Amino Acids

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General structure

Backbone

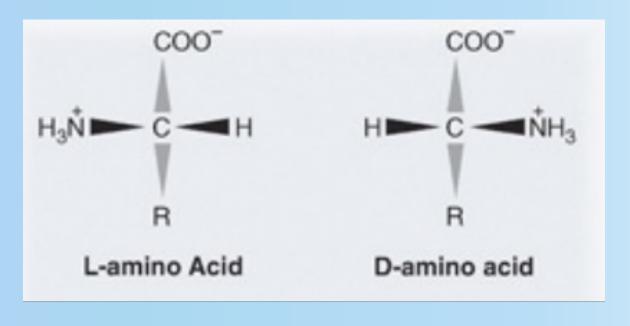
- Amino group, α-carbon, carboxyl group, hydrogen
- Unique side chains
- Zwitterions = dipolar ions
 - ion possessing both pos and neg electrical charges
 - All free aa are water soluble at physiological pH

Amino $H_3 \dot{N} - C - H$ group $H_3 \dot{N} - C - H$ R α -Carbon
Side chain



L-α-amino acids

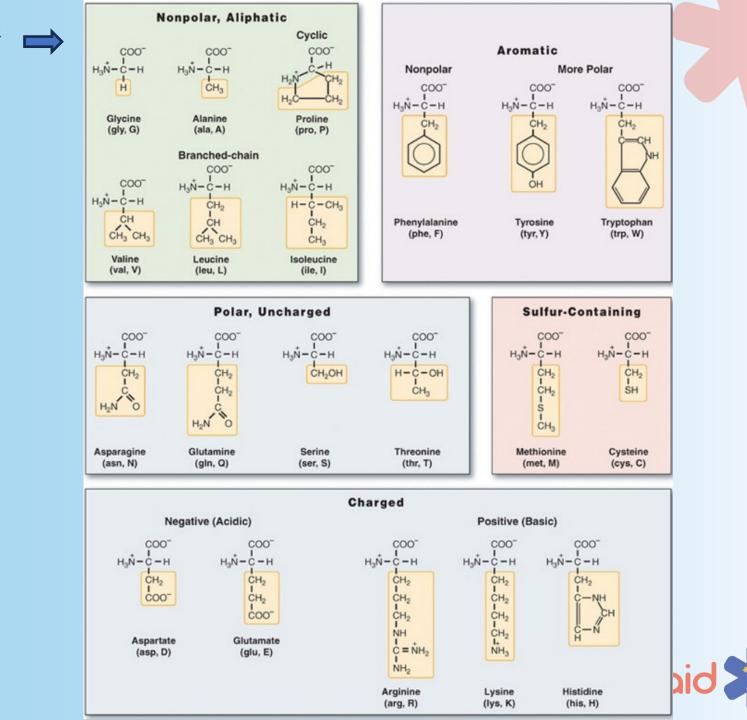
- chiral carbon = 4 single bonds and 4 different groups attached to it
- $\boldsymbol{\diamondsuit}$ amino group is attached to the $\alpha\text{-}carbon$ in the L-configuration
- L = left = life (except Glycine)

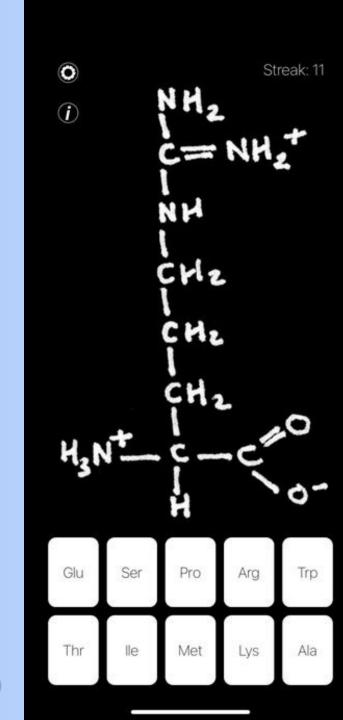


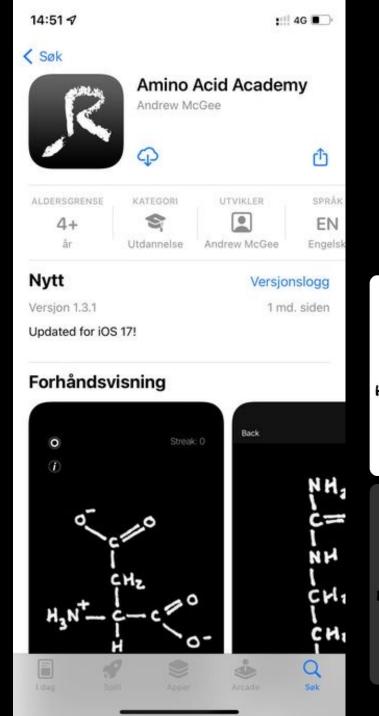


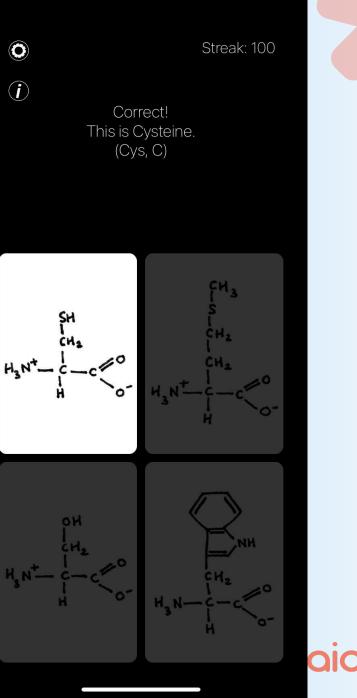
In physiological pH=7.4

Side Chain Classification



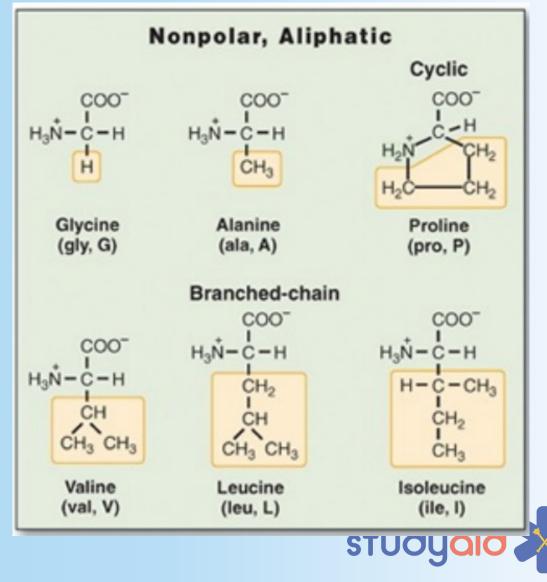






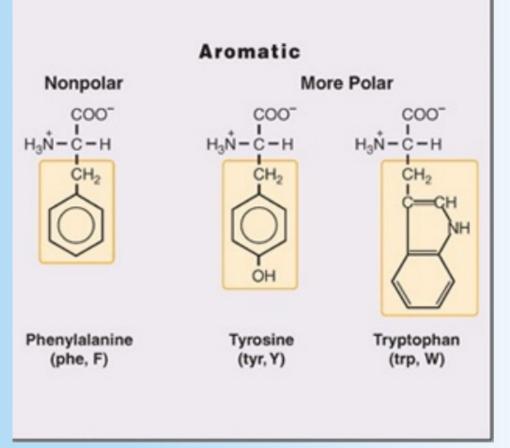
Nonpolar aliphatic

- Hydrophobic = phobia of water
- Van der Waals forces
- Aliphatic = only H and C and single bonds
- Glycine
 - Simplest aa
 - Not asymmetric
- Alanine + BCAA
 - High degree hydrophobicity
- Proline
 - Side chain forms a ring that include its backbone → restrict the conformation of the protein



Aromatic

- Aromatic = sixmembered carbon-hydrogen ring with three conjugated double bonds (benzene or phenyl)
- Absorbe UV-light
- Phenylalanine
 - Nonpolar
- Tyrosine
 - OH- group on phenyl ring \rightarrow form hydrogen bonds
 - Polar
- Tryptophan
 - N in the ring \rightarrow form hydrogen bonds
 - Polar

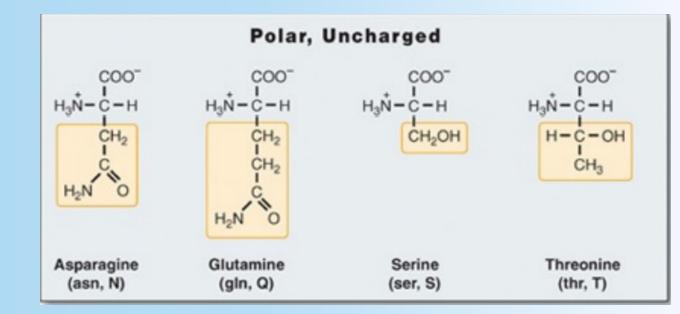




Polar, Uncharged

✤ Hydrophilic = ♥ water

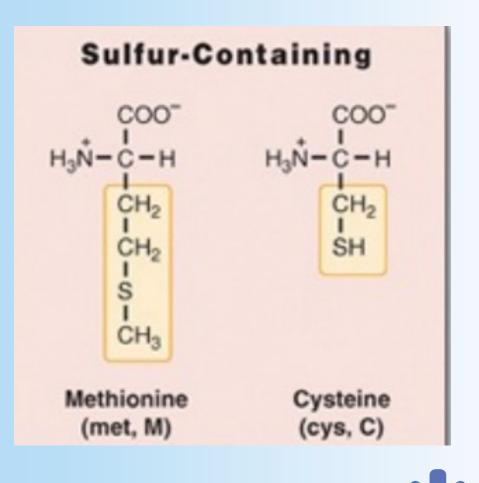
- Asparagine and Glutamine
 - Amide group \rightarrow hydrogen bonds
- Serine and Threonine
 - Hydroxyl group \rightarrow hydrogen bonds





Sulfur containing

- Cysteine
 - Sulfhydryl group → covalent disulfide bond with other cysteine
 - Polar
- Methionine
 - does not contain sulfhydryl group → cannot form disulfide bonds!
 - nonpolar



study

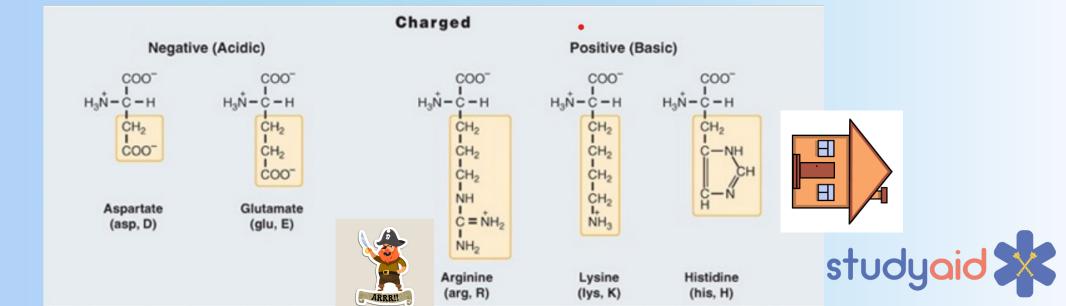
Charged

Acidic

- Carboxylic acid group
- Negative charge at physiological pH
- Polar
- Ionic and hydrogen bonds, salt bridges

Basic

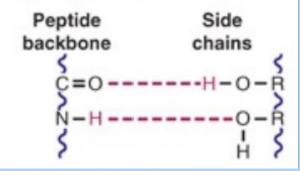
- Nitrogen that can be pronated
- **Positive** charge at physiological pH
- Polar
- Ionic and hydrogen bonds, salt bridges



Bonds from side chains

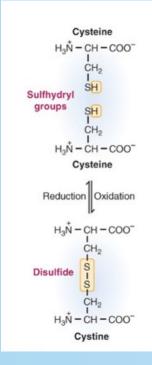
Hydrogen bonds

- Polar
- Hydrogen with NOF
- B. Hydrogen bonds



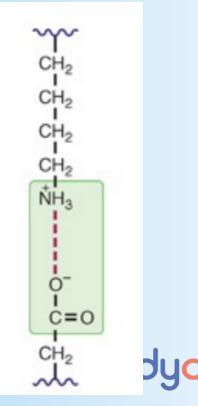
Disulfide bond

• Cys - Cys



lonic

Neg AA - pos AA



Peptide bond

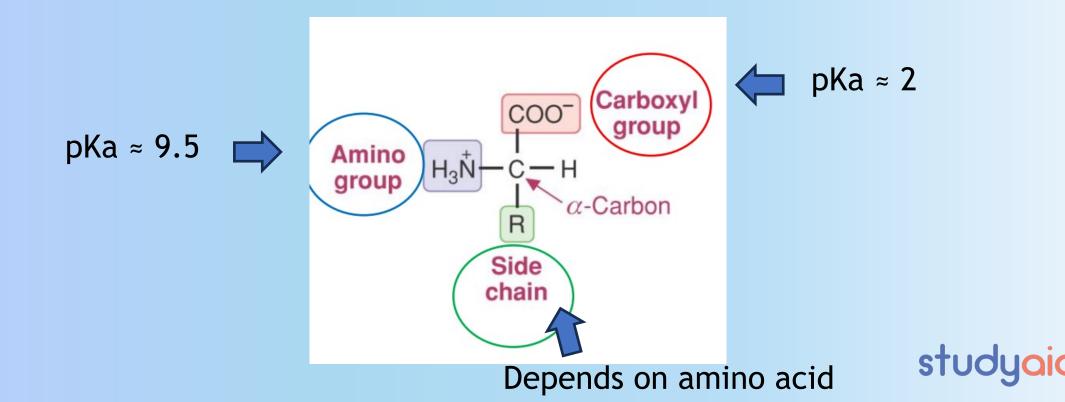
- CONH
- Condensation reaction
- \Rightarrow make polypeptides
- Always planar \rightarrow very little rotation
 - \rightarrow stabilize protein structure
- Usually trans configuration
- \clubsuit Always read from N \rightarrow C

 $H_{3}N - C - C - C - O^{-} + H_{3}N - C - C - O^{-}$ $H_{3}N - C - C - O^{-} + H_{3}N - C - C - O^{-}$ $H_{1} + H_{2}O$ $H_{3}N - C - C - N - C - C - O^{-}$ $H_{3}N - C - C - N - C - C - O^{-}$ $H_{1} + H_{1} + H_{1}$



рКа

- PKa = pH at which 50% of the protons have dissociated
- Each group that has a dissociable proton, have a pKa
 - In polypeptides only the first amino group and the last carboxyl group + side chains have pKas



Form that predominates
below the pKapKaForm that predominates
above the pKaAspartate
$$\vdash$$
 CH2 - COOH $\stackrel{3.9}{\longrightarrow}$ \vdash CH2 - COO⁻ $+$ H*Glutamate \vdash CH2 - CH2 - COOH $\stackrel{4.1}{\longrightarrow}$ \vdash CH2 - CH2 - COO⁻ $+$ H*Histidine \vdash CH2 - CH2 - COOH $\stackrel{4.1}{\longrightarrow}$ \vdash CH2 - CH2 - COO⁻ $+$ H*Visitine \vdash CH2 - CH2 - COOH $\stackrel{6.0}{\leftrightarrow}$ \vdash CH2 - CH2 - COO⁻ $+$ H*Cysteine \vdash CH2 - CH2 - CH2 - CH2 $\stackrel{6.0}{\leftrightarrow}$ \vdash CH2 - $\stackrel{1}{\leftarrow}$ H*Tyrosine \vdash CH2 - CH2 - OH $\stackrel{10.5}{\leftarrow}$ \vdash CH2 - CH2 - OT $+$ H*Lysine \vdash CH2 - NH2 $+$ H*Arginine \vdash CH2 - CH2 - CH2 - NH - $\stackrel{112.5}{\leftarrow}$ \vdash CH2 - CH2 - CH2 - NH - $\stackrel{10.5}{\leftarrow}$ H* \vdash CH2 - CH2 - CH2 - CH2 - NH - $\stackrel{10.5}{\leftarrow}$

Isoelectric point=pl/IEP

★ = the pH at which the NET charge is 0
★ If 3 pKa → use the ones on each side of net charge 0

$$pl = \frac{pKa_1 + pKa_2}{2}$$



Free H+

Molecules wants to KEEP H for themself



Molecules wants to GIVE H away

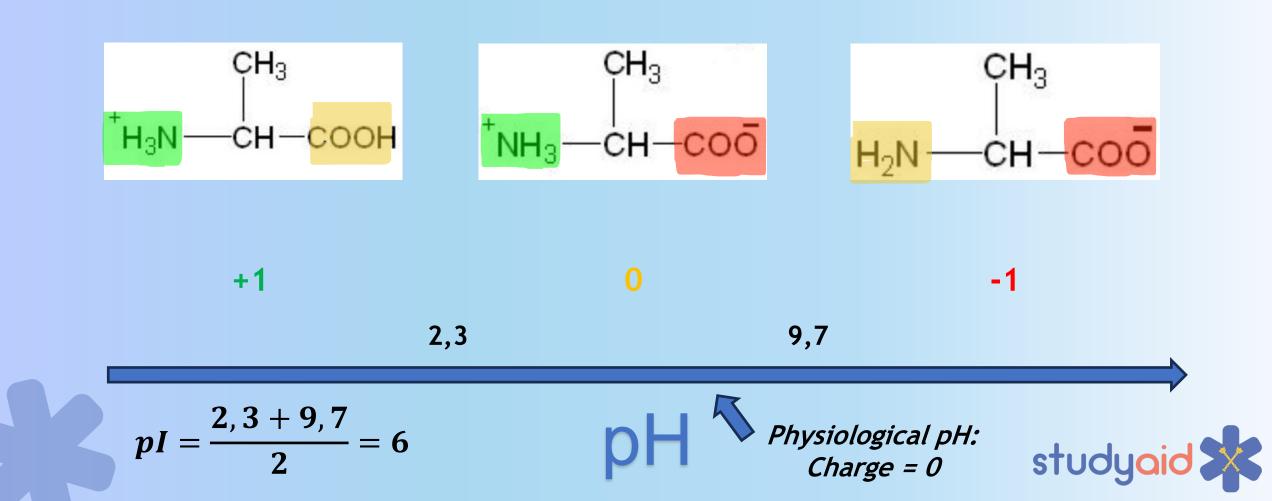




Free H+

Alanine in different pH $pKa_1 = 2, 3, pKa_2 = 9, 7$

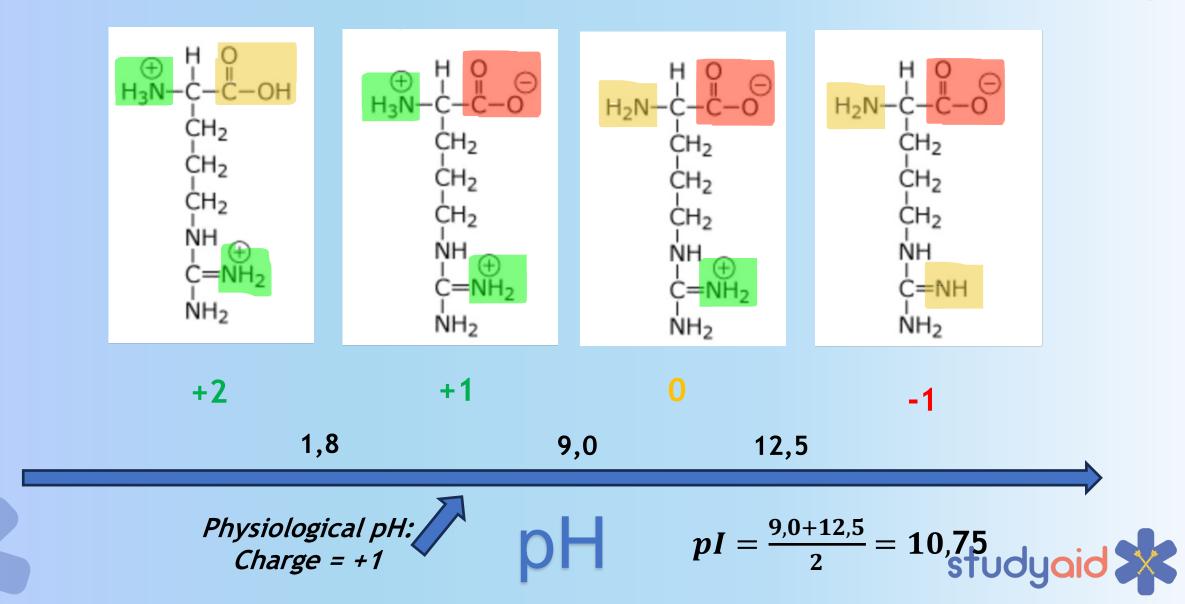




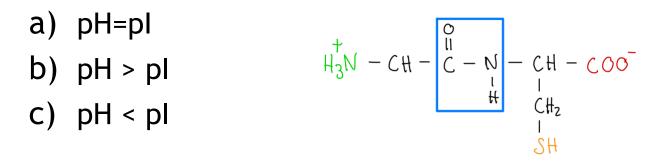
Arginine shows 3 pKas at 1.8, 9.0 and 12.5. What is the charge at physiological pH (7.4) and the pl value?



Arginine in different pH **Tree H+** $pKa_1 = 1, 8, pKa_2 = 9, 3, pKa_3 = 12, 5$ **Free H+**



Draw all possible ionic forms of dipeptide Ala-Cys and choose which form is predominant at:



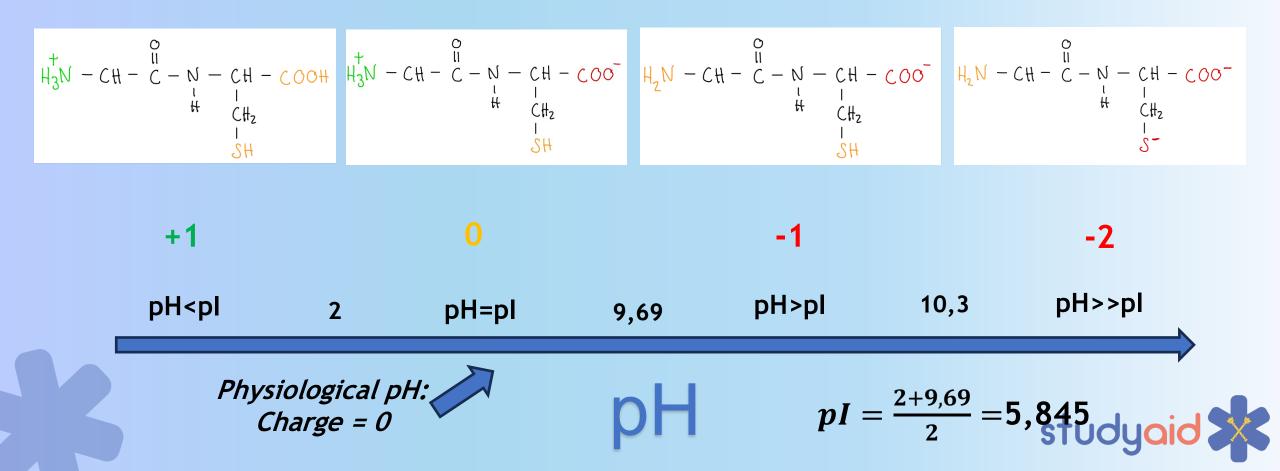
Ala: pKa(COOH)= , pKa(NH3+)= 9,69; Cys: pKa(COOH)= 2,0, pKa(NH3+)=, pKa(SH)= 10,3



Tree H+



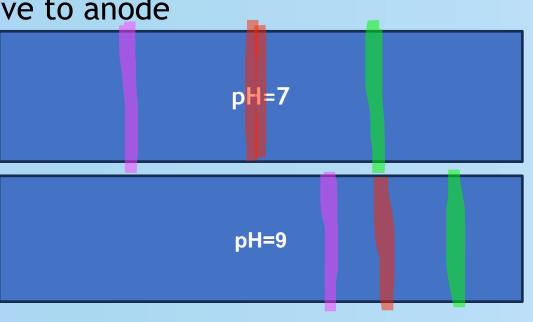
Ala: pKa(NH3+)= 9,69; Cys: pKa(COOH)= 2,0, pKa(SH)= 10,3



Electrophoretic separation

- Use electrical charge to separate AA and proteins
- If pH = pI the protein will stand still
- ♦ If pH < pI \rightarrow move to cathode
- ♦ If $pH > pI \rightarrow$ move to anode

Cathode



pl = the pH where
net charge is 0!!!

✤ pl = 6, pl = 7, pl = 8

Anode

studyaid

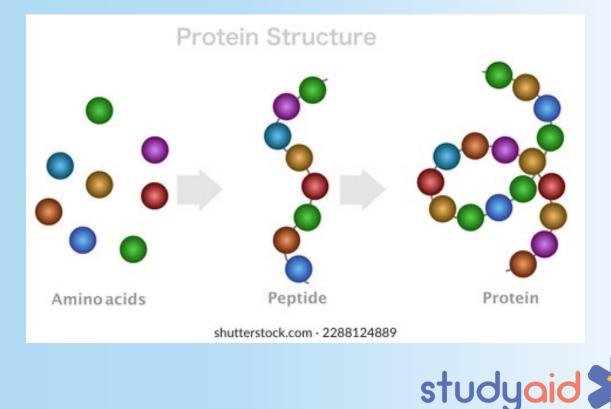
Protein and enzymes



Peptides \rightarrow Proteins

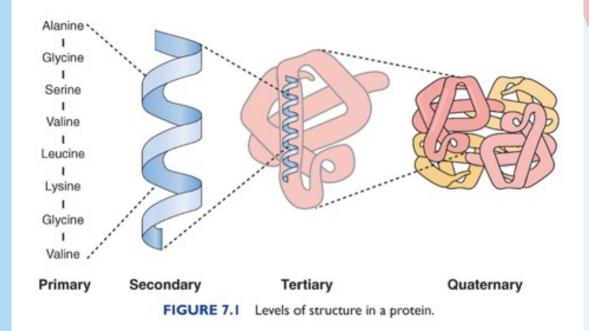
Peptides = short polymers of amino acids

- Each unit (aa) is called a residue
- 2 residues dipeptide
- 3 residues tripeptide
- 12-20 residues oligopeptide
- < 51 polypeptide
- > 51 protein



Levels of protein structure

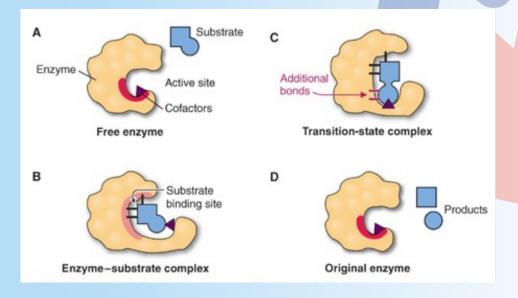
- Primary -
 - sequence of aa
- Secondary -
 - a- helix, b-sheets and turns
 - stabilized by hydrogen bonds
- Tertiary -
 - 3D configuration
 - Domains and folds
 - Makes binding site for ligands
- Quaternary -
 - two or more subunits
 - Binding site for ligands





Enzymes

- = proteins that act as catalysts
 - \Leftrightarrow \rightarrow increase the rate of chemical reactions
- Bind reactants (substrates)
 - \rightarrow convert them to products
 - \rightarrow release the products



- May be modified during their participation, but return to their original form
- Regulate the rate of metabolic pathways in the body ++



