A 3D molecular model of an enzyme active site. The enzyme's surface is shown in a grey, semi-transparent space-filling representation. An orange, flat, irregularly shaped molecule is positioned at the top of the active site. Below it, a substrate molecule is shown in a stick representation, colored green and blue. A red stick model of an amino acid residue, labeled His57, is located at the bottom left. The overall scene is set against a dark, textured background.

Aminoácidos, peptídeos e proteínas

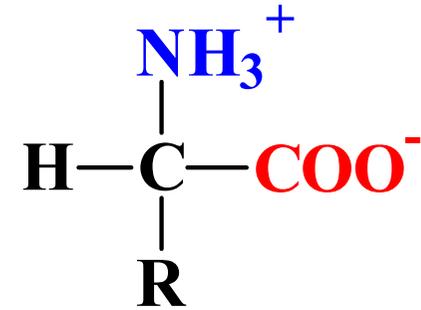
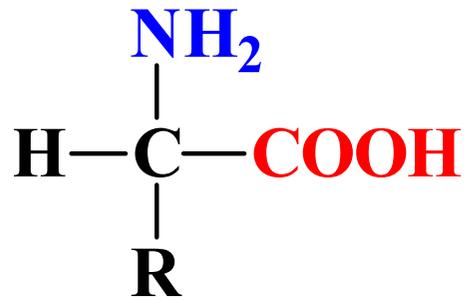
Substrate

His⁵⁷

Funções biológicas das proteínas

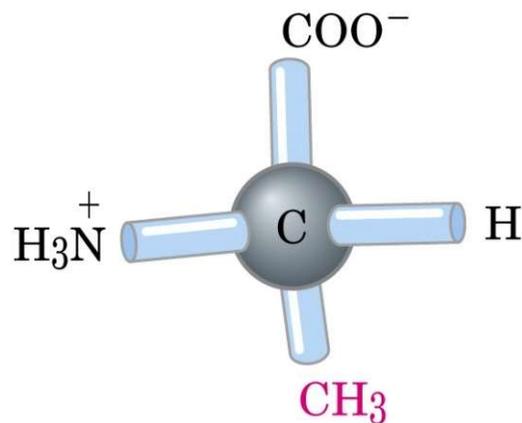
- 1) Catálise enzimática;**
- 2) Transporte e armazenamento;**
- 3) Movimento coordenado;**
- 4) Sustentação mecânica;**
- 5) Proteção imunitária;**
- 6) Geração e transmissão de impulsos nervosos;**
- 7) Controle do crescimento e da diferenciação.**

Aminoácidos

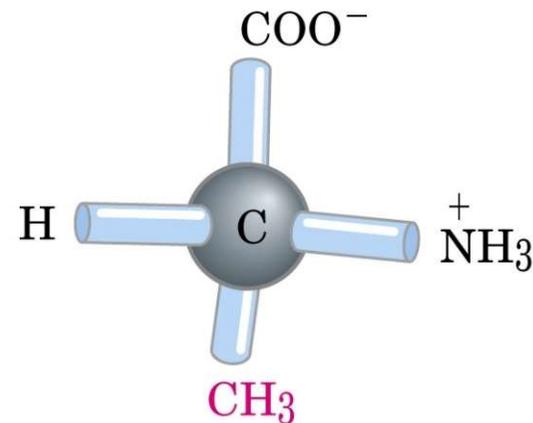


Propriedades:

- Alta solubilidade (\neq aminas orgânicas e ácidos carboxílicos)
- alto ponto de fusão (\neq aminas orgânicas e ácidos carboxílicos)



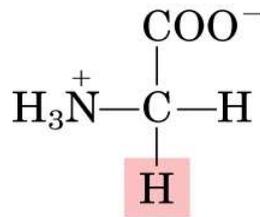
L-Alanine



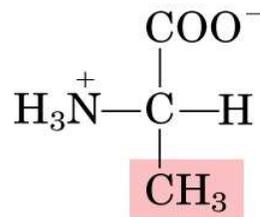
D-Alanine

(a)

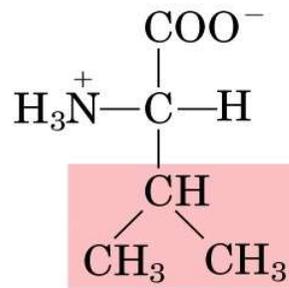
Nonpolar, aliphatic R groups



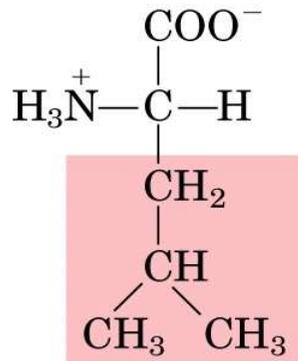
Glycine



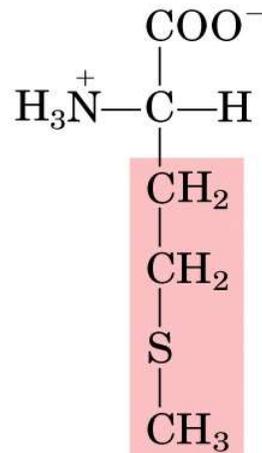
Alanine



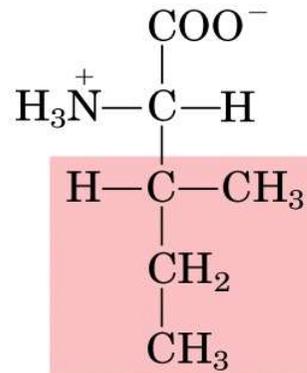
Valine



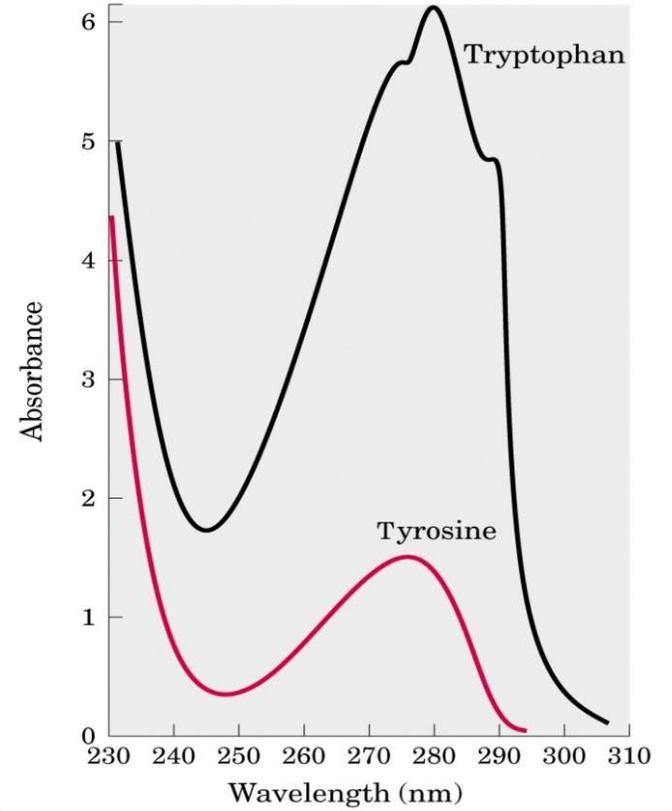
Leucine



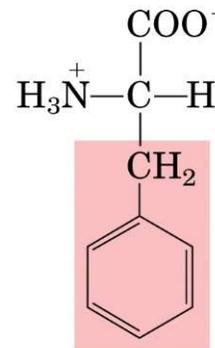
Methionine



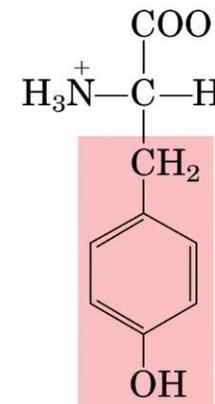
Isoleucine



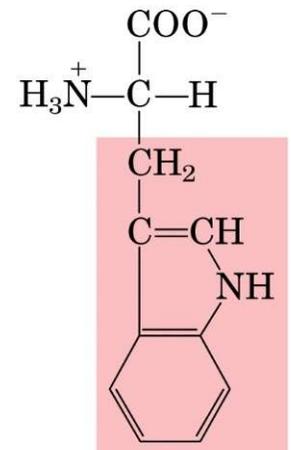
Aromatic R groups



Phenylalanine

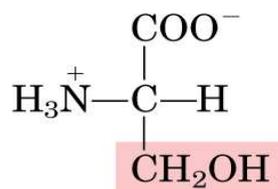


Tyrosine

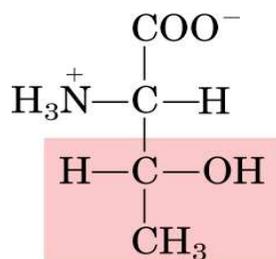


Tryptophan

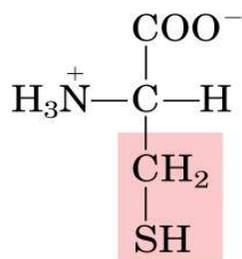
Polar, uncharged R groups



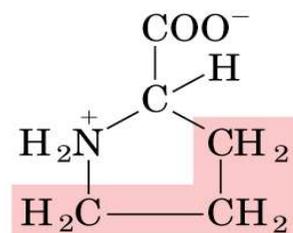
Serine



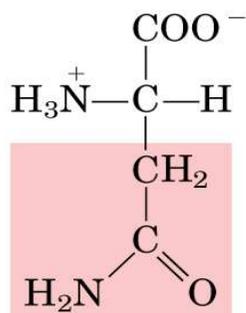
Threonine



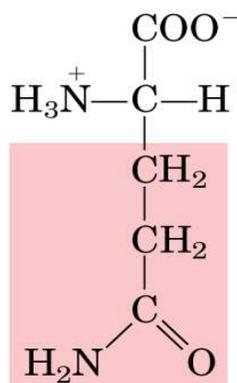
Cysteine



Proline

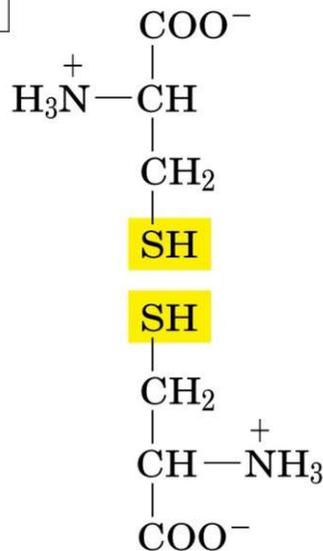


Asparagine

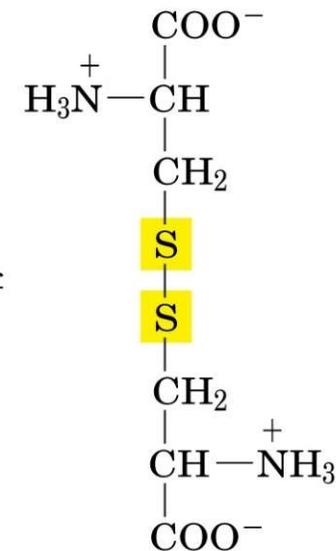
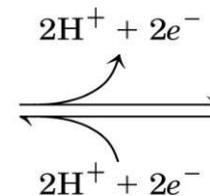


Glutamine

Cysteine

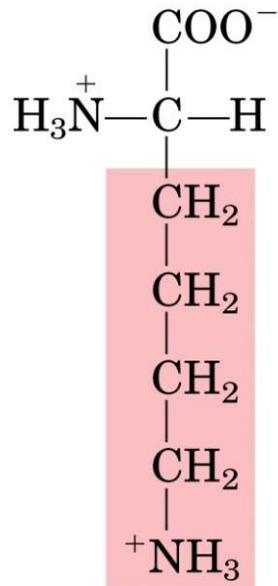


Cysteine

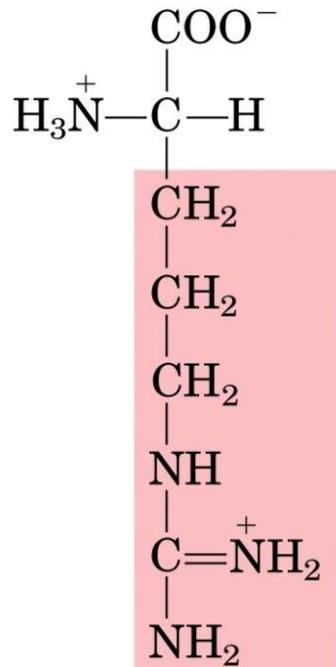


Cystine

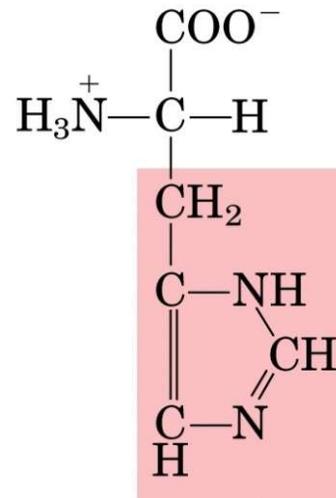
Positively charged R groups



Lysine

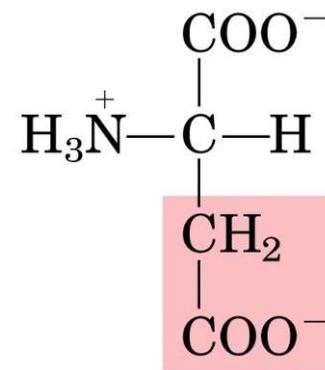


Arginine

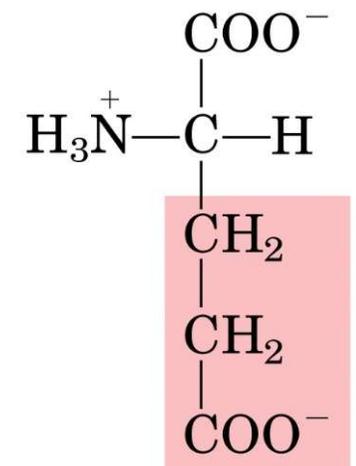


Histidine

Negatively charged R groups



Aspartate



Glutamate

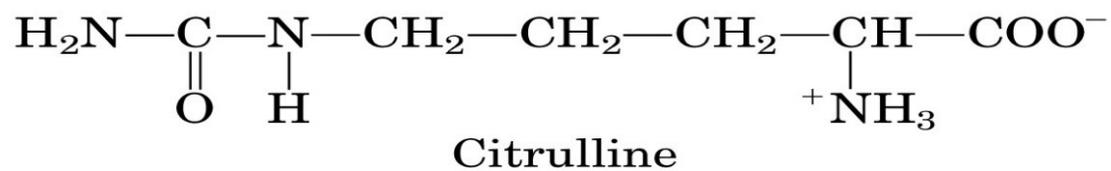
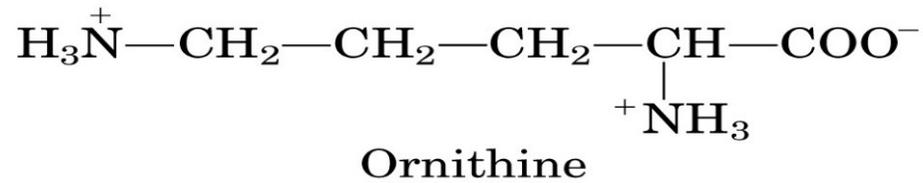
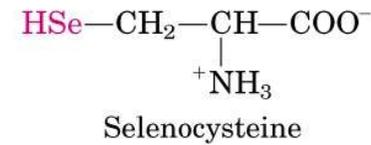
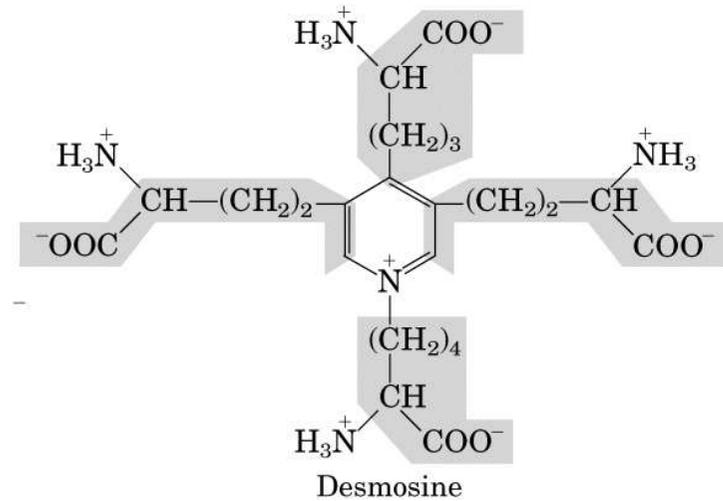
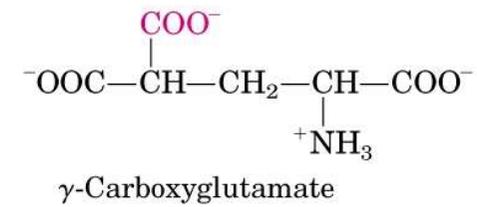
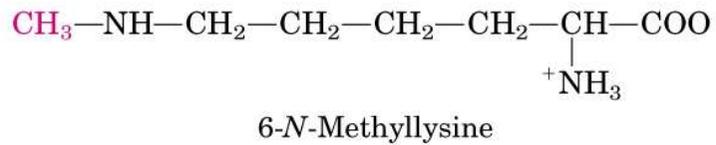
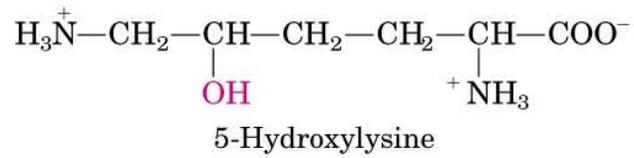
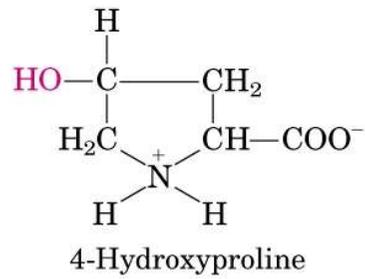
table 5-1

Properties and Conventions Associated with the Standard Amino Acids

Amino acid	Abbreviated names		M_r	pK_a values			pI	Hydropathy index*	Occurrence in proteins (%)
				pK_1 (-COOH)	pK_2 (-NH ₃ ⁺)	pK_R (R group)			
Nonpolar, aliphatic R groups									
Glycine	Gly	G	75	2.34	9.60		5.97	-0.4	7.2
Alanine	Ala	A	89	2.34	9.69		6.01	1.8	7.8
Valine	Val	V	117	2.32	9.62		5.97	4.2	6.6
Leucine	Leu	L	131	2.36	9.60		5.98	3.8	9.1
Isoleucine	Ile	I	131	2.36	9.68		6.02	4.5	5.3
Methionine	Met	M	149	2.28	9.21		5.74	1.9	2.3
Aromatic R groups									
Phenylalanine	Phe	F	165	1.83	9.13		5.48	2.8	3.9
Tyrosine	Tyr	Y	181	2.20	9.11	10.07	5.66	-1.3	3.2
Tryptophan	Trp	W	204	2.38	9.39		5.89	-0.9	1.4
Polar, uncharged R groups									
Serine	Ser	S	105	2.21	9.15		5.68	-0.8	6.8
Proline	Pro	P	115	1.99	10.96		6.48	1.6	5.2
Threonine	Thr	T	119	2.11	9.62		5.87	-0.7	5.9
Cysteine	Cys	C	121	1.96	10.28	8.18	5.07	2.5	1.9
Asparagine	Asn	N	132	2.02	8.80		5.41	-3.5	4.3
Glutamine	Gln	Q	146	2.17	9.13		5.65	-3.5	4.2
Positively charged R groups									
Lysine	Lys	K	146	2.18	8.95	10.53	9.74	-3.9	5.9
Histidine	His	H	155	1.82	9.17	6.00	7.59	-3.2	2.3
Arginine	Arg	R	174	2.17	9.04	12.48	10.76	-4.5	5.1
Negatively charged R groups									
Aspartate	Asp	D	133	1.88	9.60	3.65	2.77	-3.5	5.3
Glutamate	Glu	E	147	2.19	9.67	4.25	3.22	-3.5	6.3

*A scale combining hydrophobicity and hydrophilicity of R groups; it can be used to measure the tendency of an amino acid to seek an aqueous environment (- values) or a hydrophobic environment (+ values). See Chapter 12. From Kyte, J. & Doolittle, R.F. (1982) *J. Mol. Biol.* **157**, 105-132.

†Average occurrence in over 1150 proteins. From Doolittle, R.F. (1989) Redundancies in protein sequences. In *Prediction of Protein Structure and the Principles of Protein Conformation* (Fasman, G.D., ed) Plenum Press, NY, pp. 599-623.



pK_a

2

4

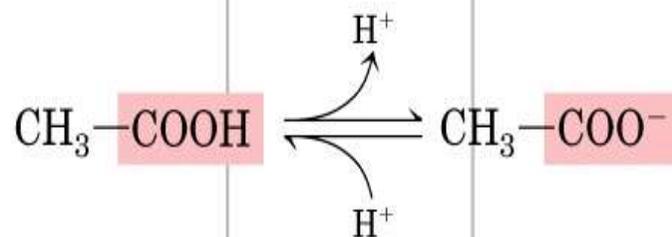
6

8

10

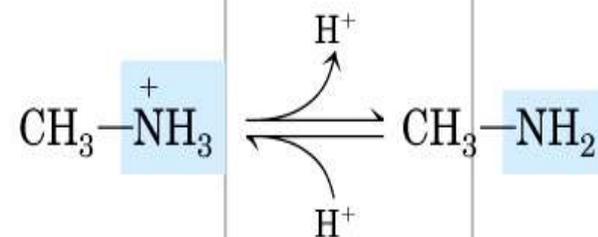
12

Methyl-substituted
carboxyl and
amino groups



Acetic acid

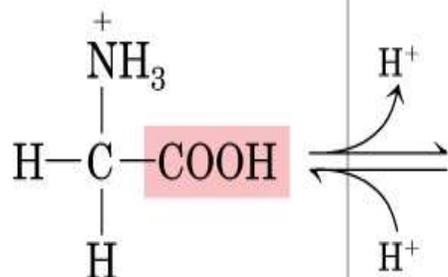
The normal pK_a for a
carboxyl group is about 4.8.



Methylamine

The normal pK_a for an
amino group is about 10.6.

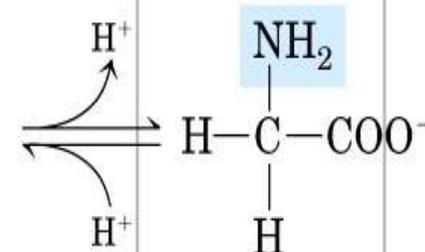
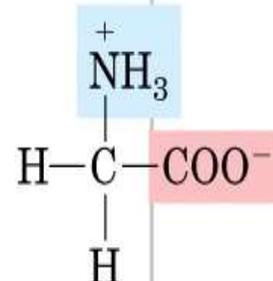
Carboxyl and
amino groups
in glycine



α -Amino acid (glycine)

$pK_a = 2.34$

Repulsion between the amino
group and the departing proton
lowers the pK_a for the carboxyl
group, and oppositely charged
groups lower the pK_a by stabi-
lizing the zwitterion.

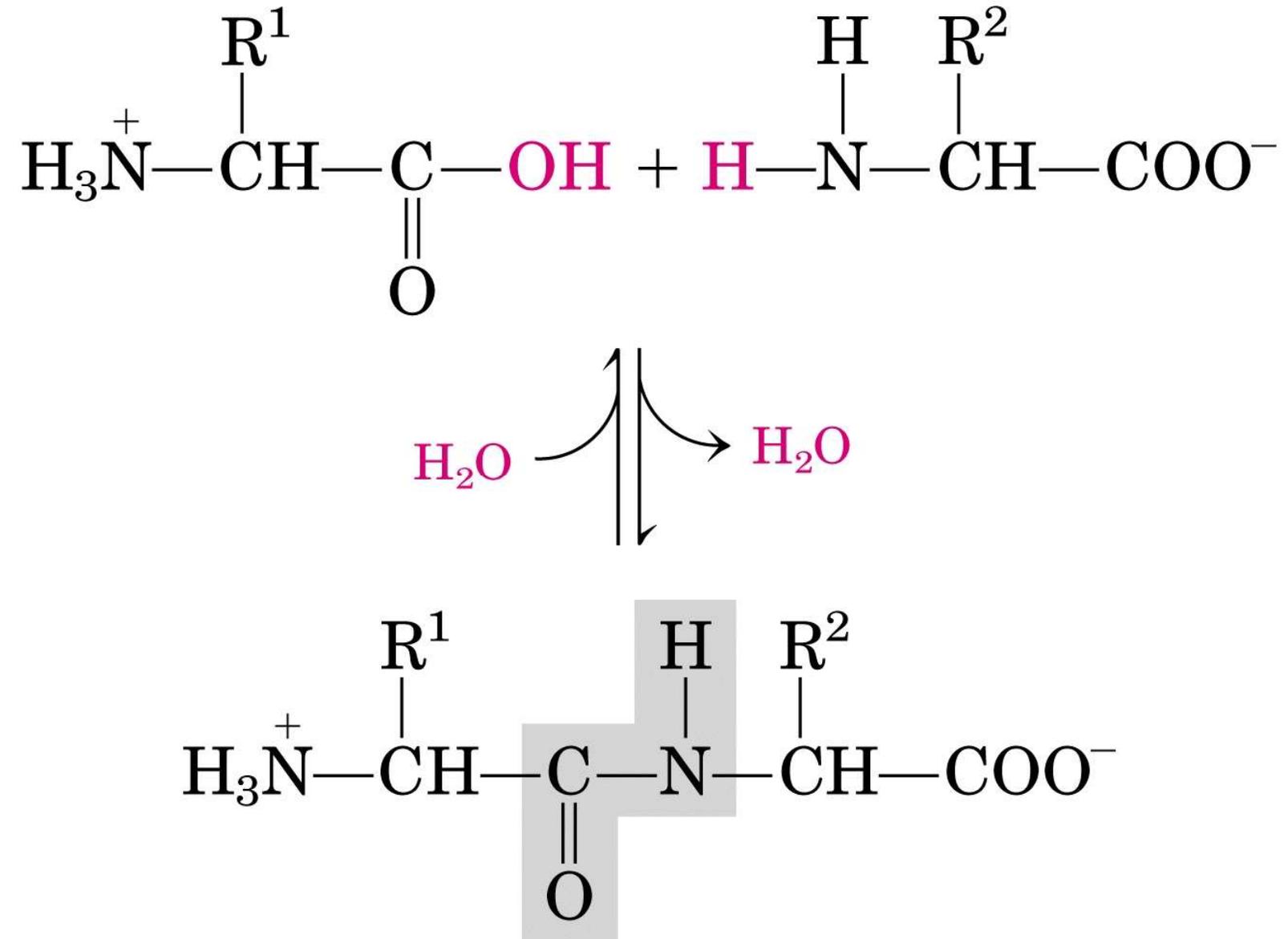


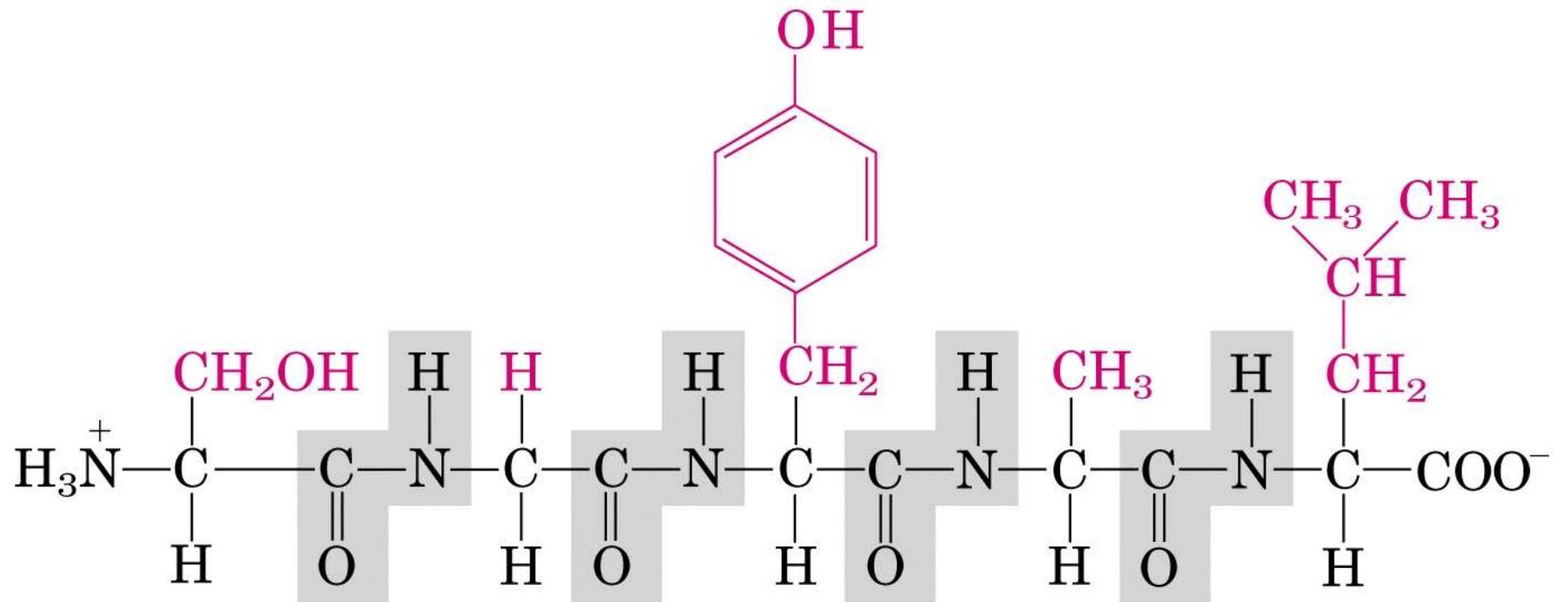
α -Amino acid (glycine)

$pK_a = 9.60$

Electronegative oxygen atoms
in the carboxyl group pull electrons
away from the amino group,
lowering its pK_a .

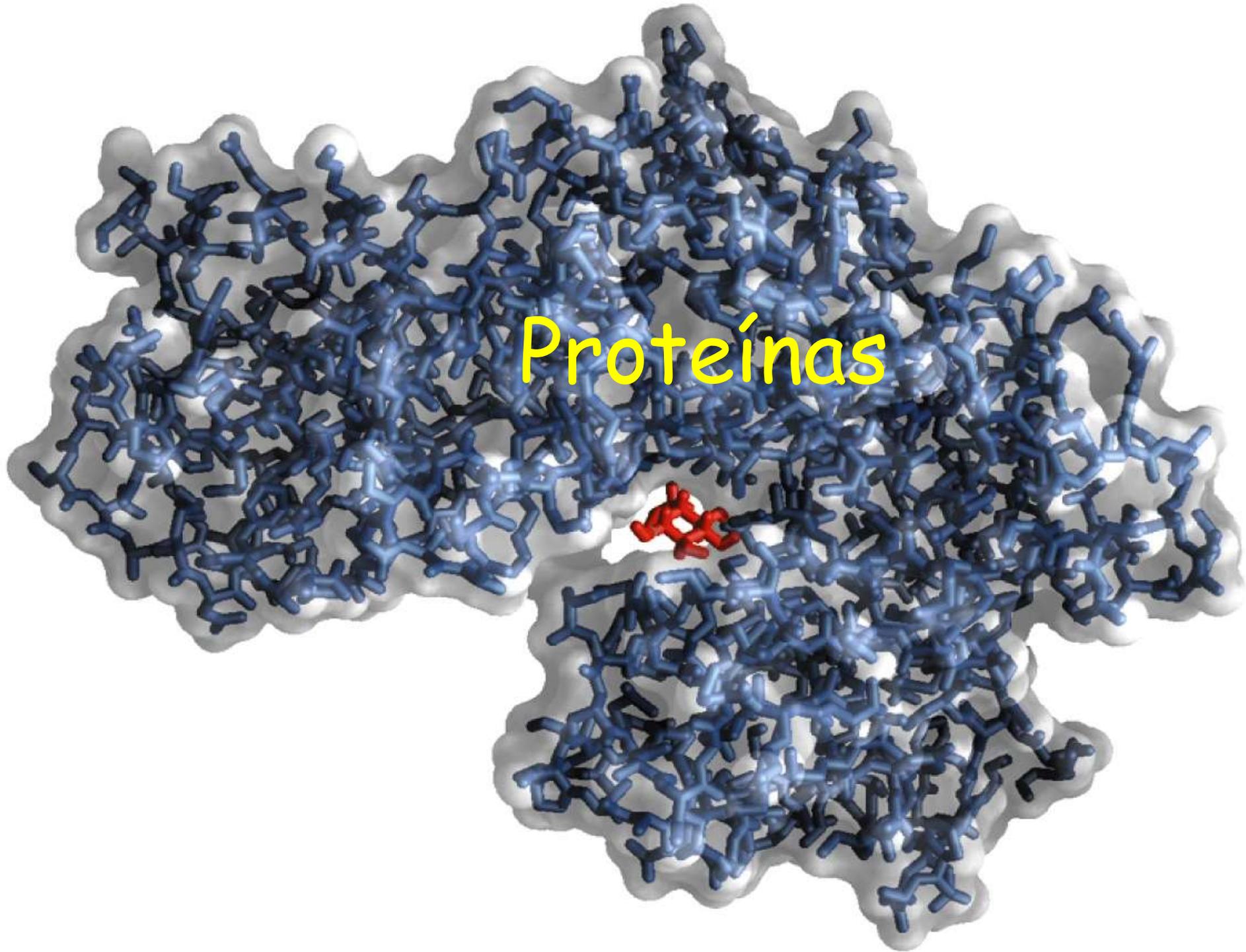
Ligações entre aminoácidos



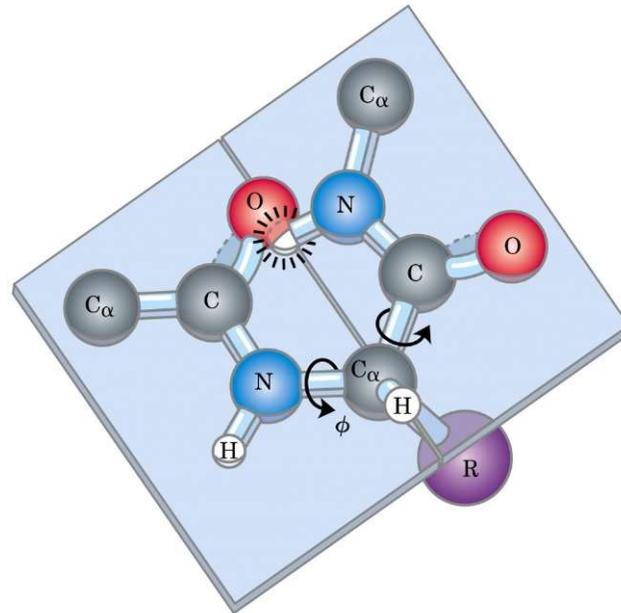
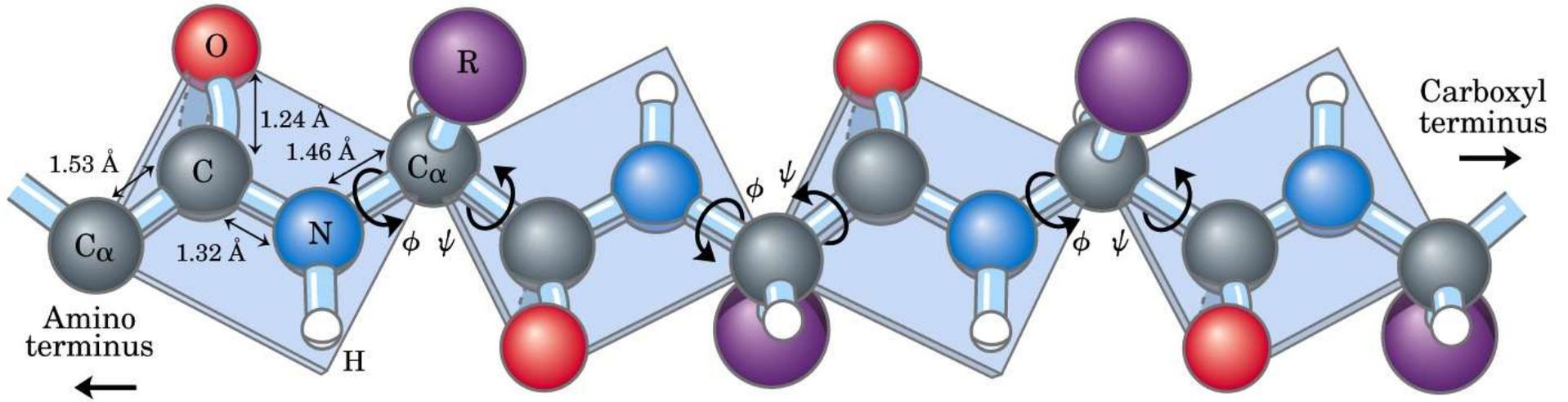
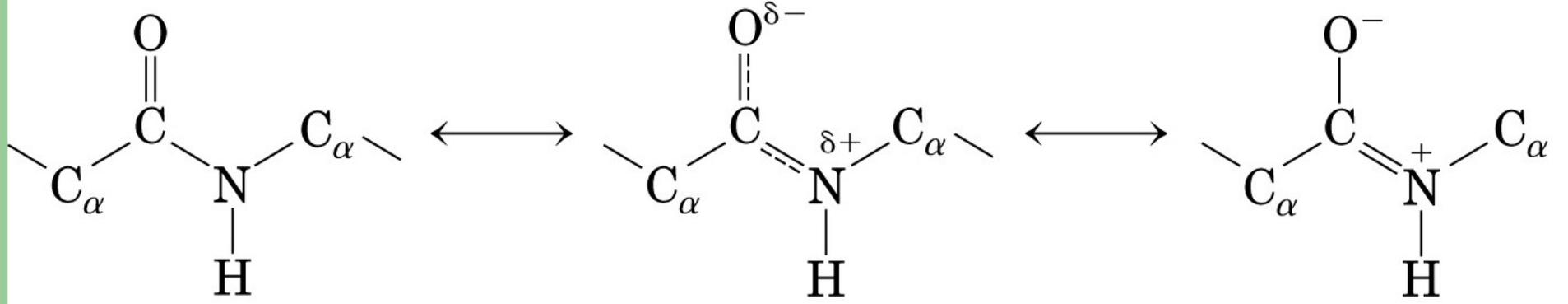


Amino-terminal end

Carboxyl-terminal end

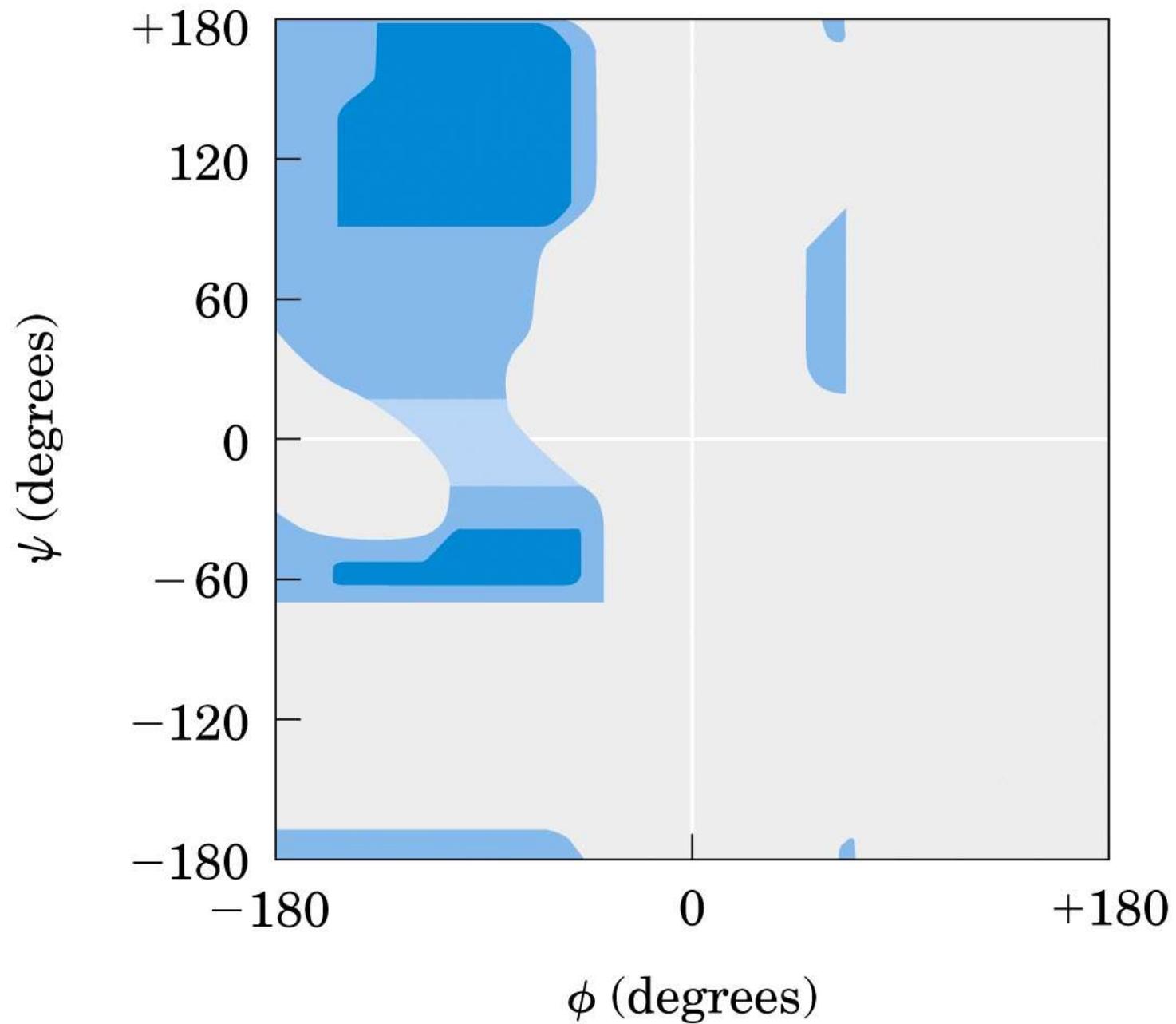


Proteínas



(e)

Gráfico de Ramachandran para L-ALA

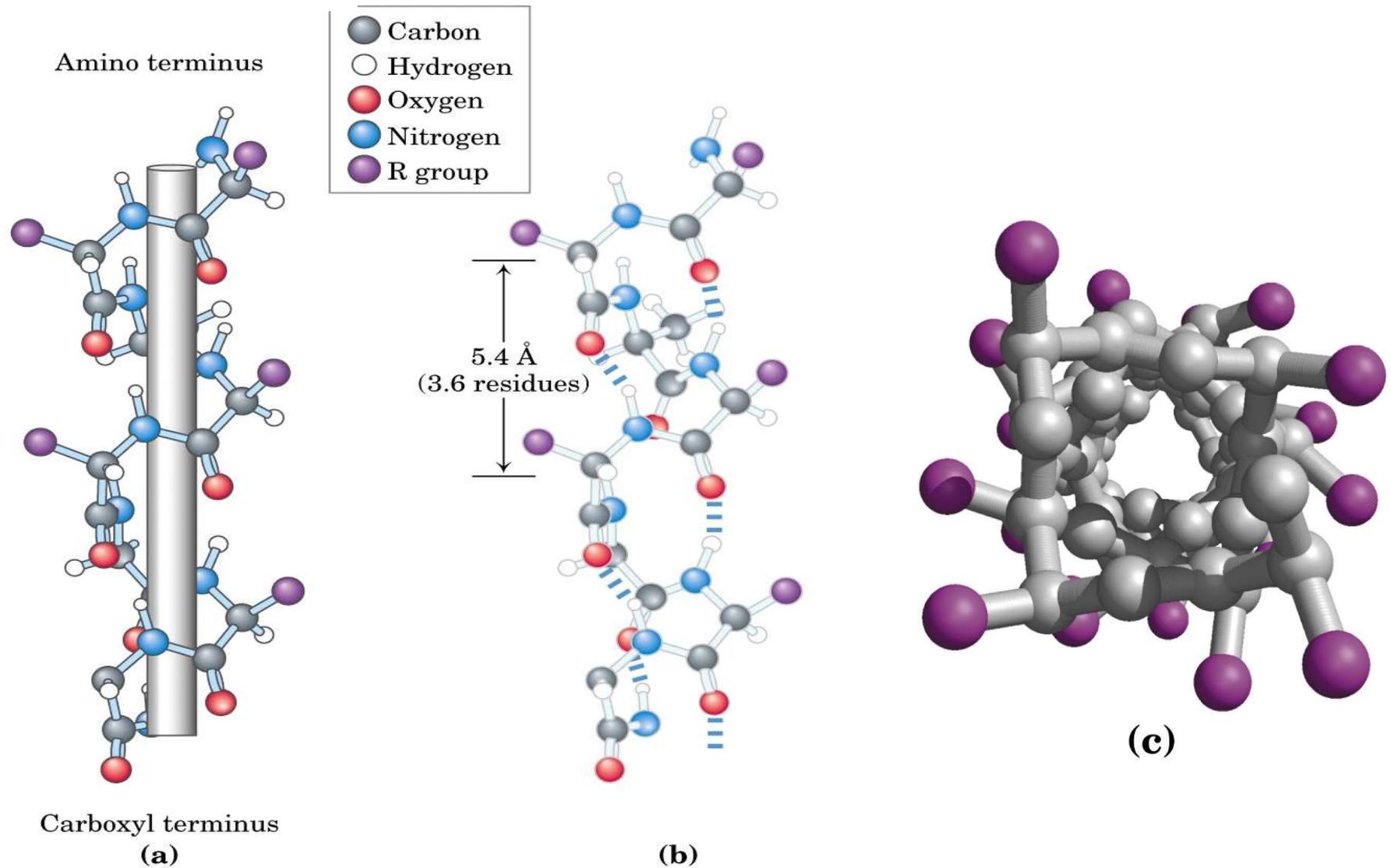


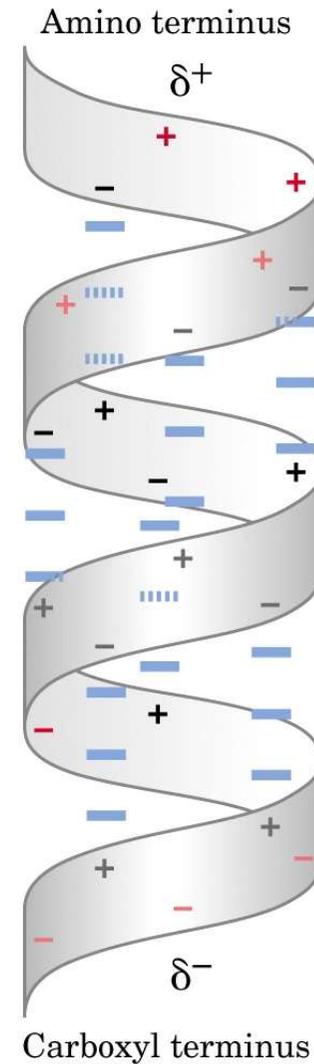
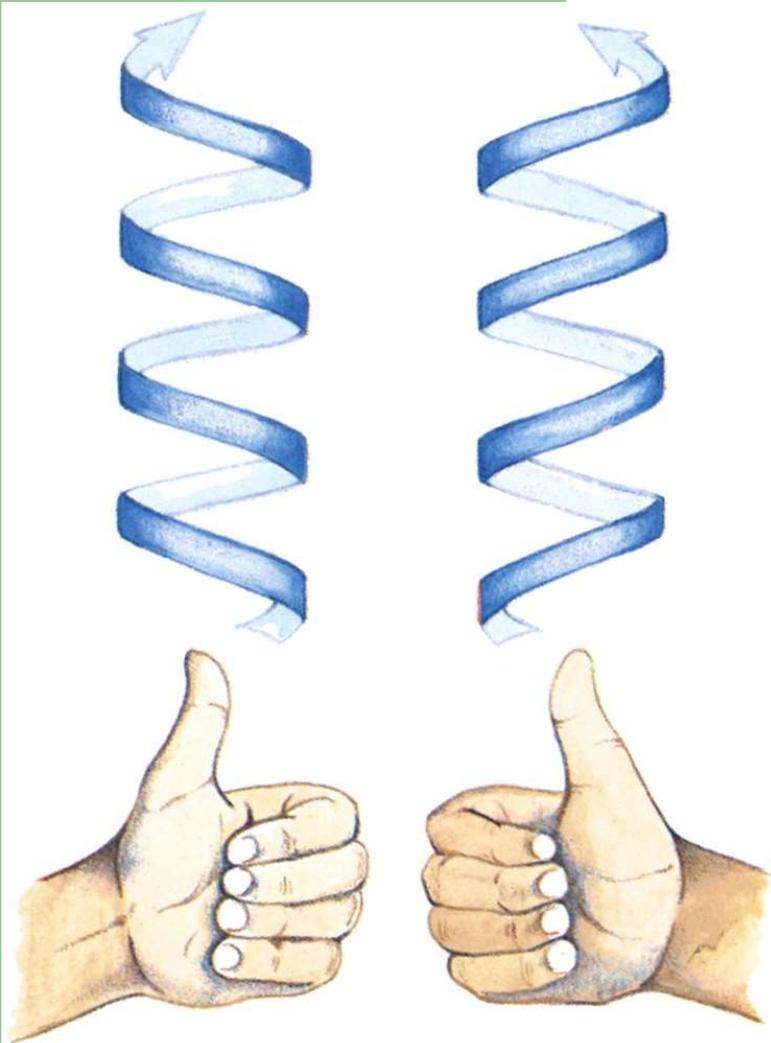
Estrutura na Arquitetura das proteínas

1) **Primária:** sequência de aminoácidos

2) **Secundária:** arranjo espacial de radicais de aminoácidos

2.1 α -hélice

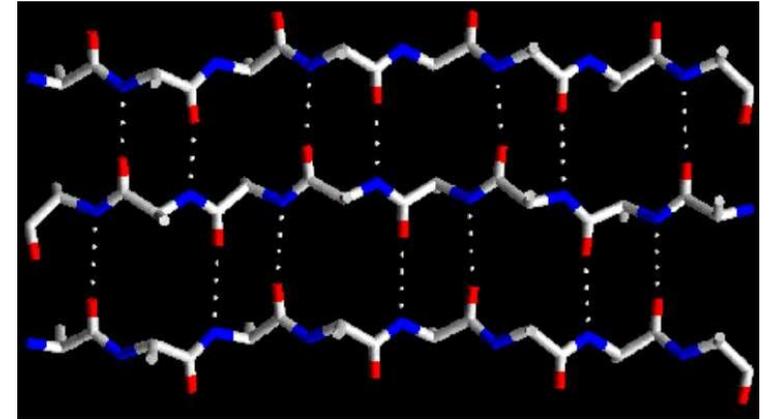




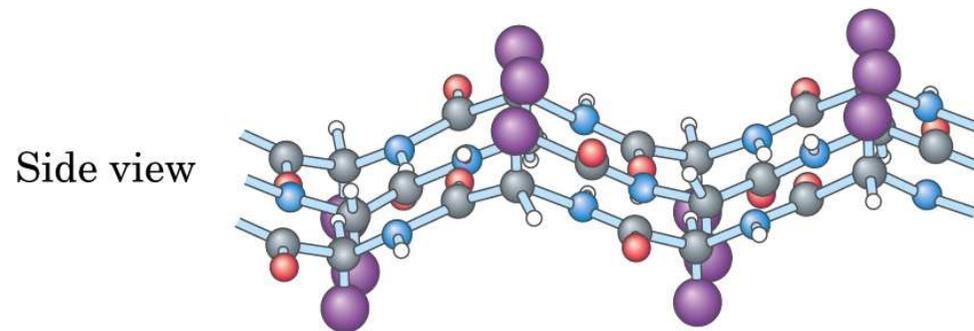
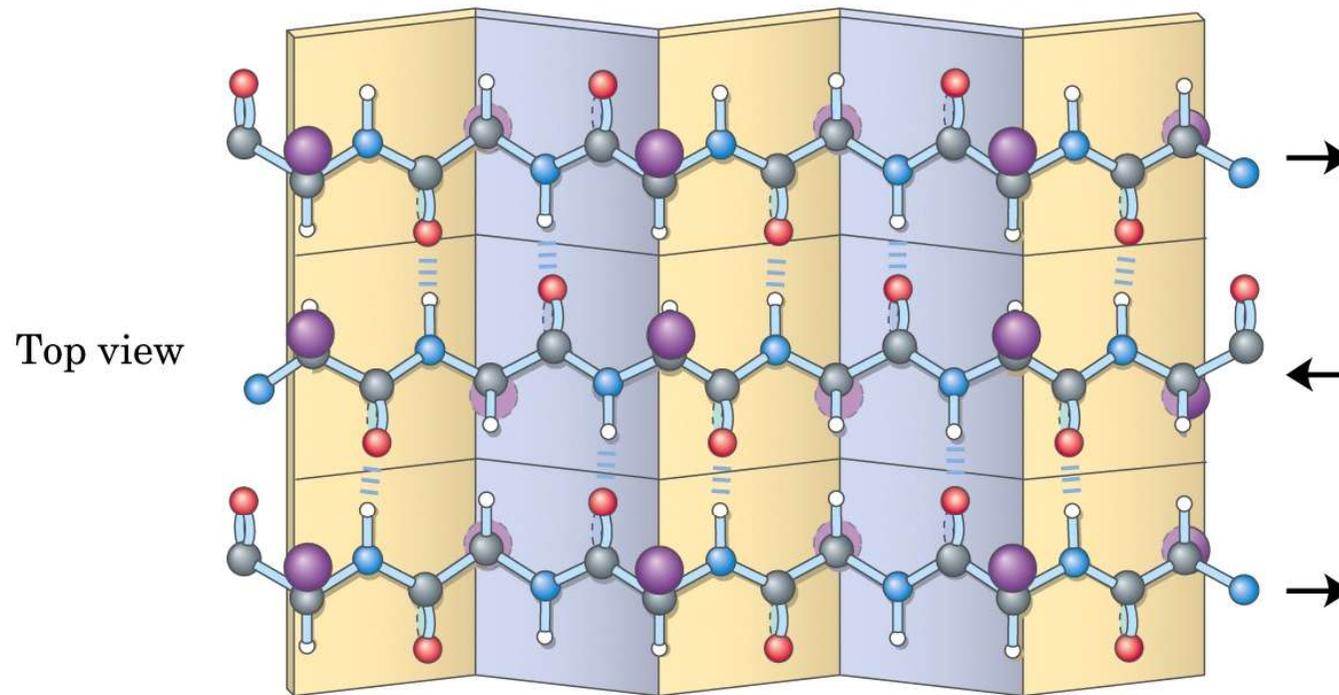
Restrições que afetam a estabilidade de uma alfa – hélice:

- 1) Repulsão eletrostática;
- 2) Ocorrência de resíduos de Pro e Gli

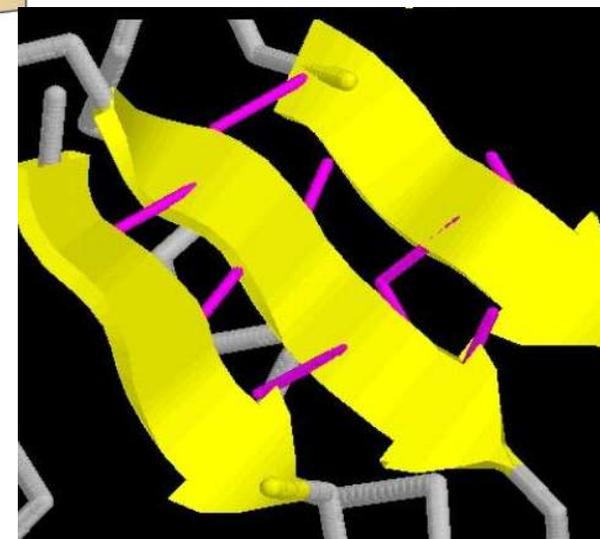
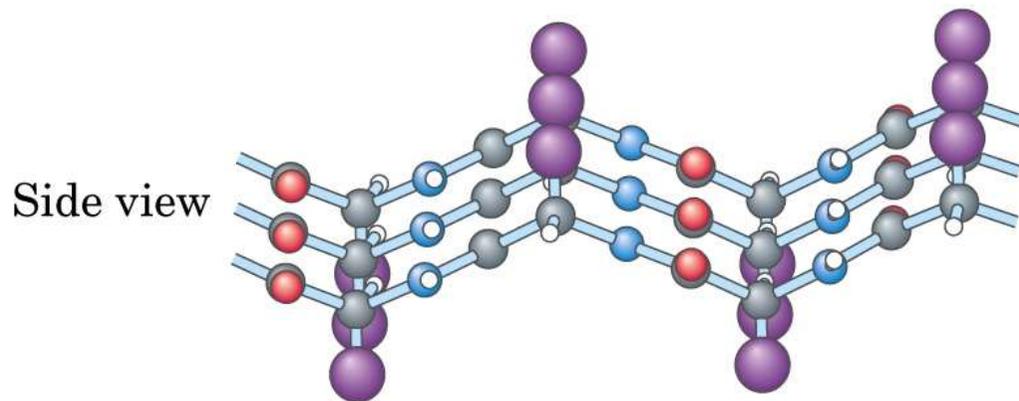
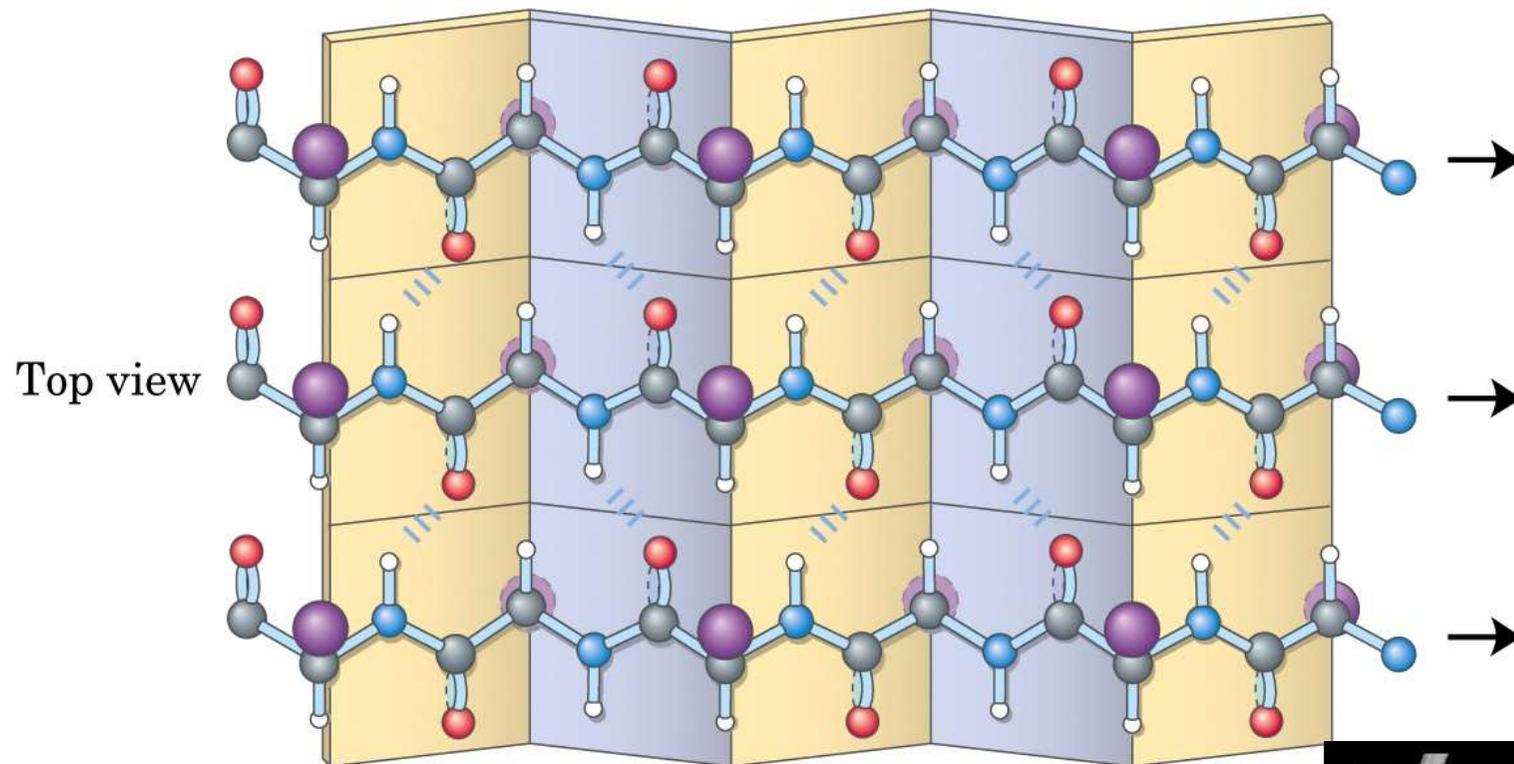
2.2 Folhas β pregueadas



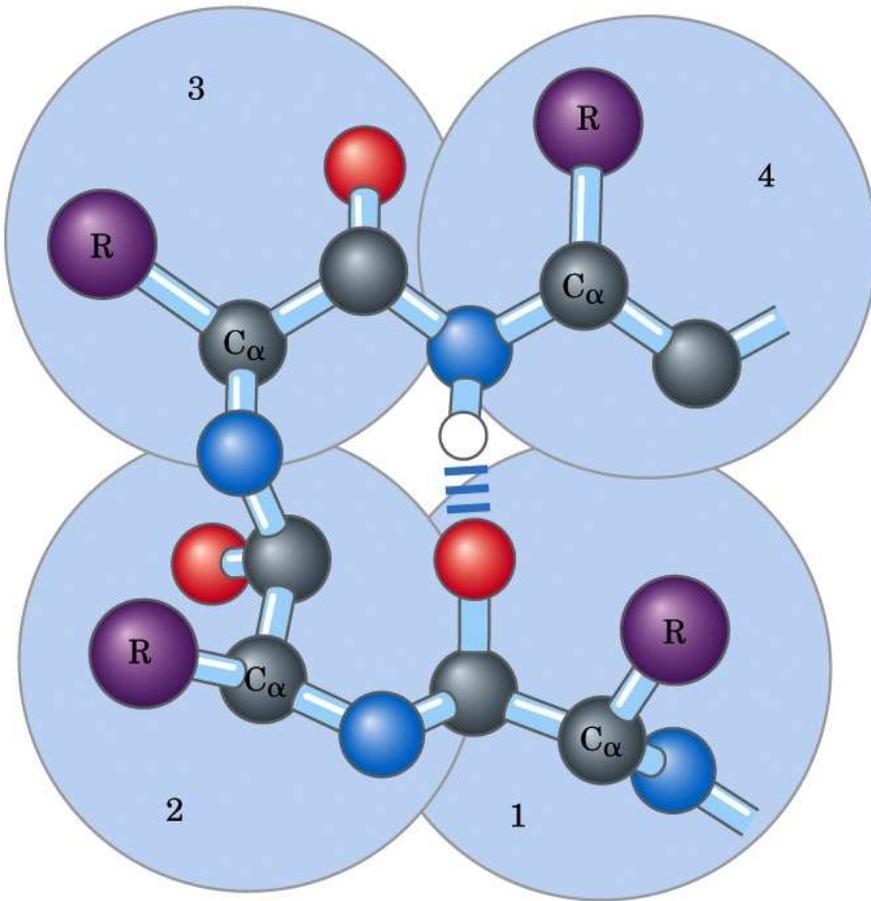
(a) Antiparallel



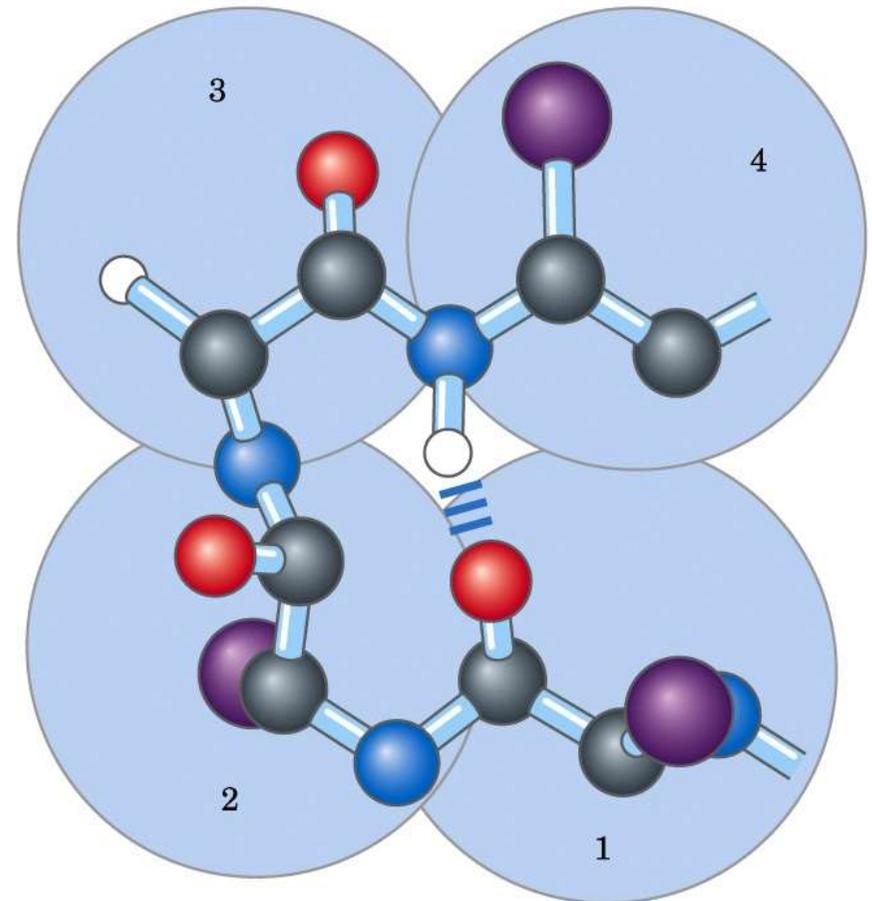
(b) Parallel



Dobras β



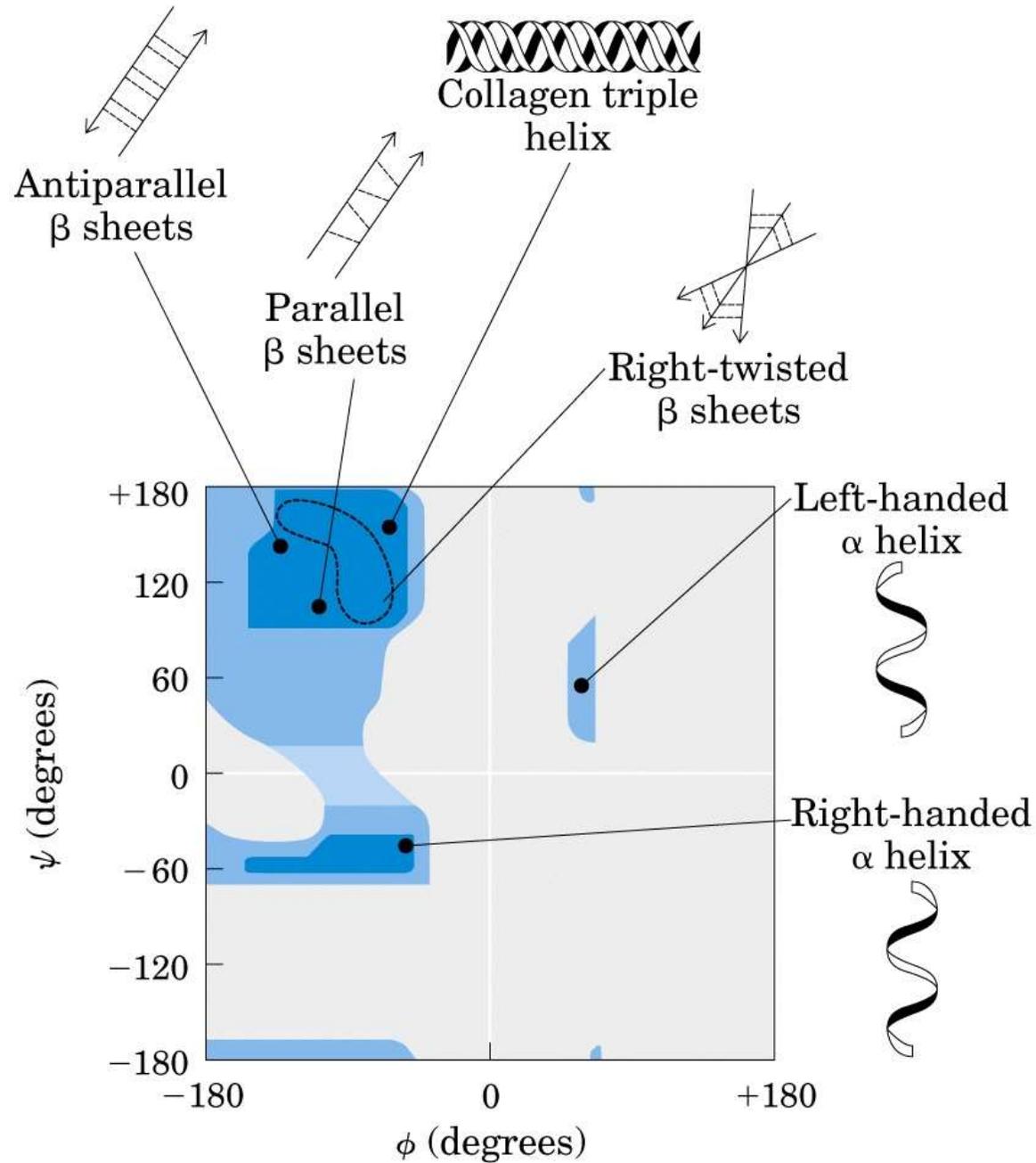
Type I



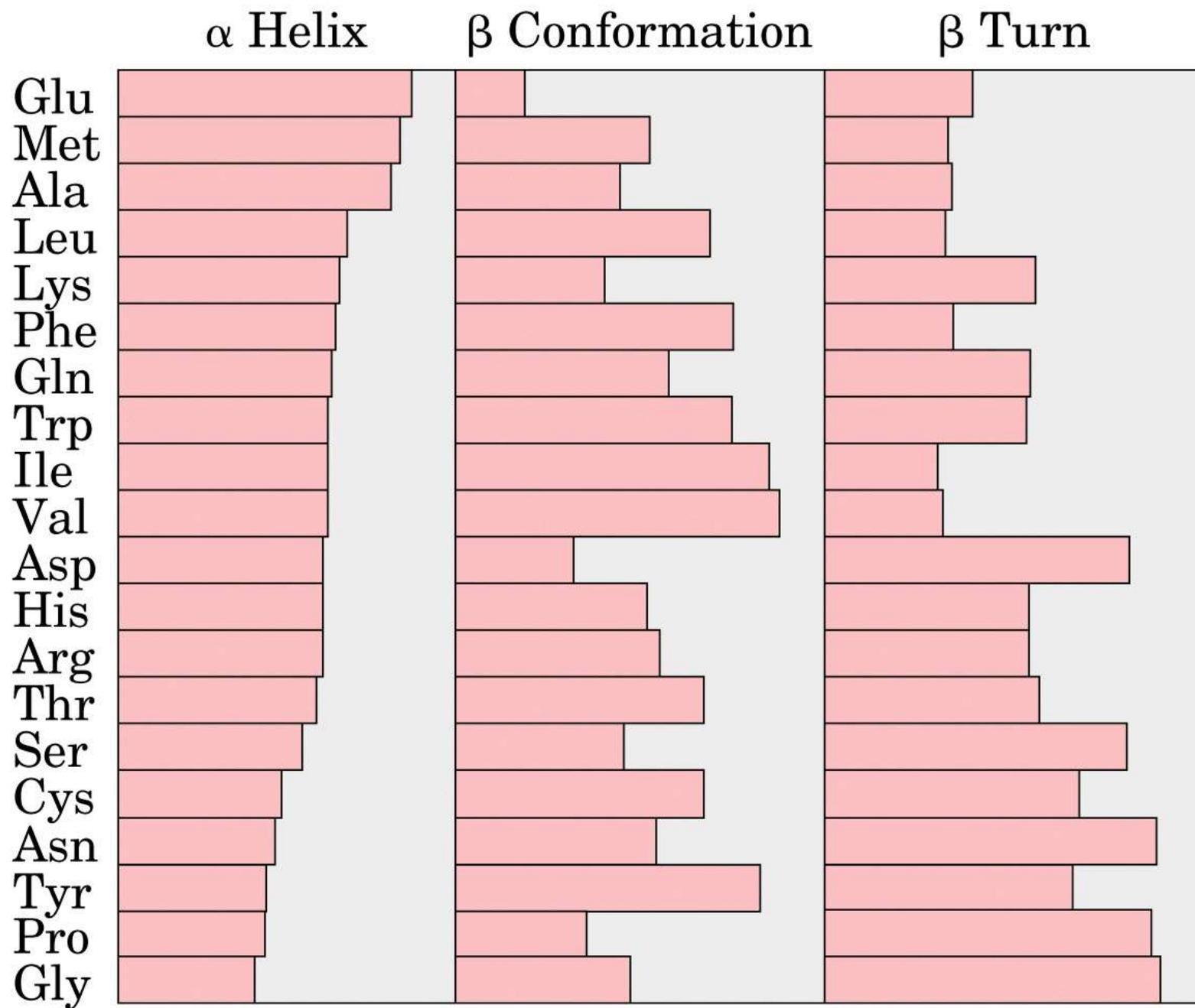
Type II

β Turns
(a)

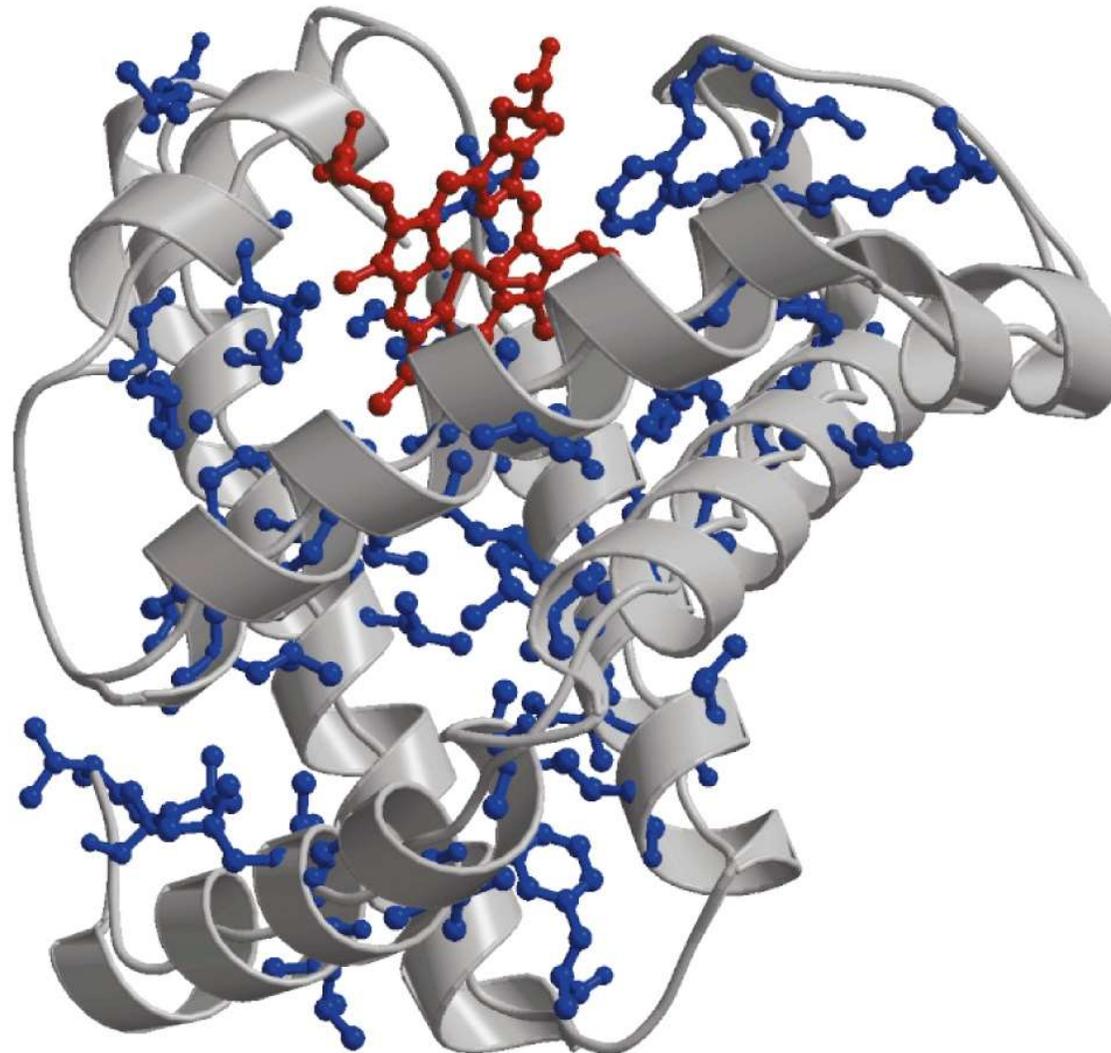
Conformações possíveis de estruturas secundárias



(a)

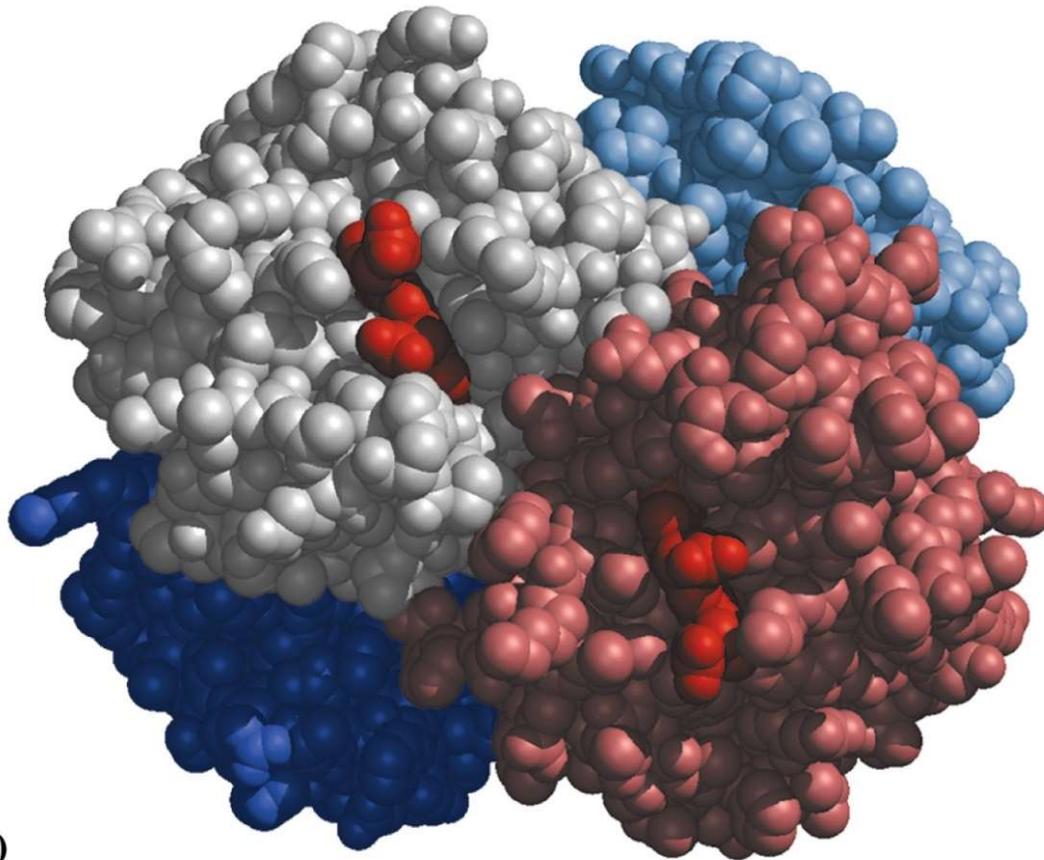


3) Terciária: arranjo tridimensional global de todos os átomos de proteína

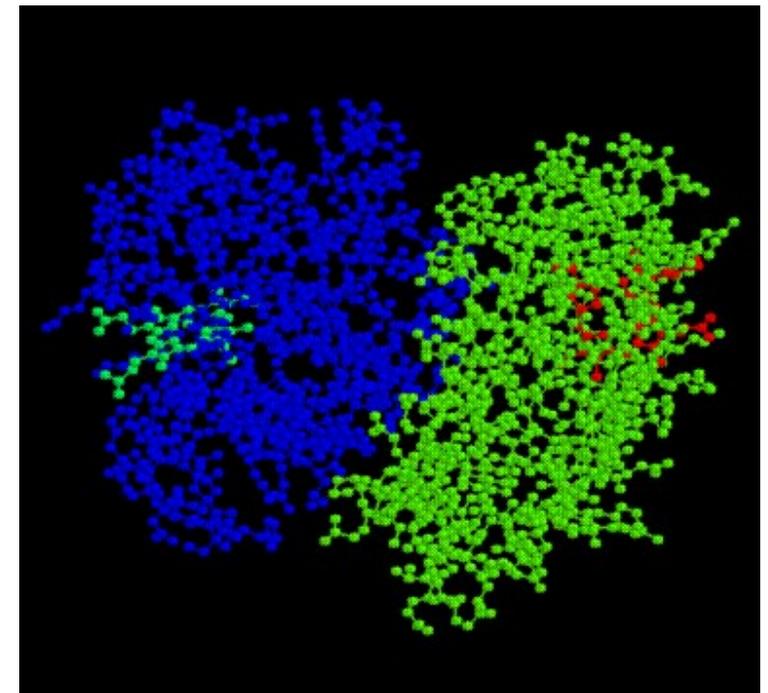
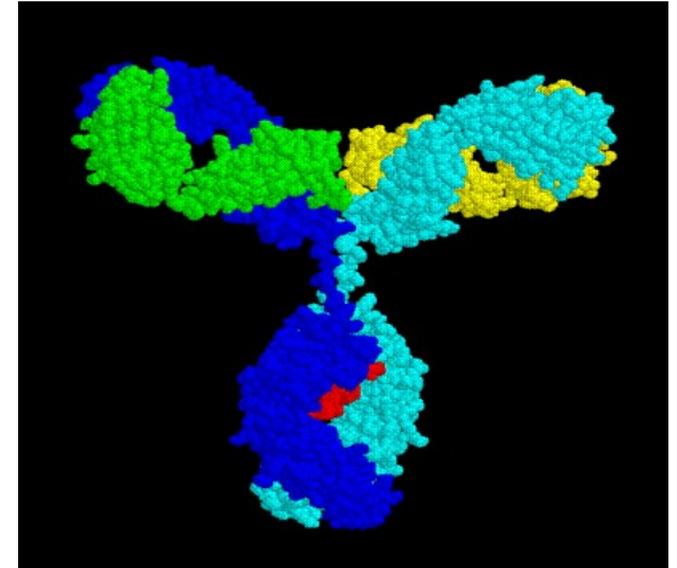


(d)

4) Quaternária: Refere-se ao arranjo espacial das subunidades polipeptídicas



(b)



PROTEÍNAS FIBROSAS E GLOBULARES

Fibrosas (α -queratina, colágeno e fibroína da seda): cadeias polipeptídicas em arranjos de folhas ou feixes

Globulares: cadeias polipeptídicas enoveladas em formas globulares

table 6-1

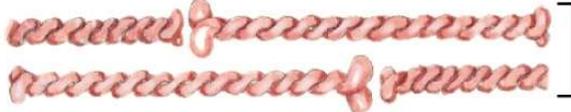
Secondary Structures and Properties of Fibrous Proteins

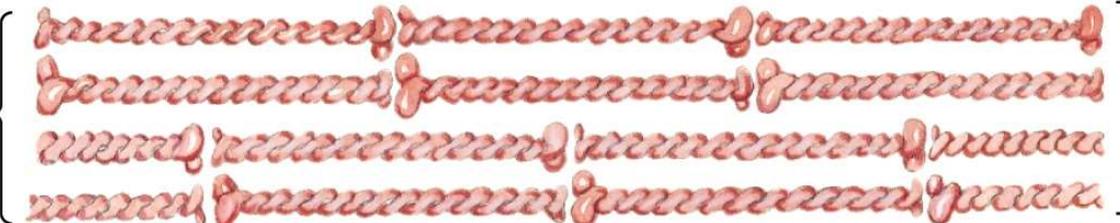
Structure	Characteristics	Examples of occurrence
α Helix, cross-linked by disulfide bonds	Tough, insoluble protective structures of varying hardness and flexibility	α -Keratin of hair, feathers, and nails
β Conformation	Soft, flexible filaments	Silk fibroin
Collagen triple helix	High tensile strength, without stretch	Collagen of tendons, bone matrix

α -queratina

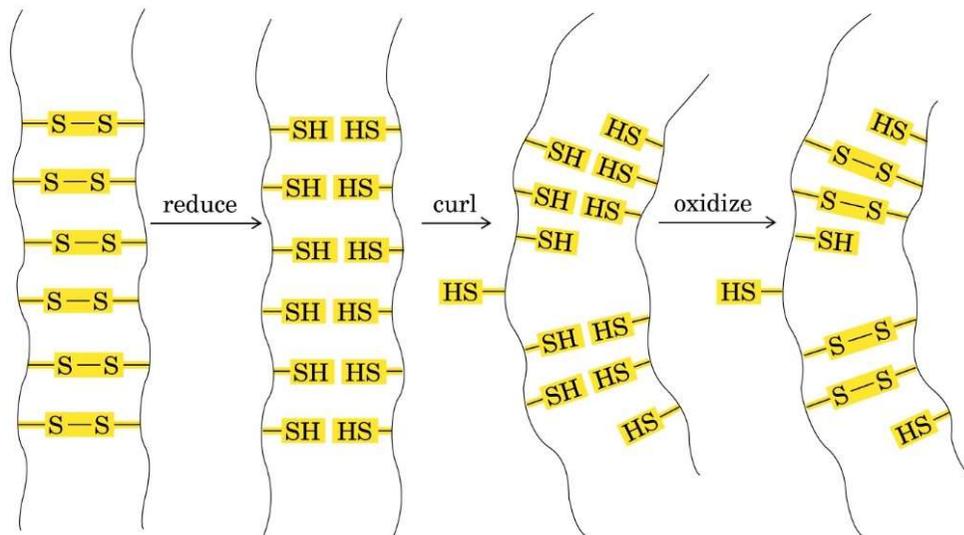
Keratin α helix — 

Two-chain coiled coil — 

Protofilament {  } 20–30 Å

Protofibril {  } 40–50 Å

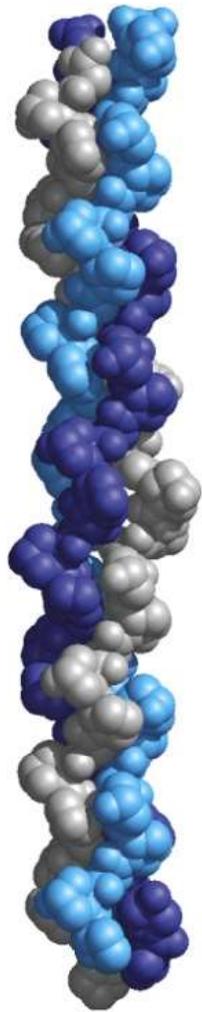
(a)



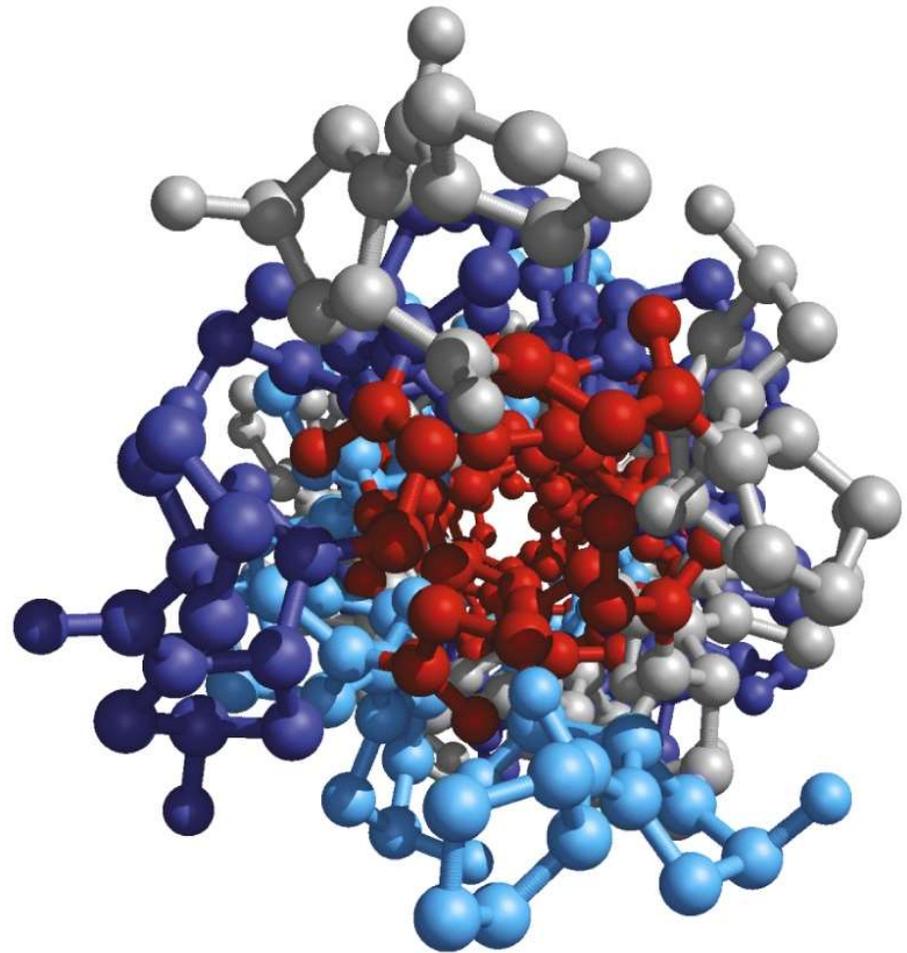
Colágeno

Encontrada em tecido conjuntivo, cartilagens, matriz orgânica dos ossos, e córnea dos olhos

Em geral apresenta uma unidade tripeptídica repetida Gly - X - Pro ou Gly - X- HyPro

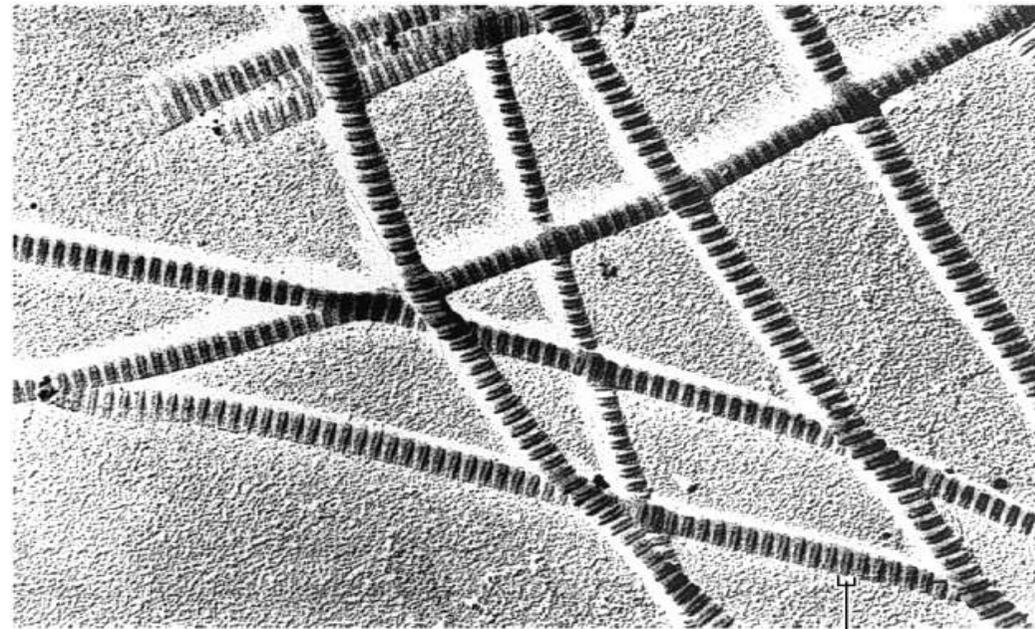


(c)



(d)

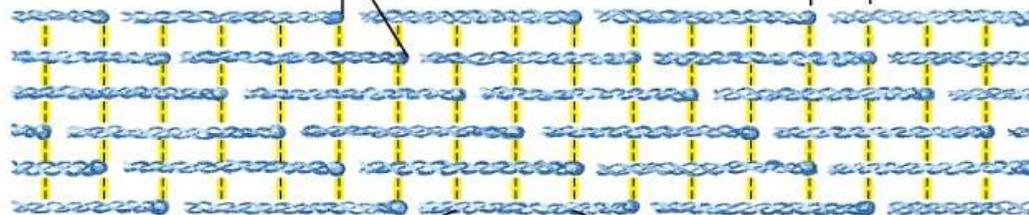
Fibrilas de colágeno



250
nm

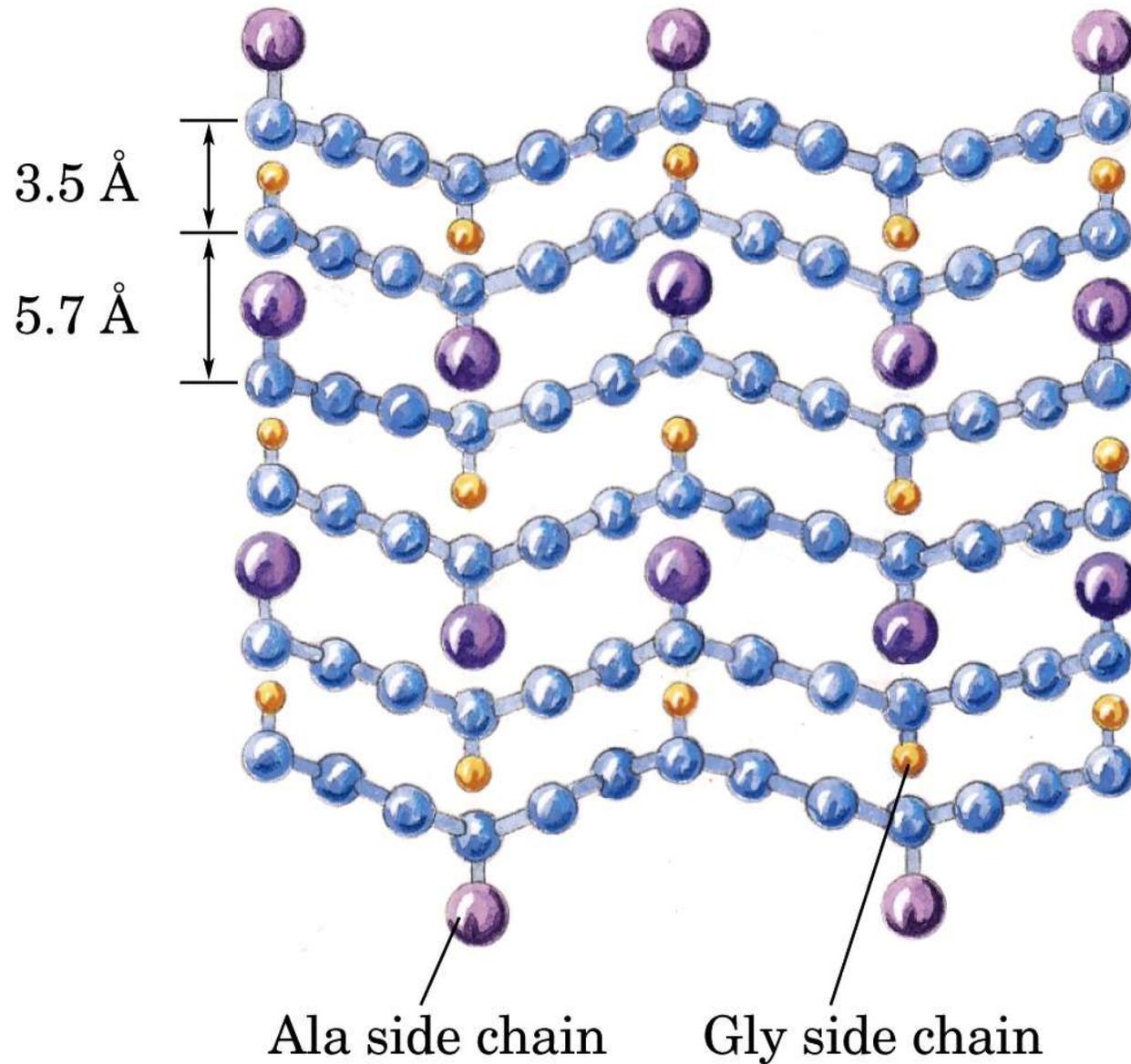
Heads of collagen
molecules

Cross-striations
640 Å (64 nm)

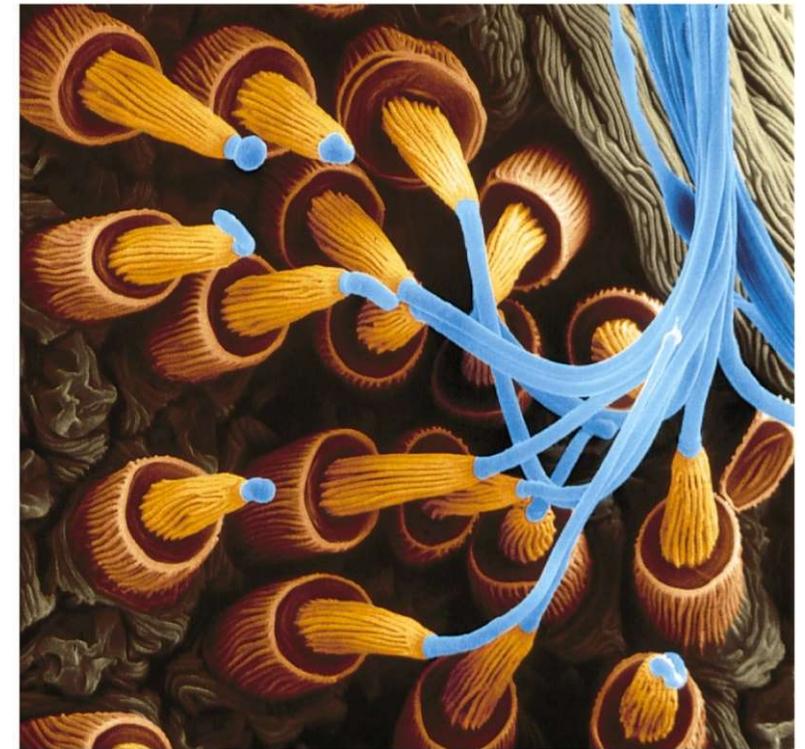


Section of collagen
molecule

Fibroína da seda



(a)



(b)

70 μm

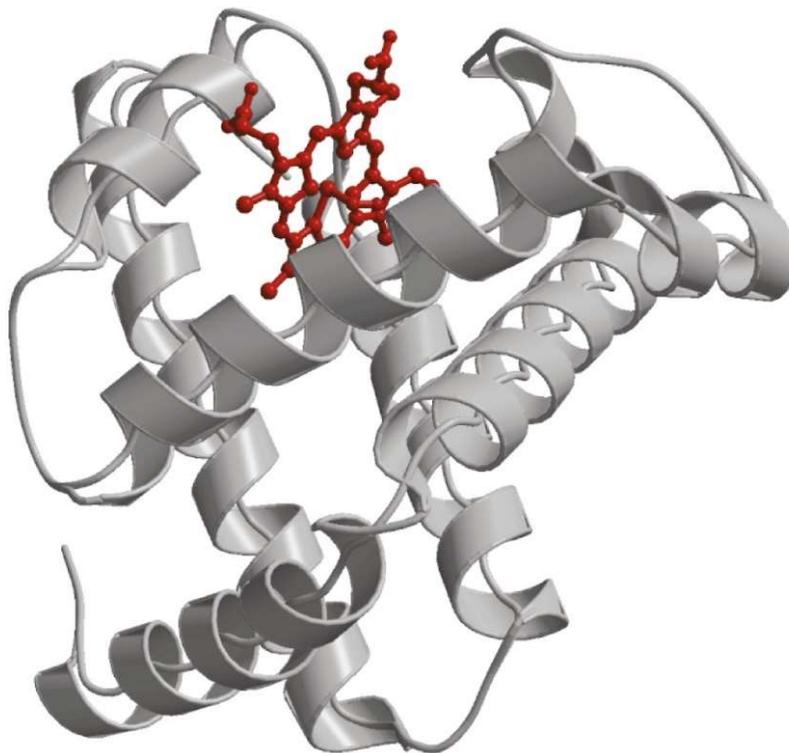
Proteínas globulares

β Conformation
 $2,000 \times 5 \text{ \AA}$

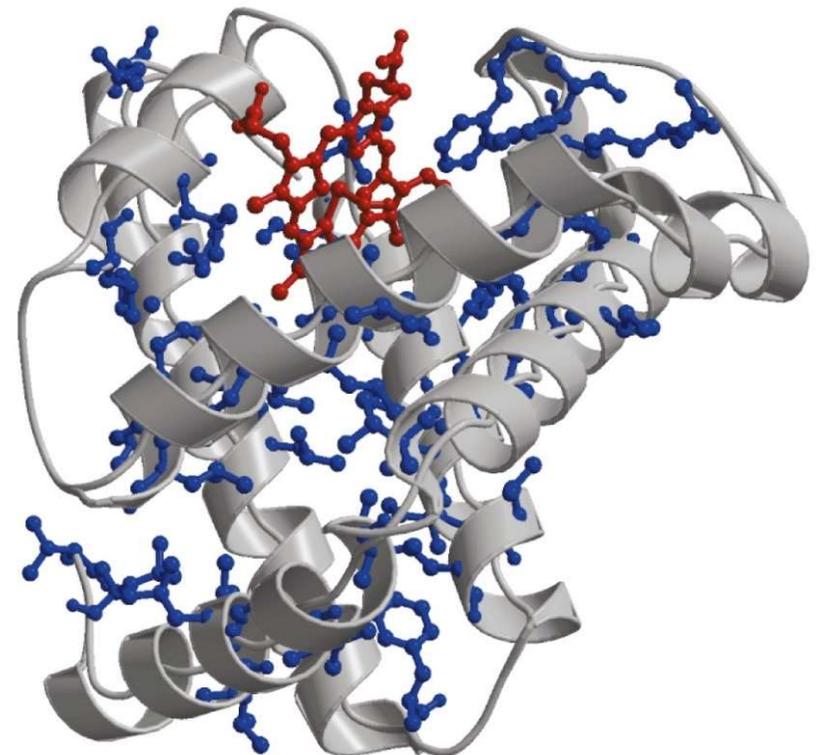
α Helix
 $900 \times 11 \text{ \AA}$

Native globular form
 $130 \times 30 \text{ \AA}$

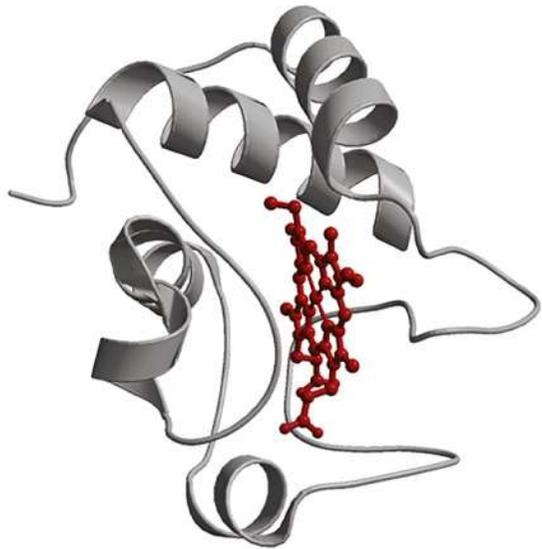
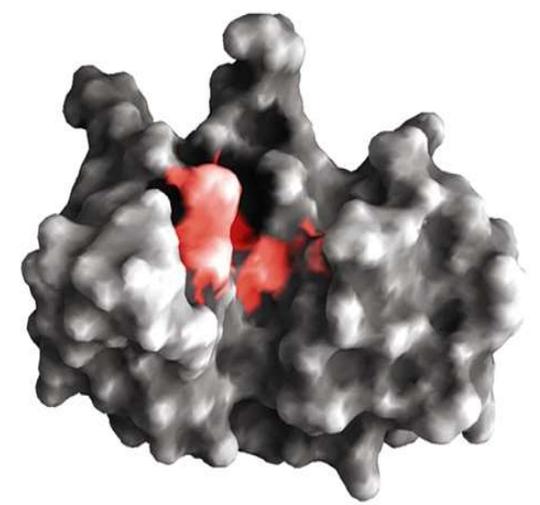
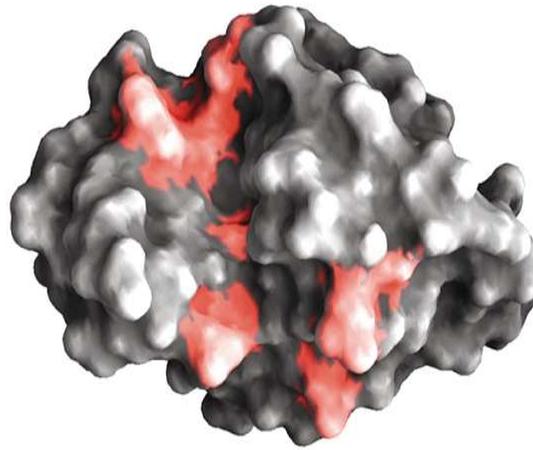
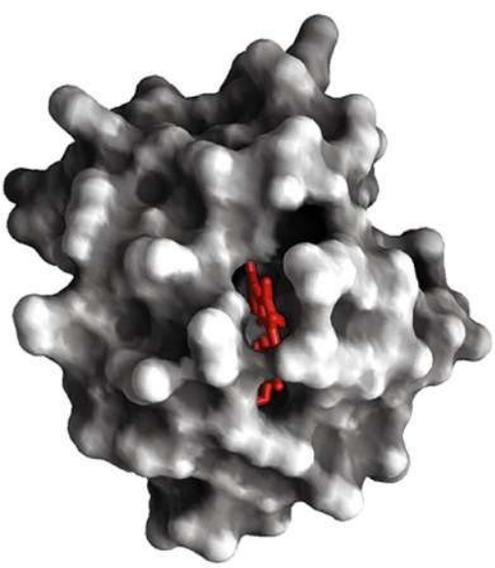
Mioglobina



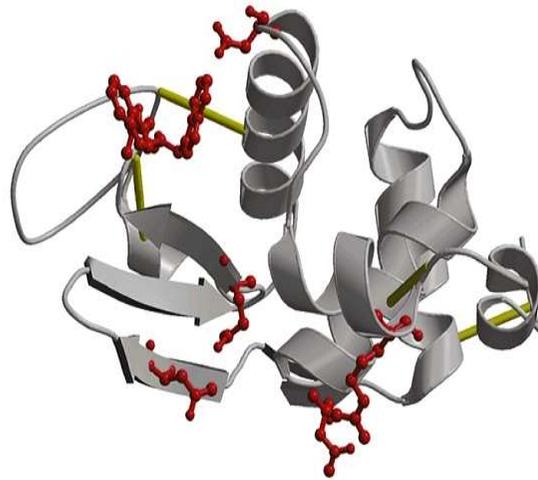
(a)



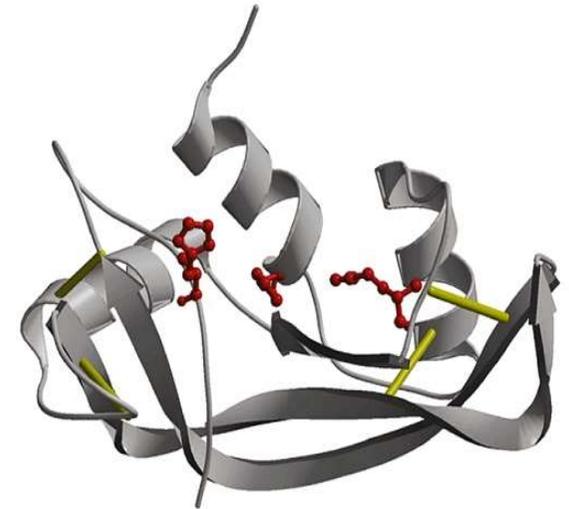
(d)



Cytochrome c



Lysozyme

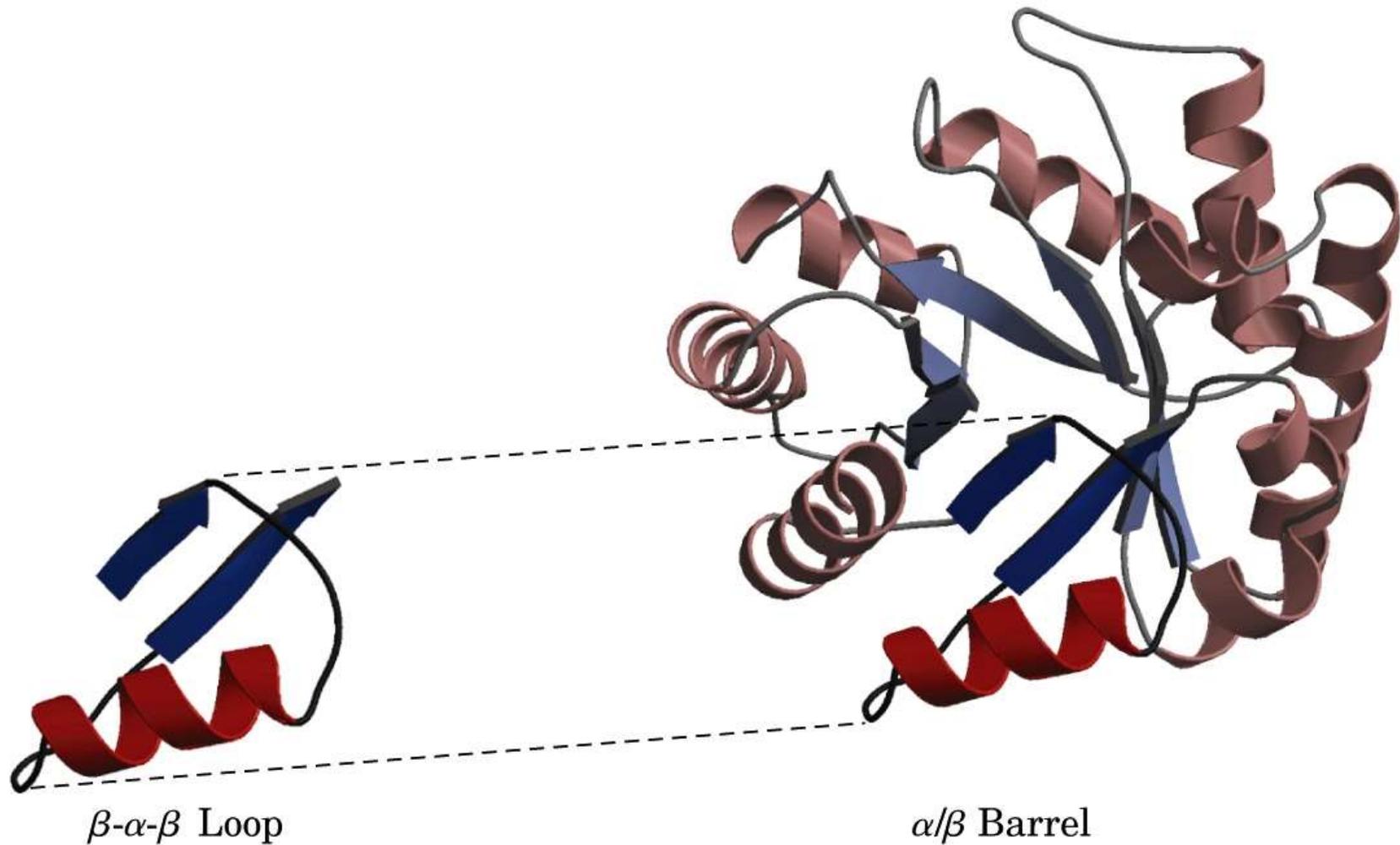


Ribonuclease

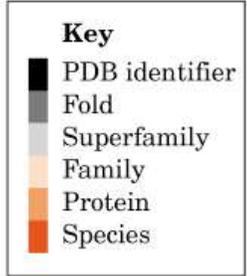
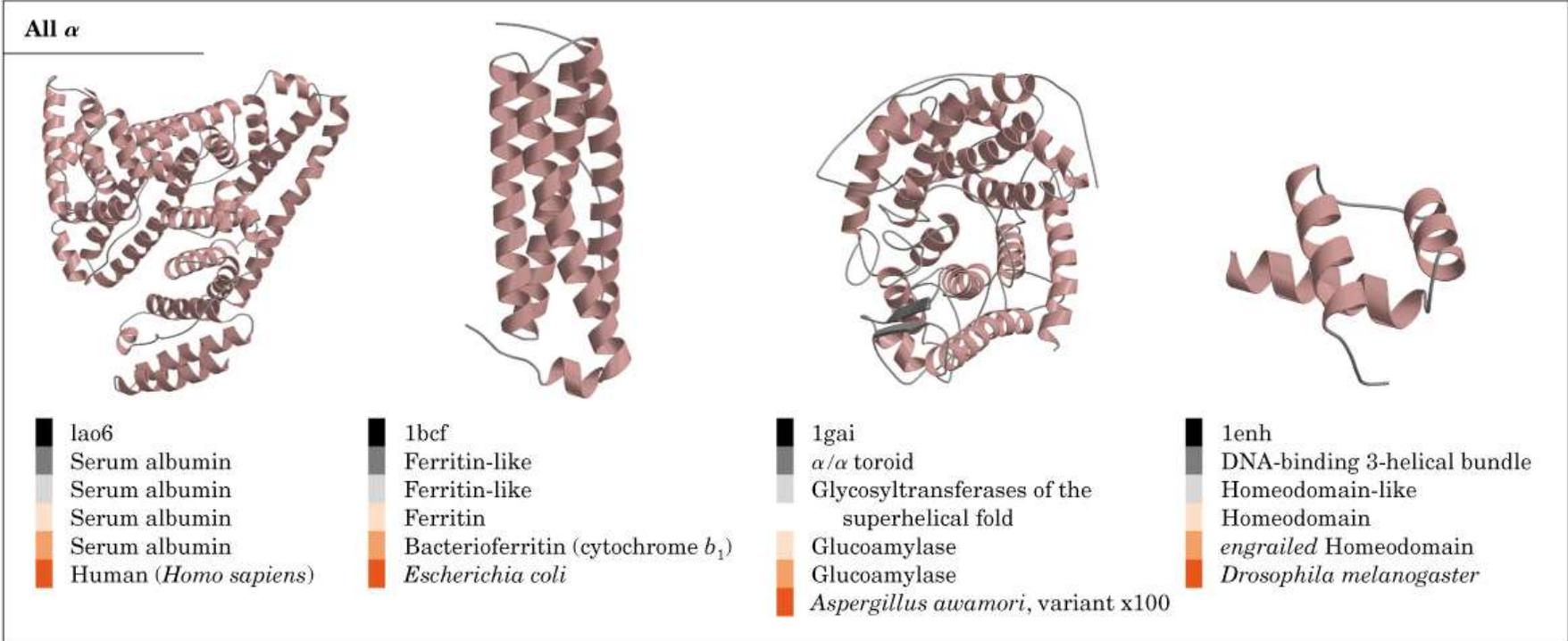
Approximate Amounts of α Helix and β Conformation in Some Single-Chain Proteins*

Protein (total residues)	Residues (%)	
	α Helix	β Conformation
Chymotrypsin (247)	14	45
Ribonuclease (124)	26	35
Carboxypeptidase (307)	38	17
Cytochrome <i>c</i> (104)	39	0
Lysozyme (129)	40	12
Myoglobin (153)	78	0

Ocultar R de aminoácidos hidrofóbicos de modo a excluir a água



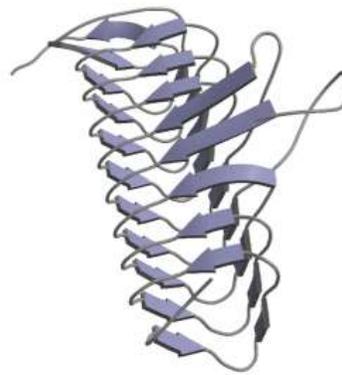
Classificação estrutural das proteínas



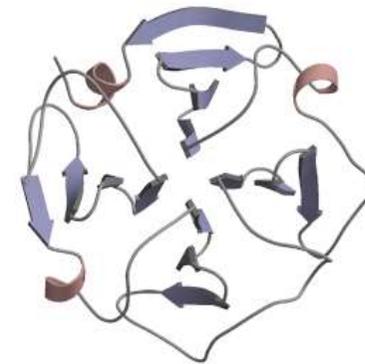
All β



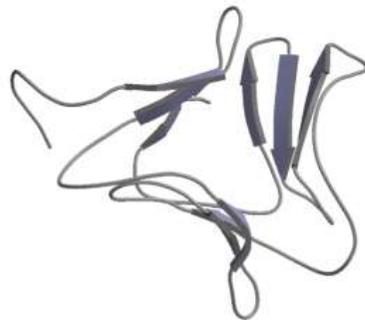
1hoe
 α -Amylase inhibitor
 α -Amylase inhibitor
 α -Amylase inhibitor
 HOE-467A
Streptomyces tendae 4158



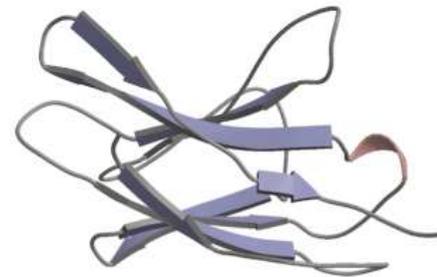
1lxa
 Single-stranded left-handed β helix
 Trimeric LpxA-like enzymes
 UDP *N*-acetylglucosamine acyltransferase
 UDP *N*-acetylglucosamine acyltransferase
Escherichia coli



1pex
 Four-bladed β propeller
 Hemopexin-like domain
 Hemopexin-like domain
 Collagenase-3 (MMP-13),
 carboxyl-terminal domain
 Human (*Homo sapiens*)



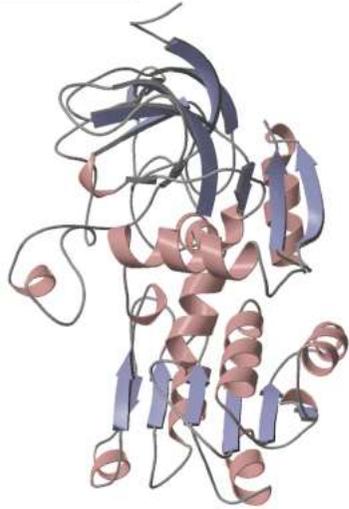
1jpc
 β -Prism II
 α -D-Mannose-specific plant lectins
 α -D-Mannose-specific plant lectins
 Lectin (agglutinin)
 Snowdrop (*Galanthus nivalis*)



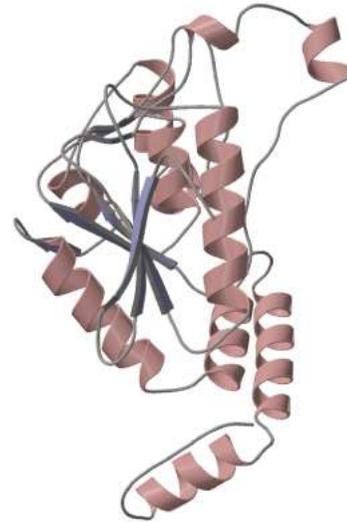
1cd8
 Immunoglobulin-like β sandwich
 Immunoglobulin
 Antibody variable domain-like
 CD8
 Human (*Homo sapiens*)

Key	
■	PDB identifier
■	Fold
■	Superfamily
■	Family
■	Protein
■	Species

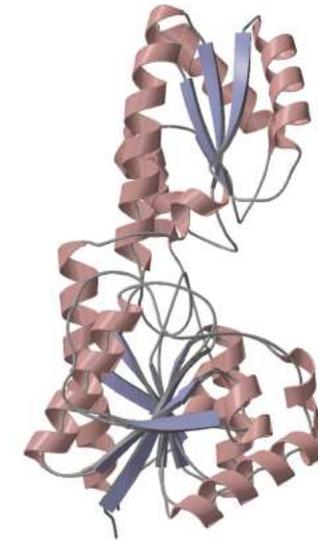
α/β



- 1deh
- NAD(P)-binding Rossmann-fold domains
- NAD(P)-binding Rossmann-fold domains
- Alcohol/glucose dehydrogenases, carboxyl-terminal domain
- Alcohol dehydrogenase
- Human (*Homo sapiens*)



- 1dub
- Crotonase-like
- Crotonase-like
- Crotonase-like
- Enoyl-CoA hydratase
- Rat (*Rattus norvegicus*)

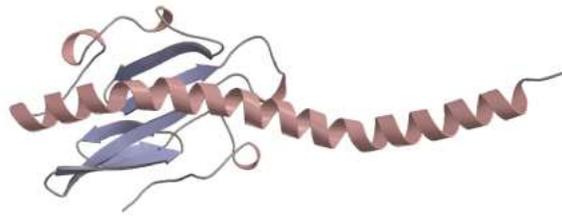


- 1pfk
- Phosphofruktokinase
- Phosphofruktokinase
- Phosphofruktokinase
- Phosphofruktokinase
- Escherichia coli*

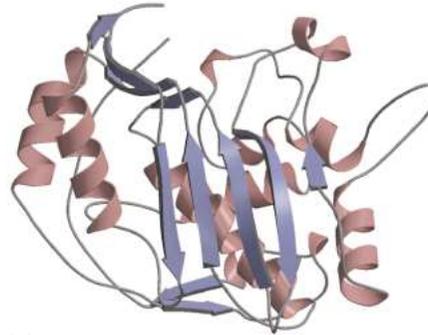
Key

- PDB identifier
- Fold
- Superfamily
- Family
- Protein
- Species

$\alpha + \beta$



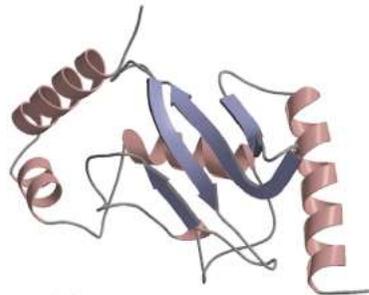
- 2pil
- Pilin
- Pilin
- Pilin
- Pilin
- Neisseria gonorrhoeae*



- 1syn
- Thymidylate synthase
- Thymidylate synthase
- Thymidylate synthase
- Thymidylate synthase
- Escherichia coli*



- 1ema
- Green fluorescent protein
- Green fluorescent protein
- Green fluorescent protein
- Green fluorescent protein
- Jellyfish (*Aequorea victoria*)



- 1u9a
- Ubiquitin-conjugating enzyme
- Ubiquitin-conjugating enzyme
- Ubiquitin-conjugating enzyme
- Ubiquitin-conjugating enzyme
- Human (*Homo sapiens*)

Key

- PDB identifier
- Fold
- Superfamily
- Family
- Protein
- Species

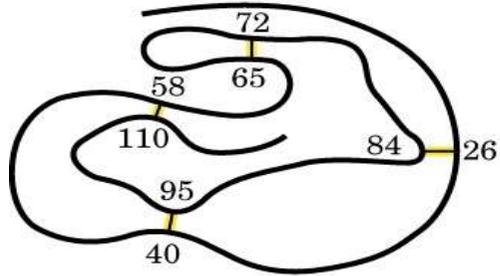
Enovelamento de proteínas

```
200 ?T(\G{+s x[A.N5~, #ATxSGpn`e□@
400 oDr'Jh7s DFR:W4l'u+^v6zpzJseOi
600 e2ih'8zs n527x8l8d_ih=Hldseb.
800 S#dh>)/s ]t3qC%lP%DK<|!^aseZ.
1000 vOth>nLs ut/isjl_kwojjwMasef.
1200 juth+nvs it is(lukh?SCw=ase5.
1400 Iithdn4s it isOl/ks/IxwLase~.
1600 M?thins it is lXk?T"_woasel.
1800 MsthinWs it is lwkN7□Kw(asel.
2000 Mhthin`s it is likv,aww_asel.
2200 MMthinns it is lik+5avwlasel.
2400 MethinXs it is likydaqw)asel.
2600 Methin4s it is lik2dasweasel.
2800 MethinHs it is like□aTweasel.
2883 Methinks it is like a weasel.
```

3. Rigor mortis. Por que o corpo enrijece

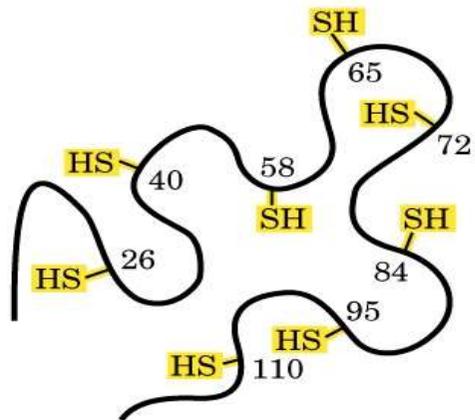
```
200 )z~hg)W4({cu!kO{d6jS!NlEyUx}p
400 "W hi\kR.<&CfA%4-YlG!iT$6({l6
600 .L=hinkm4(uMGP^lAWoE6klwW=yiS
800 AthinkaPa_vYH liR\Hb,Uo4\-"(
1000 OFthinksP)@fZO li8v) /+Eln26B
1200 6ithinksMvt -V likm+g1#K~)BFk
1400 vxthinksaEt □w like.SlGeutks.
1600 :Othinks<it MC likesN2[eaVe4.
1800 uxthinksqit Or likeQh)weaow.
2000 Y/thinks it id like7alwea)e&.
2200 Methinks it iw like a[weawel.
2400 Methinks it is like a;weasel.
2431 Methinks it is like a weasel.
```

Enovelamento de proteínas



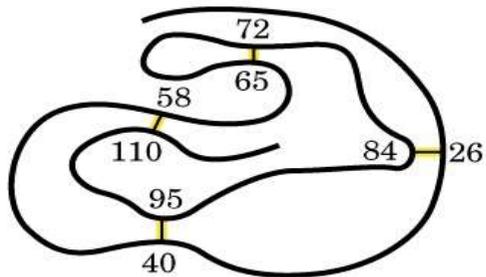
Native state;
catalytically active.

addition of
urea and
mercapto-
ethanol

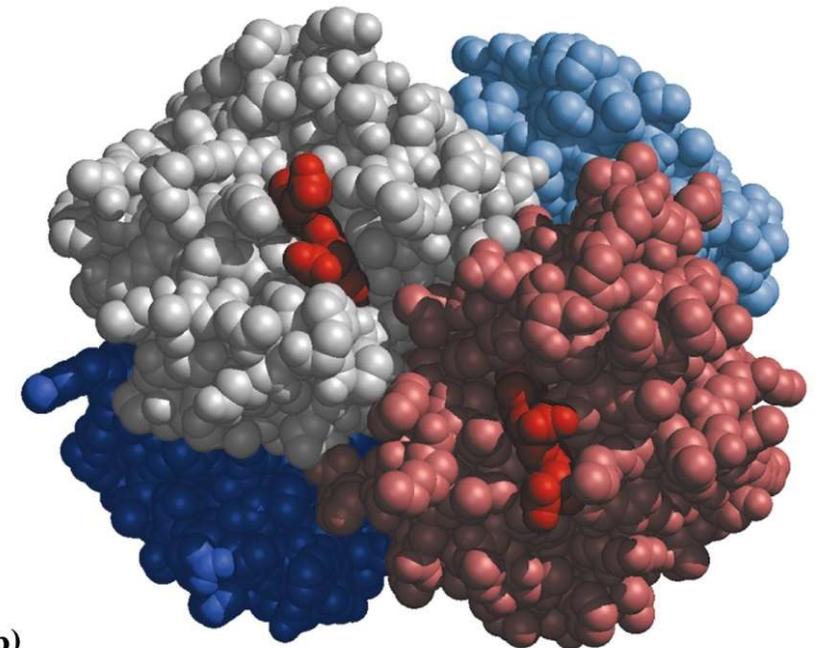


Unfolded state;
inactive. Disulfide
cross-links reduced to
yield Cys residues.

removal of
urea and
mercapto-
ethanol



Native,
catalytically
active state.
Disulfide cross-links
correctly re-formed.



(b)

Doença de príon (enovelamento incorreto)

Proteína príon (PrP)

PrP^{Sc} = conformação alterada

Encefalopatia espongiforme

