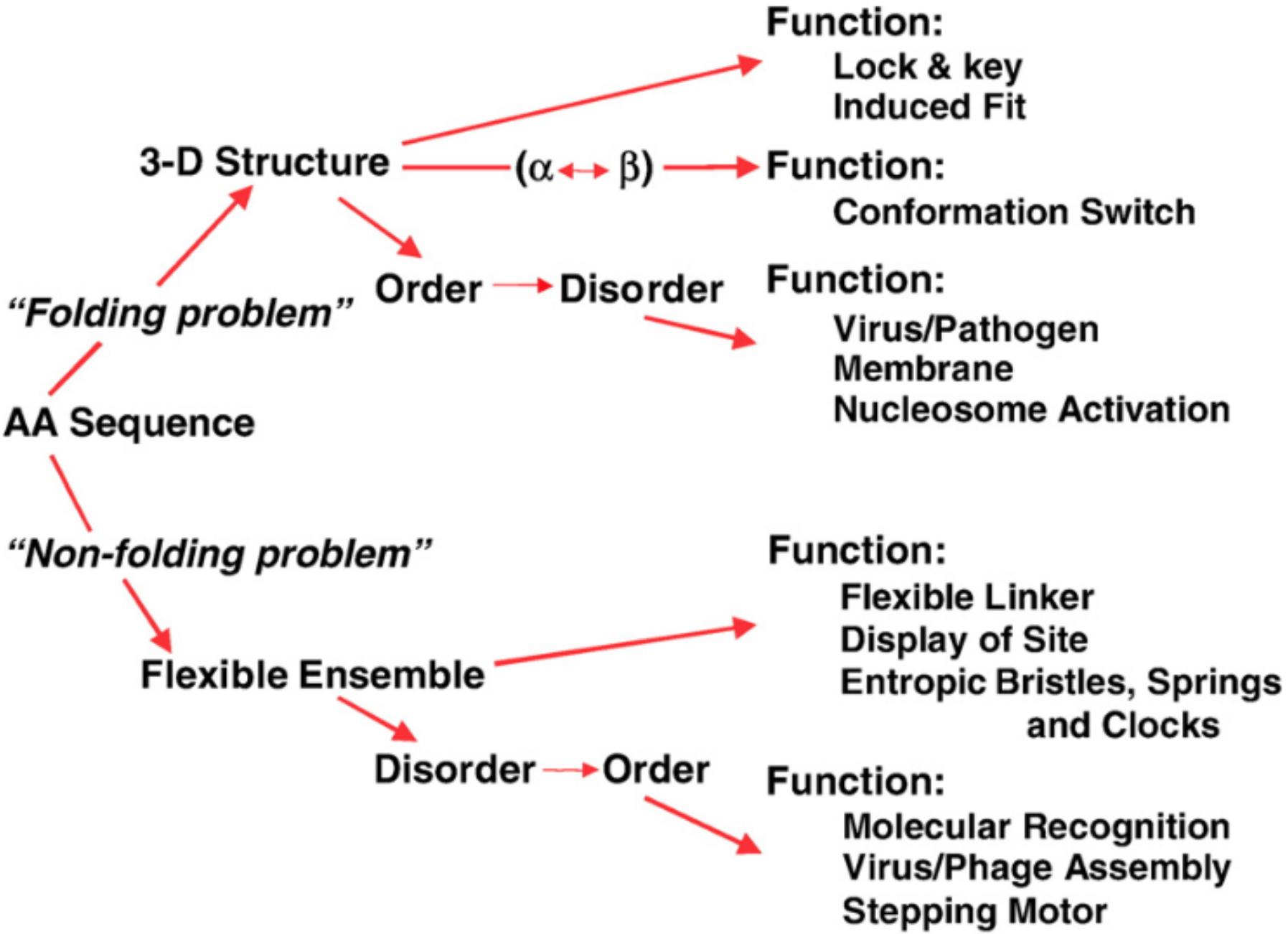
1) **NMR – nukleární (=jaderná) magnetická rezonance – měření (také) v kapalném prostředí**
2) **Rentgenová krystalografie - (měření především v krystalu)**
3) **Kryo-elektronová mikroskopie**

THE PROTEIN TRINITY



Proposal: Function can arise from any of the three protein forms and transitions between them.

J Mol Graph Model 19, 2001, 26-59



BiochimBiophysActa 1804, 2010, 1231-64

IX] Funkce proteinů:

1) Enzymy – katalyzátory biologických reakcí
2) Transportní proteiny (hemoglobin)
3) Regulační proteiny (např. hormon insulin)
4) Skladovací (storage) – např. ovalbumin – zdroj dusíku pro vyvíjející se ptačí embryo
5) “Pohybové” proteiny – actin, myosin, tubulin, dynein, kinesin
6) Strukturní proteiny – zajišťujicí vytvoření a udržení biologické struktury – α-keratin, kolagen, elastin, fibroin etc.
7) Ochranné – imunoglobuliny, fibrinogen, thrombin

X] Proteinová databáze – PDB

WWW.RCSB.ORG

XI] Vizualizační programy

1) PyMol
2) Chimera
3) VMD
4) MolMol
5) RasMol
6) Insight II