Chem 352 - Lecture 3 Part I: Amino Acids and Protein Primary Structure

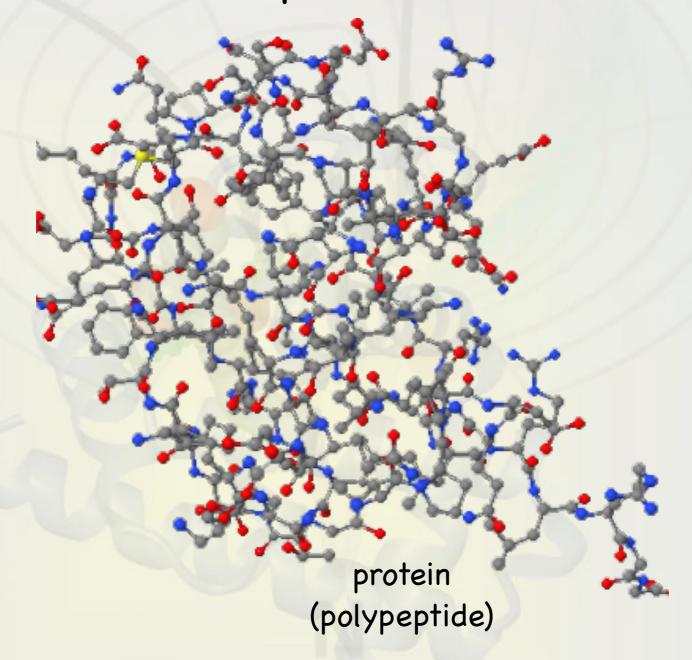
Question for the Day: Approximately how much mass is required to make just one molecule for each of the possible polypeptides with a length of 100 amino acid residues, which are made from the 20 naturally occurring L-amino acids?

Proteins are the workhorses of a living cell.

- + Biological catalysts (enzymes)
- + Storage and transport
- + Cytoskeleton
- + Cellular regulation
- + Hormones
- + Antibodies

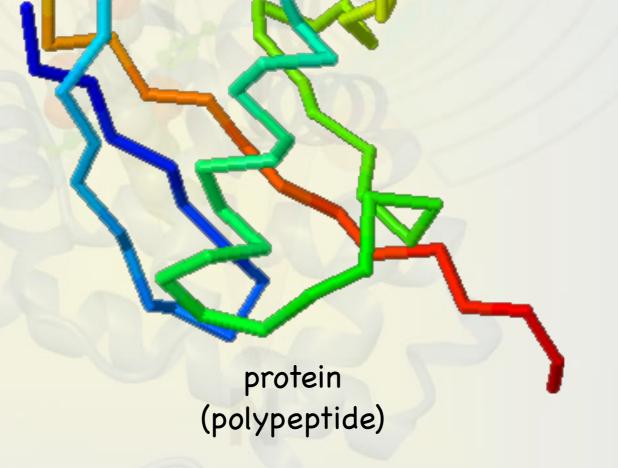
+ ...

Proteins are polymers of amino acids (polypeptides) that often have a complicated 3-D structures.



Proteins can have up to four different levels of structure:

* Primary (I°) - the anino acid sequence (defined by correct bonding)



Proteins have different levels of structure:

* Secondary (II°) - the regular arrangements of the polypeptide backbone into α-helices, β-sheets, ... (features hydrogen bonding between the backbone amide groups)

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(features hypogoling between the backbone am a secondary)

protein (polypeptide)

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 Tertiary (III°) - the 3-dimensional fold of a single polypeptide (stabilized by non-covalent side chain interactions)

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 Tertiary (III°) - the 3-dimensional fold of a single polypeptide (stabilized by non-covalent side chain interactions)

Proteins have different levels of structure:

* Quaternary (I) the assembly of multiple

(also stabilized by non-covalent side chain

interactions)

protein with two subunits (2 polypeptides)

- Proteins are made from polymers of a-amino acids.
 - * These polymers are called polypeptides.
 - + The monomers are the α -amino acids.

$$PK_a \approx 9 H_3N$$
— CH — C — OH $PK_a \approx 2$

The monomer

Problem:

Draw the titration curve (pH vs. equivalents) for glycine between pH 0 and pH 12.

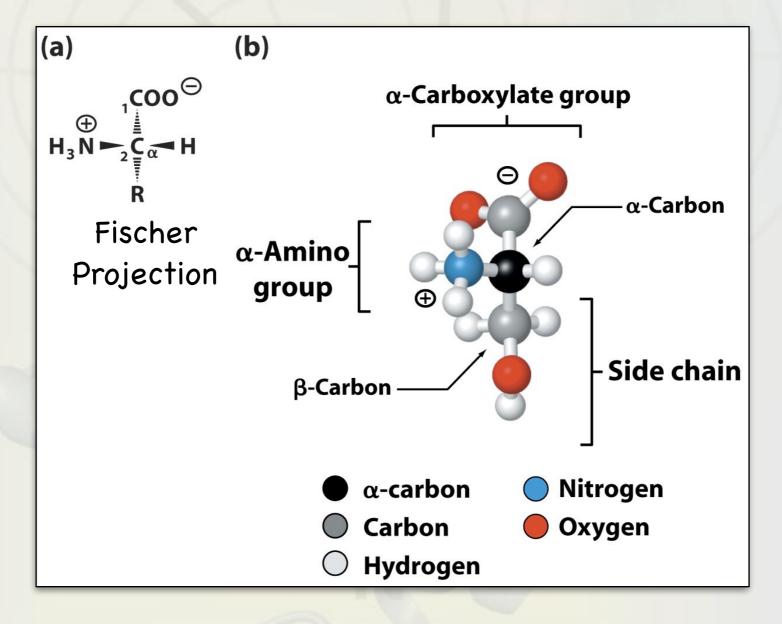
pK_a ≈ 9
$$H_3^{\dagger}N$$
— CH_2 — C — OH pK_a ≈ 2 α -carbon

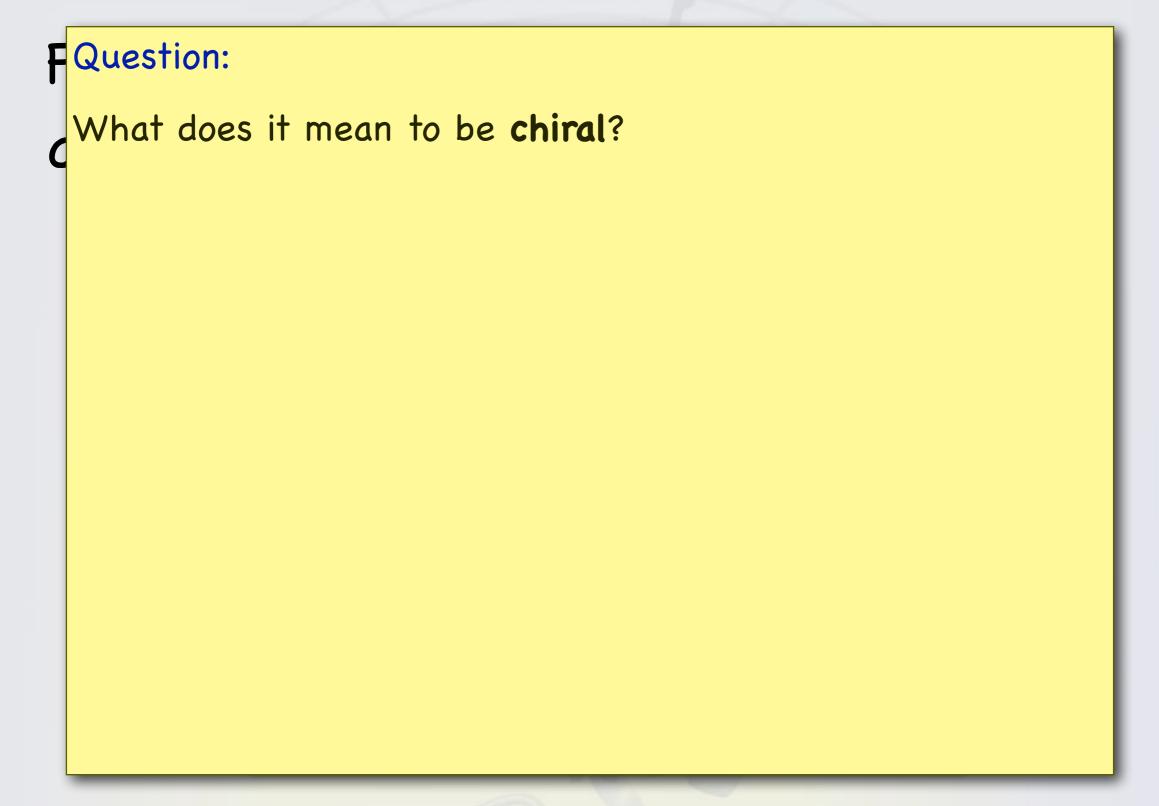
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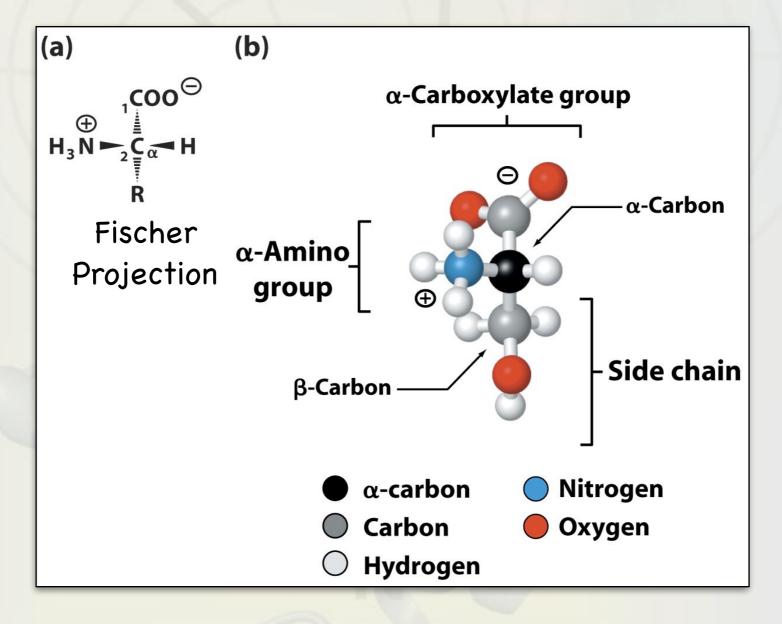
The monomer

For 19 out of the 20 common amino acids, the α -carbon is **chiral**.

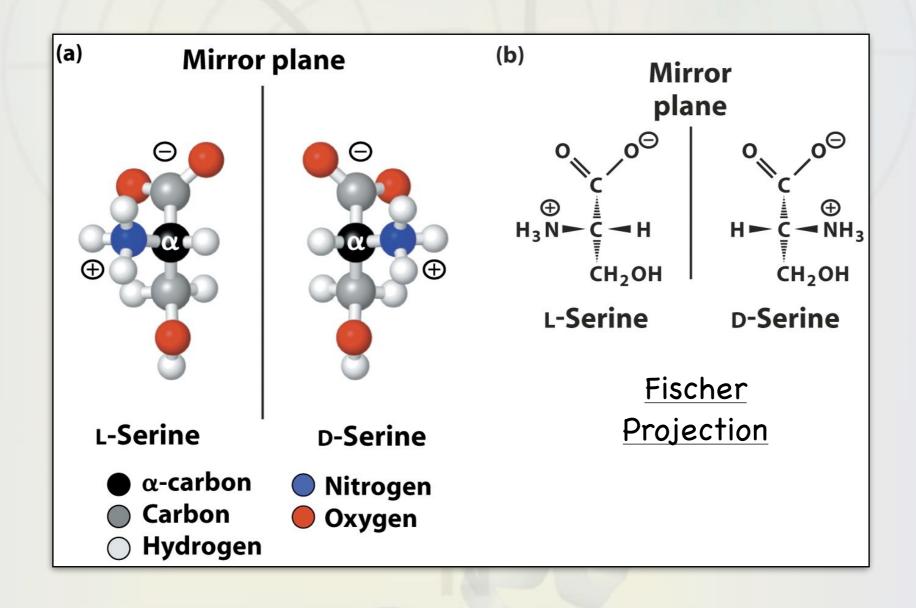




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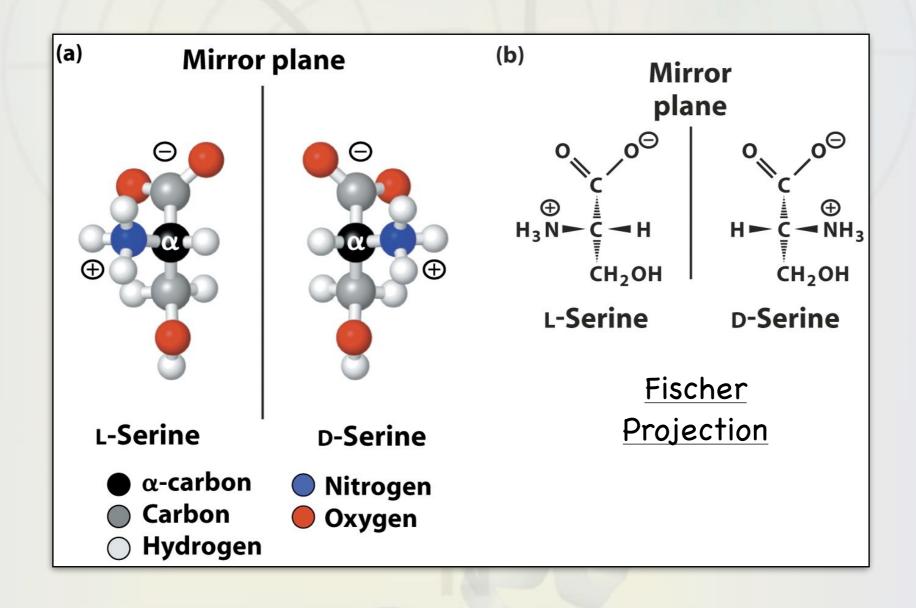


Question: Which of the 20 amino acids is not chiral?

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- + R vs S
 - Rectus versus Sinister based on the atomic mass of the substituents

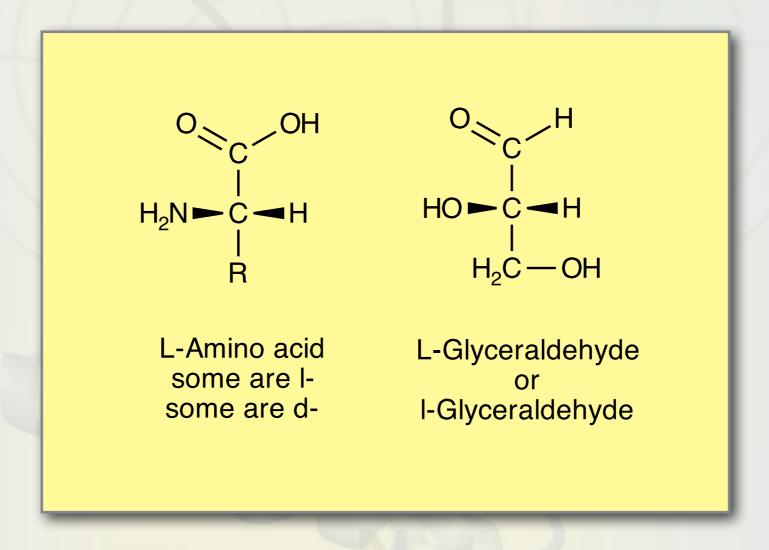
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 - dextrorotatory versus levorotatory based on the bending of plane polarized light

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- + D vs L
 - Based on how glyceraldehyde bends plane polarized light

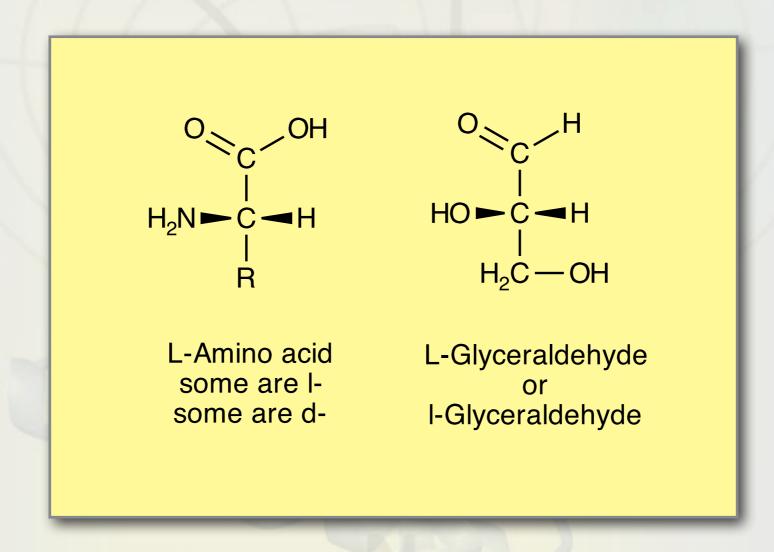
There are different wave to designate center: the ste + R vs \$ H►C OH HO ► C ← H · Rect he atom + d (+) d-Glyceraldehyde I-Glyceraldehyde D-Glyceraldehyde dext based L-Glyceraldehyde ght on t

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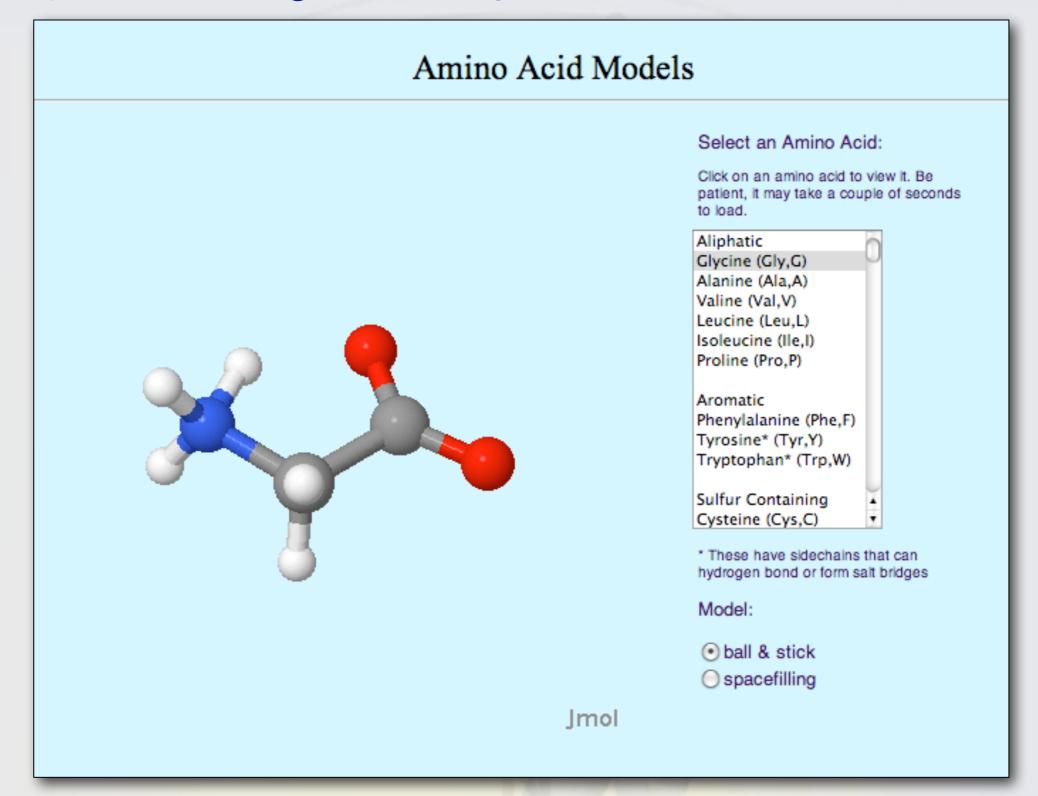


All of the amino acids used to to make proteins are L-amino acids

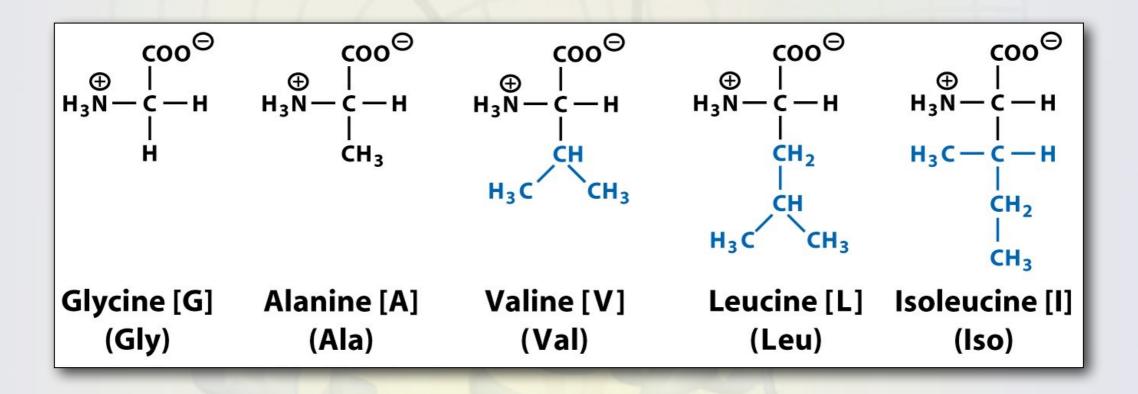


There is considerable variety in the chemical and physical properties of the the 20 different amino acid side chains.

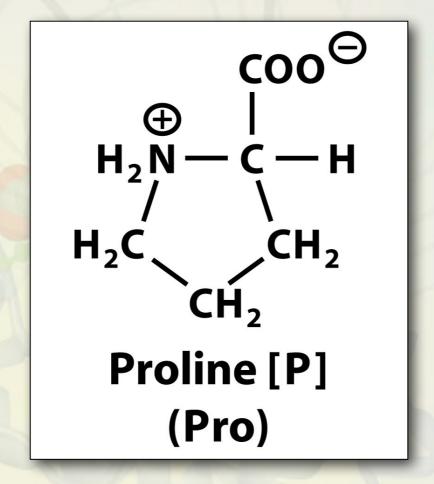
- + Aliphatic (saturated hydrocarbon) (G,A,V,L,I,P)
- + Aromatic (F,Y,W)
- + Sulfur-containing (C,M)
- + Alcohols (S,T)
- + Bases (K,R,H)
- + Acids (D,E)
- + Amides (N,Q)



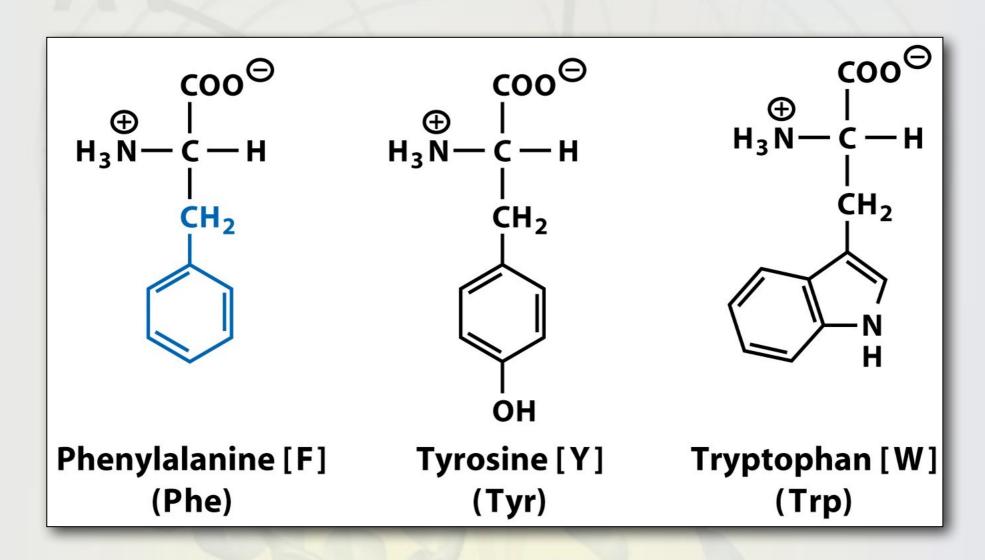
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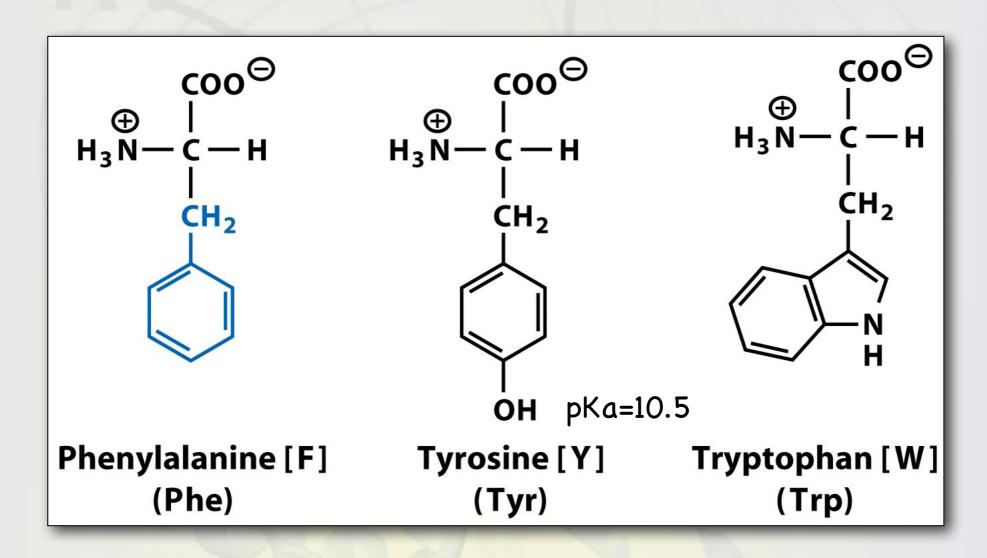
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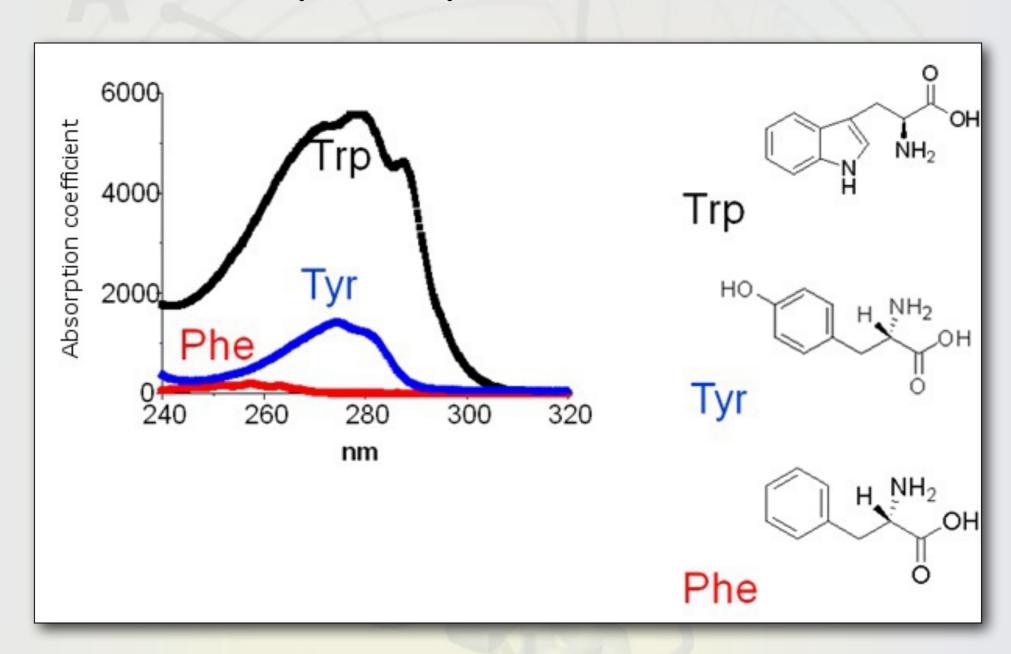
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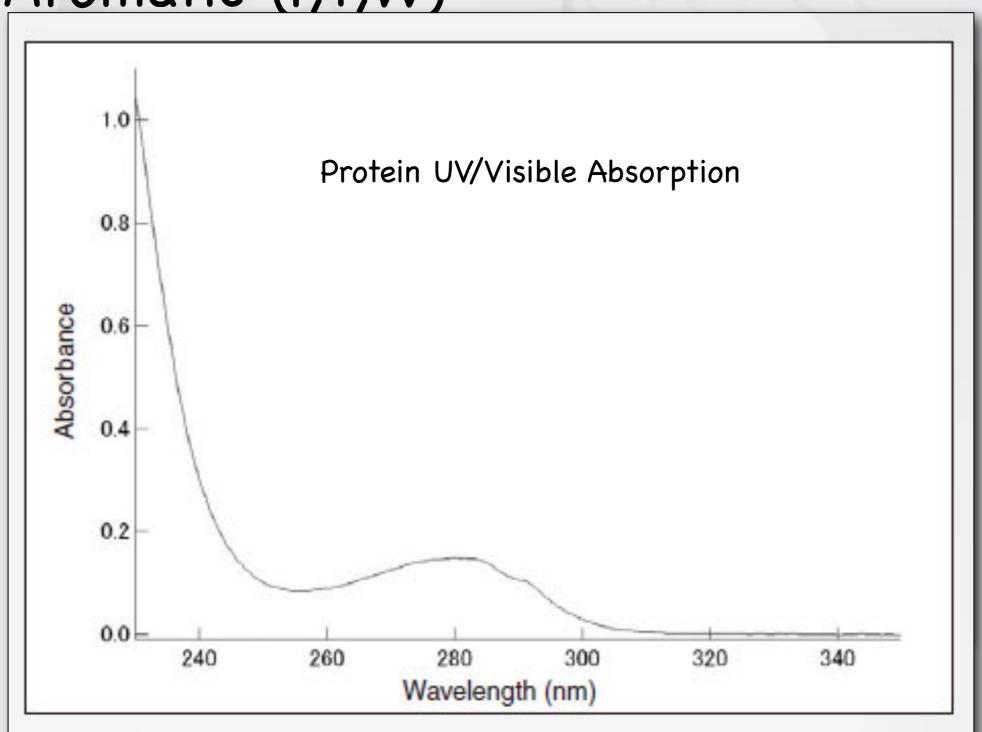
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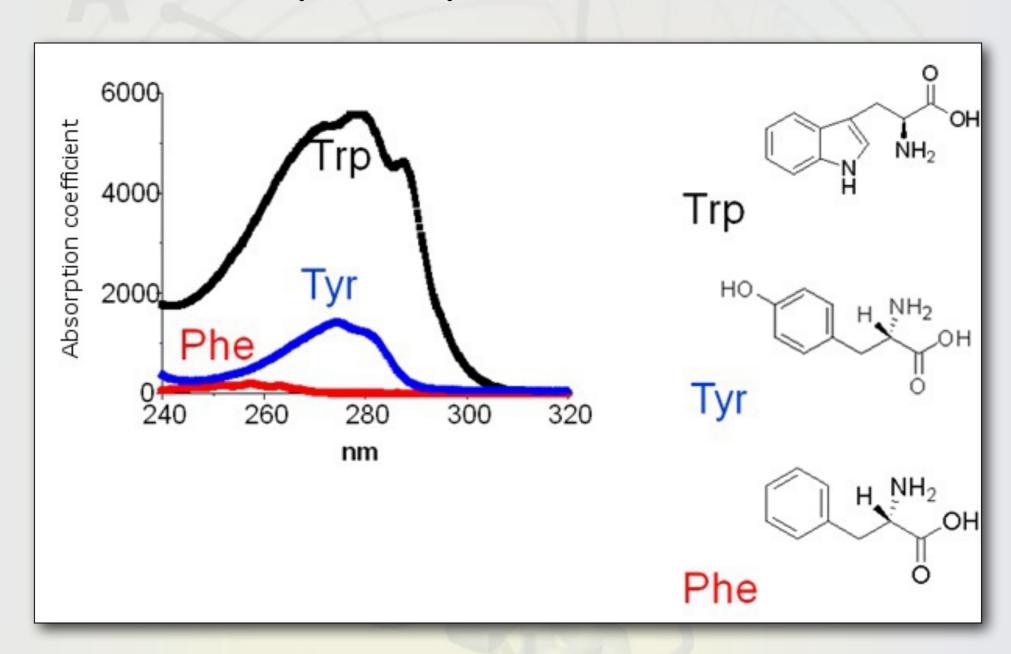
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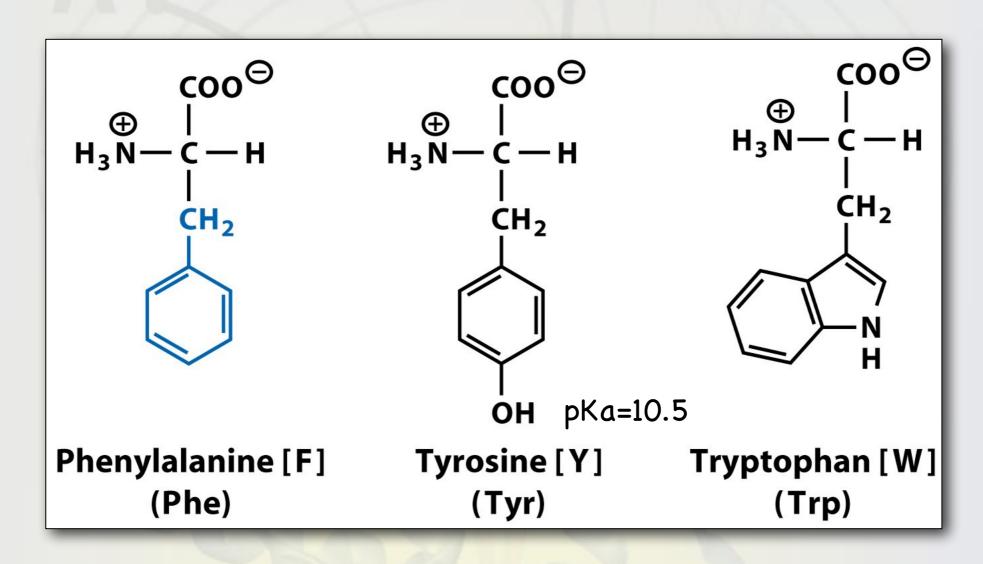
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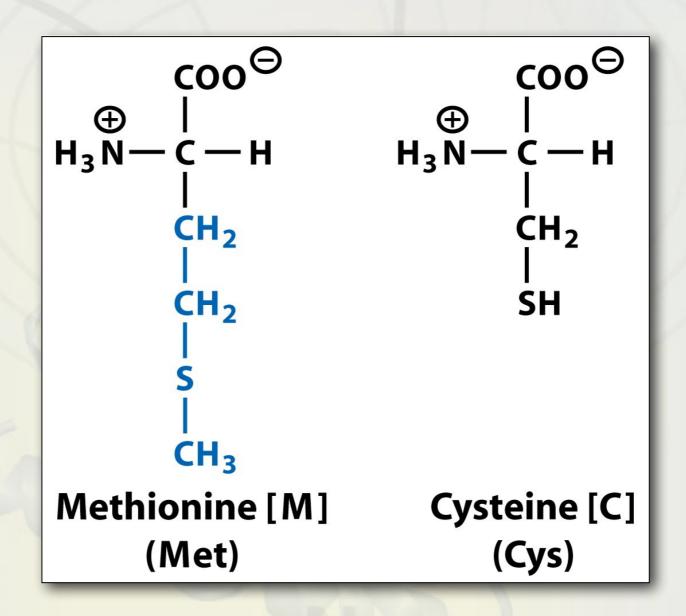
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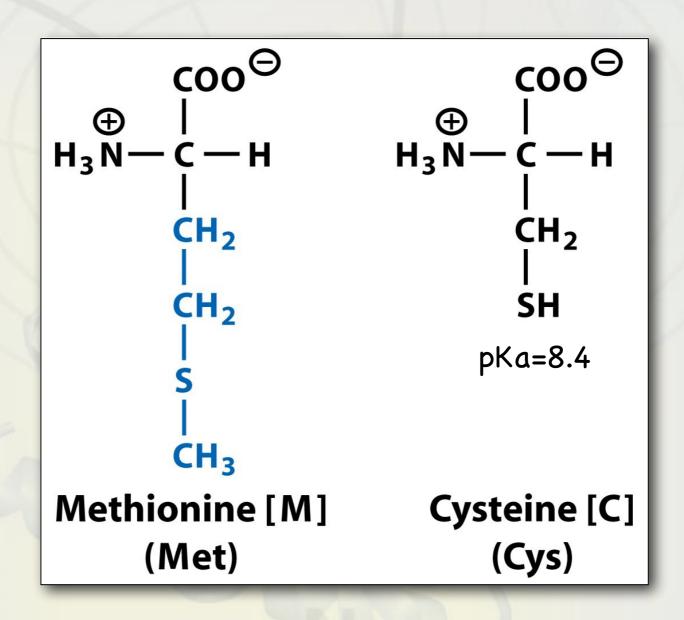
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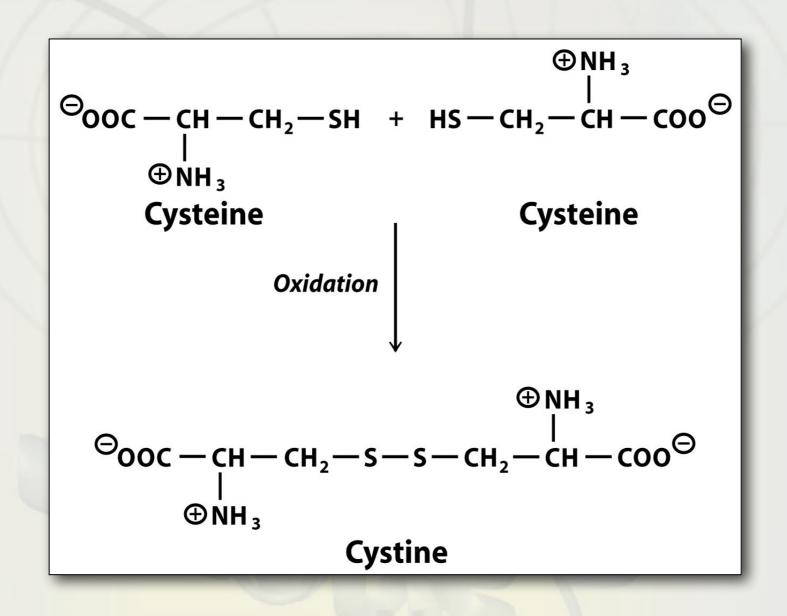
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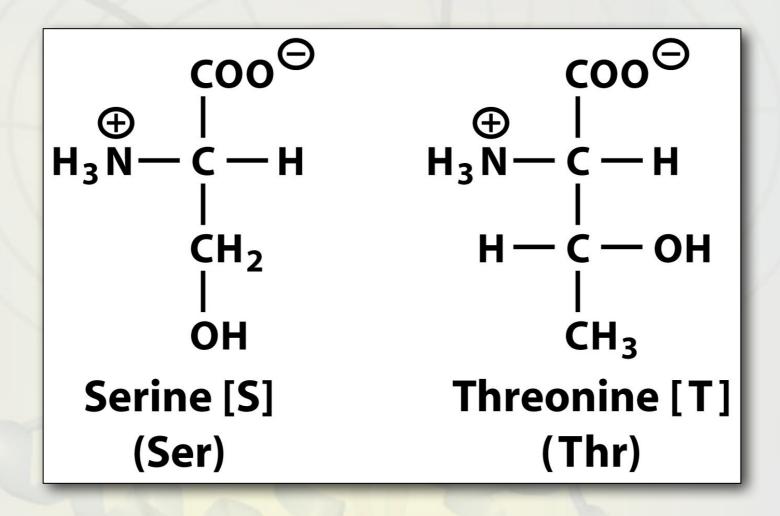
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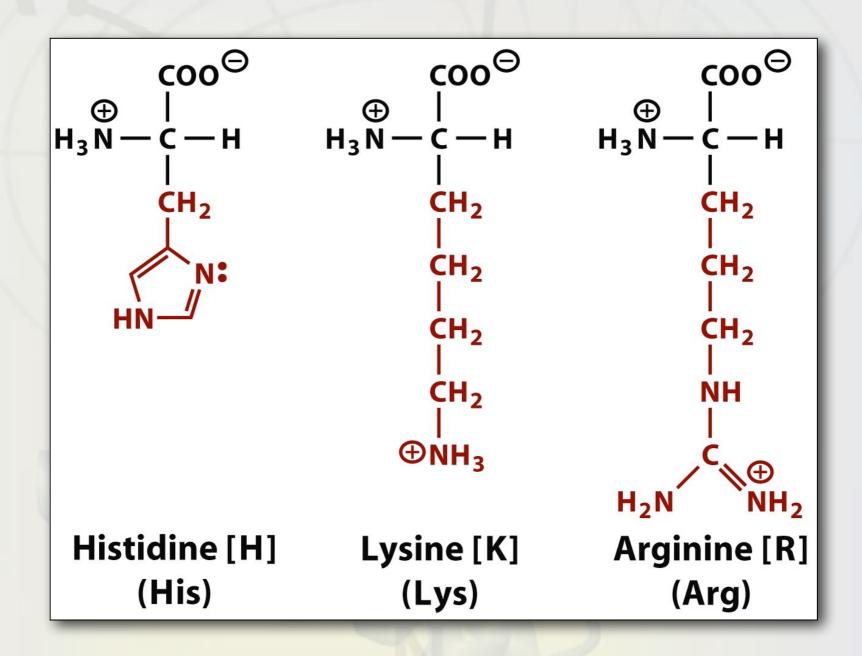
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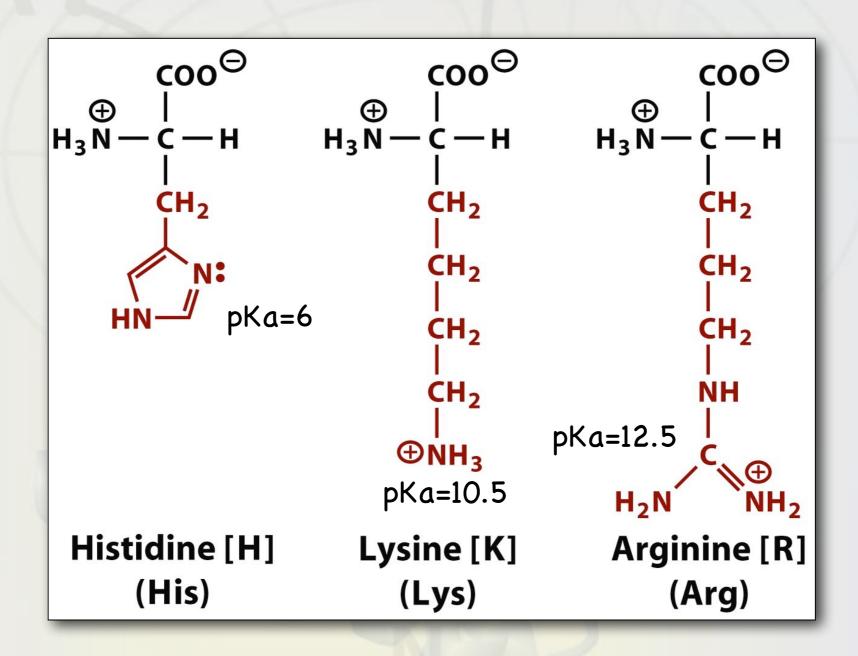
·Alcohols (S,T)



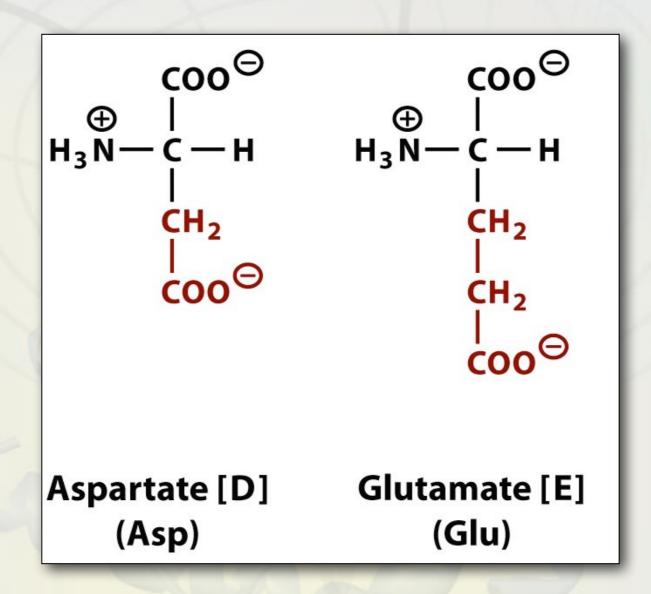
·Bases (H,K,R)



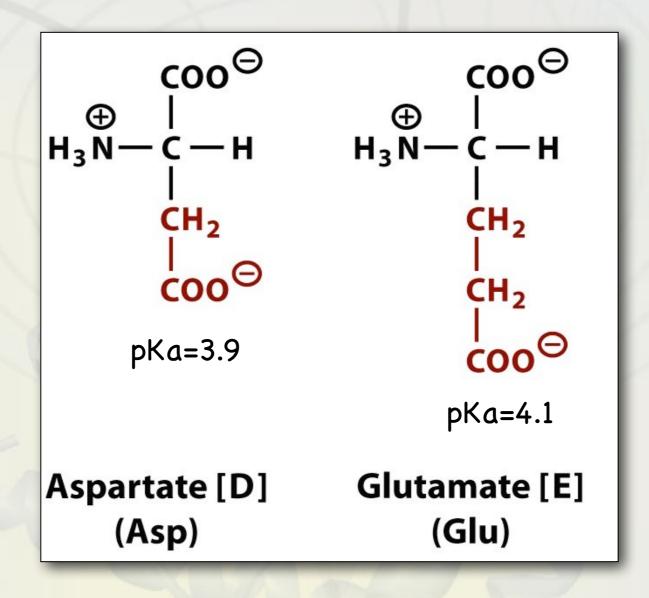
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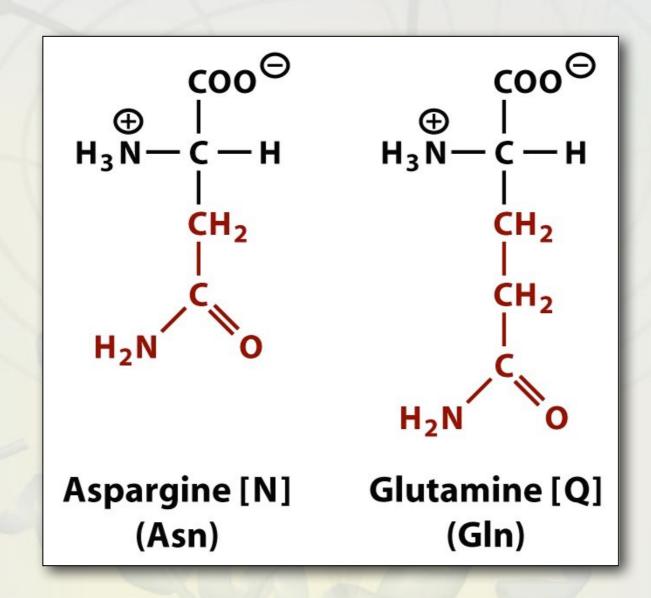
·Acids (D,E)



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·Amides (N,Q)



- ·Can also group the amino acids based on their solubility in water.
 - + Highly hydrophobic (I, P, V, L, M)
 - + Less hydrophobic (W, A, G, C, Y, P, T, S)
 - + Highly hydrophilic (H, E, N, Q, D, K, R)

·Can also on their

- + Highly h
- + Less hy
- + Highly h

TABLE 3.1	Hydropathy scale for amino acid residues			
Amino acid	Free-energy change for transfer ^{a} (kj mol ⁻¹)			
Highly hydropl	hobic			
Isoleucine	3.1			
Phenylalanin	e 2.5			
Valine	2.3			
Leucine	2.2			
Methionine	1.1			
Less hydropho	bic			
Tryptophan	1.5 ^b			
Alanine	1.0			
Glycine	0.67			
Cysteine	0.17			
Tyrosine	0.08			
Proline	-0.29			
Threonine	-0.75			
Serine	-1.1			
Highly hydrophilic				
Histidine	-1.7			
Glutamate	-2.6			
Asparagine	-2.7			
Glutamine	-2.9			
Aspartate	-3.0			
Lysine	-4.6			
Arginine	-7.5			

icids based

P, T, S) K, R)

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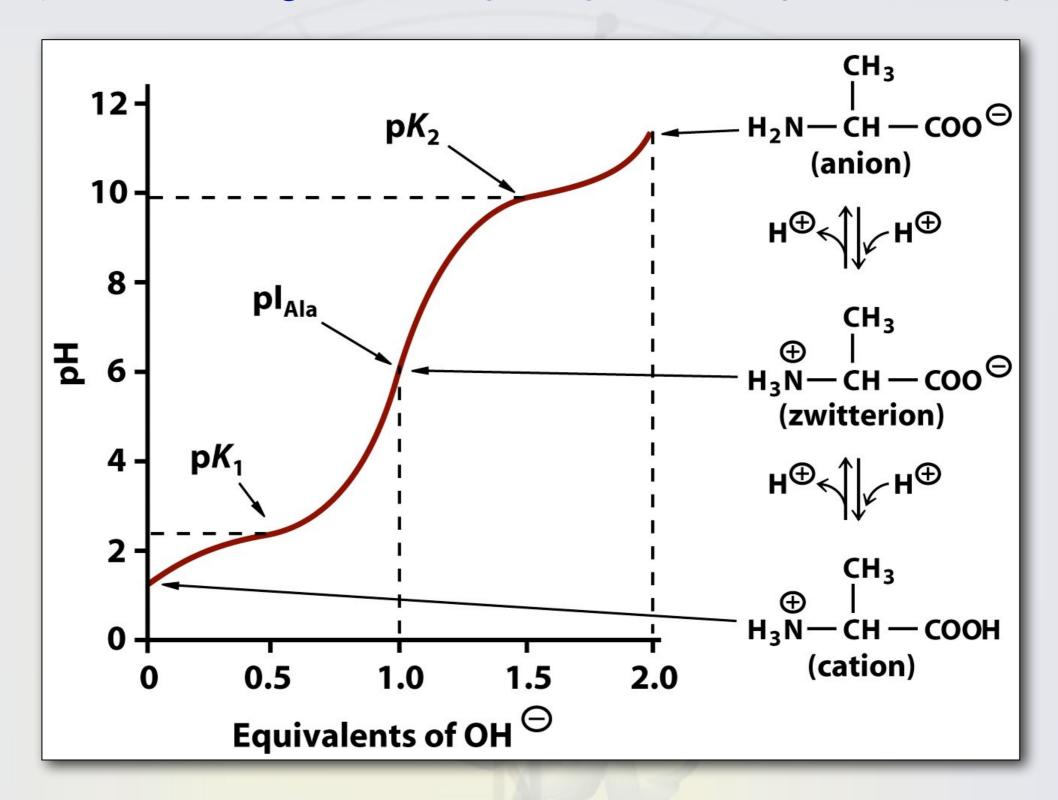
- ·Many important biological molecules are derived from amino acids, e.g.,
 - histamine (derived from His) (triggers allergic response)
 - * epinephrine (derived from Tyr) (hormone that triggers "flight or fight" response)
 - thyroxine (derived from Tyr) (thyroid hormone) (one of the few uses for iodine)
 - + GABA (derived from Glu) (neurotransmitter)

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(a)
$$(b)$$
 \oplus $CH_2-CH_2-NH_3$ $Y-Aminobutyrate$ (d) (d)

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The Amino Acids as Acids & Bases



The Amir

TABLE 3.2 pK_a values of acidic and basic constituents of free amino acids at 25°C

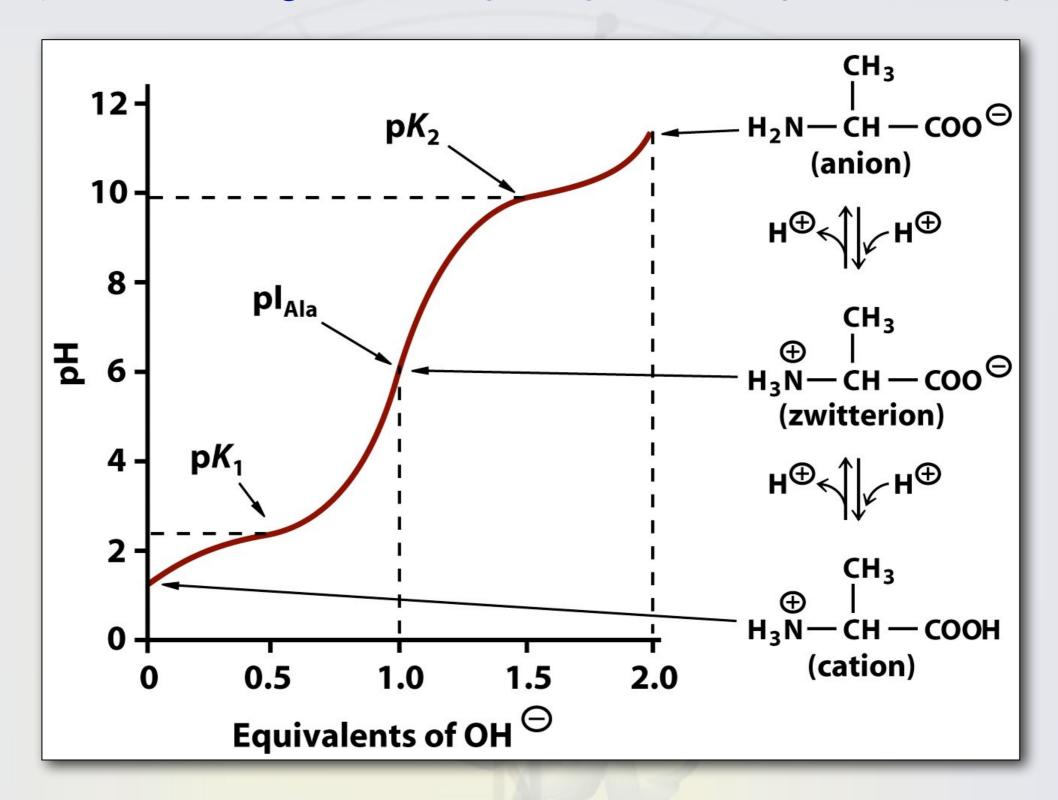
s & Bases

	12-	
,	10-	
	8 -	
표	6 -	
	4 -	р <i>К</i> ₁
	2 -	
	0 -	
1		

Amino acid		p <i>K</i> a value		
	Carboxyl group	Amino group	Side chain	
Glycine	2.4	9.8		
Alanine	2.4	9.9		
Valine	2.3	9.7		
Leucine	2.3	9.7		
Isoleucine	2.3	9.8		
Methionine	2.1	9.3		
Proline	2.0	10.6		
Phenylalanin	e 2.2	9.3		
Tryptophan	2.5	9.4		
Serine	2.2	9.2		
Threonine	2.1	9.1		
Cysteine	1.9	10.7	8.4	
Tyrosine	2.2	9.2	10.5	
Asparagine	2.1	8.7		
Glutamine	2.2	9.1		
Aspartic acid	2.0	9.9	3.9	
Glutamic acid	d 2.1	9.5	4.1	
Lysine	2.2	9.1	10.5	
Arginine	1.8	9.0	12.5	
Histidine	1.8	9.3	6.0	

CH ₃ N—CH—COO [©] (anion)
¹ [⊕] ←↑↓/✓ H [⊕]
CH ₃ ⊕ N—CH—COO [©] (zwitterion)
¹ [⊕] ←↑↓ ⊬ H⊕
CH₃ ⊕ ₃N—CH—COOH (cation)

The Amino Acids as Acids & Bases



The Peptide Bond

Amino acids are joined together by peptide (amide) bonds.

+ A peptide bond is formed from the condensation of an α -amino group from one amino acid with the α -carboxyl group of another amino acid.

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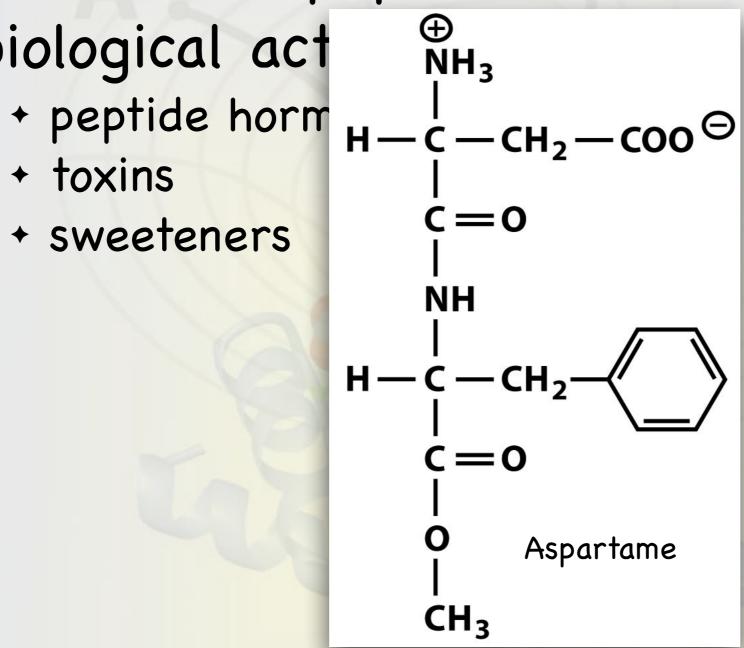
Some small peptide have important biological activities.

- + peptide hormones
- + toxins
- + sweeteners

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biological act

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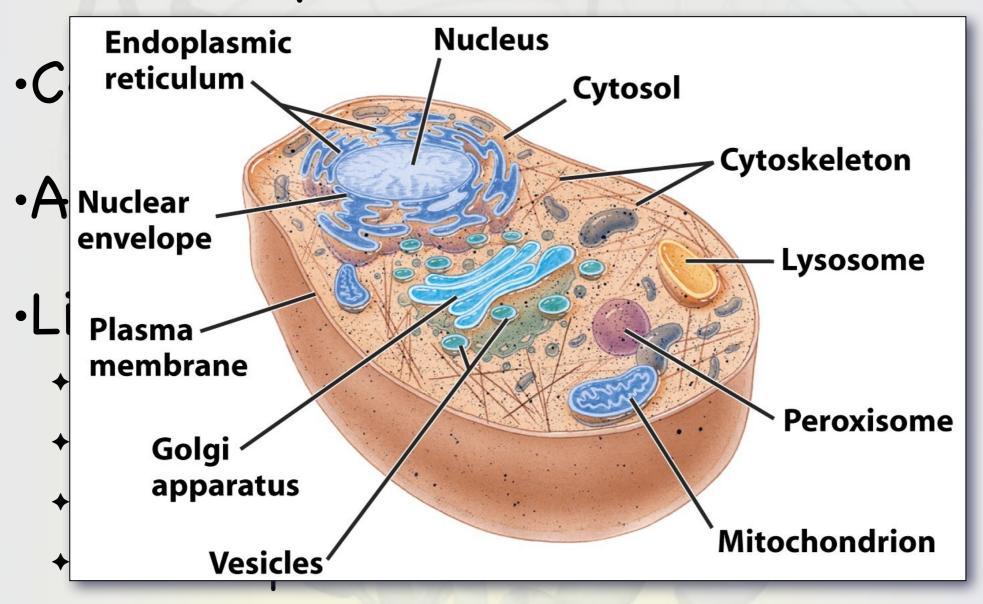
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Problem:

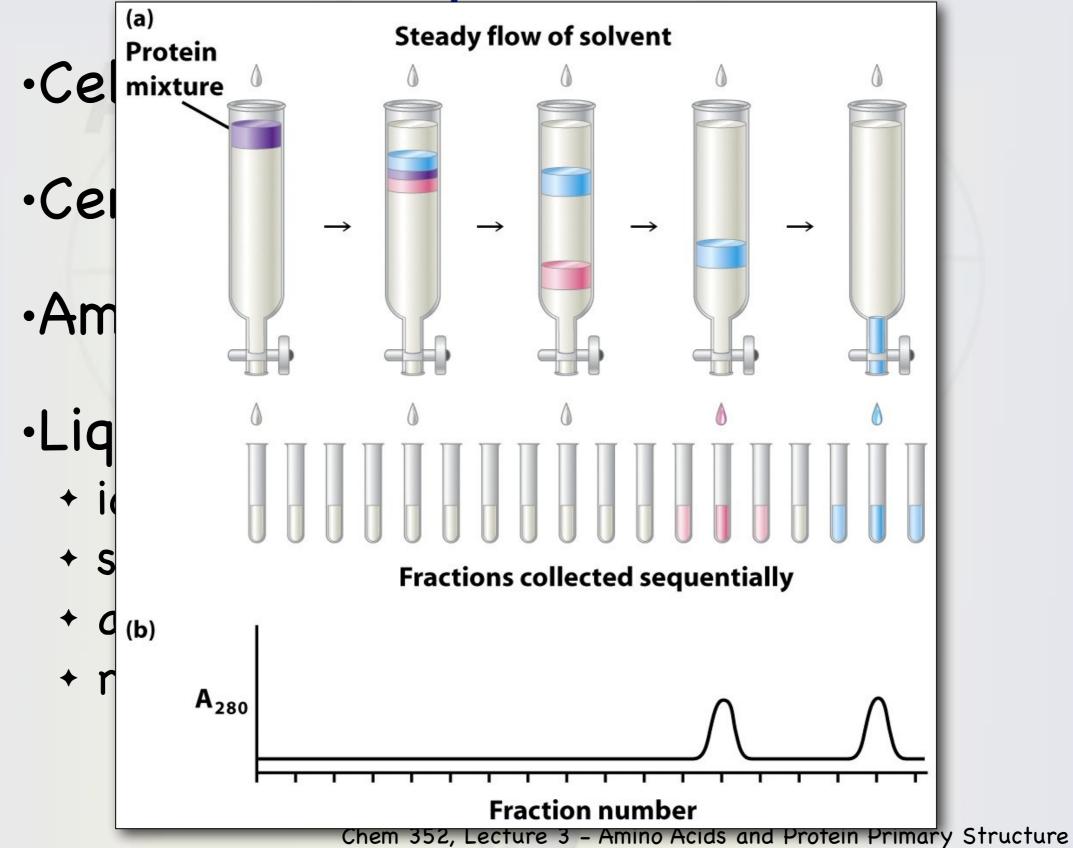
Sketch the titration curve for the dipeptide cysteinylaspartic acid and draw the structures of the predominant species that exists at each of the endpoints. Confirm your answers using Marvinsketch.

- ·Cell disruption
- ·Centrifugation
- ·Ammonium sulfate precipitation
- ·Liquid chromatography
 - + ion exchange
 - + size exclusion (gel filtration)
 - + affinity chromatography
 - + reverse phase.

·Cell disruption



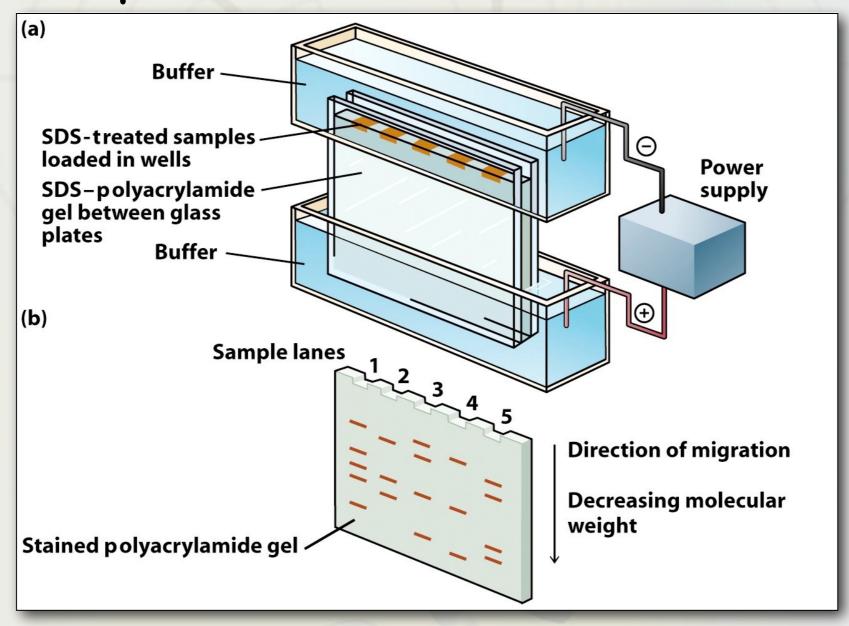
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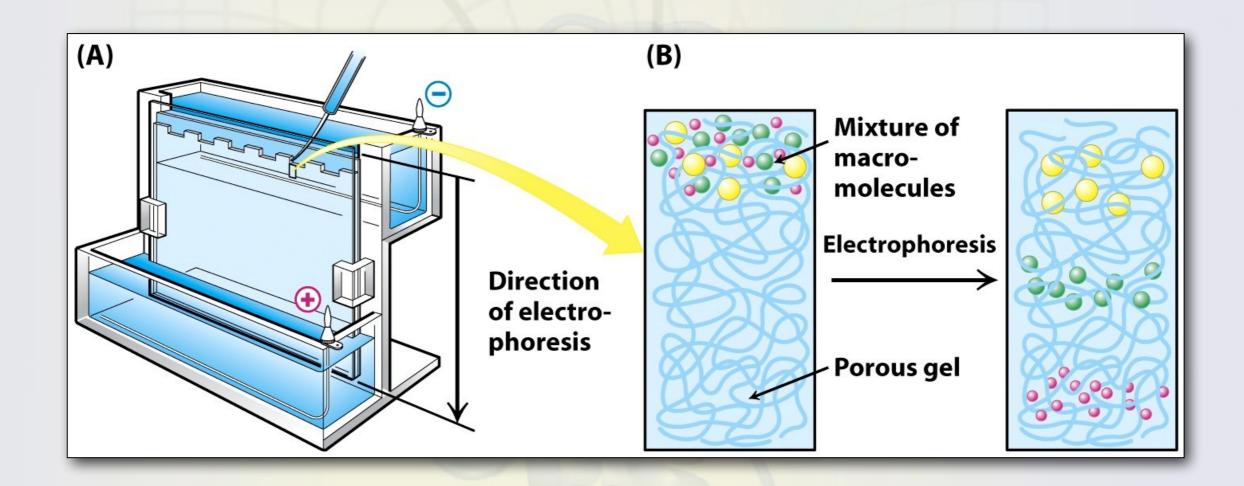
Protein Isolation and Analysis

·SDS-PAGE (SDS-polyacrylamide gel electrophoresis)



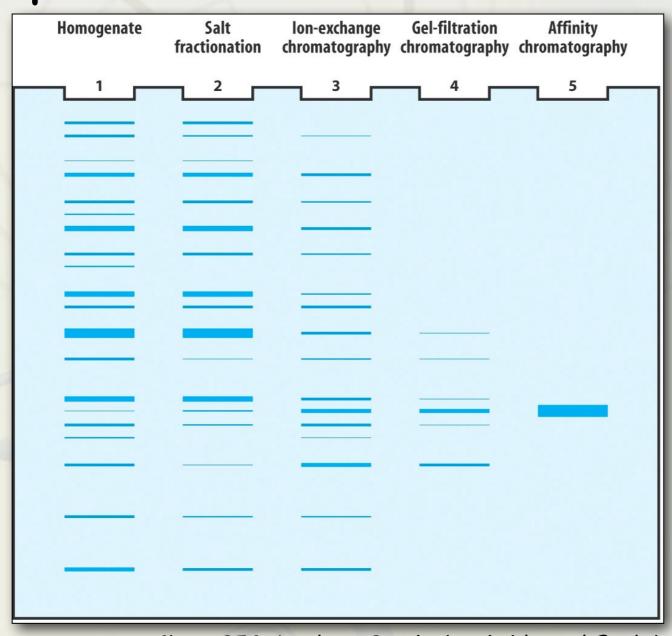
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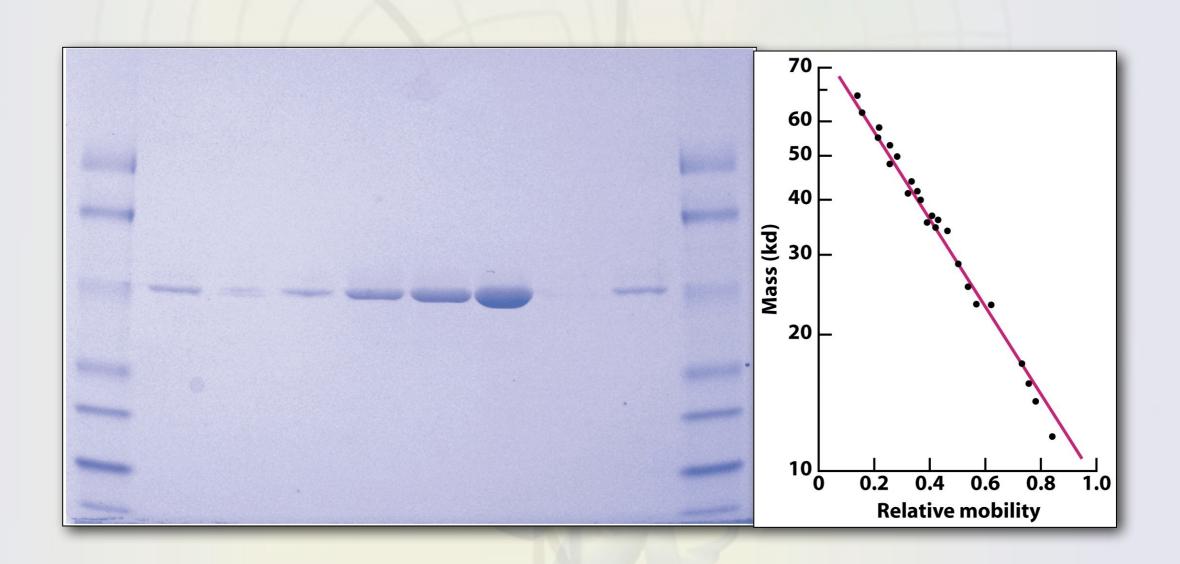
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Protein Isolation and Analysis

·SDS-PAGE (SDS-polyacrylamide gel electrophoresis)



·Mass spectroscopy

MALDI

Ionization

Laser **Detector**. Time of flight Matrix tube **Electric** field generator

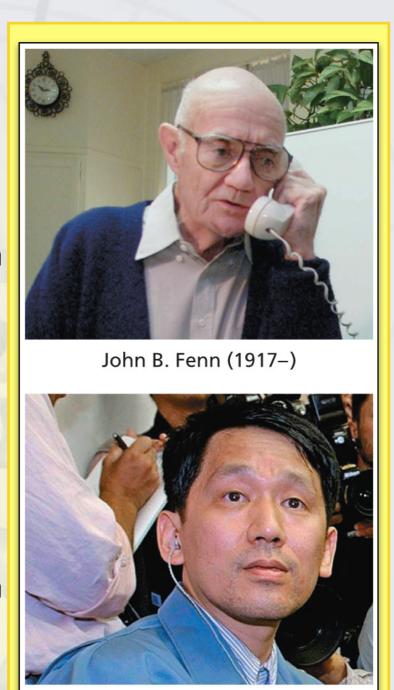
·Mass spectroscopy



·Mass spectroscopy

ESI Ionization

MALDI Ionization



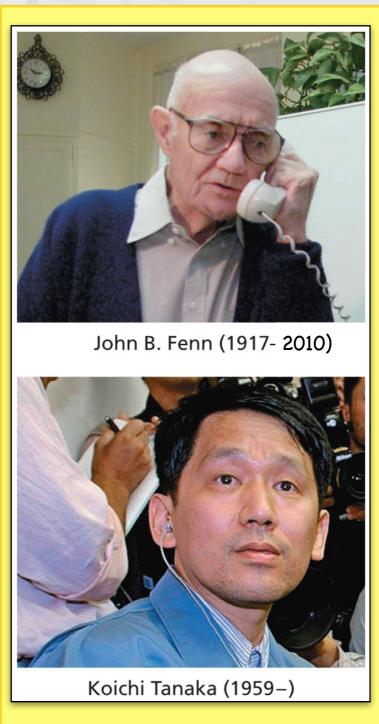
Nobel Prize in Chemistry, 2002

Koichi Tanaka (1959-)

·Mass spectroscopy

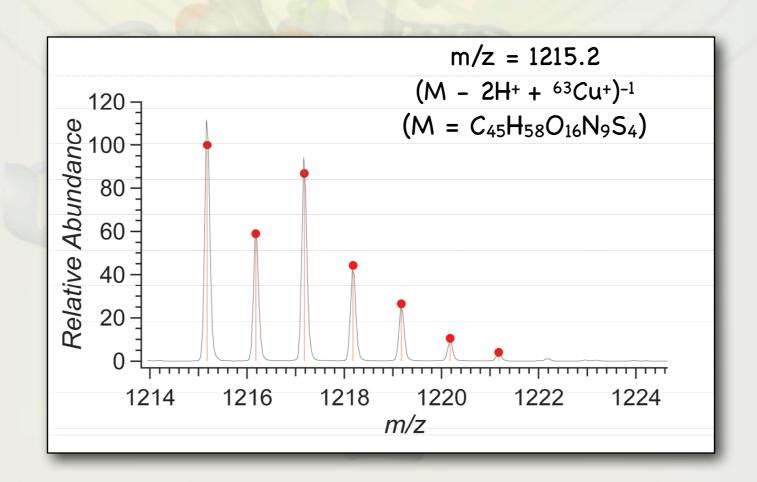
ESI Ionization

MALDI Ionization



Nobel Prize in Chemistry, 2002

Methanobactin



A peptide bond is formed from the condensation of an α -amino group from one amino acid with the α-carboxyl group of another amino acid.

CH₃

$$H_3N-CH-COO^{\circleddash} + H_3N-CH-COO^{\circleddash}$$

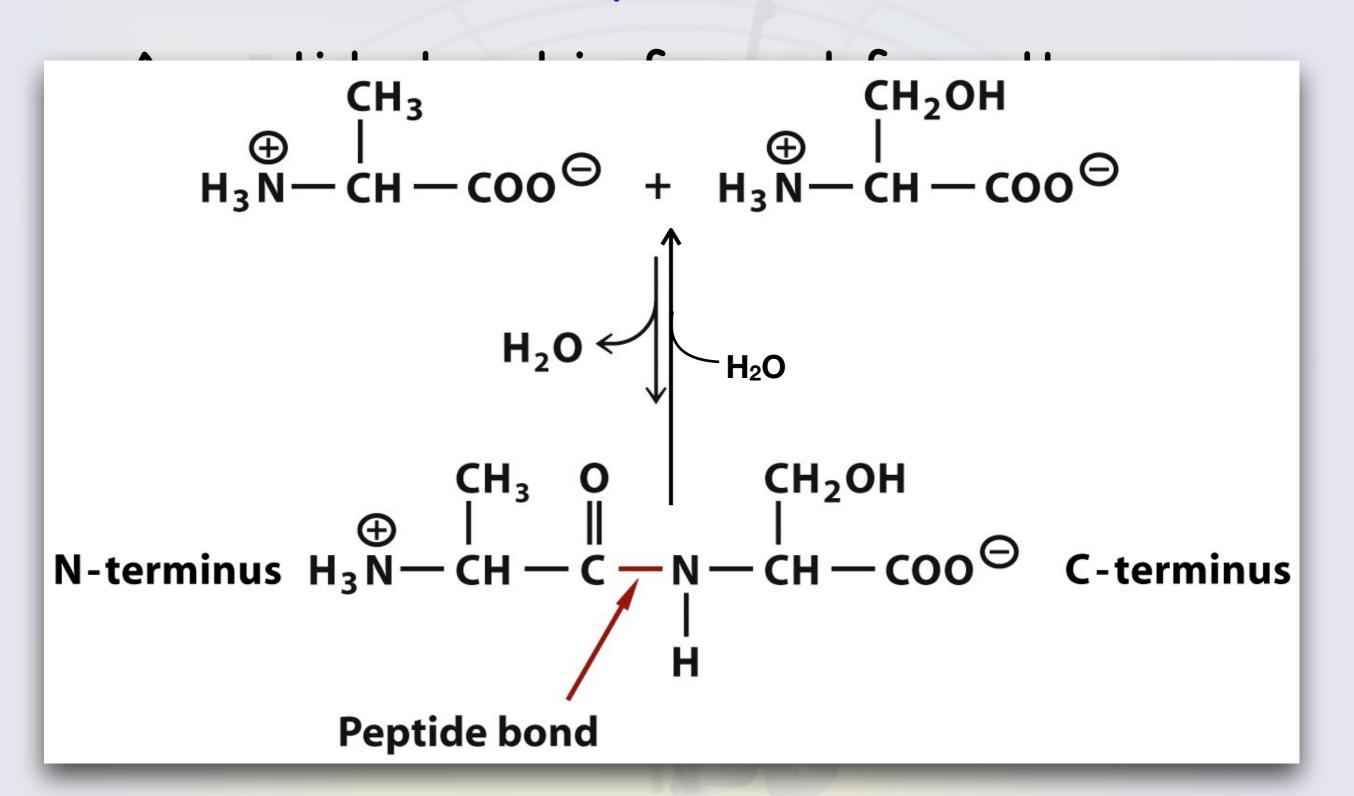
$$H_2O \longleftrightarrow$$

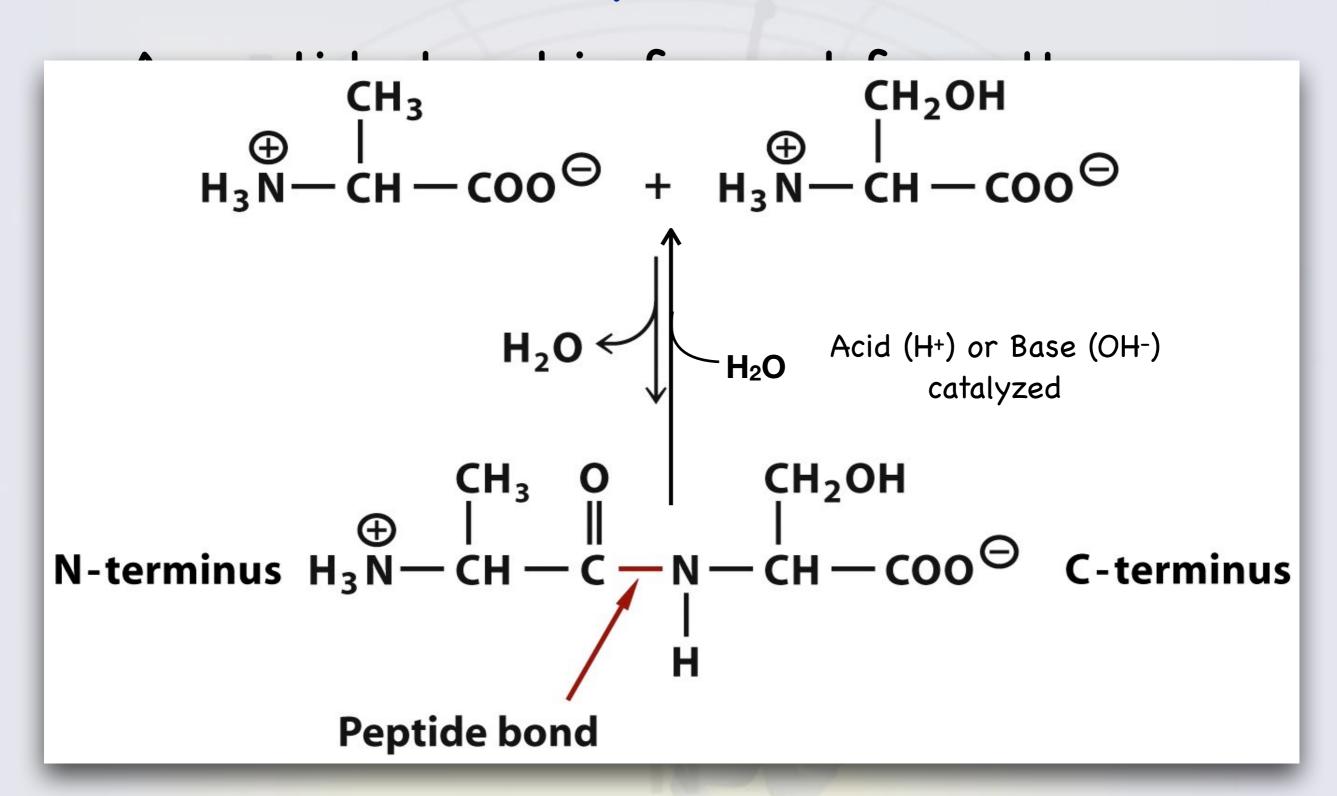
$$CH_3 O CH_2OH$$

$$H_3N-CH-COO^{\circleddash} - N-CH-COO^{\bigodot} - C-terminus$$

$$H_3N-CH-C-N-CH-COO^{\bigodot} - C-terminus$$

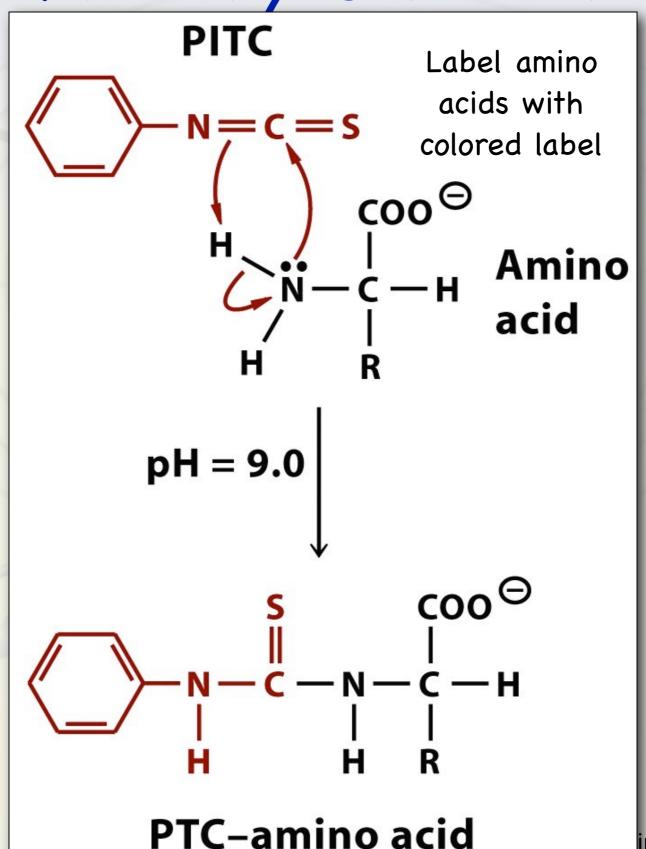
$$H$$
Peptide bond



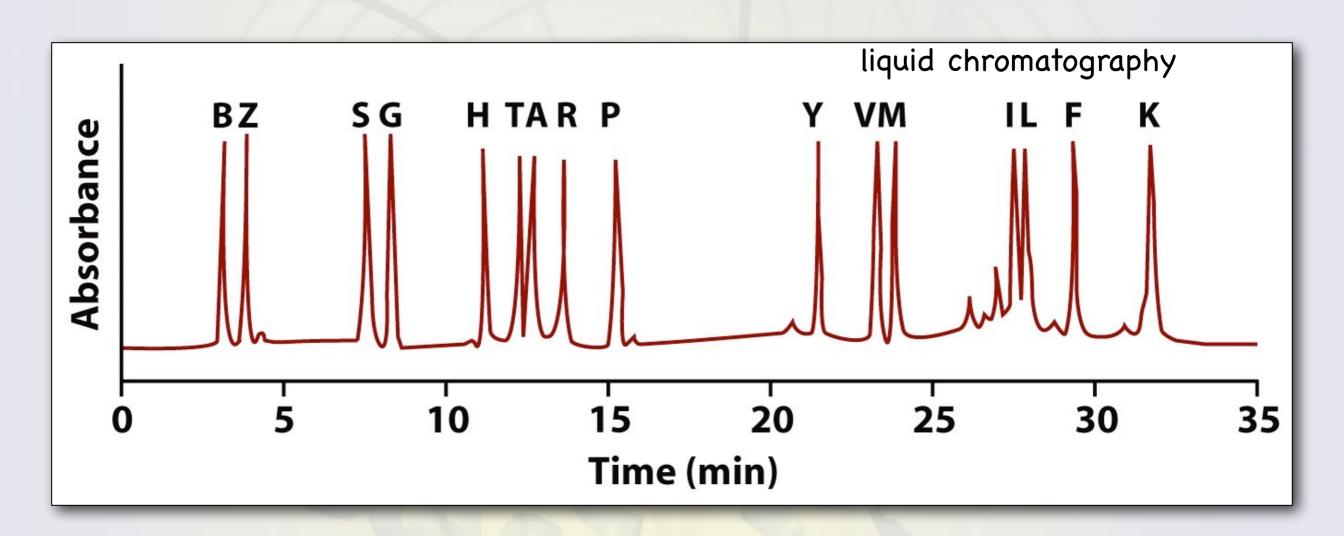


·Amino acid composition

·Amino



·Amino acid composition



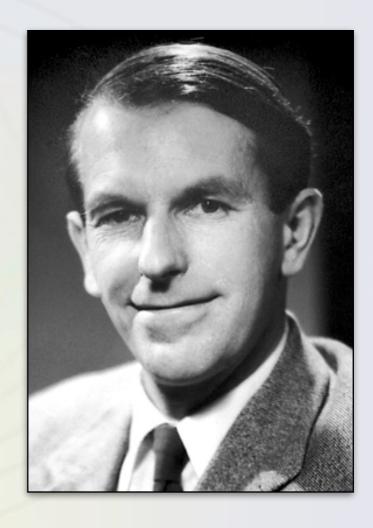
Fredrick Sanger was the first person to sequence a complete protein

+ Insulin (1953)

GIVEQCCASVCSLYQLENYCN A chain (21 amino acids)

FVNQHLCGSHLVEALYLVCGERGFFYTPKA B chain (30 amino acids)

FIGURE 1.—The structure of bovine insulin.



1956 Nobel Prize in Chemistry

Perspectives on Genetics: Antony Stretton, "The First Sequence: Fred Sanger and Insulin", Genetics 2002, 162, 527-532.

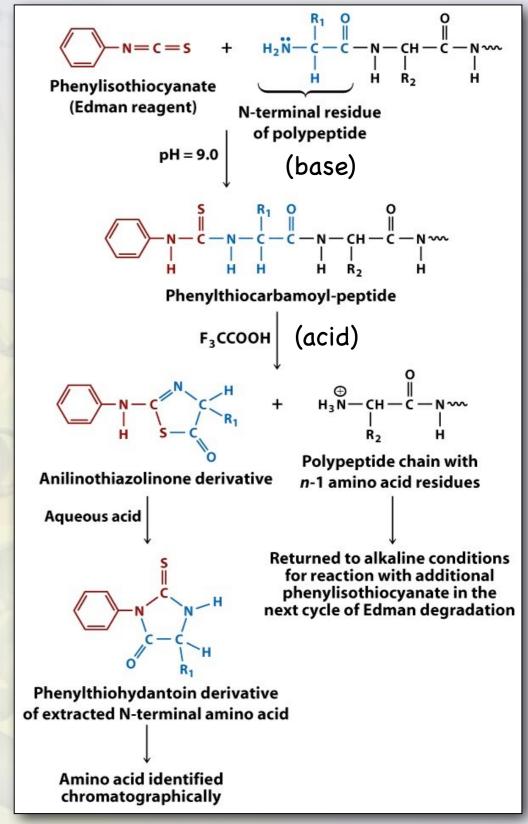
- ·Sanger's Reagent
 - + (DNFB, 2,4-dinitrofluorobenzene)

·Cleavage of disulfide bonds with β-mercaptoenthanol.

(a)
$$H$$
 O H O

- ·Amino acid sequence
 - + Edman Degradation

- ·Amino acid sequence
 - + Edman Degradation



Amino acid sequence

- + Edman Degradation
- + Can only sequence up to around 30 amino acids at a time, therefore, for larger proteins, the polypeptide is cleaved into smaller segments.
 - · CNBr (cyanogen bromide) cleaves at Met
 - · Trypsin protease cleaves at Lys & Arg (+)
 - Chymotrypsin cleaves at Phe, Tyr & Trp (aromatic)

Amino acid sequence

+ Edman Degradation

$$H_{3}^{\bigoplus} - Gly - Arg - Phe - Ala - Lys - Met - Trp - Val - COO^{\bigoplus}$$

$$BrCN (+ H_{2}O) \downarrow$$

$$H_{3}^{\bigoplus} - Gly - Arg - Phe - Ala - Lys - N - C$$

$$H_{2}^{\bigoplus} - C = O$$

$$H_{2}^{\bigoplus} - C = O$$

$$+ H_{3}^{\bigoplus} - Trp - Val - COO^{\bigoplus} + H_{3}CSCN + H^{\bigoplus} + Br^{\bigoplus}$$

$$H_{2}^{\bigoplus} - C = O$$

$$Peptidyl homoserine lactone$$

- Trypsin protease cleaves at Lys & Arg (+)
- Chymotrypsin cleaves at Phe, Tyr & Trp (aromatic)

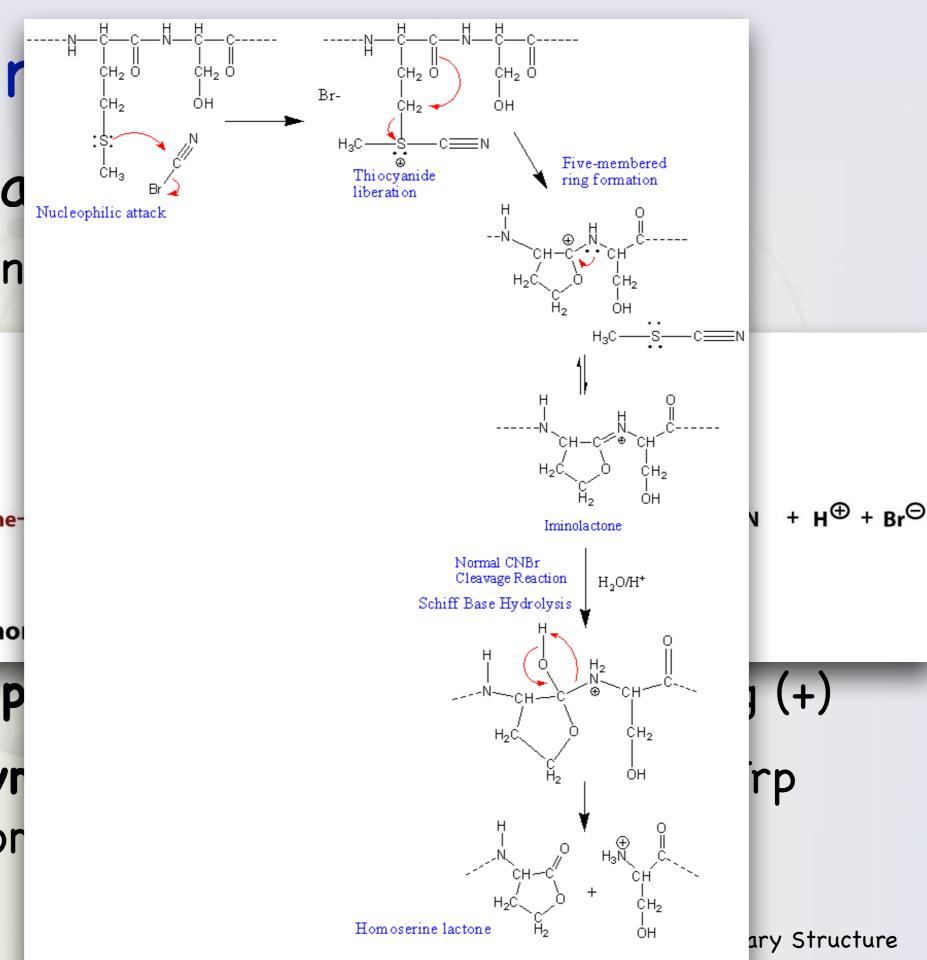
Proteir

Amino a

+ Edman

Peptidyl ho

- · Tryp
- · Chyr (aror



Amino acid sequence

+ Edman Degradation

$$H_{3}^{\bigoplus} - Gly - Arg - Phe - Ala - Lys - Met - Trp - Val - COO^{\bigoplus}$$

$$BrCN (+ H_{2}O) \downarrow$$

$$H_{3}^{\bigoplus} - Gly - Arg - Phe - Ala - Lys - N - C$$

$$H_{2}^{\bigoplus} - C = O$$

$$H_{2}^{\bigoplus} - C = O$$

$$+ H_{3}^{\bigoplus} - Trp - Val - COO^{\bigoplus} + H_{3}CSCN + H^{\bigoplus} + Br^{\bigoplus}$$

$$H_{2}^{\bigoplus} - C = O$$

$$Peptidyl homoserine lactone$$

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Amino acid sequence

Question:

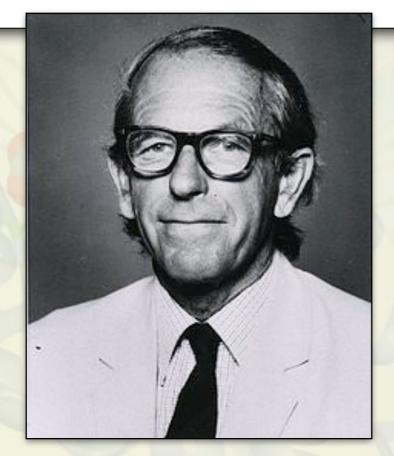
You have isolated a decapeptide called FP, which has anticancer activity. Determine the sequence of the peptide using the following information:

- a. One cycle of Edman degradation of intact FP yields 2 mol of PTH-aspartate per mole of FP.
- b. Treatment of a solution of FP with 2-mercaptoethanol followed by addition of trypsin yields three peptides with the composition (Ala, Cys,Phe), (Arg,Asp), and (Asp,Cys,Gly,Met,Phe). The intact (Ala,Cys,Phe) peptide yields PTH-cysteine in the first cycle of Edman degradation.
- c. Treatment of 1 mol of FP with carboxypeptidase (which cleave the C-terminal residue from peptides) yields 2 mol of phenylalanine.
- d. Treatment of the intact pentapeptide (Asp,Cys,Gly,Met,Phe) with CNBr yields two peptides with the composition (homoserine lactone, Asp) and (Cys,Gly,Phe). The (Cys,Gly,Phe) peptide yields PTH-glycine in the first cycle of Edman degradation.

~~~AAGAGTGAACCTGTC~~~ DNA

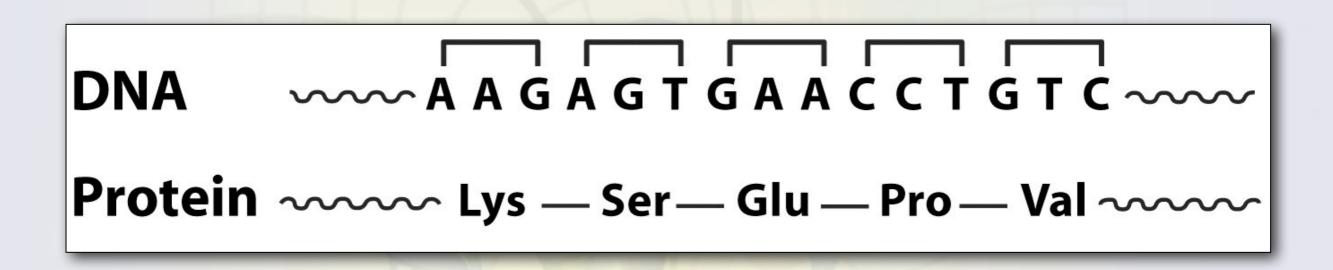
#### **DNA**

# ~~~AAGAGTGAACCTGTC~~~

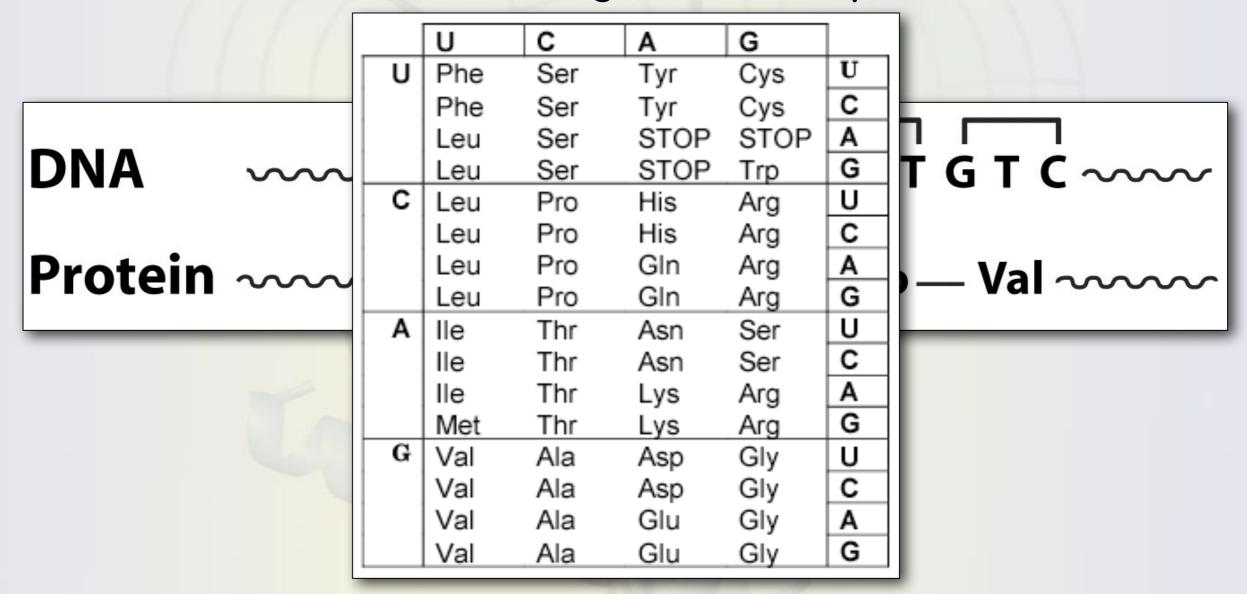


1956 Nobel Prize in Chemistry 1980 Nobel Prize in Chemistry

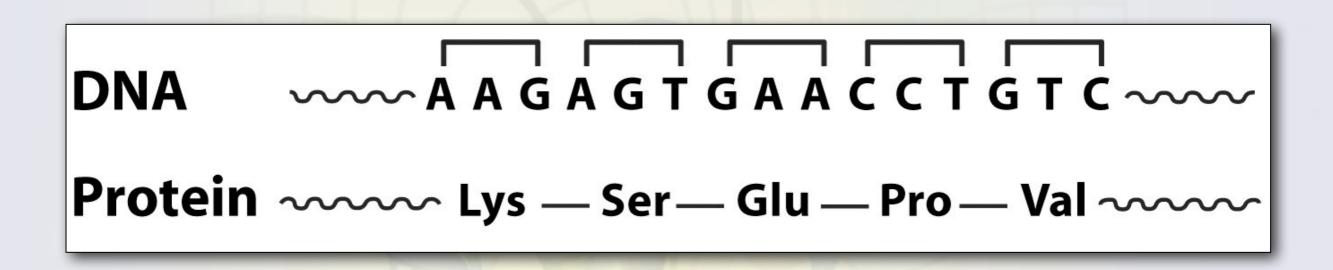
- ·Amino acid sequence
  - + Reverse translating a DNA sequence



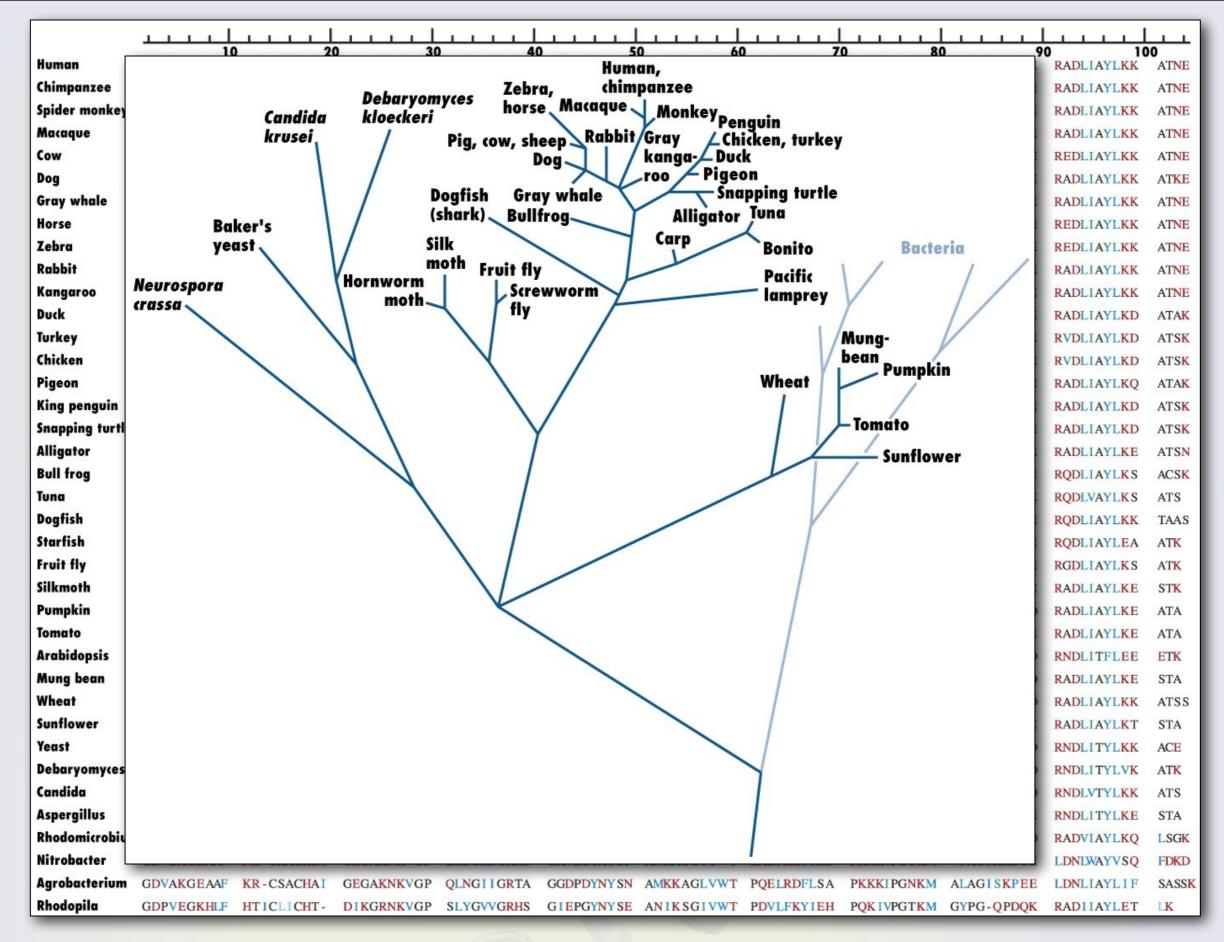
- ·Amino acid sequence
  - + Reverse translating a DNA sequence



- ·Amino acid sequence
  - + Reverse translating a DNA sequence



|                 | 1            | 1             | 1          | 1                  | 1                                      | 1            | 1                  | 1           |             | 1          |       |
|-----------------|--------------|---------------|------------|--------------------|----------------------------------------|--------------|--------------------|-------------|-------------|------------|-------|
|                 | 10           |               | 30         | 4(                 | 0 5                                    | 0 60         | 7                  | 0 80        | 9           | 0 10       | 00    |
| Human           | GDVEKGKKIF   | IMKCSQCHTV    |            |                    |                                        | ANKNKGI I WG |                    |             |             | RADLIAYLKK | ATNE  |
| Chimpanzee      | GDVEKGKKIF   | IMKCSQCHTV    | EKGGKHKTGP |                    |                                        | ANKNKGI I WG |                    |             | IFVGIKKKEE  | RADLIAYLKK | ATNE  |
|                 | GDVFKGKRIF   | IMKCSQCHTV    |            | NLHGLFGRKT         | ************************************** | ANKNKGIIWG   |                    | PKKYIPGTKM  | IFVGIKKKEE  | RADLIAYLKK | ATNE  |
| Macaque         | GDVEKGKKIF   | IMKCSQCHTV    | EKGGKHKTGP |                    | erediction and administration          | ANKNKGITWG   |                    | PKKYIPGTKM  | IFVGIKKKEE  | RADLIAYLKK | ATNE  |
| Cow             | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAPGFSYTD                             | ANKNKGITWG   | EETLMEYLEN         | PKKYIPGTKM  | IFAGIKKKGE  | REDLIAYLKK | ATNE  |
| Dog             | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | and the same and the same and          |              |                    | PKKYIPGTKM  | IFAGIKKTGE  | RADLIAYLKK | ATKE  |
|                 | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAVGFSYTD                             | ANKNKGITWG   | EETLMEYLEN         | PKKYIPGTKM  | I FAGIKKKGE | RADLIAYLKK | ATNE  |
|                 | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAPGFTYTD                             | ANKNKGITWK   | EETLMEYLEN         | PKKYIPGTKM  | IFAGIKKKTE  | REDLIAYLKK | ATNE  |
| Zebra           | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAPGFSYTD                             | ANKNKGITWK   | EETLMEYLEN         | PKKYIPGTKM  | IFAGIKKKTE  | REDLIAYLKK | ATNE  |
| Rabbit          | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAVGFSYTD                             | ANKNKGITWG   | EDTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKDE  | RADLIAYLKK | ATNE  |
| Kangaroo        | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLHGIFGRKT         | GQAPGFTYTD                             | ANKNKGI I WG | EDTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKGE  | RADLIAYLKK | ATNE  |
| Duck            | GDVEKGKKIF   | VQKCSQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAEGFSYTD                             | ANKNKGITWG   | EDTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKSE  | RADLIAYLKD | ATAK  |
| Turkey          | GDIEKGKKIF   | VQKCSQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAEGFSYTD                             | ANKNKGITWG   | EDTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKSE  | RVDLIAYLKD | ATSK  |
| Chicken         | GDIEKGKKIF   | VQKCSQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAEGFSYTD                             | ANKNKGITWG   | EDTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKSE  | RVDLIAYLKD | ATSK  |
| Pigeon          | GDIEKGKKIF   | VQKCSQCHTV    | EKGGKHKTGP | NLHGLFGRKT         | GQAEGFSYTD                             | ANKNKGITWG   | EDTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKAE  | RADLIAYLKQ | ATAK  |
|                 | GDIEKGKKIF   | VQKCSQCHTV    | EKGGKHKTGP | NLHGIFGRKT         | GQAEGFSYTD                             | ANKNKGITWG   | EDTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKSE  | RADLIAYLKD | ATSK  |
| Snapping turtle | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLNGL I GRKT       | GQAEGFSYTE                             | ANKNKGITWG   | EETLMEYLEN         | PKKYIPGTKM  | IFAGIKKKAE  | RADLIAYLKD | ATSK  |
| Alligator       | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKTGP | NLHGL I GRKT       | GQAPGFSYTE                             | ANKNKGITWG   | EETLMEYLEN         | PKKYIPGTKM  | IFAGIKKKPE  | RADLIAYLKE | ATSN  |
| Bull frog       | GDVEKGKKIF   | VQKCAQCHTV    | EKGGKHKVGP | NLYGL I GRKT       | GQAAGFSYTD                             | ANKNKGITWG   | EDTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKGE  | RQDLIAYLKS | ACSK  |
| Tuna            | GDVAKGKKTF   | VQKCAQCHTV    | ENGGKHKVGP | NLWGLFGRKT         | GQAEGYSYTD                             | ANKSKGIVWN   | ENTLMEYLEN         | PKKYIPGTKM  | IFAGIKKKGE  | RQDLVAYLKS | ATS   |
| Dogfish         | GDVEKGKKVF   | VQKCAQCHTV    | ENGGKHKTGP | NLSGLFGRKT         | GQAQGFSYTD                             | ANKSKGITWQ   | QETLR IYLEN        | PKKYIPGTKM  | IFAGIKKKSE  | RQDLIAYLKK | TAAS  |
| Starfish        | GQVEKGKKIF   | VQRCAQCHTV    | EKAGKHKTGP | NLNGILGRKT         | GQAAGFSYTD                             | ANRNKGITWK   | NETLFEYLEN         | PKKYIPGTKM  | VFAGLKKQKE  | RQDLIAYLEA | ATK   |
| Fruit fly       | GDVEKGKKLF   | VQRCAQCHTV    | EAGGKHKVGP | NLHGL I GRKT       | GQAAGFAYTD                             | ANKAKGITWN   | EDTLFEYLEN         | PKKYIPGTKM  | I FAGLKKPNE | RGDLIAYLKS | ATK   |
| Silkmoth        | GNAENGKKIF   | VQRCAQCHTV    | EAGGKHKVGP | NLHGFYGRKT         | GQAPGFSYSN                             | ANKAKGITWG   | DOTLFEYLEN         | PKKYIPGTKM  | VFAGLKKANE  | RADLIAYLKE | STK   |
| Pumpkin         | GNSKAGEKIF   | KTKCAQCHTV    | DKGAGHKQGP | NLNGLFGRQS         | GTTPGYSYSA                             | ANKNRAVIWE   | EKTLYDYLLN         | PKKYIPGTKM  | VFPGLKKPQD  | RADLIAYLKE | ATA   |
| Tomato          | GNPKAGEKIF   | KTKCAQCHTV    | EKGAGHKEGP | NLNGLFGRQS         | GTTAGYSYSA                             | ANKNMAVNWG   | ENTLYDYLLN         | PKKYIPGTKM  | VFPGLKKPQE  | RADLIAYLKE | ATA   |
| Arabidopsis     | GDAKKGANLF   | KTRCAQCHTL    | KAGEGNKIGP | ELHGLFGRKT         | GSVAGYSYTD                             | ANKQKGIEWK   | DDTLFEYLEN         | PKKYIPGTKM  | AFGGLKKPKD  | RNDLITFLEE | ETK   |
| Mung bean       | GNSKSGEKIF   | KTKCAQCHTV    | DKGAGHKQGP | NLNGL I GRQS       | GTTAGYSYST                             | ANKNMAV I WE | EKTLYDYLLN         | PKKYIPGTKM  | VFPGLKKPQD  | RADLIAYLKE | STA   |
| Wheat           | GNPDAGAKIF   | KTKCAQCHTV    | DAGAGHKQGP | NLHGLFGRQS         | GTTAGYSYSA                             | ANKNKAVEWE   | ENTLYDYLLN         | PKKYIPGTKM  | VFPGLKKPQD  | RADLIAYLKK | ATSS  |
| Sunflower       | GNPTTGEKIF   | KTKCAQCHTV    | EKGAGHKQGP | <b>NLNGLFGRQS</b>  | GTTAGYSYSA                             | GNKNKAVIWE   | ENTLYDYLLN         | PKKYIPGTKM  | VFPGLKKPQE  | RADLIAYLKT | STA   |
| Yeast           | GSAKKGATLF   | KTRCLQCHTV    | EKGGPHKVGP | NLHGIFGRHS         | GQAEGYSYTD                             | ANIKKNVLWD   | <b>ENNMS EYLTN</b> | PKKYIPGTKM  | AFGGLKKEKD  | RNDLITYLKK | ACE   |
| Debaryomyces    | GSEKKGANLF   | KTRCLQCHTV    | EKGGPHKVGP | NLHGVVGRTS         | GQAQGFSYTD                             | ANKKKGVEWT   | EQDLSDYLEN         | PKKYIPGTKM  | AFGGLKKAKD  | RNDLITYLVK | ATK   |
| Candida         | GSEKKGATLF   | KTRCLQCHTV    | EKGGPHKVGP | <b>NLHGVFGRKS</b>  | GLAEGYSYTD                             | ANKKKGVEWT   | EQTMSDYLEN         | PKKYIPGTKM  | AFGGLKKPKD  | RNDLVTYLKK | ATS   |
| Aspergillus     | GDAK - GAKLF | QTRCAQCHTV    | EAGGPHKVGP | NLHGLFGRKT         | GQSEGYAYTD                             | ANKQAGVTWD   | ENTLFSYLEN         | PKKFIPGTKM  | AFGGLKKGKE  | RNDLITYLKE | STA   |
| Rhodomicrobium  | GDPVKGEQVF   | KQ-CKICHQV    | GPTAKNGVGP | EQNDVFGQKA         | GARPGFNY SD                            | AMKNSGLTWD   | EATLDKYLEN         | PKAVVPGTKM  | VFVGLKNPQD  | RADVIAYLKQ | LSGK  |
| Nitrobacter     | GDVEAGKAAF   | NK - CKACHE I | GESAKNKVGP | ELDGLDGRHS         | GAVEGYAYSP                             | ANKASGITWT   | EAEFKEYIKD         | PKAKVPGTKM  | VFAGIKKDSE  | LDNLWAYVSQ | FDKD  |
| Agrobacterium   | GDVAKGEAAF   | KR-CSACHAI    | GEGAKNKVGP | <b>QLNGII GRTA</b> | GGDPDYNY SN                            | AMKKAGLVWT   | PQELRDFLSA         | PKKKI PGNKM | ALAGISKPEE  | LDNLIAYLIF | SASSK |
| Rhodopila       | GDPVEGKHLF   | HTICLICHT-    | DIKGRNKVGP | SLYGVVGRHS         | GIEPGYNYSE                             | ANIKSGIVWT   | PDVLFKYIEH         | PQK IVPGTKM | GYPG-QPDQK  | RADIIAYLET | LK    |



#### Question:

The functional diversity of proteins results from the large number of possible polypeptides that can be built using the 20 different amino acids

Question: What is the minimum mass it would take to construct one molecule each of all of the possible polypeptides that contain 100 amino acids?

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| Ougstion                       |                            |  |  |  |  |  |
|--------------------------------|----------------------------|--|--|--|--|--|
| Number of polypeptides (20100) | 1.26 X 10 <sup>130</sup>   |  |  |  |  |  |
| Avg. Mass of each polypeptide  | 1.83 x 10 <sup>-22</sup> g |  |  |  |  |  |
| Total mass needed              | 2.32 X IO <sup>108</sup> g |  |  |  |  |  |
| Number of Earths               | 3.9 X 10 <sup>80</sup>     |  |  |  |  |  |
| Number of Suns                 | I.2 X IO <sup>75</sup>     |  |  |  |  |  |
| Number of Galaxies             | 9.7 X 10 <sup>29</sup>     |  |  |  |  |  |

#### Question:

The functional diversity of proteins results from the large number of possible polypeptides that can be built using the 20 different amino acids

Question: What is the minimum mass it would take to construct one molecule each of all of the possible polypeptides that contain 100 amino acids?

# Next up

Lecture 3, Part II - Protein Structure and Function

+ Read Chapter 4 of Moran et al.