

Bioquímica Avançada (QBQ-5751) 2023

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Aminoácidos e Peptídeos

Princípios de termodinâmica
e Forças Intermoleculares



Estrutura covalente de
proteínas

(Estrutura e função
/evolução química)



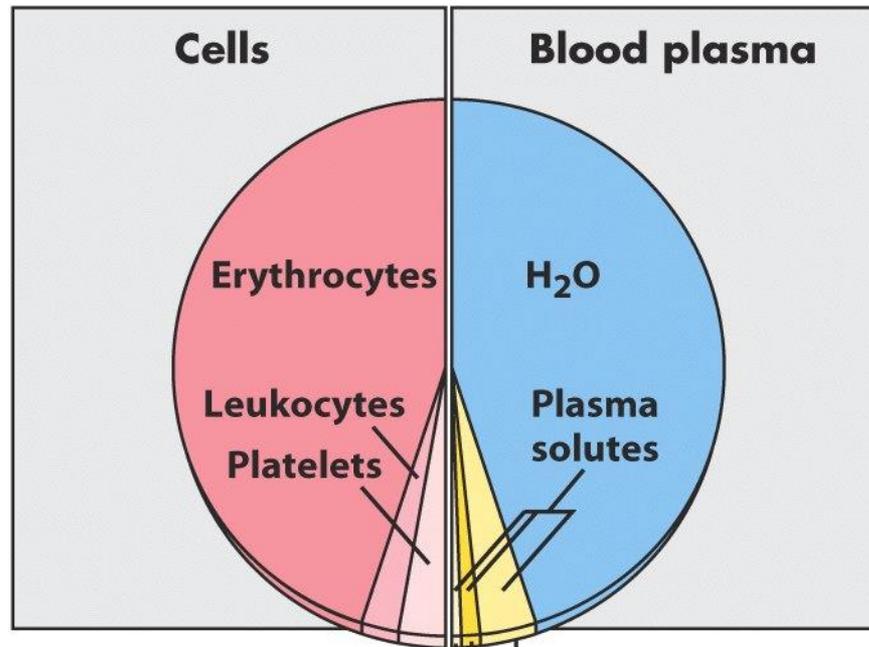
Estrutura 3D de proteínas



... Enzimas



Folding e dinâmica de proteínas



Inorganic components (10%)

NaCl, bicarbonate, phosphate,
CaCl₂, MgCl₂, KCl, Na₂SO₄

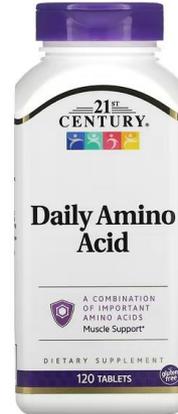
Organic metabolites and waste products (20%)

glucose, amino acids, lactate, pyruvate,
ketone bodies, citrate, urea, uric acid

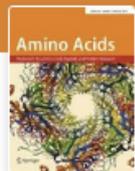
Plasma proteins (70%)

Major plasma proteins: serum albumin, very-low-density lipoproteins (VLDL), low-density lipoproteins (LDL), high-density lipoproteins (HDL), immunoglobulins (hundreds of kinds), fibrinogen, prothrombin, many specialized transport proteins such as transferrin

Funções + Aplicações de aminoácidos → Pesquisa, Terapêutica, Alimentação, Nutrição, Indústria



- Fontes de energia metabólica
- Blocos construtivos das proteínas e peptídeos:
20 α -aminoácidos usuais/ "essenciais" aos humanos (9): F, H, I, L, K, M, T, W, V
aminoácidos não usuais
- Intermediários biossintéticos: síntese de aminoácidos, nucleotídeos, compostos nitrogenados
- Ações biológicas: algumas já citadas
- Marcador de envelhecimento
- Suplementos alimentares
- Compostos neuroativos
- Reagentes para sínteses orgânicas (heterociclos e β -lactamas)
- Síntese química de aminoacil-resinas, peptídeos e proteínas
- Preparação de colunas quirais p/ cromatografia
- Cosmética



Amino Acids

The Forum for Amino Acid, Peptide and Protein Research

 [Editorial board](#)  [Aims & scope](#)  [Journal updates](#)

Amino Acids publishes contributions from all fields of amino acid and protein research: analysis, separation (proteomics), synthesis, biosynthesis, evolution, folding, structure, stability, dynamics, medicinal chemistry, catabolism, cross linking amino acids, racemization/enantiomers, modification of amino acids such as phosphorylation, methylation, acetylation, hydroxylation and glycosylation. The *journal* also welcomes papers on new roles for amino acids and proteins in physiology and pathophysiology, biology, amino acid analogues, polyamines, labeled amino acids, peptides, stable and radioactive isotopes of amino acids, excitatory amino acids, unusual amino acids, and peptides. Applications include medicine (gastroenterology, nephrology, psychiatry, neurology, oncology), biochemistry, structural biology, agriculture and plants, food chemistry, nutrition, microbiology, neurochemistry, pharmacology, and sports. We also encourage the submissions of computational papers and interdisciplinary research such as economic, social sciences and humanities. — [show all](#)

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Ellen I. Closs

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3.844 (2021)

Five year impact factor

34 days

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(Median)

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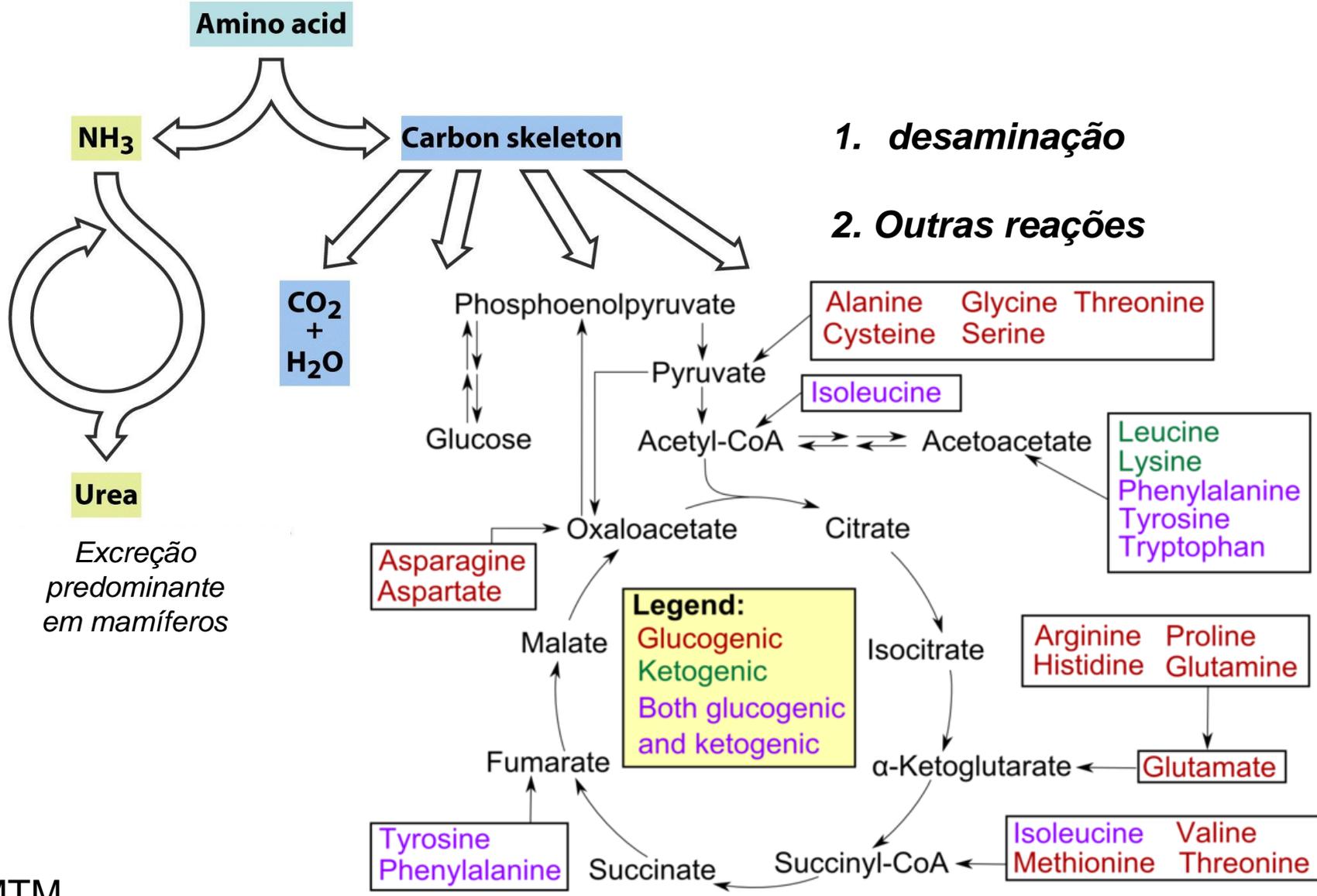
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Aminoácidos: blocos construtivos de proteínas → Metabolismo de *proteínas* endógenas e da dieta

metabolismo de aminoácidos (degradação e biossíntese)

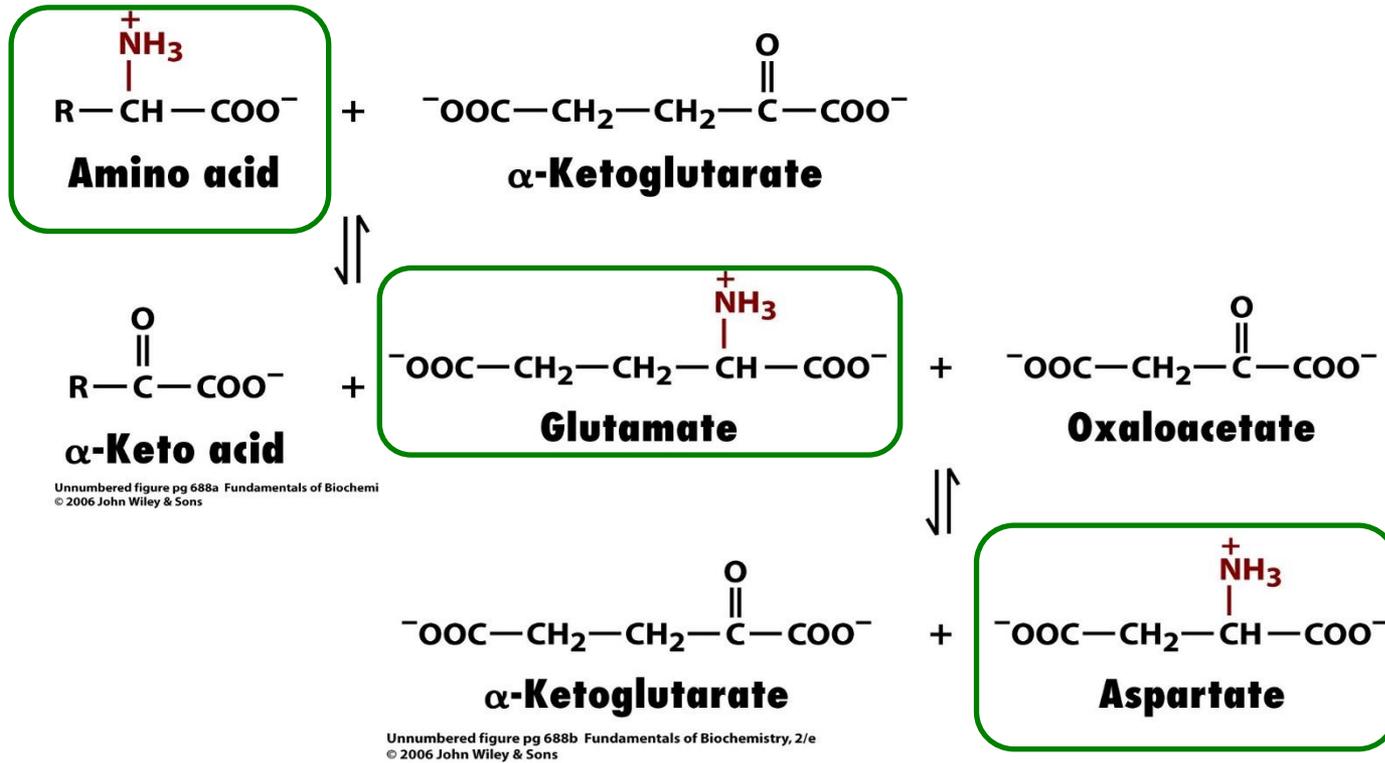


1. *desaminação*

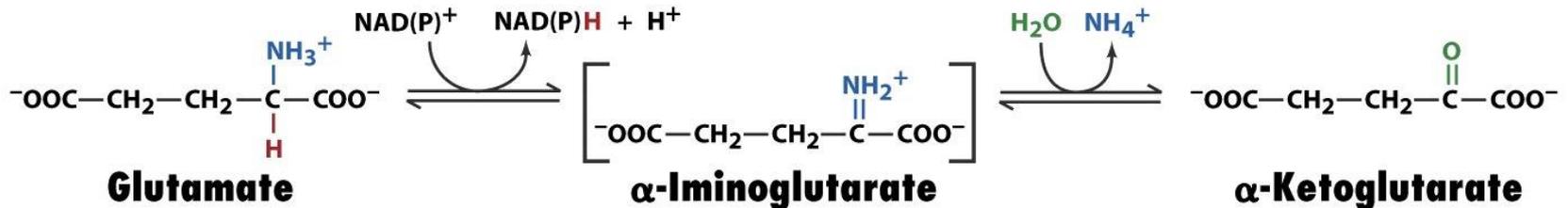
2. *Outras reações*

Excreção predominante em mamíferos

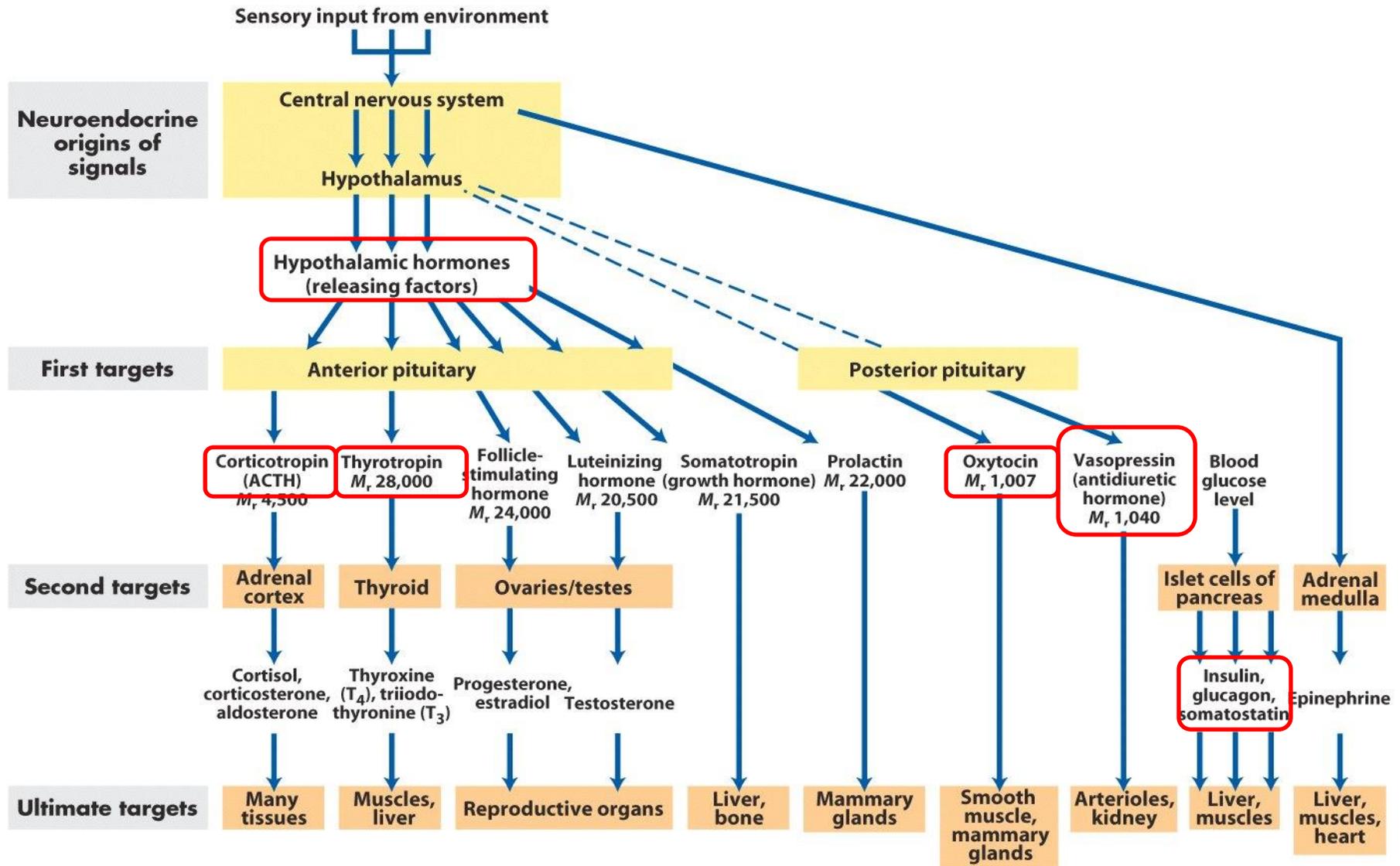
Desaminação → reações catalisadas por **transaminases**



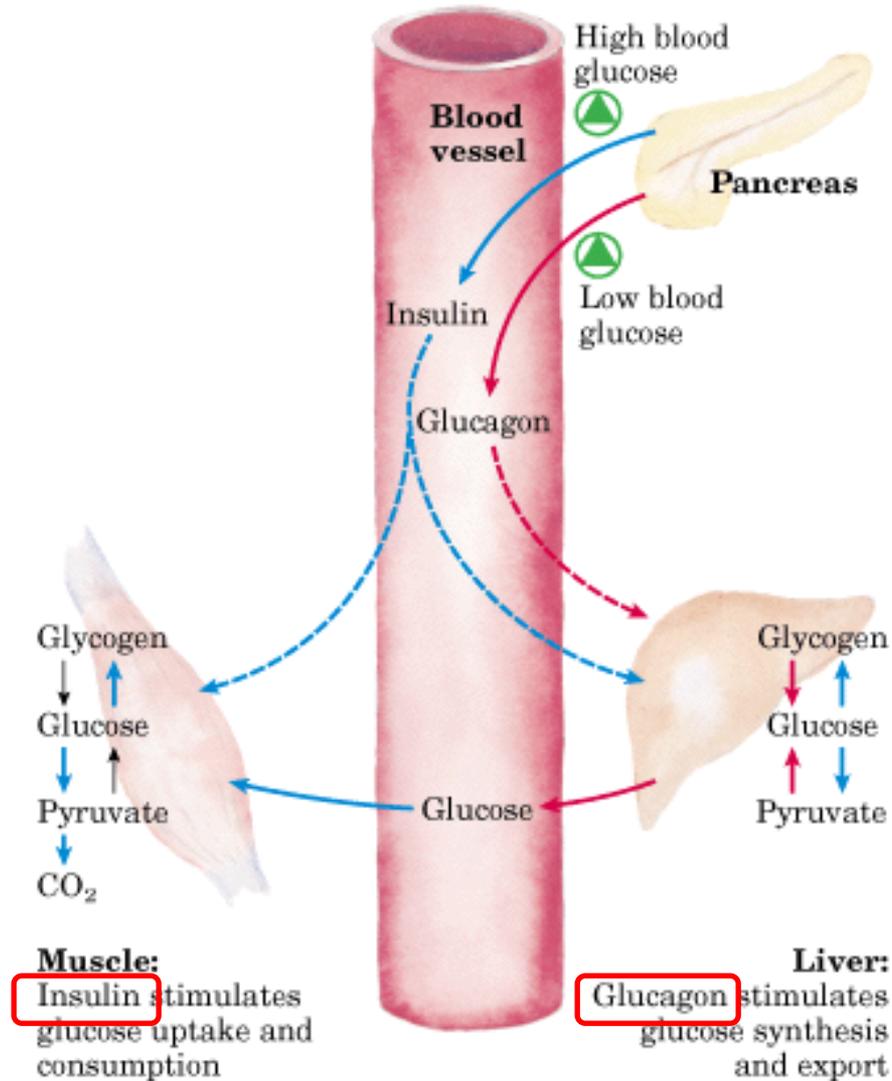
Desaminação → reação catalisada por **glutamato desidrogenase (GDH)**



Aminoácidos: blocos construtivos de fatores liberadores de hormônios/ hormônios peptídicos em prol do controle de funções vitais



Aminoácidos: blocos construtivos dos hormônios peptídicos envolvidos no controle da glicemia → metabolismo de mamíferos



Aminoácidos: blocos construtivos de inibidores sintéticos de proteases → ciência terapêutica

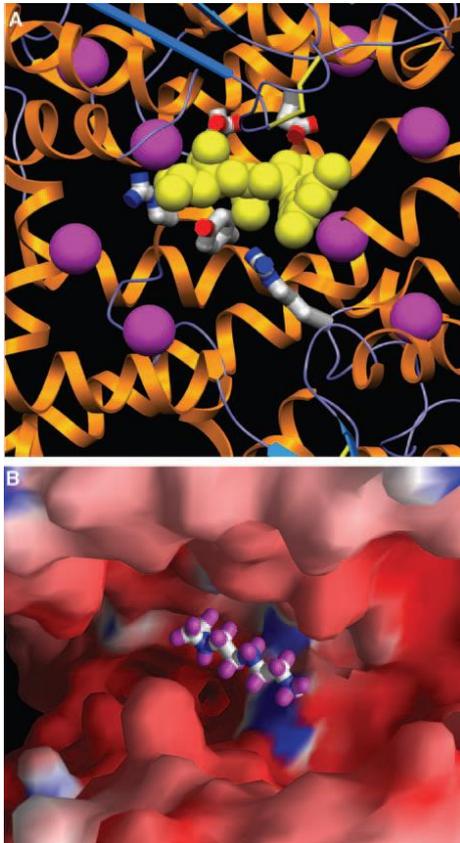


Figure 1. A novel ACE2 inhibitor identified by molecular docking. A, The active site residues of ACE2 are displayed. ACE2-strands are colored blue and -helices are colored gold. Yellow spheres indicate the position of a known ACE2 inhibitor used as a guide for targeting small molecules. Magenta spheres mark the boundary of the scoring grid used to calculate energy scores for molecularly docked small molecules. B, The top scoring compound, N-(2-aminoethyl)-1-aziridine-ethanamine (NAAE), is shown in the ACE2 active site. ACE2

Angiotensin-converting enzyme (**ACE**) inhibitors: are widely used for cardiovascular diseases, including high blood pressure, heart failure, heart attack and kidney failure, and have combined annual sales in excess of US \$6 billion.

Para desenvolver um inibidor é preciso saber:

Protease: especificidade/modo de ação/estrutura

Proteólise e estruturas de proteínas

Geração de fragmentos/peptídeos

Identificação e estruturas

Síntese/purificação/caracterização de peptídeos

Inibição da função catalítica

Busca de análogos não peptídicos

Ação inibitória específica



Química, estrutura, propriedades de aminoácidos



<http://www.haircareresources.com/amino-acid.html>

Aminoácidos: **componentes de produtos da cosmética**

..... Certain amino acids have been determined to contribute to the thinning and thickening of hair.

...Some of the amino acids that the body needs to produce healthier hair are **methionine, cysteine, cystine, and tyrosine**.

Methionine

Methionine, an essential amino acid, is a powerful antioxidant. This amino acid is a good source of sulfur which helps in the prevention of hair disorders as well as skin and nail disorders..... Methionine prevents the premature loss of hair.....

Cysteine

The non essential amino acid **cysteine** is important for the proper growth of hair. Cysteine has been found to increase the growth of hair by 100%.

Cysteine also acts as a powerful antioxidant and protects the body from damage brought about by radiation.

Gutiérrez-Preciado et al, (2010) Nature Education 3(9):29
An Evolutionary Perspective on Amino Acids

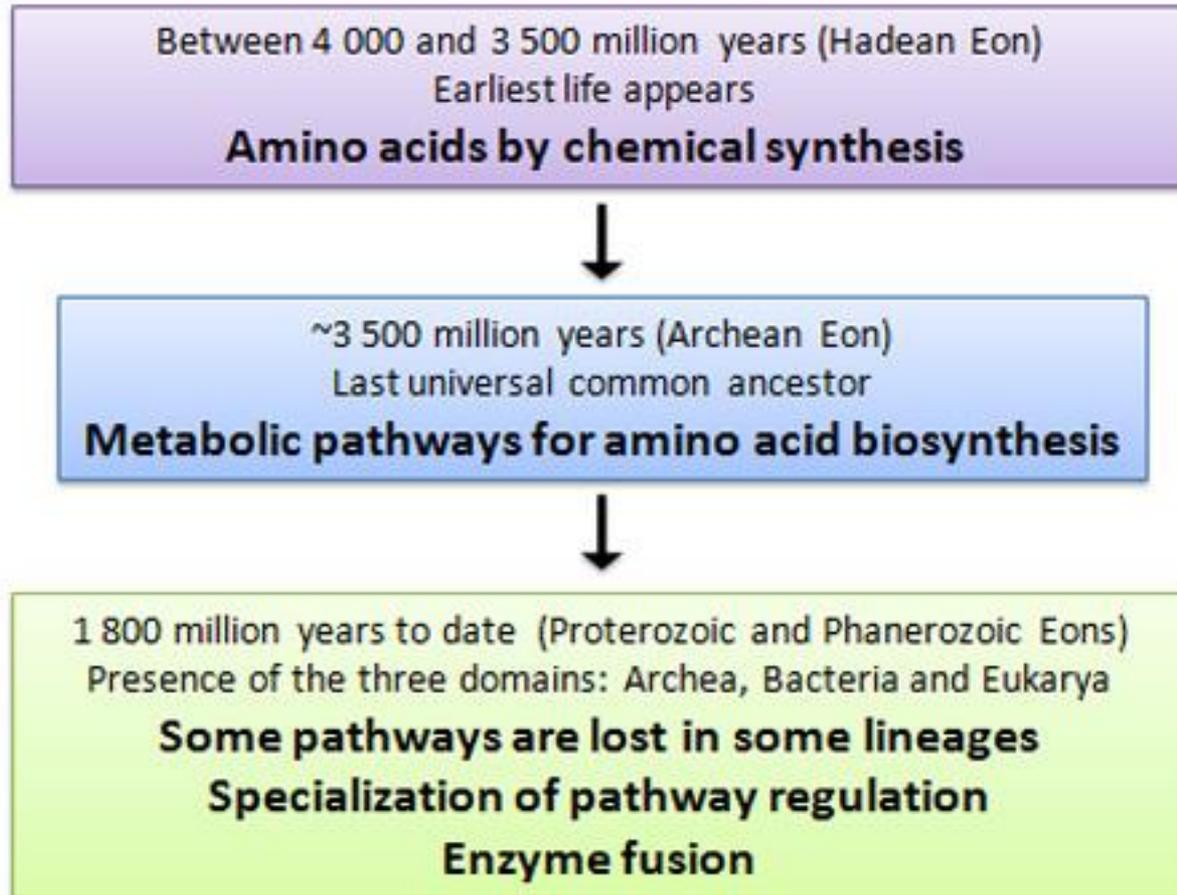


Figure 1: Major events in the evolution of amino acid synthesis

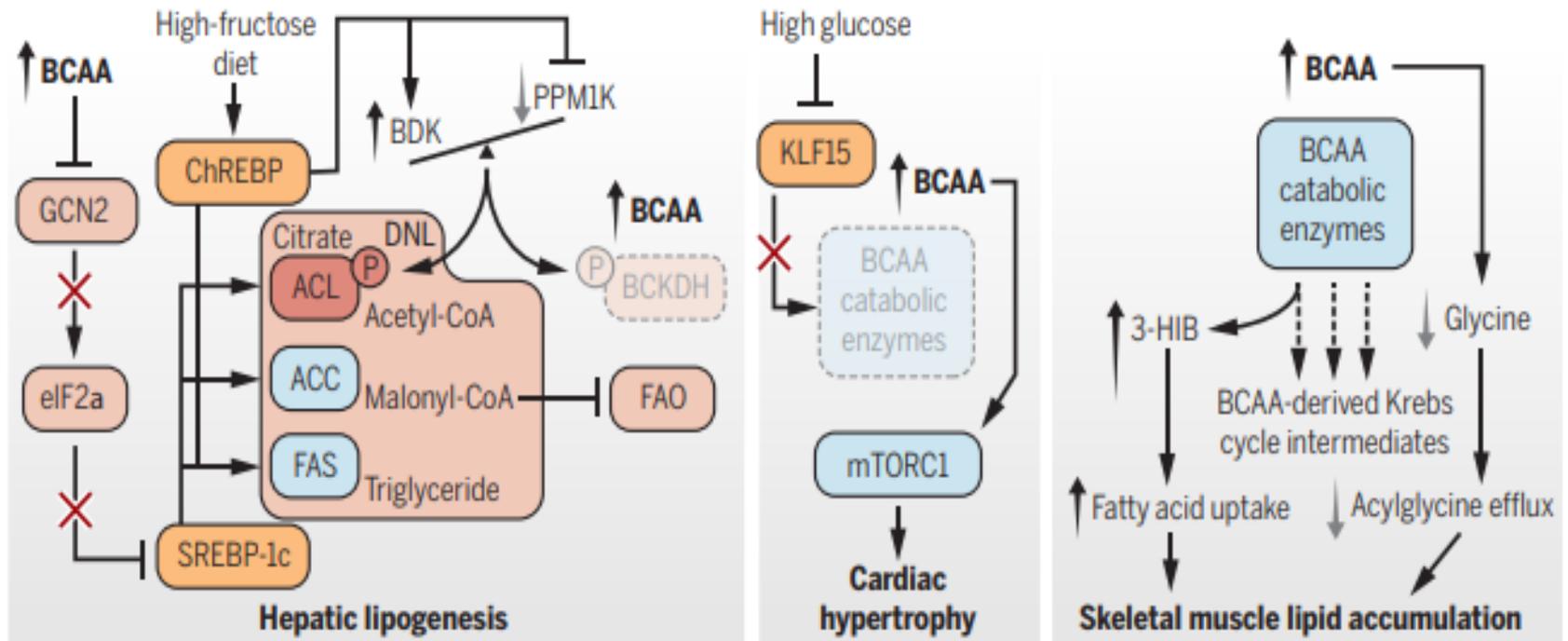
The way amino acids are synthesized has changed during the history of Earth. The Hadean Eon represents the time from which Earth first formed. The subsequent Archean Eon (approximately 3,500 million years ago) is known as the age of bacteria and archaea. The Proterozoic Eon was the gathering up of oxygen in Earth's atmosphere, and the Phanerozoic Eon coincides with the major diversification of animals, plants, and fungi.

P.J. White & C.B. Newgard, *Science* 2019, 363 (6427), 582-583

Branched-Chain Amino Acids in disease: Leu, Ile, Val

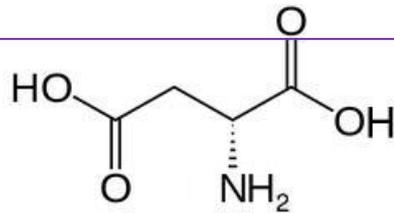
BCAAs: biomarkers and causal agents of cardiometabolic disease

Diet, obesity, the gut microbiota, and genetics can increase circulating BCAAs. BCAAs are proposed to promote increased hepatic lipid storage, cardiac hypertrophy, and muscle lipid accumulation contributing to insulin resistance.

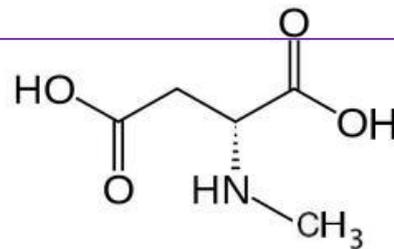


Localization of D-beta-aspartic acid-containing proteins in human eyes

Biologically uncommon **D-beta-aspartic acid (D-beta-Asp)** has been detected in proteins from various human tissues in elderly donors. Previous studies have identified D-beta-Asp residues at four different specific sites in alpha-crystallin from aged human lenses and an **increased amount of D-beta-Asp residues with age**. D-beta-Asp is formed as a result of racemization and accumulates with age; therefore, it is thought to be a potential marker of aging. To reveal the role of the D-beta-Asp formation in the aging process of eyes, immunohistochemical localization of D-beta-Asp was investigated in ocular samples of various ages.



D-Aspartic Acid



N-Methyl-D-Aspartate (NMDA)

Melville GW et al., [PLoS ONE 12\(8\): e0182630 \(2017\)](#)

The effects of d-aspartic acid supplementation in resistance-trained men over a three months training period: A randomised controlled trial.

D-aspartic acid (D-AA) is an amino acid regulator of testosterone synthesis and may act on a stimulatory receptor (NMDA). D-AA shows promise in aiding male fertility. Healthy men supplementing D-AA experience only temporary increases in testosterone, which limits its use.

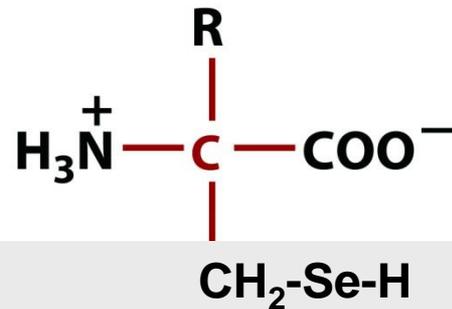
D-AA works in the central brain region to cause a release of hormones, such as luteinizing hormone, follicle-stimulating hormone, and growth hormone.

Aminoácidos modificados e não usuais

Código genético: 20 α -aminoácidos usuais

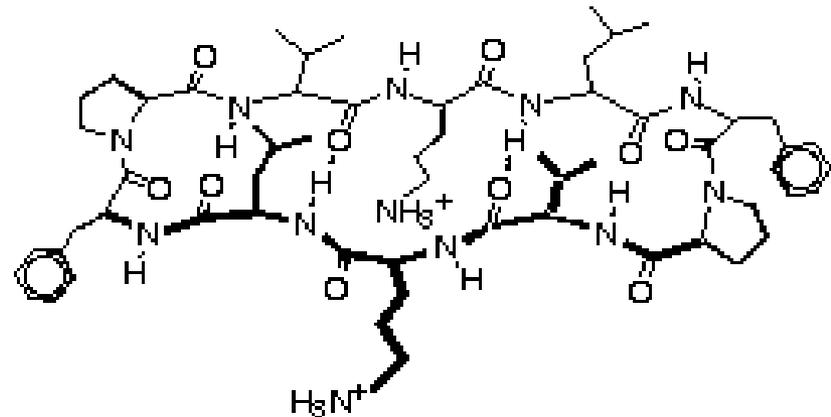
α -Aminoácidos modificados (não usuais) em peptídeos/proteínas?
modificação pós-tradução

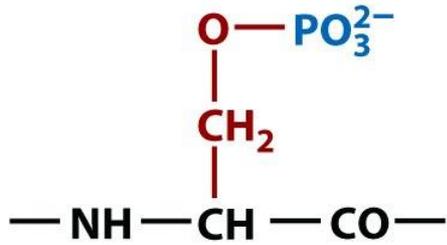
Exceção: **Sec** ou **SeCys**



21º. Aminoácido proteico

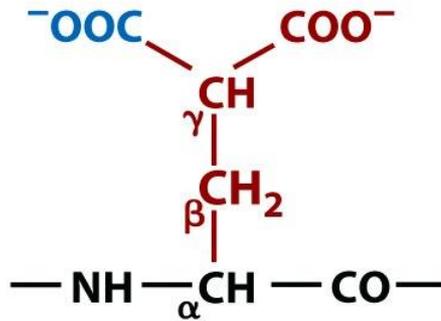
**D-Phe: peptídeo antibiótico
gramicidina A**





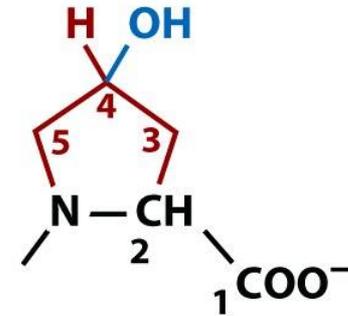
O-Phosphoserine

Proteínas fosforiladas

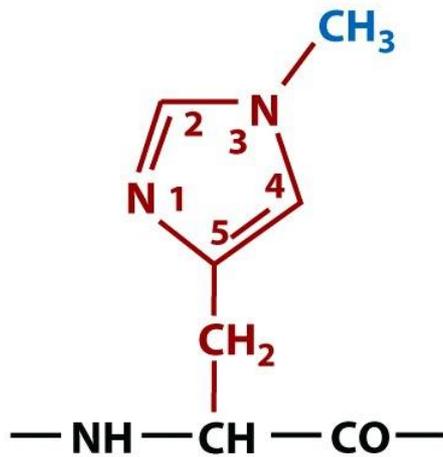


γ-Carboxyglutamate

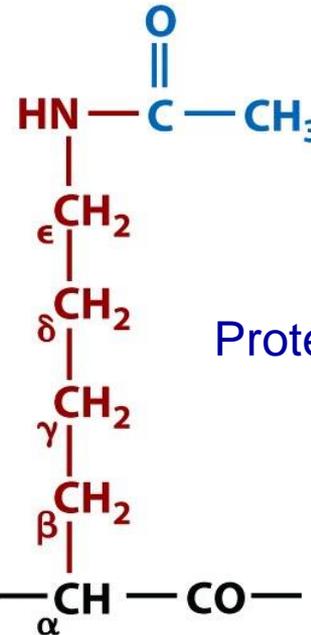
conotoxinas



4-Hydroxyproline colágeno



3-Methylhistidine

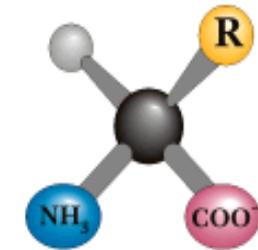
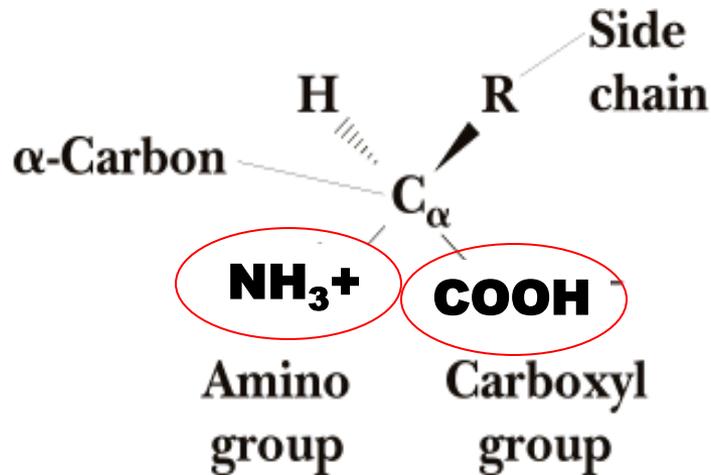


ε-N-Acetyllysine

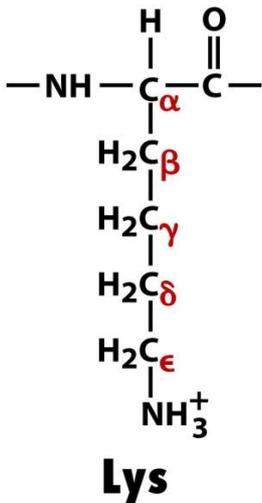
Proteínas Ribossomais
Cromossomais

Figure 4-15 Fundamentals of Biochemistry, 2/e
© 2006 John Wiley & Sons

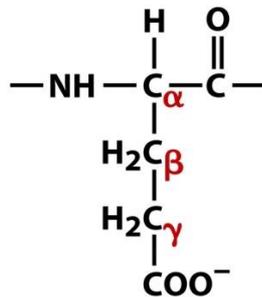
Estrutura geral dos α -aminoácidos



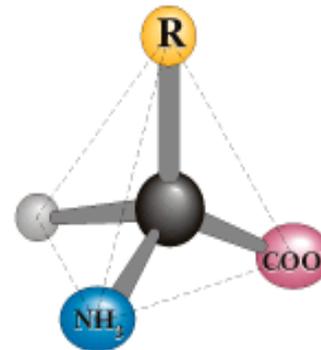
Ball-and-stick model



Lys



Glu

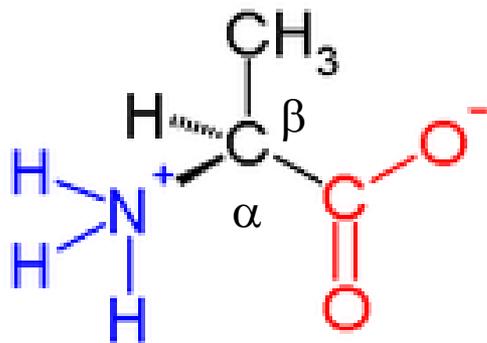


Amino acids are tetrahedral structures

Figure 4-9 Fundamentals of Biochemistry, 2/e

➤ 700 diferentes aminoácidos na natureza (plantas, bactérias e fungos)

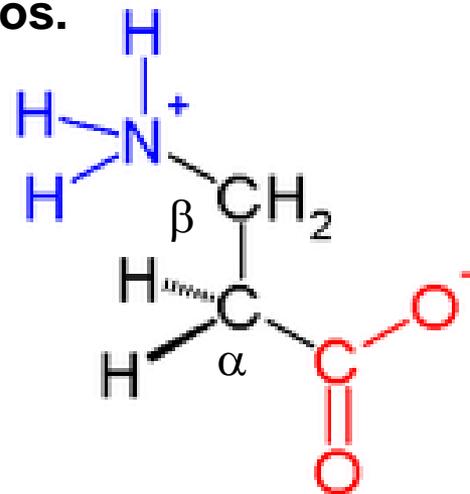
A maioria é α -aminoácidos, mas existem outros.



L- α -alanine

em MICROCISTINA

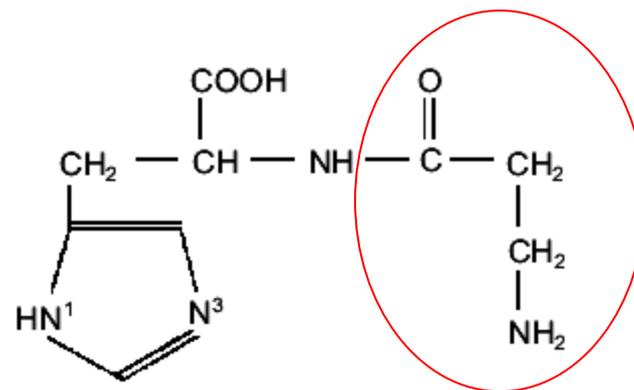
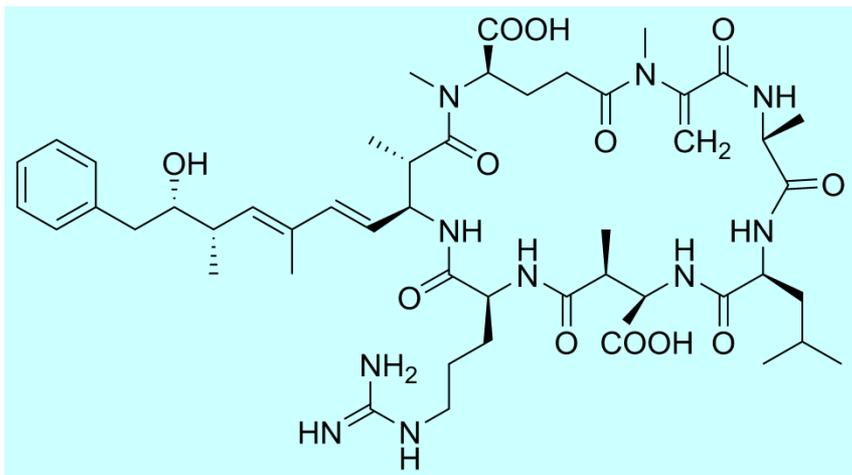
(toxina de alga *Microcystis aeruginosa*)



β -alanine

em CARNOSINA

(dipeptídeo de glia e neurônios)



Propriedades físico-químicas dos α -aminoácidos

MTM

- Capacidade de formar ligações de H
- Capacidade de se envolver em ligações S-S
- Reatividade química
- Acidez X Basicidade
- Polaridade
- Aromaticidade
- Volume
- Capacidade de absorver/emitir luz
- Capacidade de desviar luz plano polarizada
- Quiralidade
- Flexibilidade conformacional

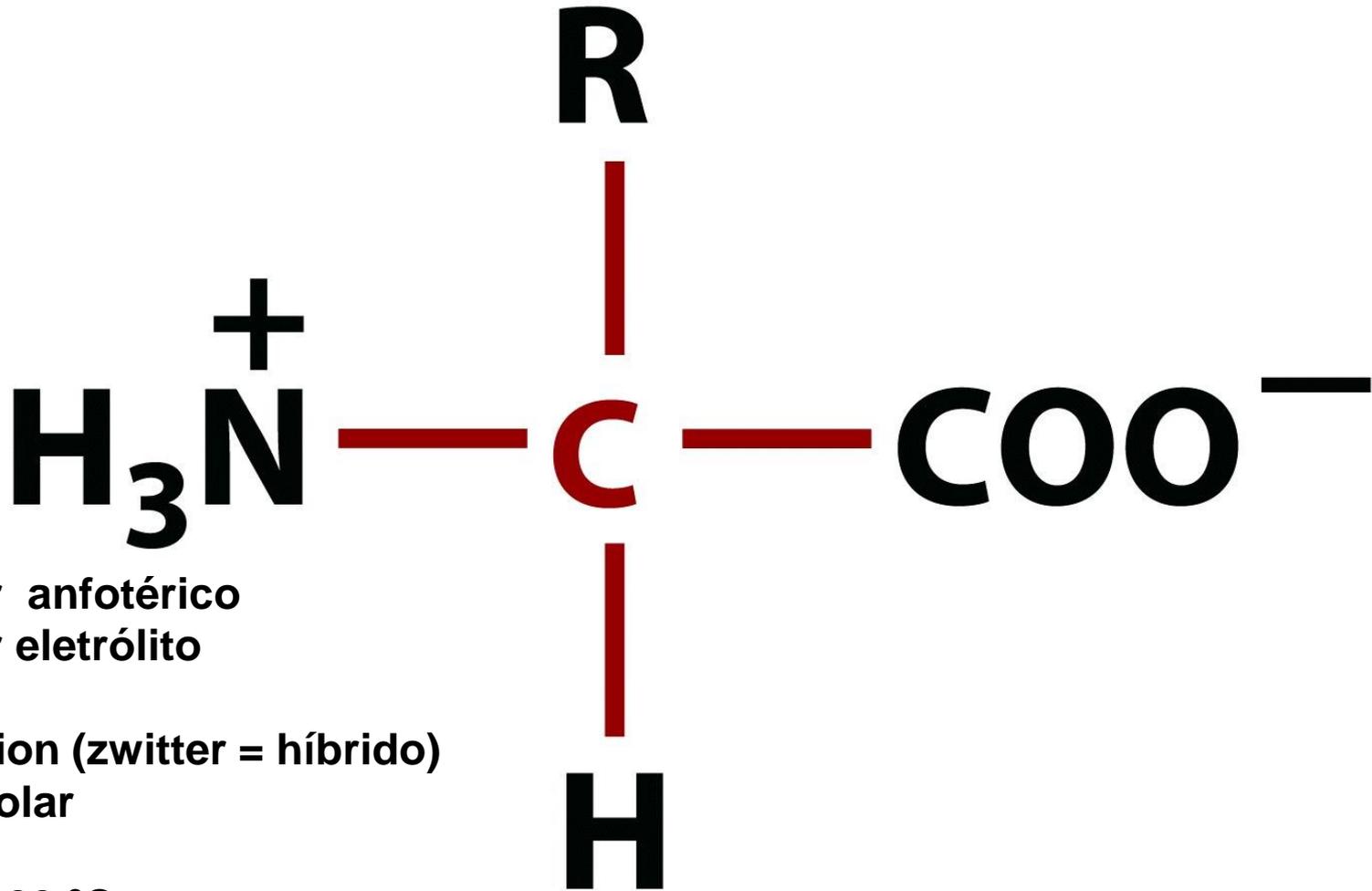
Solubility

Amino acids are **generally soluble in water** and insoluble in non-polar organic solvents such as hydrocarbons.

Melting points

The amino acids are **crystalline solids with surprisingly high melting points**. It is difficult to pin the melting points down exactly because the amino acids tend to decompose before they melt. Decomposition and melting tend to be in the **200 - 300°C** range.

Propriedades ácido-base



Caráter anfotérico
Caráter eletrólito

Zwitterion (zwitter = híbrido)
Íon dipolar

PF = ~300 °C
(compostos iônicos típicos)

Solúveis em solventes polares

Por isso,

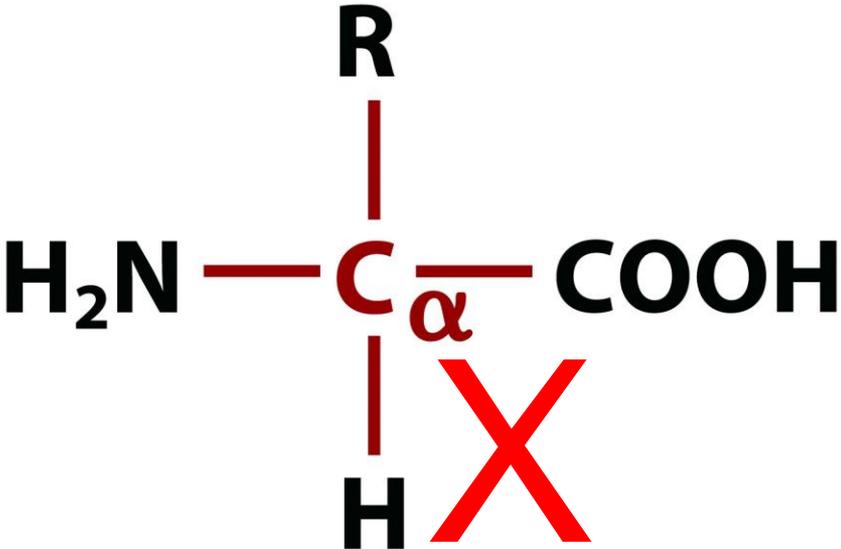


Figure 4-1 Fundamentals of Biochemistry, 2/e
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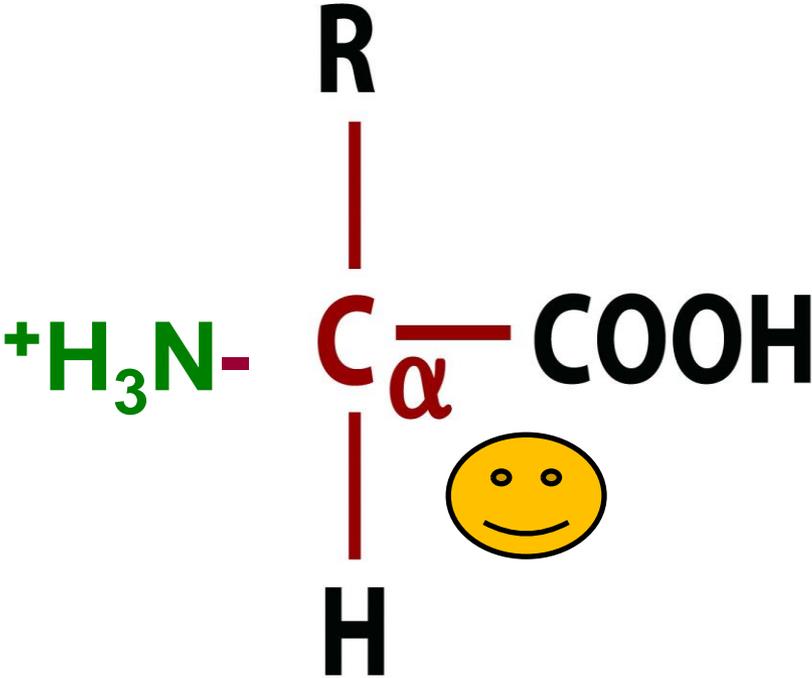


Figure 4-1 Fundamentals of Biochemistry, 2/e
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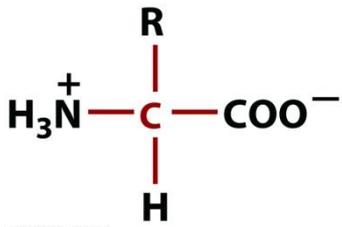
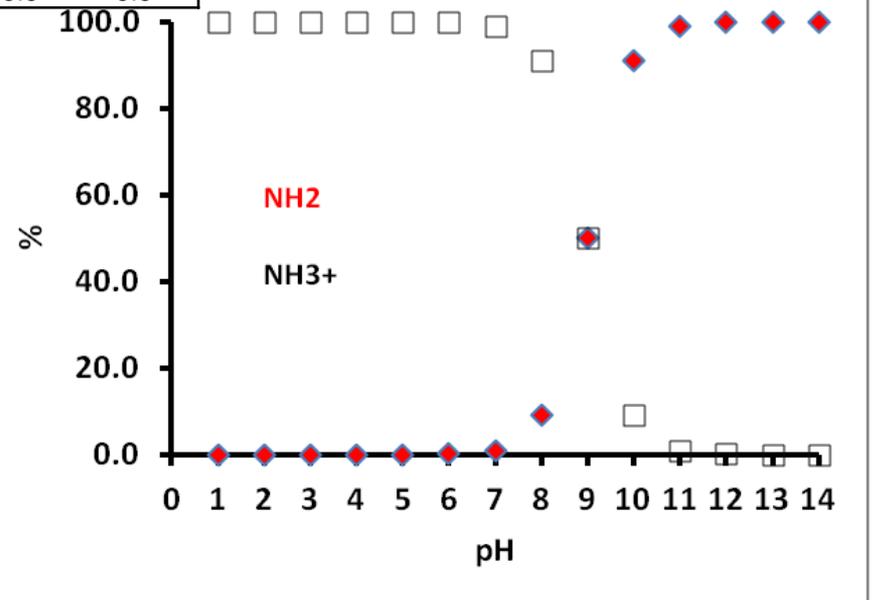
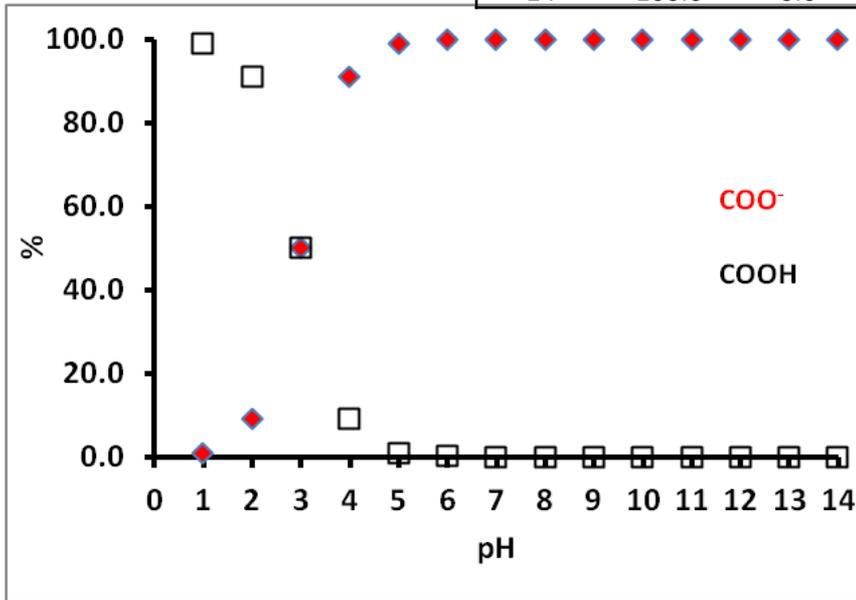


Figure 4.2 Fundamentals of Biochemistry, 2/e
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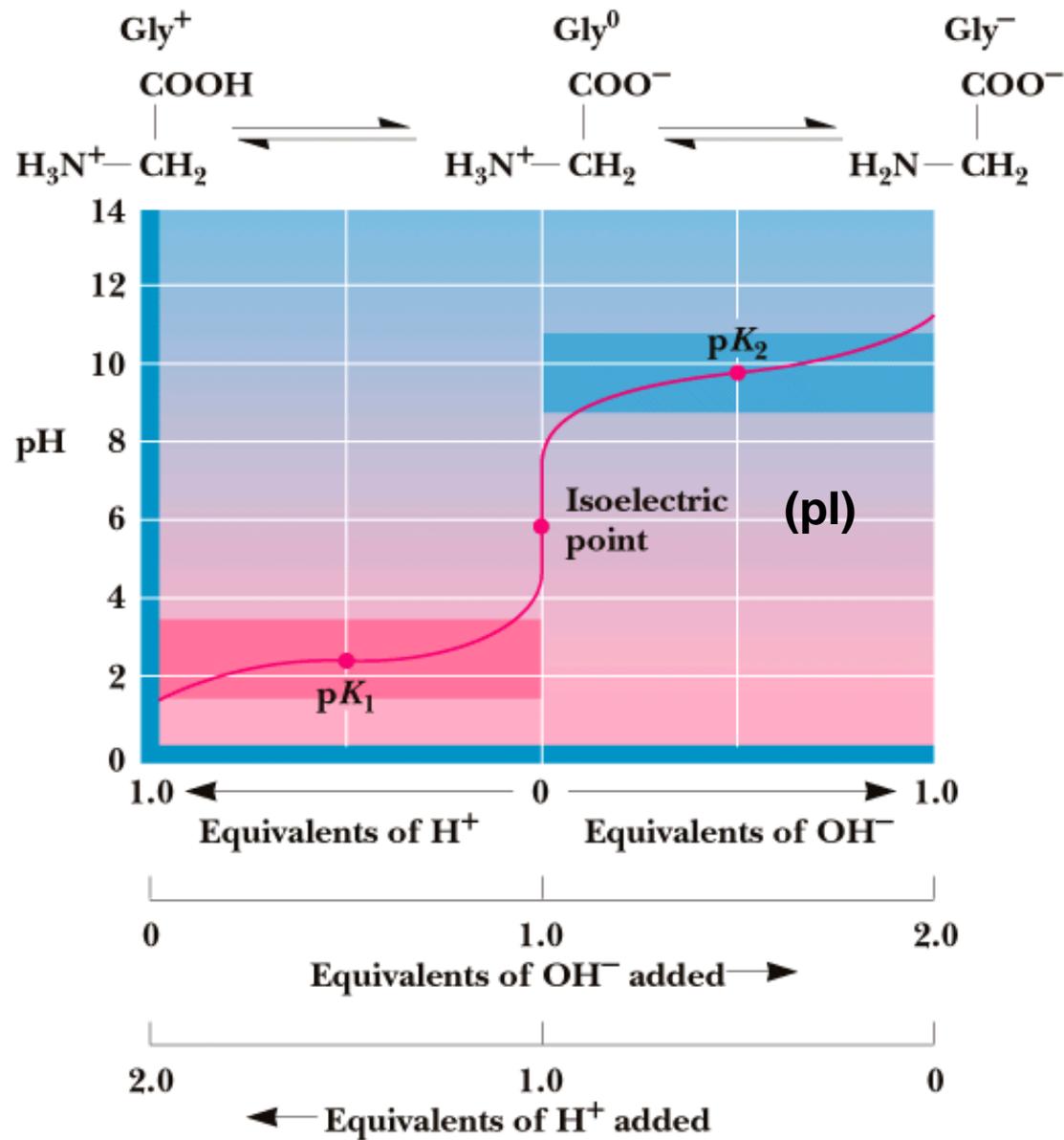
- COOH
pK_a = 3

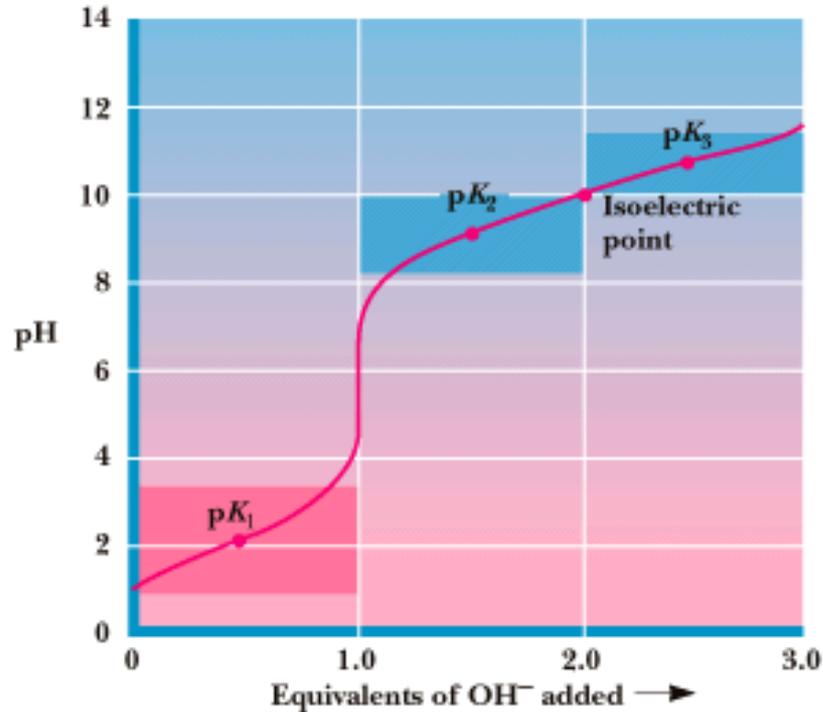
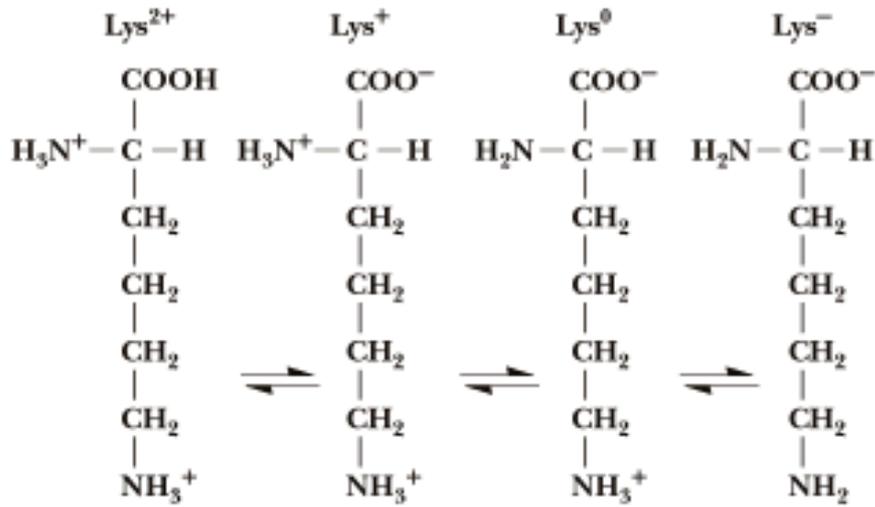
- NH₃⁺
pK_a = 9

pH	%B - COO ⁻	%A - COOH	%B - NH ₂	%A - NH ₃ ⁺
1	1.0	99.0	0.0	100.0
2	9.1	90.9	0.0	100.0
3	50.0	50.0	0.0	100.0
4	90.9	9.1	0.0	100.0
5	99.0	1.0	0.0	100.0
6	99.9	0.1	0.1	99.9
7	100.0	0.0	1.0	99.0
8	100.0	0.0	9.1	90.9
9	100.0	0.0	50.0	50.0
10	100.0	0.0	90.9	9.1
11	100.0	0.0	99.0	1.0
12	100.0	0.0	99.9	0.1
13	100.0	0.0	100.0	0.0
14	100.0	0.0	100.0	0.0



pH = pKa + log [A⁻]/[HA]; qdo [A⁻] = [HA]: pH = pKa





Cálculo de pI
Capacidade tamponante

pK_a Values of Polyfunctional Amino Acids

Amino Acid	α -CO ₂ H pK_a^1	α -NH ₃ pK_a^2	Side Chain pK_a^3	pI
Arginine	2.1	9.0	12.5	10.8
Aspartic Acid	2.1	9.8	3.9	3.0
Cysteine	1.7	10.4	8.3	5.0
Glutamic Acid	2.2	9.7	4.3	3.2
Histidine	1.8	9.2	6.0	7.6
Lysine	2.2	9.0	10.5	9.8
Tyrosine	2.2	9.1	10.1	5.7

Estrutura, polaridade, volume, aromaticidade

Ala Usuais apolares (9): G, A, V, L, I, M, P, F, W

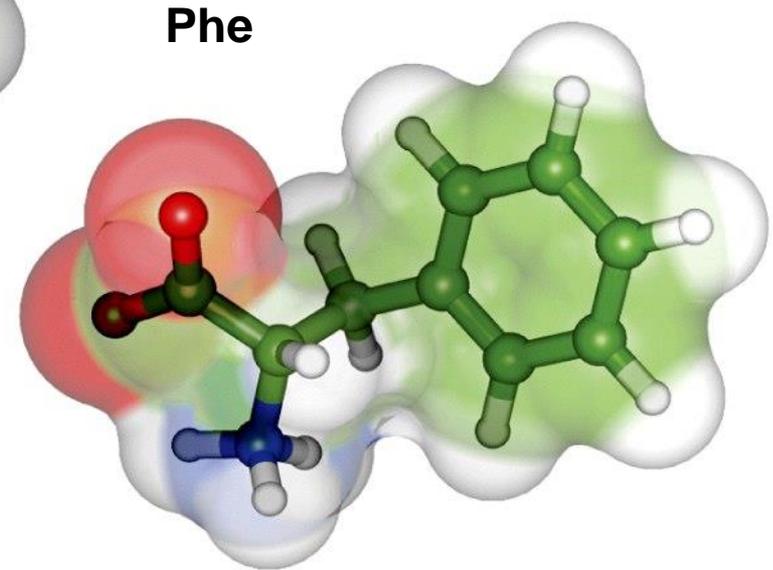
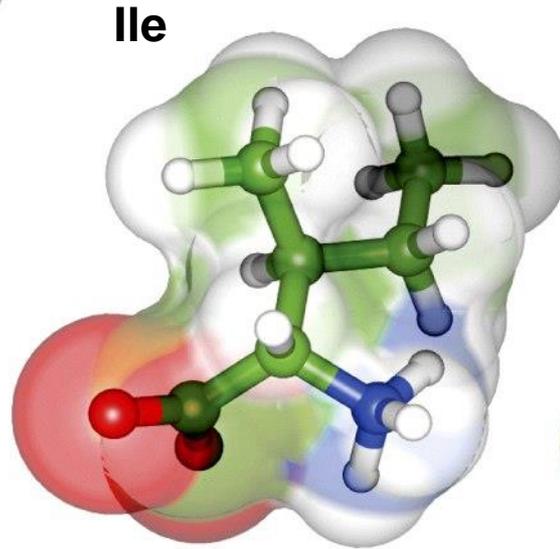
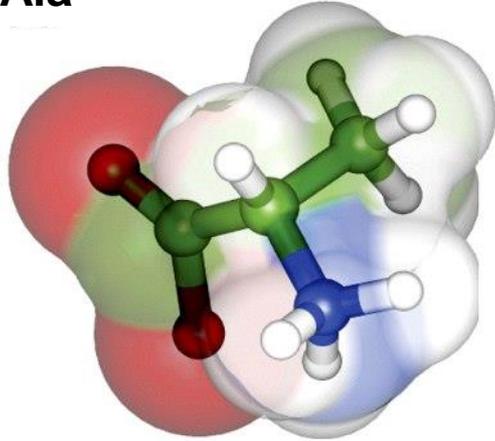


Figure 4-4 Fundamentals of Biochemistry, 2/e
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Table 4-1 Key to Structure. Covalent Structures and Abbreviations of the “Standard” Amino Acids of Proteins, Their Occurrence, and the pK Values of Their Ionizable Groups

Name, Three-letter Symbol, and One-letter Symbol	Structural Formula ^a	Residue Mass (D) ^b	Average Occurrence in Proteins (%) ^c	pK ₁ α-COOH ^d	pK ₂ α-NH ₃ ⁺ ^d	pK _R Side Chain ^d
<i>Amino acids with nonpolar side chains</i>						
Glycine Gly G	$\begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{H} \\ \\ \text{NH}_3^+ \end{array}$	57.0	7.2	2.35	9.78	
Alanine Ala A	$\begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_3 \\ \\ \text{NH}_3^+ \end{array}$	71.1	7.8	2.35	9.87	
Valine Val V	$\begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH} \\ \quad \diagup \quad \diagdown \\ \text{NH}_3^+ \quad \text{CH}_3 \quad \text{CH}_3 \end{array}$	99.1	6.6	2.29	9.74	

^aThe ionic forms shown are those predominating at pH 7.0 (except for that of histidine^f) although residue mass is given for the neutral compound. The C_α atoms, as well as those atoms marked with an asterisk, are chiral centers with configurations as indicated according to Fischer projection formulas (Section 4-2). The standard organic numbering system is provided for heterocycles.

^bThe residue masses are given for the neutral residues. For the molecular masses of the parent amino acids, add 18.0 D, the molecular mass of H₂O, to the residue masses. For side chain masses, subtract 56.0 D, the formula mass of a peptide group, from the residue masses.

^cCalculated from a database of nonredundant proteins containing 300,688 residues as compiled by Doolittle, R.F. in Fasman, G.D. (Ed.), *Predictions of Protein Structure and the Principles of Protein Conformation*, Plenum Press (1989).

^dData from Dawson, R.M.C., Elliott, D.C., Elliott, W.H., and Jones, K.M., *Data for Biochemical Research* (3rd ed.), pp. 1–31, Oxford Science Publications (1986).

Table 4-1 Key to Structure. Covalent Structures and Abbreviations of the “Standard” Amino Acids of Proteins, Their Occurrence, and the p*K* Values of Their Ionizable Groups

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<i>Amino acids with nonpolar side chains</i>						
Leucine Leu L	$ \begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_2-\text{CH} \\ \qquad \quad / \quad \backslash \\ \text{NH}_3^+ \qquad \text{CH}_3 \quad \text{CH}_3 \end{array} $	113.2	9.1	2.33	9.74	
Isoleucine Ile I	$ \begin{array}{c} \text{COO}^- \quad \text{CH}_3 \\ \qquad \quad \\ \text{H}-\text{C}-\text{C}^*-\text{CH}_2-\text{CH}_3 \\ \qquad \quad \\ \text{NH}_3^+ \quad \text{H} \end{array} $	113.2	5.3	2.32	9.76	
Methionine Met M	$ \begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_2-\text{CH}_2-\text{S}-\text{CH}_3 \\ \\ \text{NH}_3^+ \end{array} $	131.2	2.2	2.13	9.28	

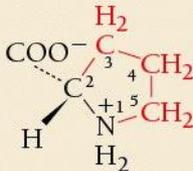
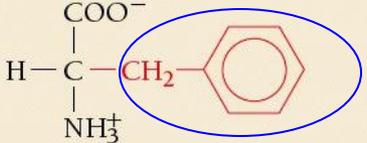
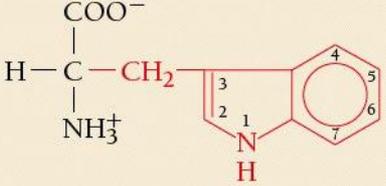
^aThe ionic forms shown are those predominating at pH 7.0 (except for that of histidine^f) although residue mass is given for the neutral compound. The C_α atoms, as well as those atoms marked with an asterisk, are chiral centers with configurations as indicated according to Fischer projection formulas (Section 4-2). The standard organic numbering system is provided for heterocycles.

^bThe residue masses are given for the neutral residues. For the molecular masses of the parent amino acids, add 18.0 D, the molecular mass of H₂O, to the residue masses. For side chain masses, subtract 56.0 D, the formula mass of a peptide group, from the residue masses.

^cCalculated from a database of nonredundant proteins containing 300,688 residues as compiled by Doolittle, R.F. in Fasman, G.D. (Ed.), *Predictions of Protein Structure and the Principles of Protein Conformation*, Plenum Press (1989).

^dData from Dawson, R.M.C., Elliott, D.C., Elliott, W.H., and Jones, K.M., *Data for Biochemical Research* (3rd ed.), pp. 1–31, Oxford Science Publications (1986).

Table 4-1 Key to Structure. Covalent Structures and Abbreviations of the “Standard” Amino Acids of Proteins, Their Occurrence, and the pK Values of Their Ionizable Groups

Name, Three-letter Symbol, and One-letter Symbol	Structural Formula ^a	Residue Mass (D) ^b	Average Occurrence in Proteins (%) ^c	pK ₁ α-COOH ^d	pK ₂ α-NH ₃ ⁺ ^d	pK _R Side Chain ^d
<i>Amino acids with nonpolar side chains</i>						
Proline Pro P		97.1	5.2	1.95	10.64	
Phenylalanine Phe F		147.2	3.9	2.20	9.31	
Tryptophan Trp W		186.2	1.4	2.46	9.41	

^aThe ionic forms shown are those predominating at pH 7.0 (except for that of histidine^f) although residue mass is given for the neutral compound. The C_α atoms, as well as those atoms marked with an asterisk, are chiral centers with configurations as indicated according to Fischer projection formulas (Section 4-2). The standard organic numbering system is provided for heterocycles.

^bThe residue masses are given for the neutral residues. For the molecular masses of the parent amino acids, add 18.0 D, the molecular mass of H₂O, to the residue masses. For side chain masses, subtract 56.0 D, the formula mass of a peptide group, from the residue masses.

^cCalculated from a database of nonredundant proteins containing 300,688 residues as compiled by Doolittle, R.F. in Fasman, G.D. (Ed.), *Predictions of Protein Structure and the Principles of Protein Conformation*, Plenum Press (1989).

^dData from Dawson, R.M.C., Elliott, D.C., Elliott, W.H., and Jones, K.M., *Data for Biochemical Research* (3rd ed.), pp. 1–31, Oxford Science Publications (1986).

Estrutura, polaridade, volume, aromaticidade

Usuais polares não carregados (6): S,T, N, Q, Y, C

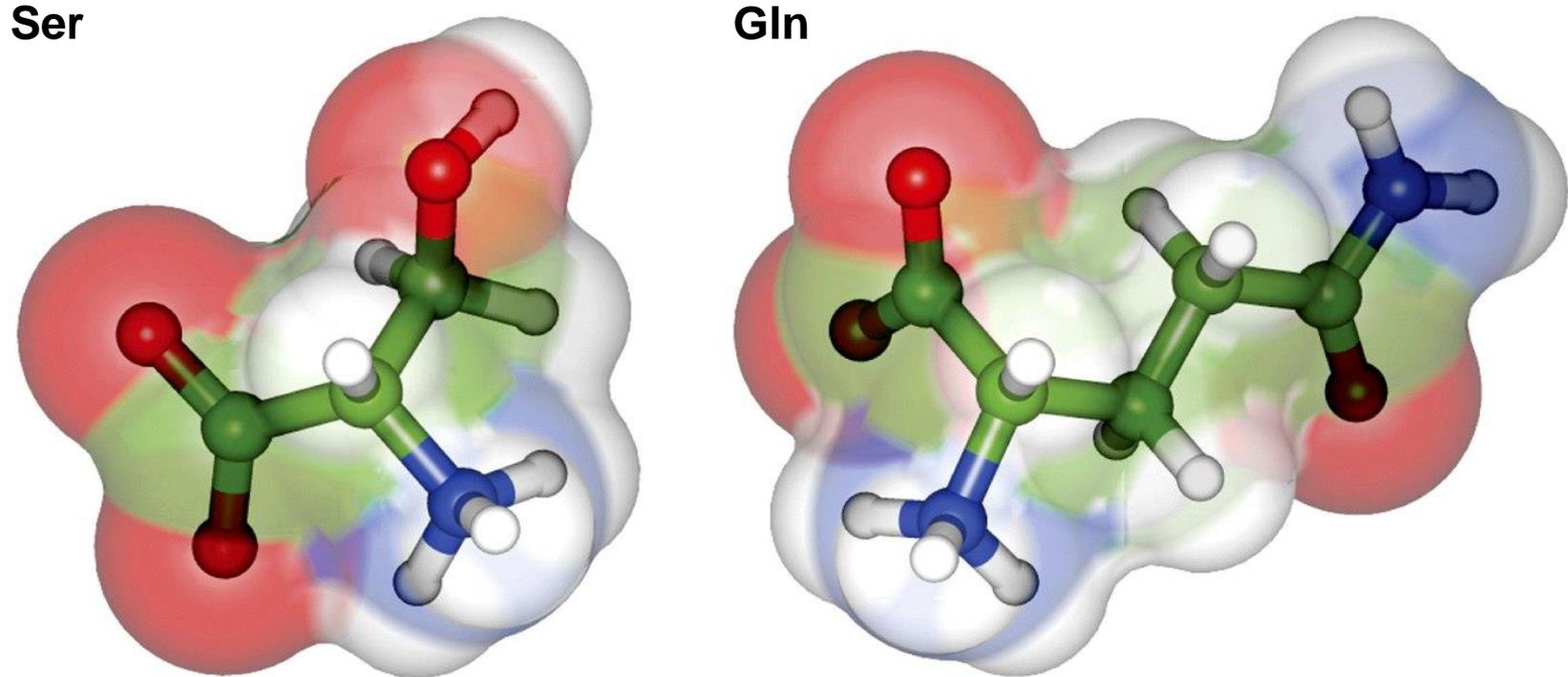


Figure 4-5 Fundamentals of Biochemistry, 2/e
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Table 4-1 (continued)

Name, Three-letter Symbol, and One-letter Symbol	Structural Formula ^a	Residue Mass (D) ^b	Average Occurrence in Proteins (%) ^c	pK ₁ α-COOH ^d	pK ₂ α-NH ₃ ⁺ ^d	pK _R Side Chain ^d
<i>Amino acids with uncharged polar side chains</i>						
Serine Ser S	$ \begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_2-\text{OH} \\ \\ \text{NH}_3^+ \end{array} $	87.1	6.8	2.19	9.21	
Threonine Thr T	$ \begin{array}{c} \text{COO}^- \quad \text{H} \\ \quad \quad \\ \text{H}-\text{C}-\text{C}^*-\text{CH}_3 \\ \quad \quad \\ \text{NH}_3^+ \quad \text{OH} \end{array} $	101.1	5.9	2.09	9.10	
Asparagine ^e Asn N	$ \begin{array}{c} \text{COO}^- \quad \quad \text{O} \\ \quad \quad \quad // \\ \text{H}-\text{C}-\text{CH}_2-\text{C} \\ \quad \quad \quad \backslash \\ \text{NH}_3^+ \quad \quad \text{NH}_2 \end{array} $	114.1	4.3	2.14	8.72	

^eThe three- and one-letter symbols for asparagine *or* aspartic acid are Asx and B, whereas for glutamine *or* glutamic acid they are Glx and Z. The one-letter symbol for an undetermined or “nonstandard” amino acid is X.

^fBoth neutral and protonated forms of histidine are present at pH 7.0, since its pK_R is close to 7.0.

Table 4-1 part 4 Fundamentals of Biochemistry, 2/e

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Table 4-1 (continued)

Name, Three-letter Symbol, and One-letter Symbol	Structural Formula ^a	Residue Mass (D) ^b	Average Occurrence in Proteins (%) ^c	pK ₁ α-COOH ^d	pK ₂ α-NH ₃ ⁺ ^d	pK _R Side Chain ^d
<i>Amino acids with uncharged polar side chains</i>						
Glutamine ^e Gln Q		128.1	4.3	2.17	9.13	
Tyrosine Tyr Y		163.2	3.2	2.20	9.21	10.46 (phenol)
Cysteine Cys C		103.1	1.9	1.92	10.70	8.37 (sulfhydryl)

^eThe three- and one-letter symbols for asparagine *or* aspartic acid are Asx and B, whereas for glutamine *or* glutamic acid they are Glx and Z. The one-letter symbol for an undetermined or “nonstandard” amino acid is X.

^fBoth neutral and protonated forms of histidine are present at pH 7.0, since its pK_R is close to 7.0.

Table 4-1 part 5 Fundamentals of Biochemistry, 2/e
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Natureza dos R dos α-aminoácidos:
determinantes para a estrutura tridimensional das proteínas

Estrutura, polaridade, volume, aromaticidade

Usuais polares carregados (5): K, R, H, D, E

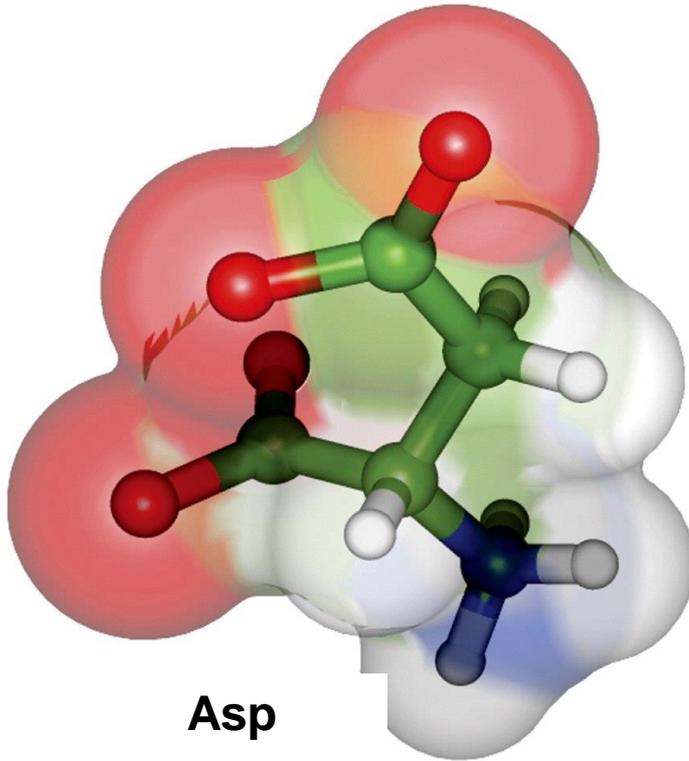


Figure 4-7a Fundamentals of Biochemistry, 2/e
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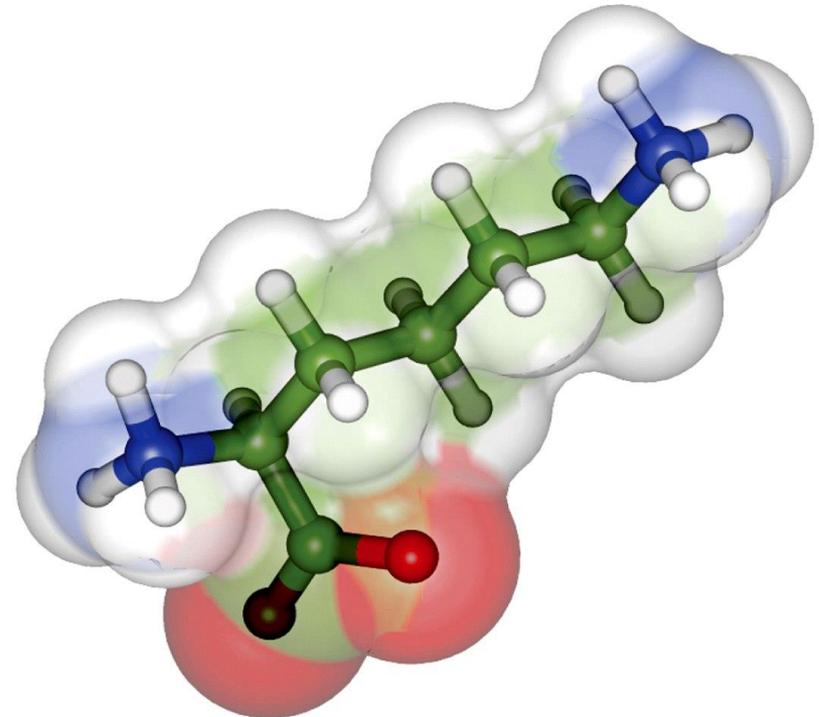


Figure 4-7b Fundamentals of Biochemistry, 2/e
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Table 4-1 (continued)

Name, Three-letter Symbol, and One-letter Symbol	Structural Formula ^a	Residue Mass (D) ^b	Average Occurrence in Proteins (%) ^c	pK ₁ α-COOH ^d	pK ₂ α-NH ₃ ⁺ ^d	pK _R Side Chain ^d
<i>Amino acids with charged polar side chains</i>						
Lysine Lys K	$ \begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_2-\text{CH}_2-\text{CH}_2-\text{CH}_2-\text{NH}_3^+ \\ \\ \text{NH}_3^+ \end{array} $	128.2	5.9	2.16	9.06	10.54 (ε-NH ₃ ⁺)
Arginine Arg R	$ \begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_2-\text{CH}_2-\text{CH}_2-\text{NH}-\text{C} \begin{array}{l} \text{NH}_2 \\ \text{NH}_2^+ \end{array} \\ \\ \text{NH}_3^+ \end{array} $	156.2	5.1	1.82	8.99	12.48 (guanidino)
Histidine ^f His H	$ \begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_2-\text{Imidazole}^+ \\ \\ \text{NH}_3^+ \end{array} $	137.1	2.3	1.80	9.33	6.04 (imidazole)
Aspartic acid ^e Asp D	$ \begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_2-\text{C} \begin{array}{l} \text{O} \\ \text{O}^- \end{array} \\ \\ \text{NH}_3^+ \end{array} $	115.1	5.3	1.99	9.90	3.90 (β-COOH)
Glutamic acid ^e Glu E	$ \begin{array}{c} \text{COO}^- \\ \\ \text{H}-\text{C}-\text{CH}_2-\text{CH}_2-\text{C} \begin{array}{l} \text{O} \\ \text{O}^- \end{array} \\ \\ \text{NH}_3^+ \end{array} $	129.1	6.3	2.10	9.47	4.07 (γ-COOH)

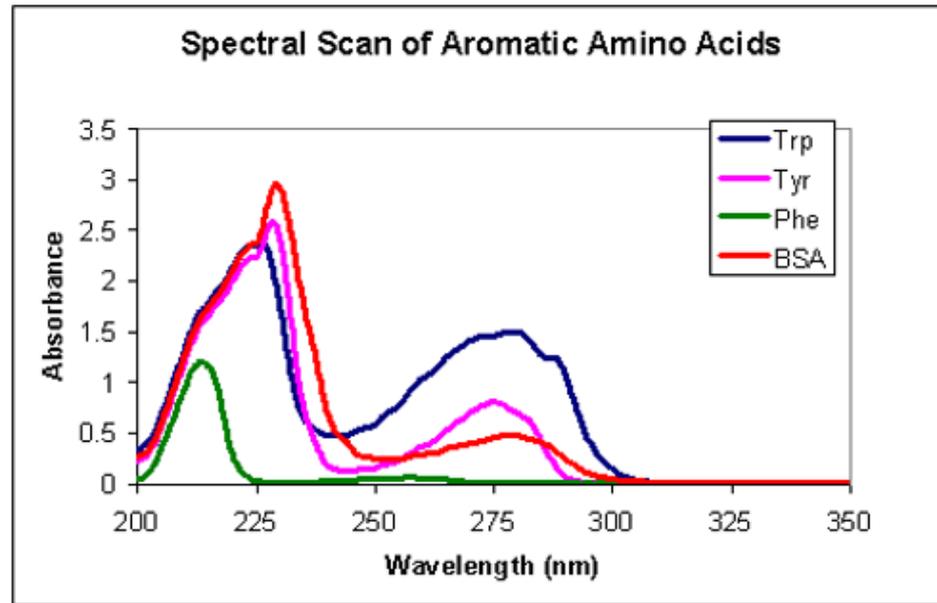
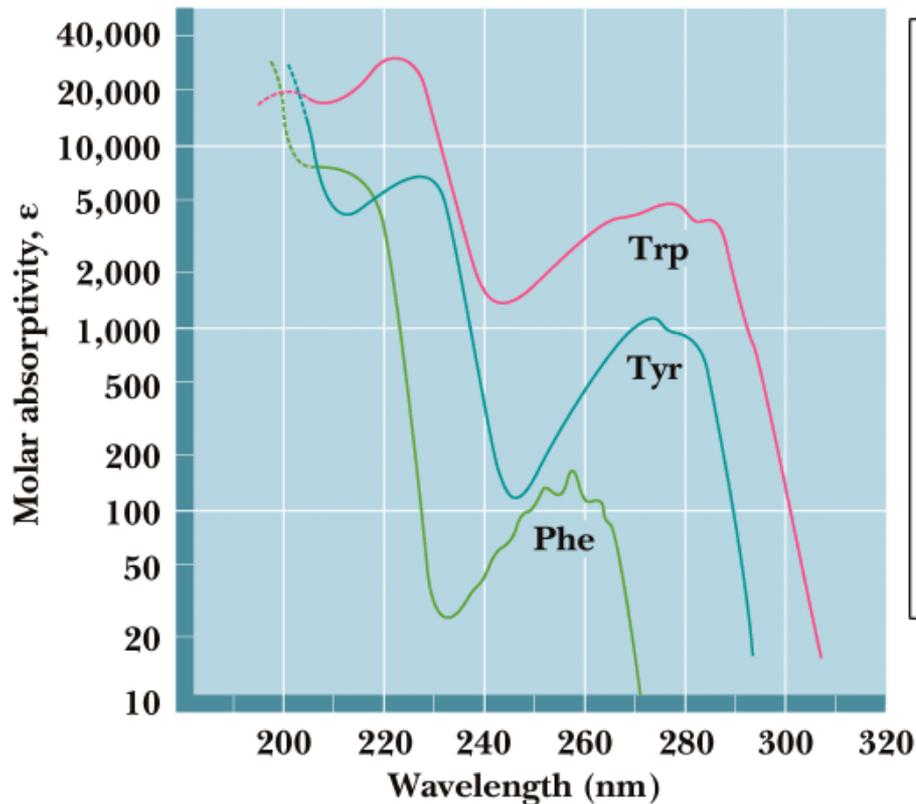
^eThe three- and one-letter symbols for asparagine *or* aspartic acid are Asx and B, whereas for glutamine *or* glutamic acid they are Glx and Z. The one-letter symbol for an undetermined or “nonstandard” amino acid is X.

^fBoth neutral and protonated forms of histidine are present at pH 7.0, since its pK_R is close to 7.0.

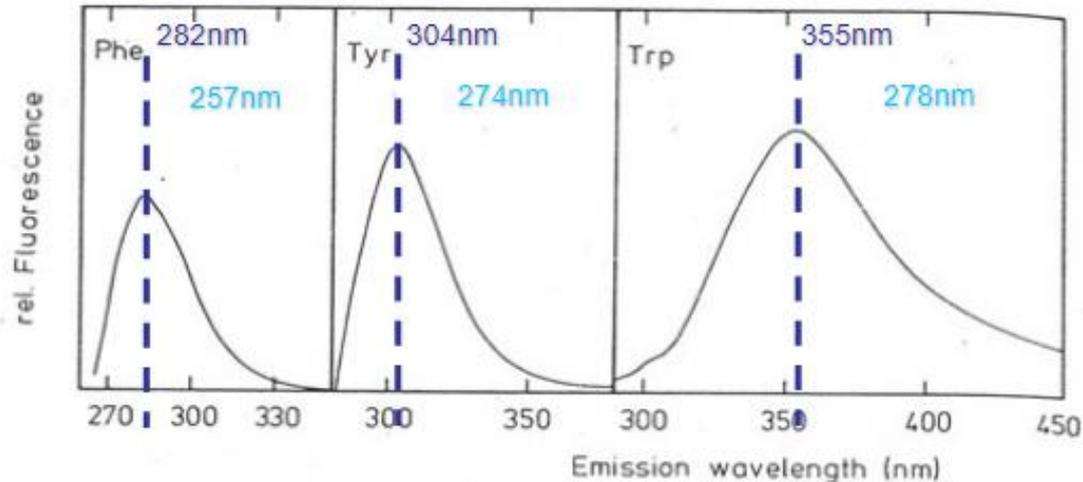
Absorção de luz

Todos: absorvem em 200-220 nm; alguns absorvem em 250-280 nm

Importância: detecção e dosagem
(deles e dos biopolímeros formados por eles)



Fluorescência de aminoácidos



Amino acid	Absorbance		Fluorescence		Sensitivity
	λ_{\max} (nm)	ϵ_{\max} ($M^{-1}cm^{-1}$)	λ_{\max} (nm)	φ_F^b	$\epsilon_{\max} \times \varphi_F^b$ ($M^{-1}cm^{-1}$)
Tryptophan	280	5600	355	0.13	730
Tyrosine	275	1400	304	0.14	200
Phenylalanine	258	200	282	0.02	4

Quiralidade → Atividade óptica

MTM

Aminoácidos são substâncias opticamente ativas pq desviam
a luz plano-polarizada

dextrorrotatórias: d (dexter = direita) = + (sentido horário)

levorrotatórias: l (laeves = esquerda) = - (sentido anti-horário)

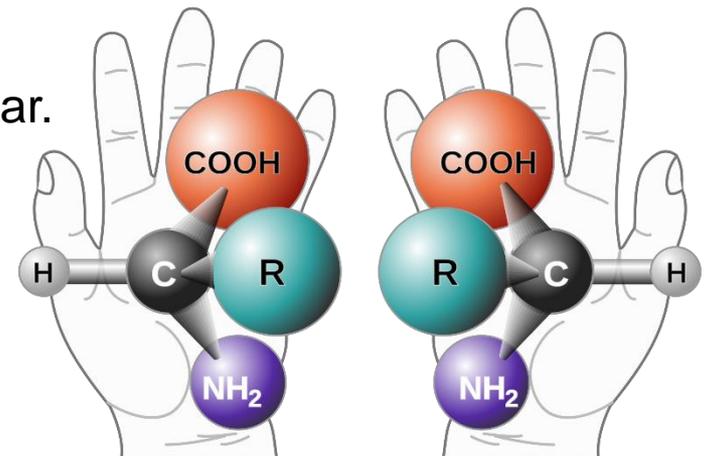
Porque isso ocorre? Possuem assimetria/quiralidade

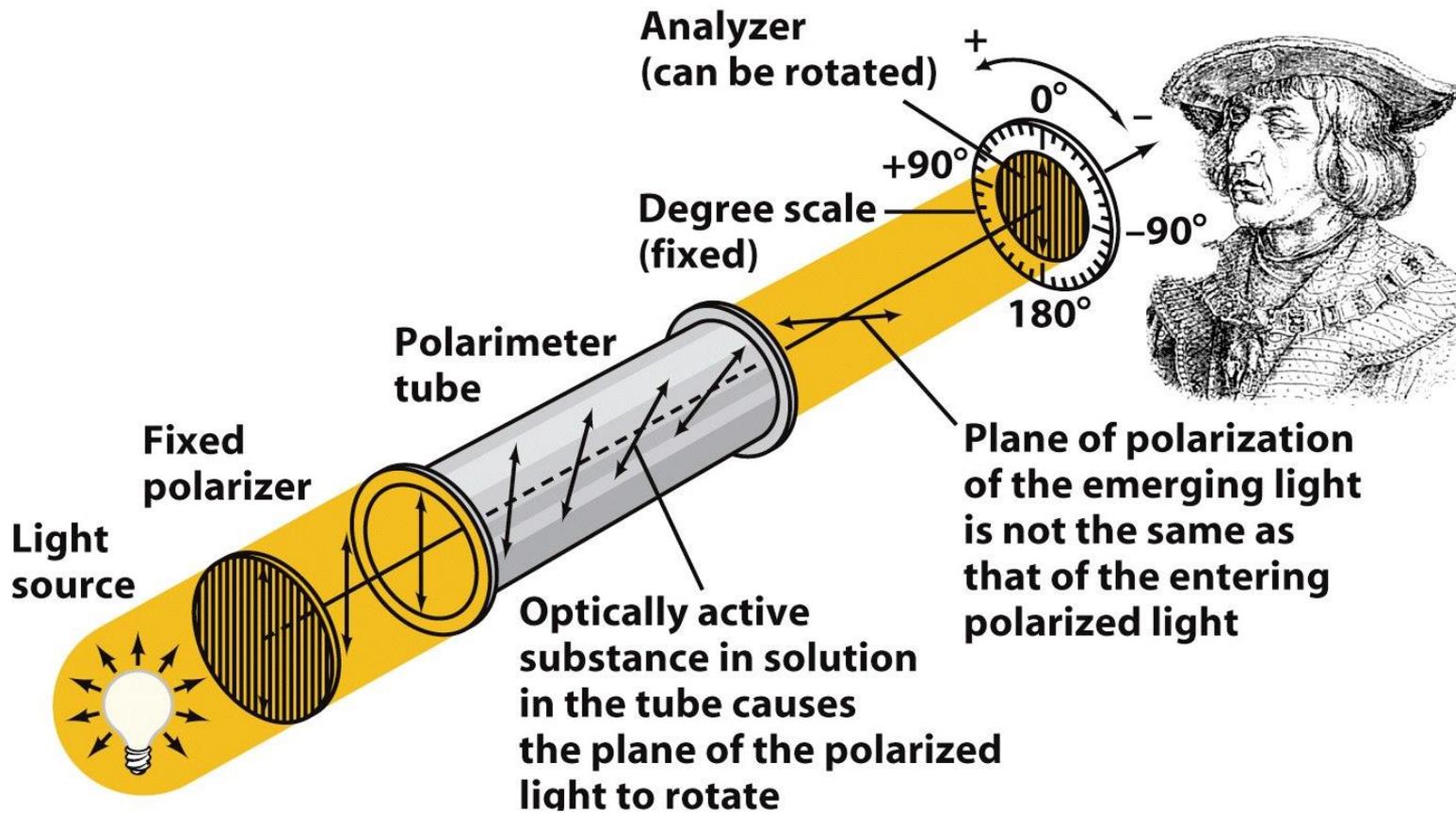
característica típica de substâncias que contém } centro(s) assimétrico(s)/quirálico(s)
} carbono(s) assimétrico(s) / **C***

impossibilita a sobreposição à sua imagem especular.

no. de possíveis estereoisômeros = 2^n

(2 possíveis configurações; n = no. de **C***):





$$[\alpha]_D^{25} = \frac{\% \text{ rotação observada } (^{\circ})}{\text{caminho óptico (dm)} \times \text{concentração (g/ml)}}$$

$D = \text{linha } D \text{ do espectro do Na: } \lambda = 598,3\text{nm}$

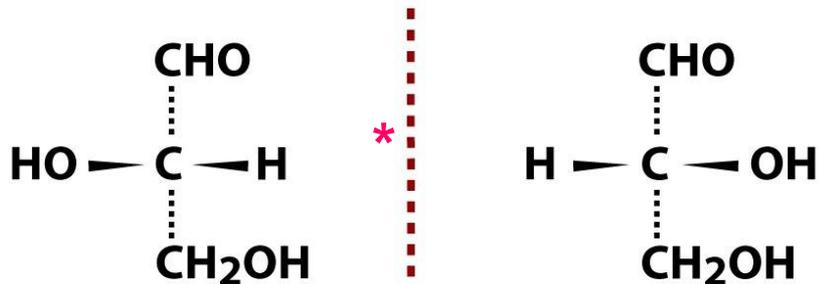
L- Pro	-86,2°	D- Pro	+ 86,2 °
L- Leu	-10,4 °	D- Leu	+10,4 °
L- Arg	+12,5 °	D- Arg	-12,5 °

Nomenclatura para especificar configuração absoluta:

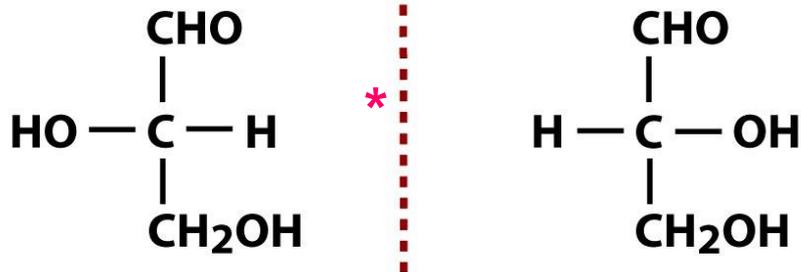
(disposição espacial dos grupos ao redor do C*)

sistema D, L; *Emil Fischer, 1891*: configuração de um composto de referência

Geometric formulas



Fischer projection



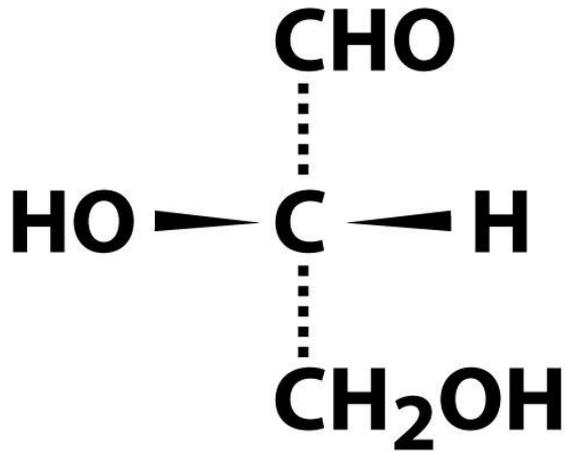
Mirror plane

L-Glyceraldehyde

D-Glyceraldehyde

(50% de chance de erro)

Configuração absoluta dos aminoácidos segundo sistema D,L:

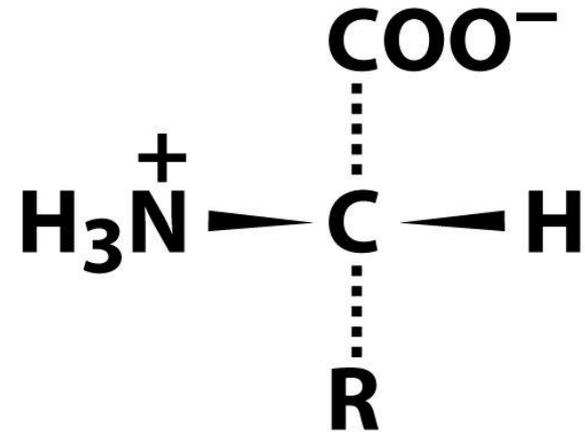


L-Glyceraldehyde

Unnumbered figure pg 87 Fundamentals of Biochemistry, 2/e
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(forma – ou l)

1949: configuração absoluta confirmada por cristalografia de raios X



L- α -Amino acid

(configuração dos grupos ao redor do C* está relacionada com aquela dos grupos do L-gliceraldeído:

reações químicas convertem os diferentes grupos com os quais são comparados em relação à configuração)

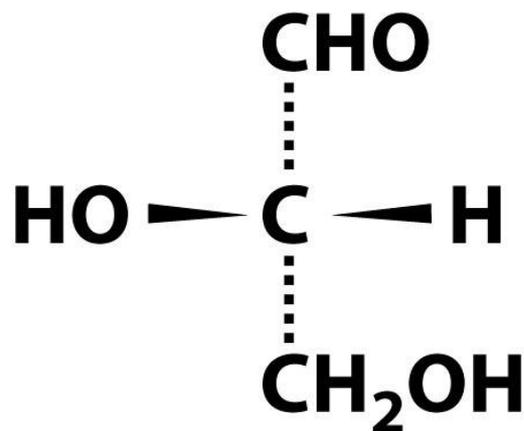
Todos os aminoácidos proteicos: L

Nomenclatura para especificar configuração absoluta:

sistema R (rectus), S (sinistre); *Cahn-Ingold-Prelog, 1956*:

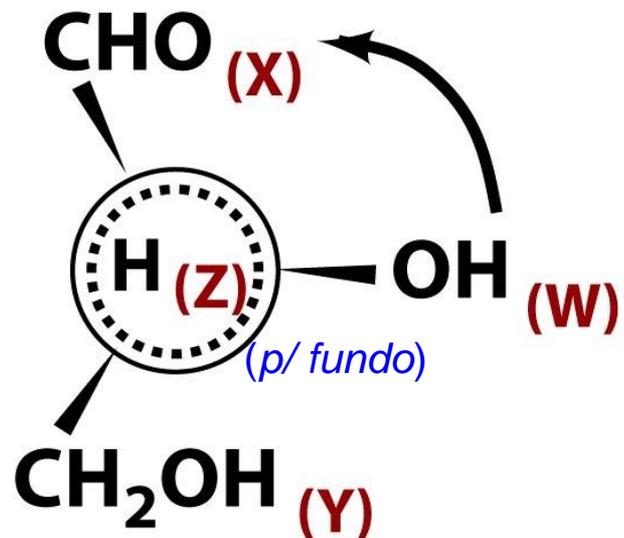
ordem de prioridade dos átomos: nos. atômicos dos grupos ligados a um C*
 $\text{SH} > \text{OH} > \text{NH}_2 > \text{COOH} > \text{CHO} > \text{CH}_2\text{OH} > \text{C}_6\text{H}_5 > \text{CH}_3 > {}^2\text{H} > {}^1\text{H}$

mais adequada para moléculas com mais de um C*.



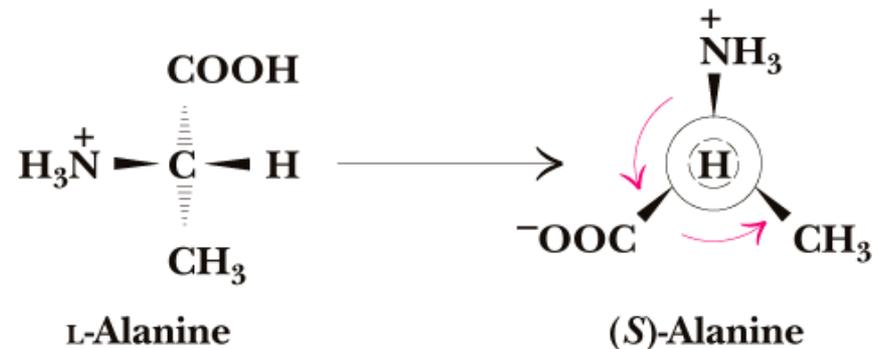
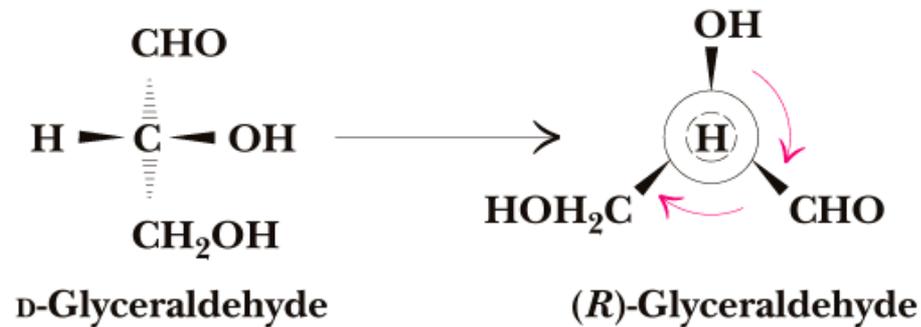
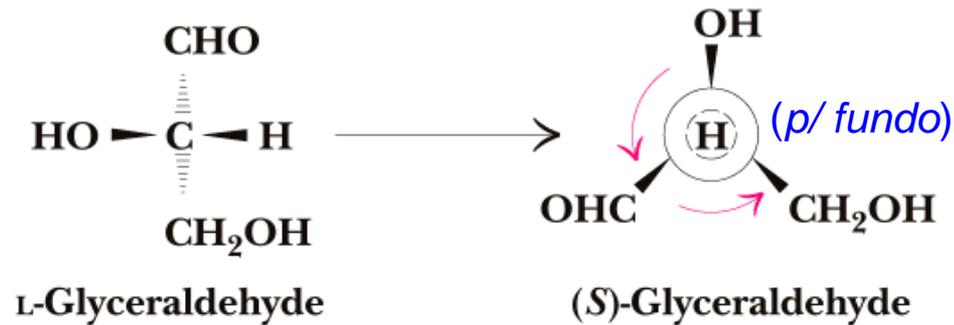
L-Glyceraldehyde

≡

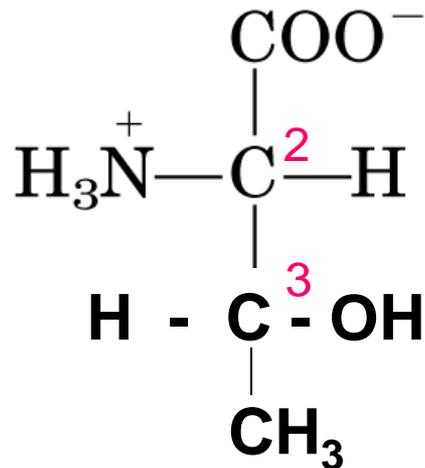


(S)-Glyceraldehyde

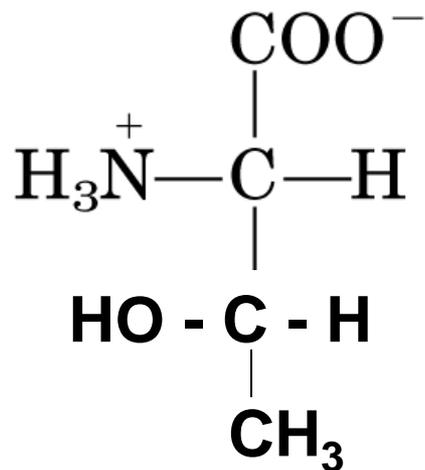
Sistemas L,D e S, R aplicados aos aminoácidos



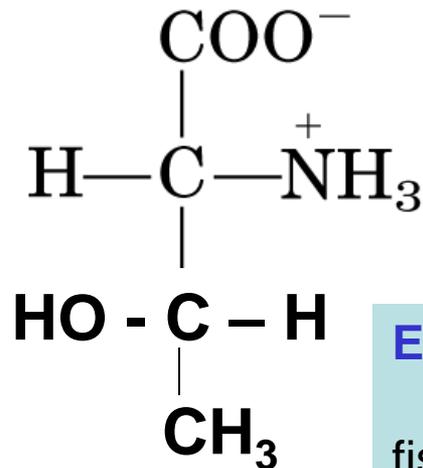
Com exceção de Cys, todos os 20 L-aminoácidos de pept/prot são S!



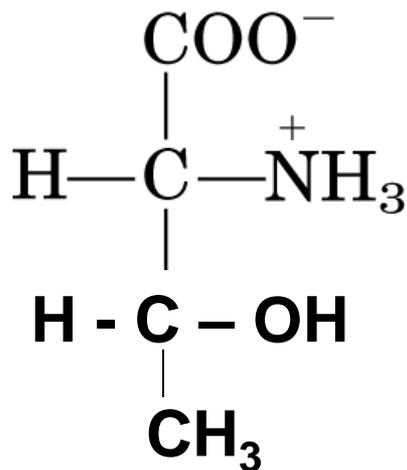
L-Thr
(2S, 3R)-Thr



L-allo-Thr



D-Thr

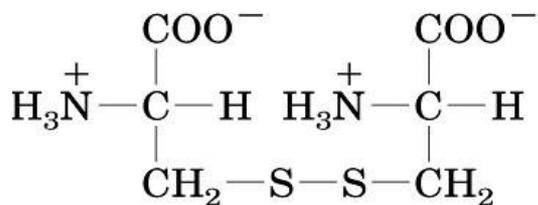


D-allo-Thr

$2^n = 2^2 = 4$ isômeros

Enantiômeros: imagens especulares não sobreponíveis; física- e quimicamente indistinguíveis.

Diastereisômeros: imagens especulares entre si, mas não de L- ou D-Thr física- e quimicamente distinguíveis (*PF, espectros, reatividade química diferentes*).



Mirror plane

L-Cystine

L-Cystine:

Optical

rotation:

-218° to -224°

(c = 2, 1 N HCl,

20°C) EMD

Millipore

-215 to -230

deg

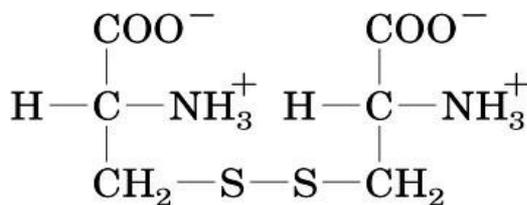
(C=1, 1mol/L

HCl) [α]_{20/D}

Chemical

Industry Co.,

Ltd. Tokyo



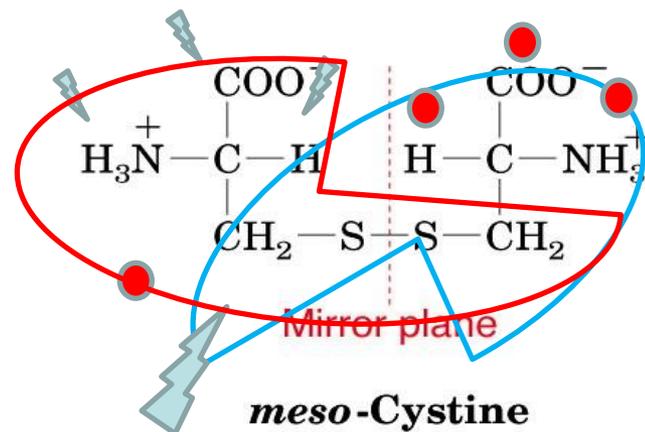
D-Cystine

D-Cystine: Optical

rotation: [α]_{20/D} +212°

(c = 1, 1 M HCl, 20°C)

Merck



meso-Cystine

Isômero meso ou allo ou internamente compensado:

Oticamente inativo

2 centros assimétricos quimicamente idênticos

uma parte da molécula não se sobrepõe à outra parte → as partes são imagens especulares uma da outra

A molécula é sobreponível à sua imagem especular

Como separar/analisar/quantificar aminoácidos? MTM

1) Separação por diferença de polaridade:

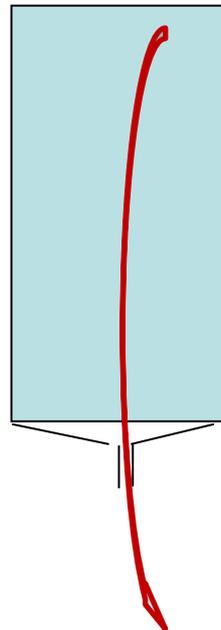
Cromatografia em papel (fase estacionária = celulose)

Cromatografia em camada delgada (CCD; TLC): sílica, celulose, alumina

Revelação: reação química que gera produtos coloridos ou fluorescentes
comparação com aminoácidos de concentração conhecida e entre Rfs

Cromatografia em coluna (preenchida com material não iônico polar ou apolar)

(Coluna =
fase estacionária)



(eluente = fase móvel)

comparação da amostra
com mistura-padrão de
concentração conhecida,
seus tr (tempos de retenção)
e áreas dos seus picos

Neste caso: Derivatização ou revelação dos aminoácidos

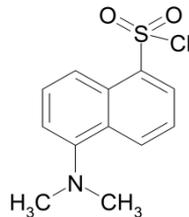
pré-coluna: antes da cromatografia

pós-coluna: depois da cromatografia

Que reagentes?

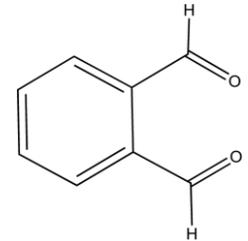
cloreto de dansila

produto fluorescente



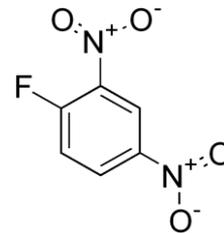
o-ftaldeído (OPA)

produto fluorescente



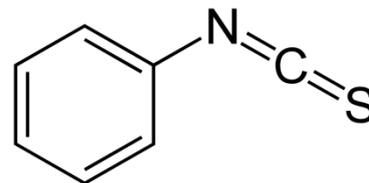
2,4 dinitrofluorobenzeno
(DTNB; reagente de Sanger)

produto colorido



fenilisotiocianato (PITC)

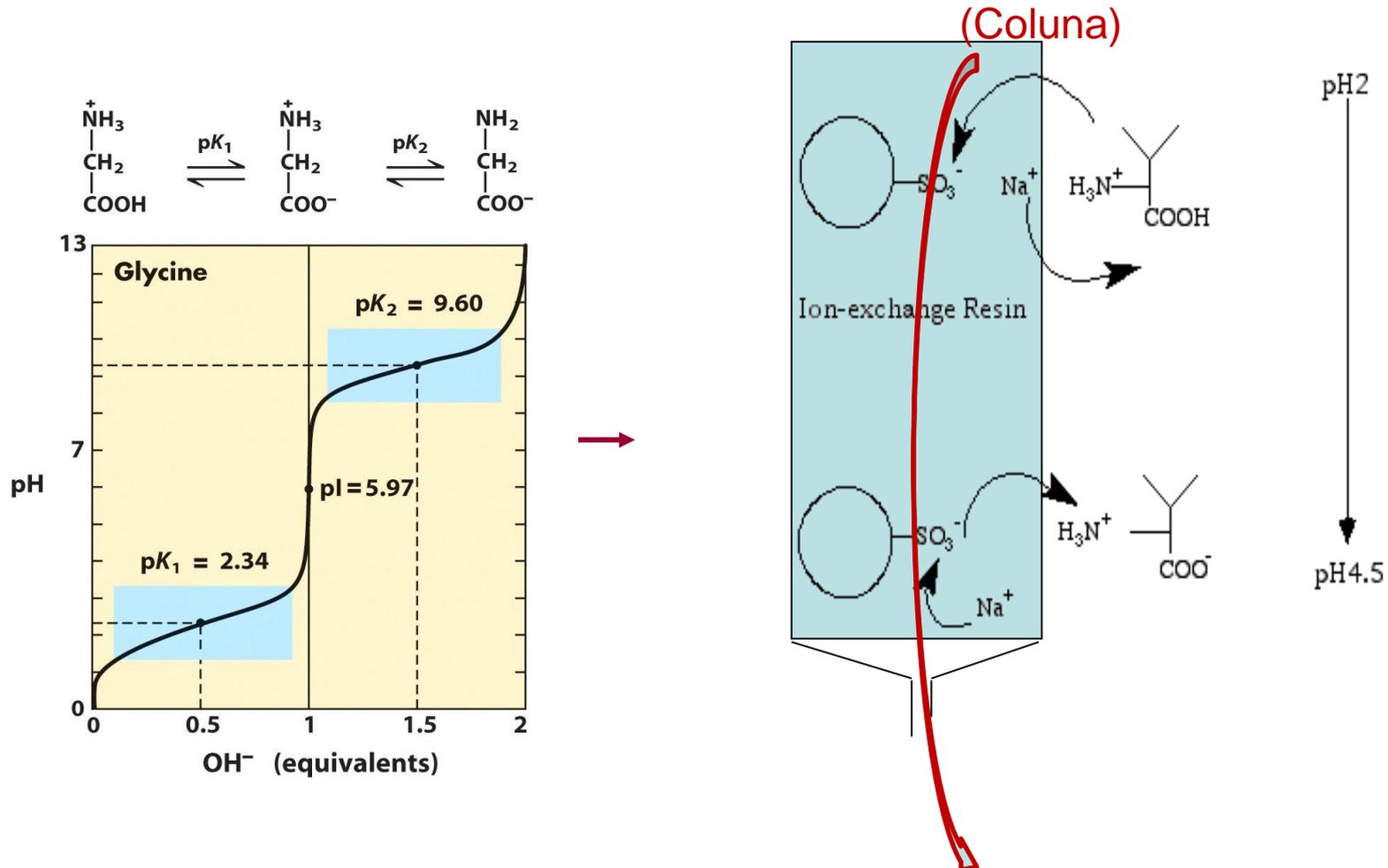
produto que absorve em 254 nm



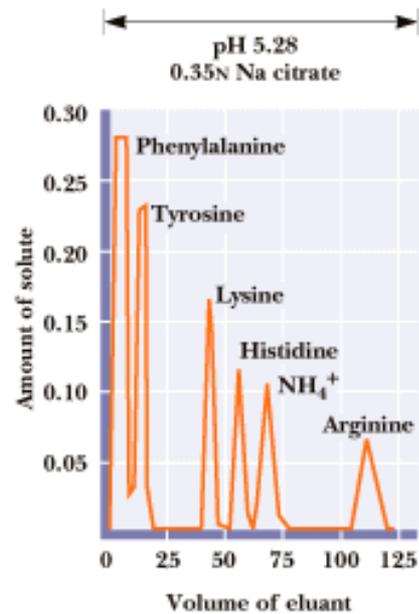
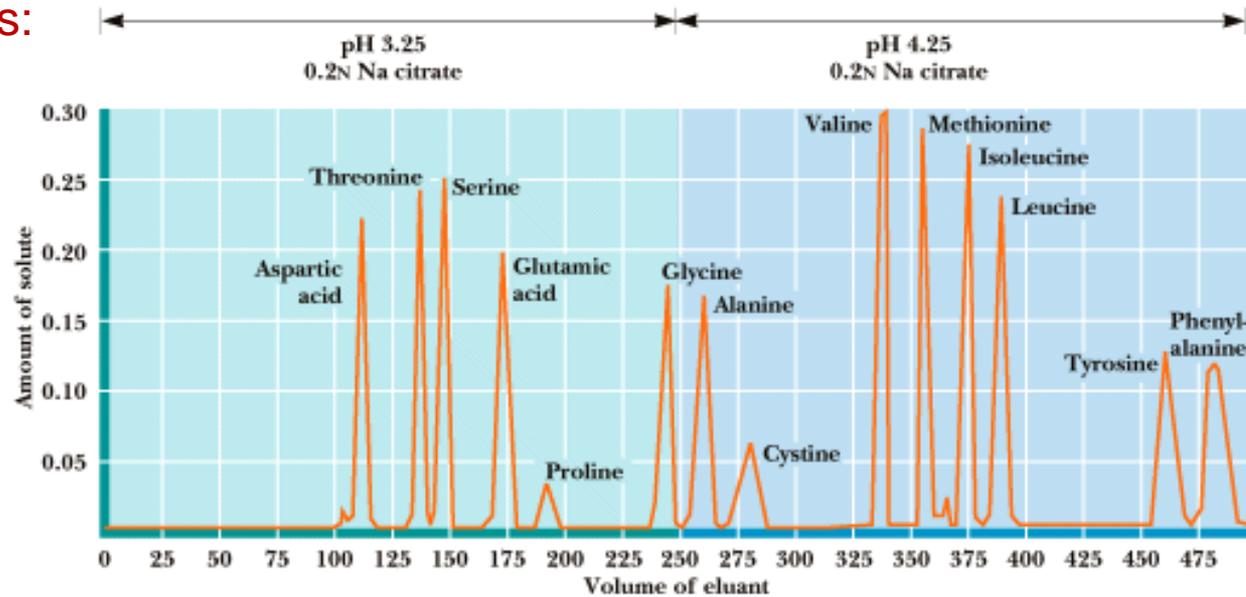
2) Separação por diferença de carga líquida em dado pH:

propriedades ácido-base dos aminoácidos

- cromatografia dos aminoácidos em coluna (preenchida com material iônico)
- uso de NaCl ou KCl para eluir os aminoácidos retidos na coluna
- comparação com aminoácidos-padrão de concentração conhecida e entre volume do eluente e áreas dos picos



cromatografia de troca iônica catiônica: sem pré-derivatização da mistura de aminoácidos:



Comparação com padrões de concentração conhecida!