

Lecture 2

Protein Composition and Structure

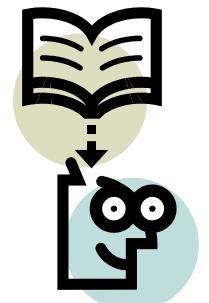
From last lecture...

- **Overview the major classes of biomolecules:**
 - proteins
 - carbohydrates
 - lipids
 - DNA/RNA
- **Weak bonds that keep them together:**
 - ionic
 - H-bonds
 - van der Waals
 - hydrophobic effect
- **pH in biology**
 - buffers
 - Henderson-Hasselbach Equation

Protein Composition and Structure

In Lecture 2:

- Building Blocks of Proteins (Amino Acids)
- Structure of Common Amino Acids
- Peptide bonds and polypeptide chains
- Protein Structure: primary, secondary, tertiary, and quaternary
- When protein folding goes wrong...



Readings:

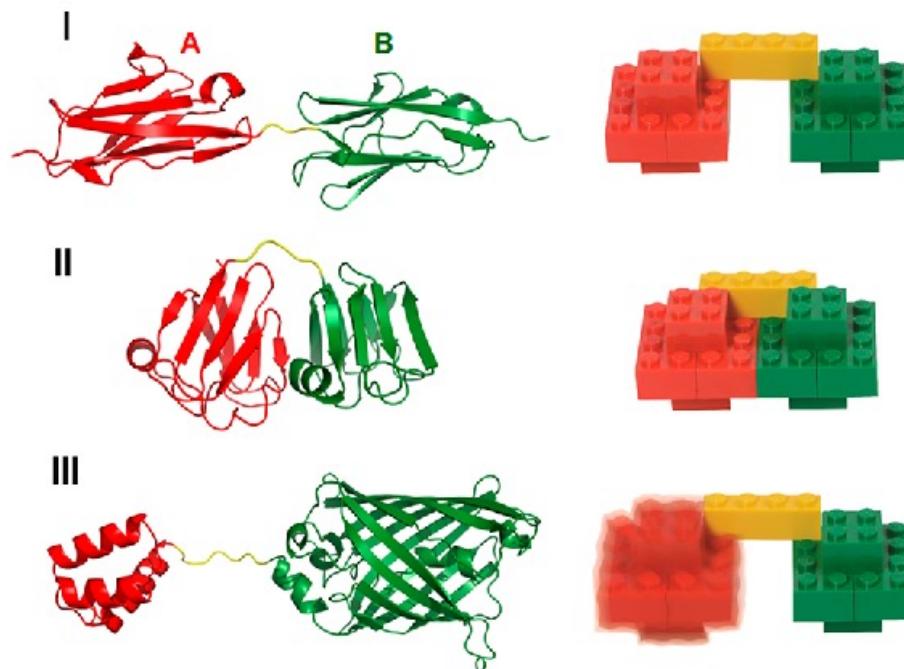
Biochemistry, 2nd Edition,
Ch. 3 - 4, pp. 33 - 60
3rd Edition, Ch. 3 - 4, pp. 37 - 68
4th Edition, Ch. 3 - 4, pp. 37 - 66

Proteins are fundamental to every biological process!

- **Structural Support:** collagen and keratin provide structural integrity
- **Catalysis:** enzymes catalyze biochemical reactions essential for life
- **Transport:** hemoglobin transport molecules such as O₂
- **Communication:** hormones and receptors facilitate cell signaling
- **Defense:** antibodies defend the body against pathogens
- **Movement:** actin and myosin enable movement (muscle contraction)
- **Regulation:** proteins help regulate gene expression (polymerases)

Proteins are large, complex molecules that perform a wide range of essential functions in living organisms....

How do proteins form?



Biochemistry > Vol 56/Issue 38 > Article

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PERSPECTIVE | August 15, 2017

Protein Assembly and Building Blocks: Beyond the Limits of the LEGO Brick Metaphor

Yaakov Levy*

Hierarchy of protein structure

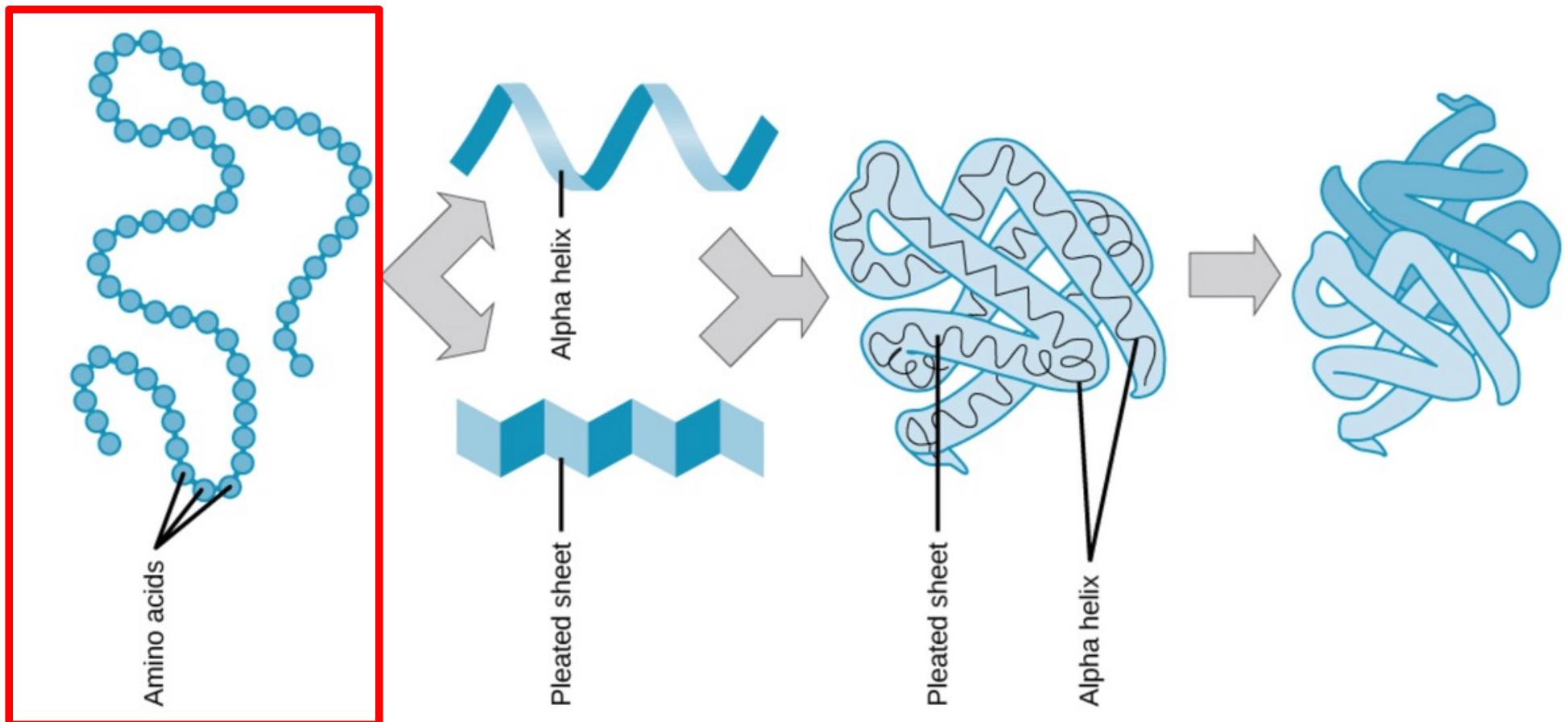
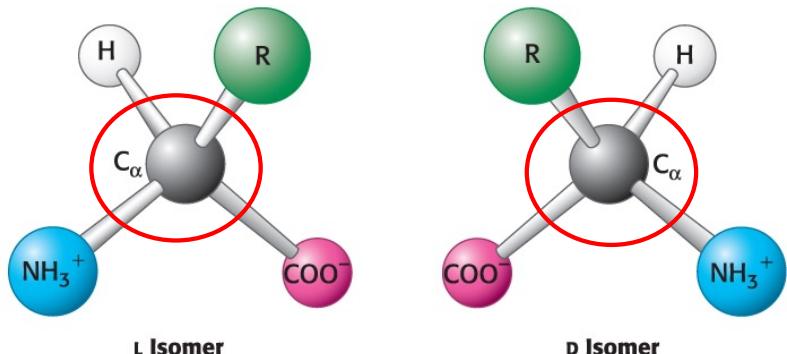
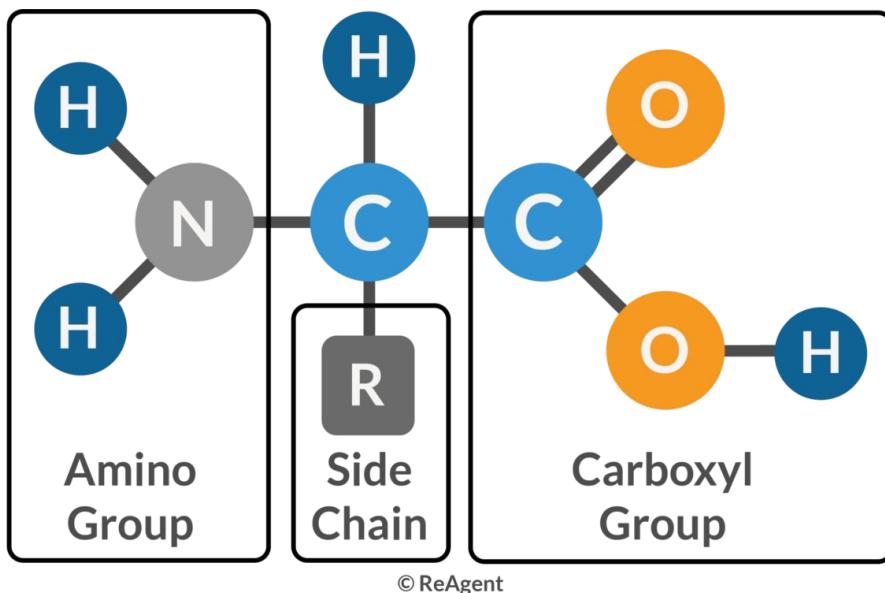


Image by Dillon Daudert

Amino acids are the basic unit of proteins

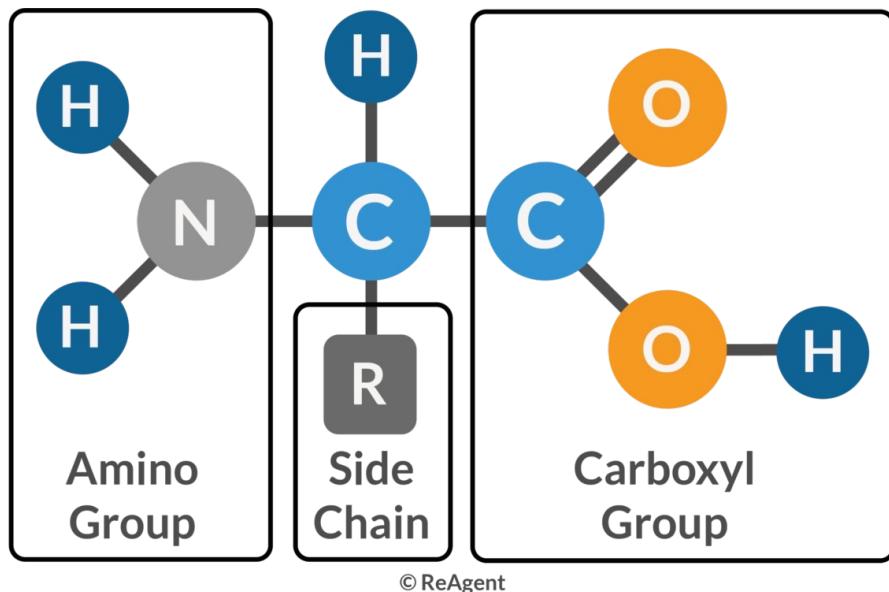
- **amino acid:** small molecule containing an amino group ($-\text{NH}_2$), a carboxylate group ($-\text{COO}^-$), and a variable side chain (R group)



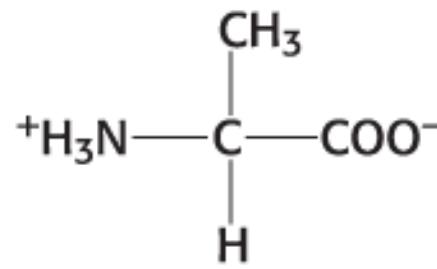
- The chirality of amino acids results from asymmetry of the alpha carbon. They exist as a pair of **enantiomers**.
- Only L amino acids are constituents of proteins.
- Pure L and D are slightly more soluble than DL.

Building blocks of proteins

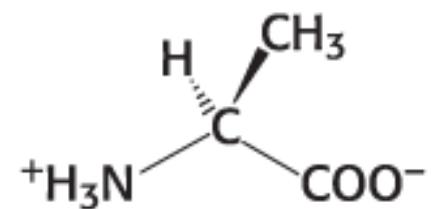
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© ReAgent

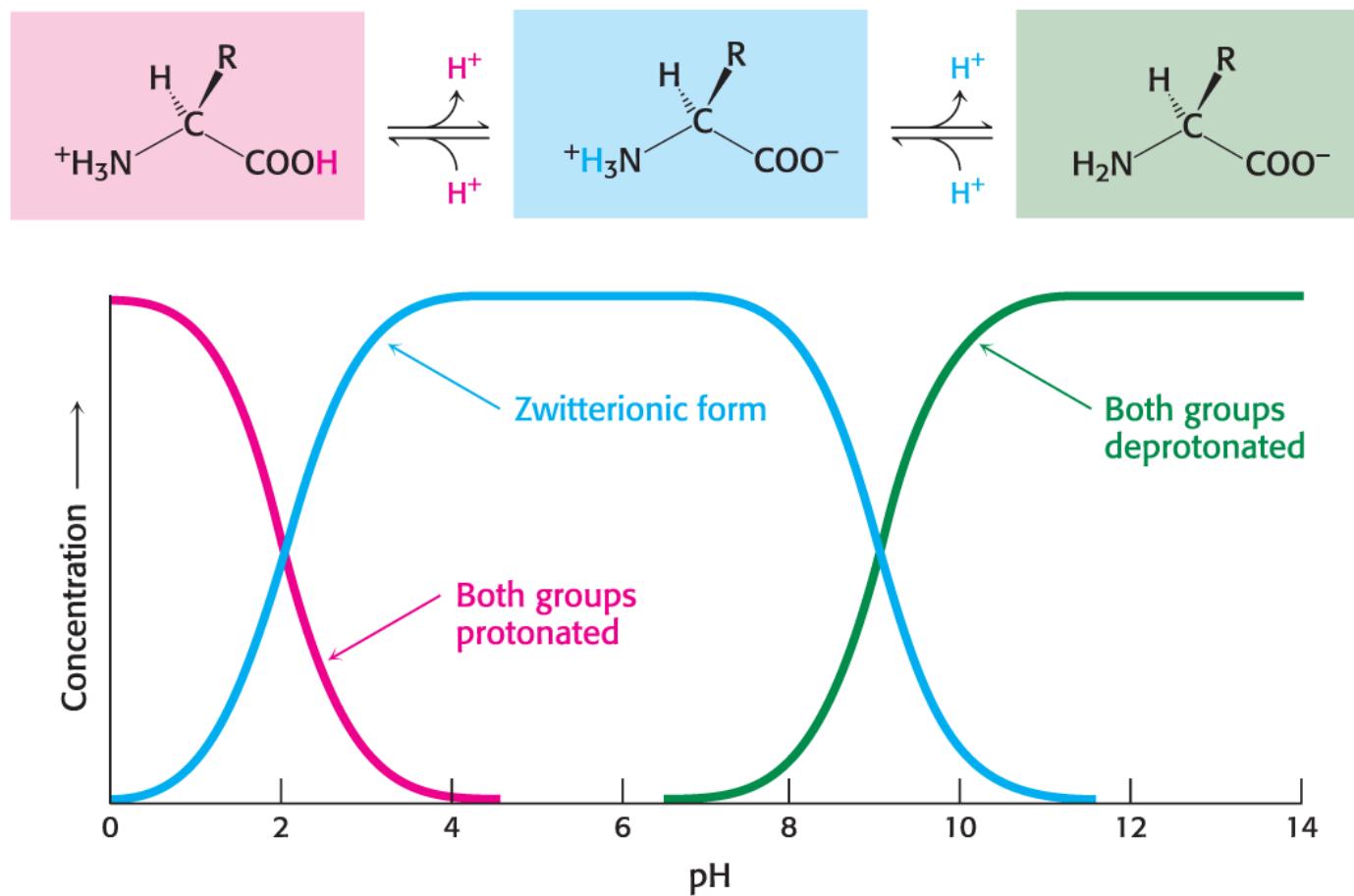


Fischer projection
of alanine



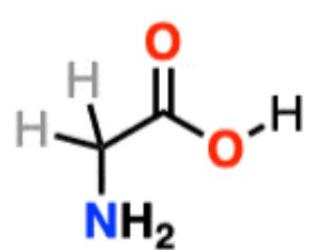
Stereochemical rendering
of alanine

pH-dependence ionization state of amino acid

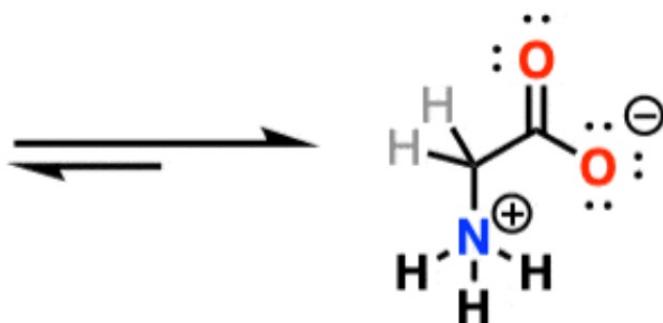


Tymoczko et al., *Biochemistry: A Short Course*, 4e, © 2019 W. H. Freeman and Company

Zwitterion



“neutral” form

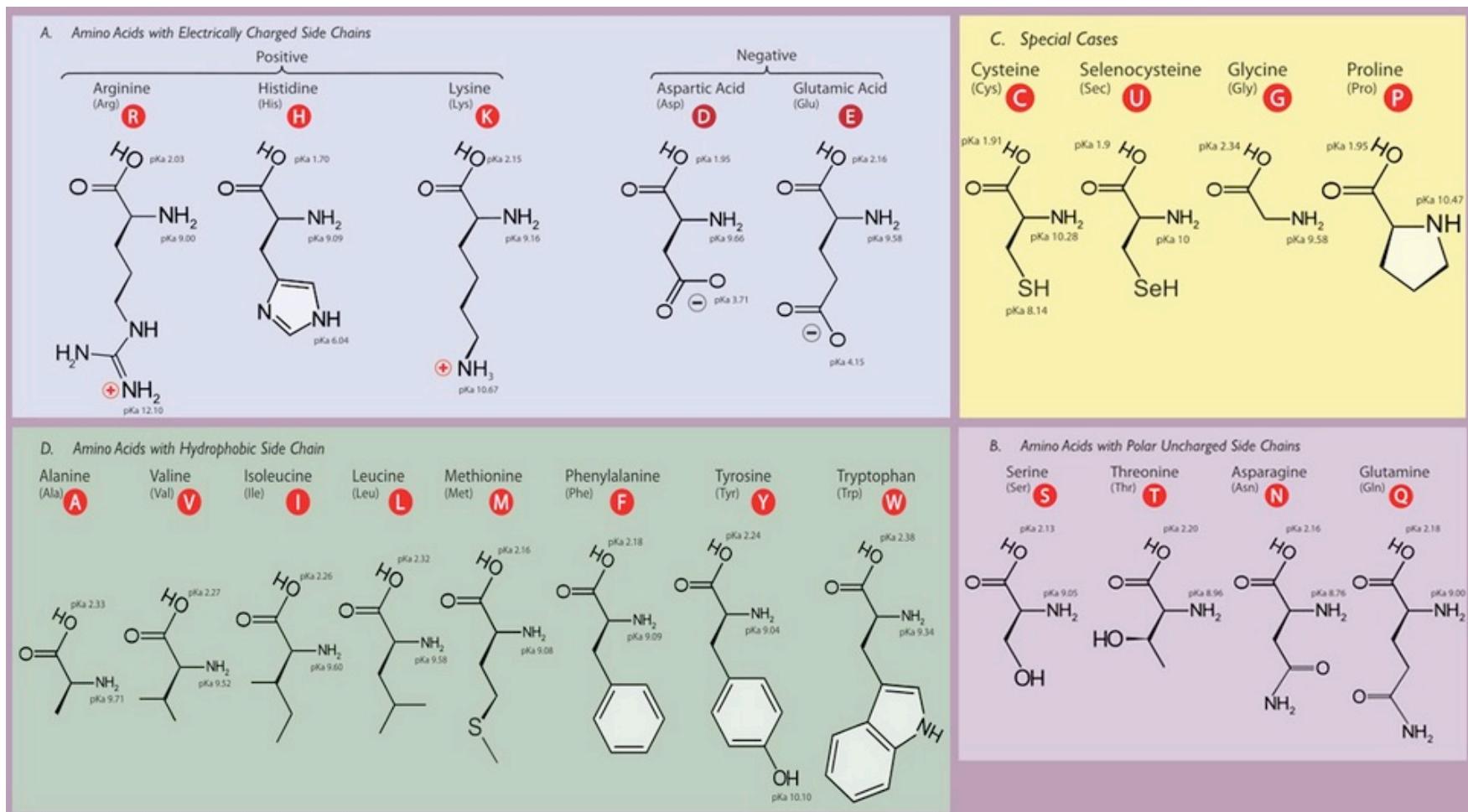


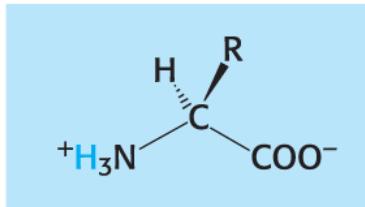
“zwitterionic” form

a **zwitterion** contains two point charges but is **neutral** overall

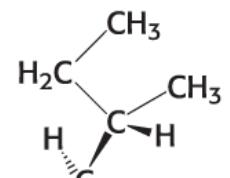
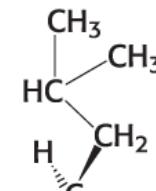
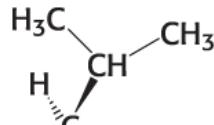
this is also a better representation of the structure of amino acids in **water** at physiological pH (7.4)

Amino acids contain a wide array of functional groups

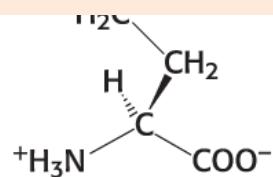




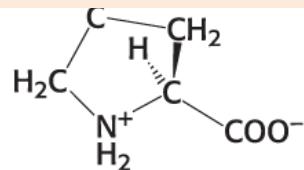
Hydrophobic amino acids



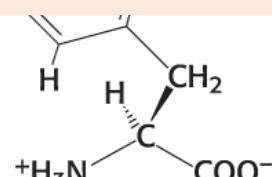
Different sizes and shapes of the hydrophobic side chains → facilitates efficient packing (compact structures with little empty spaces)



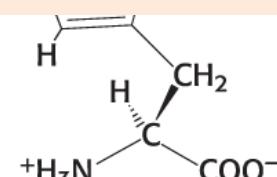
Methionine
(Met, M)



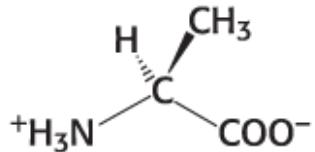
Proline
(Pro, P)



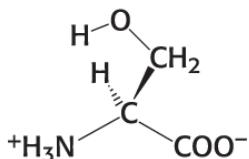
Phenylalanine
(Phe, F)



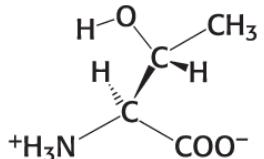
Tryptophan
(Trp, W)



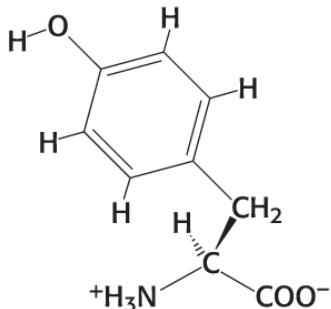
Stereochemical rendering
of alanine



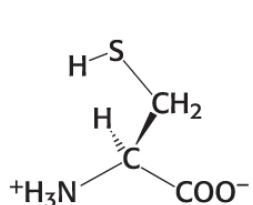
Serine
(Ser, S)



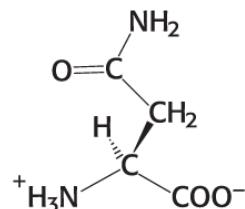
Threonine
(Thr, T)



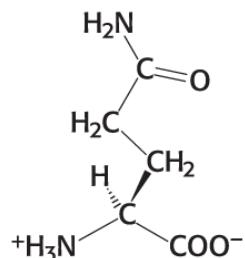
Tyrosine
(Tyr, Y)



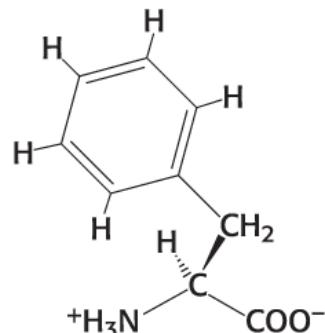
Cysteine
(Cys, C)



Asparagine
(Asn, N)



Glutamine
(Gln, Q)



Phenylalanine
(Phe, F)

Polar Amino Acids

➤ Serine is a version of alanine with hydroxyl (-OH) instead of methyl (-CH₃)

➤ compare tyrosine and phenylalanine

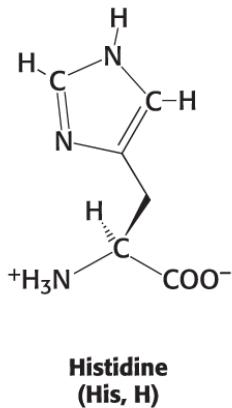
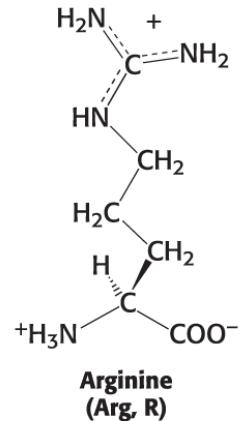
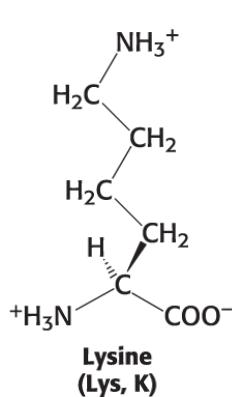
➤ presence of -OH in the side chain makes amino acids more **hydrophilic**

➤ compare

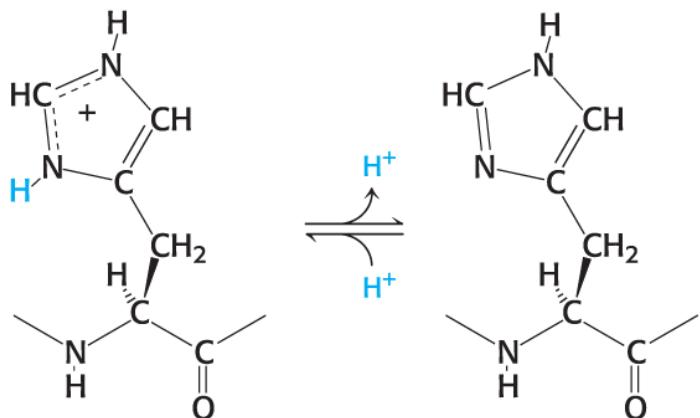
➤ -SH is more polar than -OH

➤ two -SH groups can form a disulfide bond

Positively charged Amino Acids are hydrophilic

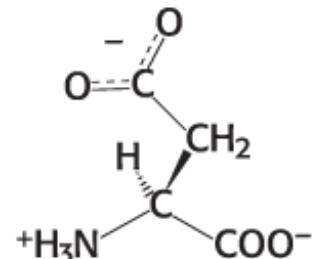


- Side chains of lysine and arginine have dual properties
- histidine contains an imidazole group ($\text{pK}_a \sim 6$)
- What is histidine's charge near neutral pH?
- Histidine is often found in the active site of enzymes

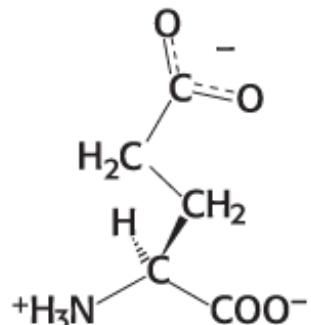


Histidine can bind or release protons near physiological pH.

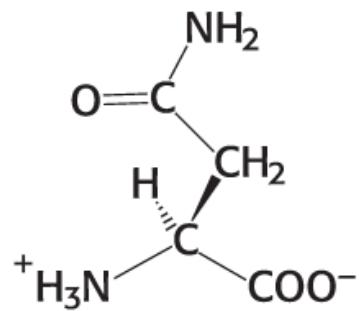
Negatively charged Amino Acids have acidic side chains



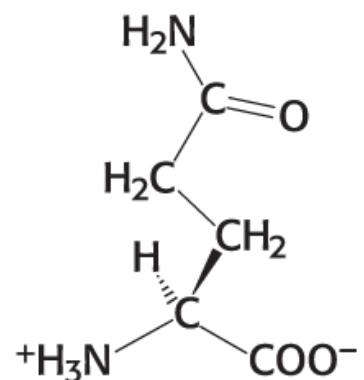
Aspartate
(Asp, D)



Glutamate
(Glu, E)



Asparagine
(Asn, N)



Glutamine
(Gln, Q)

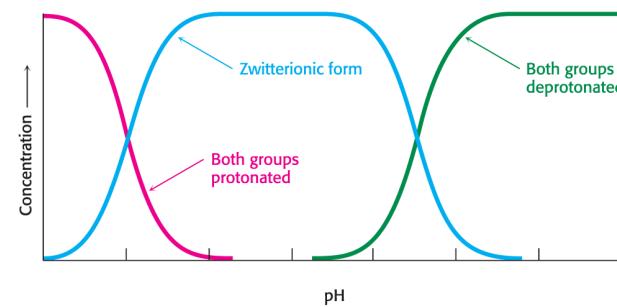
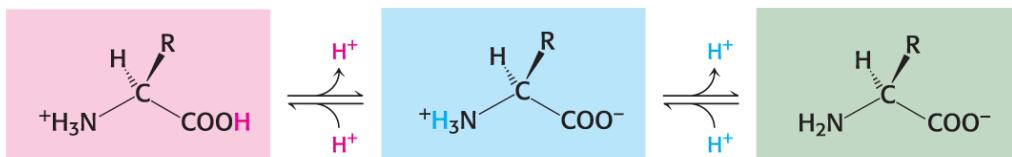
- Aspartate and glutamate have acidic side chains
- side chain is negatively charged (can accept protons → neutralize the negative charge)
- compare to Asn and Glu

Typical pK_a values of ionizable groups in proteins

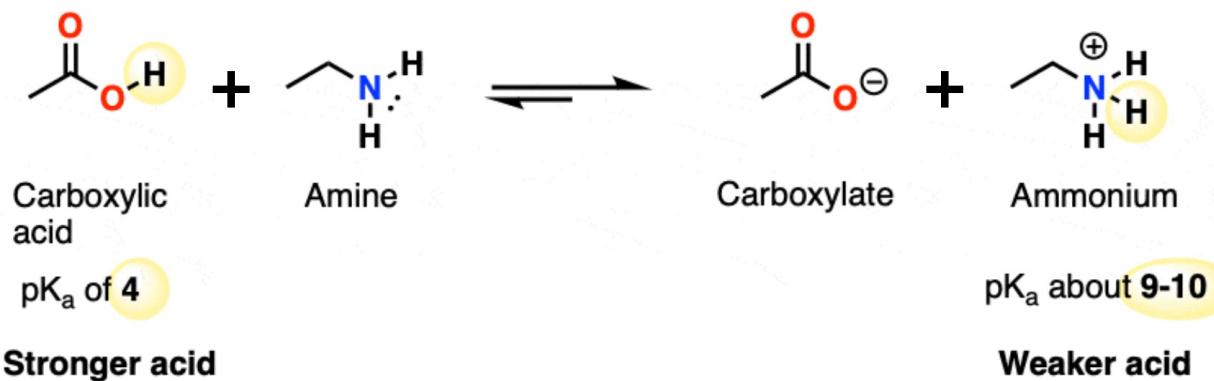
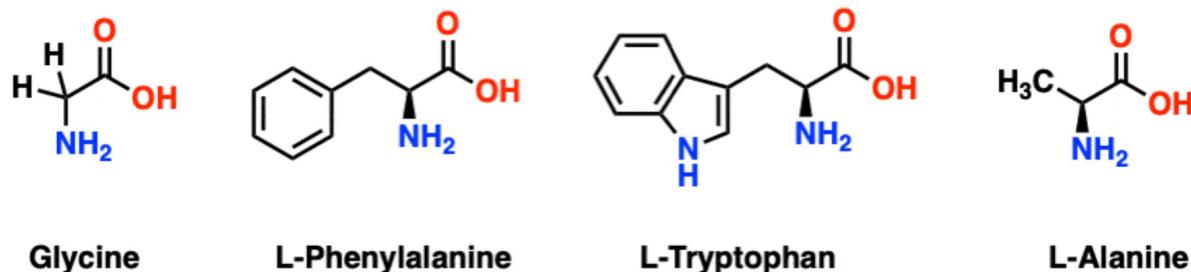
Group	Acid	Base	Typical pK_a
Terminal α -carboxyl group			3.1
Aspartic acid Glutamic acid			4.1
Histidine			6.0
Terminal α -amino group			8.0

Group	Acid	Base	Typical pK_a
Cysteine			8.3
Lysine			10.8
Tyrosine			10.9
Arginine			12.5

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Isoelectric point of amino acids



<https://www.masterorganicchemistry.com/2023/02/09/isolectric-point-calculation/>

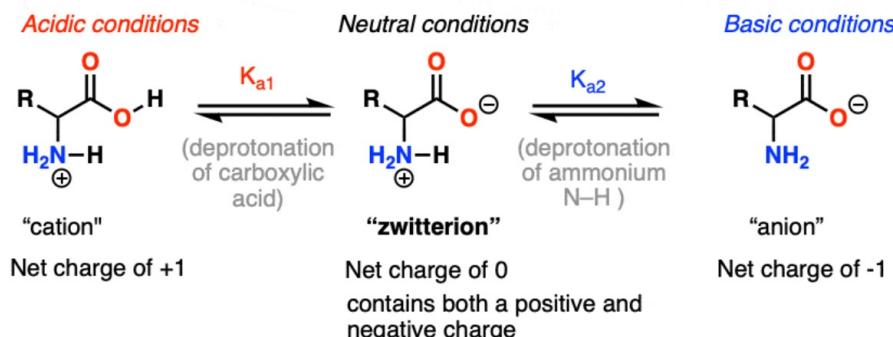
Isoelectric point of amino acids

Summary - How To Calculate Isoelectric Points

Typical amino acids are “**zwitterions**” at neutral pH

An internal acid-base reaction between the basic amino group and acidic carboxylic acid results in a **salt** with two point charges but a net charge of **zero**.

Typical amino acids have two acidity constants (K_a) - one for the carboxylic acid (K_{a1}) and one for the ammonium salt (K_{a2}).



The **isoelectric point** of an amino acid is the **pH** at which it bears a **net charge of zero**.

For amino acids with non-acidic or non-basic sidechains, the isoelectric point **pI** can be calculated by averaging the two **pK_a** values.

$$\text{pK}_{\text{a}1} = \text{pK}_a \text{ of carboxylic acid}$$

$$\text{pK}_{\text{a}2} = \text{pK}_a \text{ of ammonium}$$

Amino acids with **acidic** or **basic** sidechains have **three** pK_a values

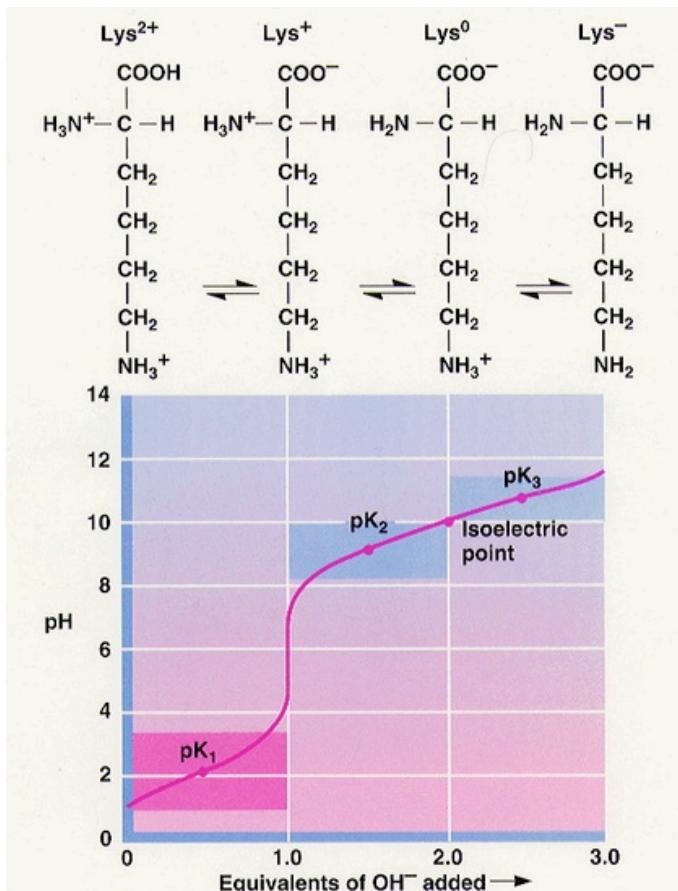
The pI of an **acidic** amino acid is obtained by averaging the two **most acidic** pK_a values.

The **pl** of a **basic** amino acid is obtained by averaging the two **least acidic** pK_a values

<https://www.masterorganicchemistry.com/2023/02/09/isoelectric-point-calculation/>

Isoelectric point of amino acids

- The **isoelectric point** (pI), is the pH at which a particular molecule carries no net electrical charge.
- pI is a critical parameter for many analytical biochemistry and proteomics techniques, especially for 2D gel electrophoresis (2D-PAGE), capillary isoelectric focusing (cIEF) and liquid chromatography-mass spectrometry (LC-MS)



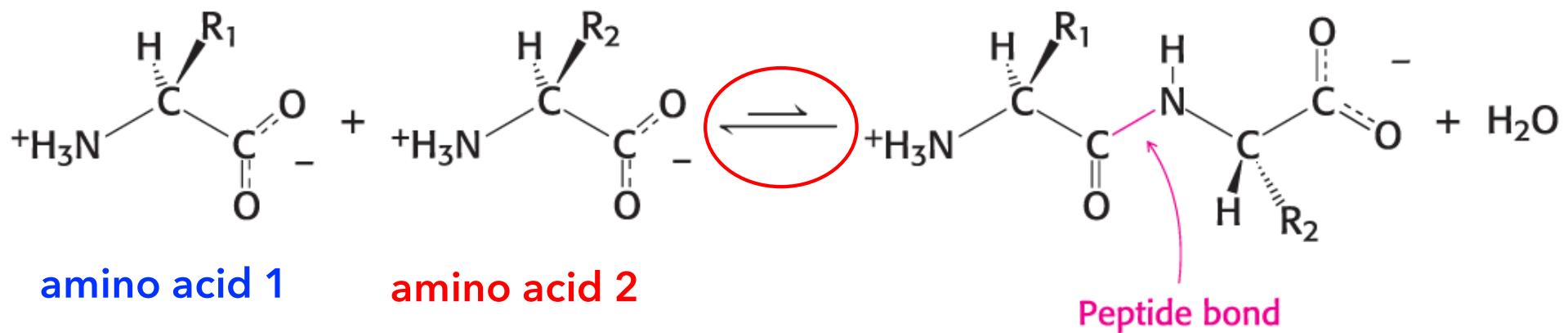
Amino Acids Contain a Wide Array of Functional Groups

- Proteins contain 20 amino acids, each with unique side chains varying in size, shape, charge, hydrophobicity, and reactivity.
- Hydrophobic amino acids have nonpolar side chains, while polar amino acids interact with water via hydrogen bonds.
- Ten amino acids are essential and must be obtained through the diet.

Essential	Conditionally Non-Essential	Non-Essential
Histidine	Arginine	Alanine
Isoleucine	Asparagine	Aspartate
Leucine	Glutamine	Cysteine
Methionine	Glycine	Glutamate
Phenylalanine	Proline	
Threonine	Serine	
Tryptophan	Tyrosine	
Valine		
Lysine		

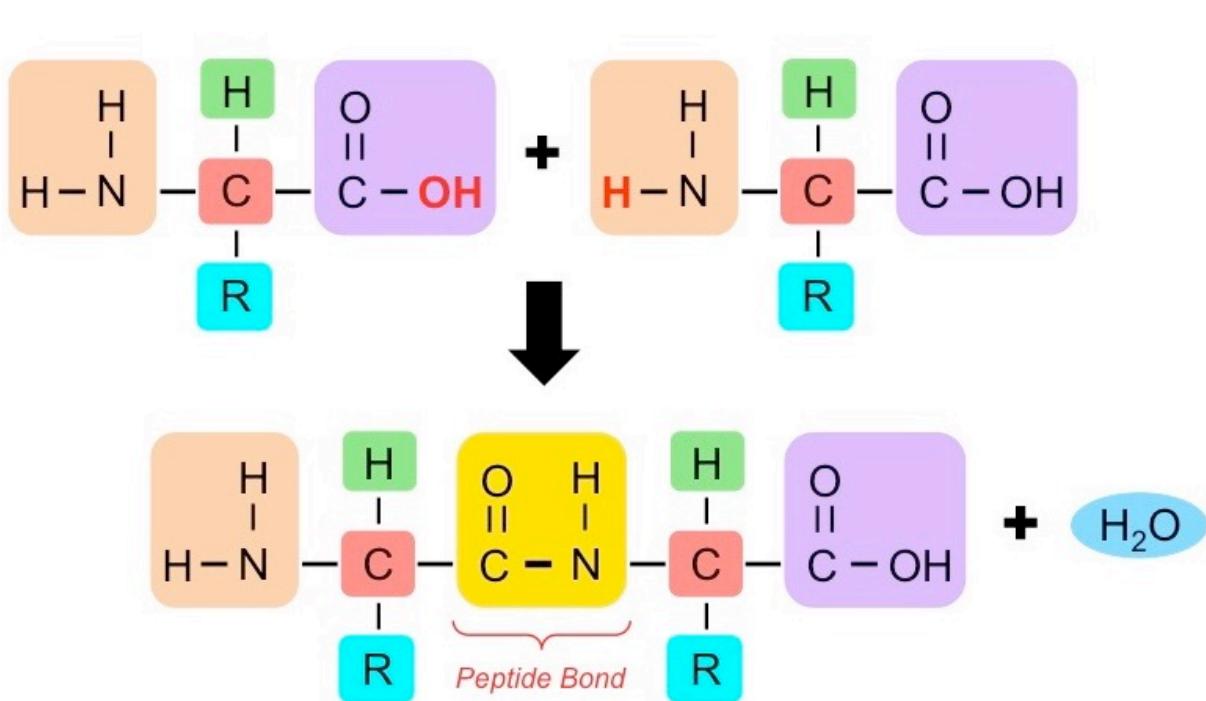
When amino acids link together...

- A **protein** is a biological molecule that consist of one or more **polypeptides**, which are chains of polymerized amino acids.



- equilibrium lies on the side of hydrolysis rather than synthesis
- peptide bond formation requires an input of energy
- peptide bonds are still stable as rate of hydrolysis is extremely low

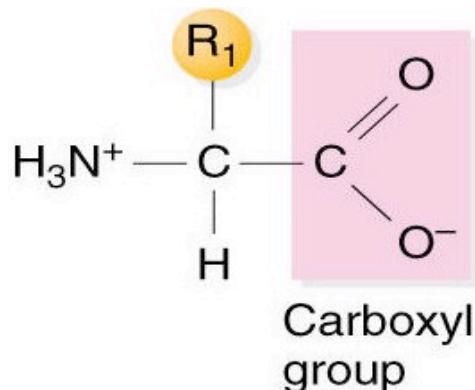
When amino acids link together



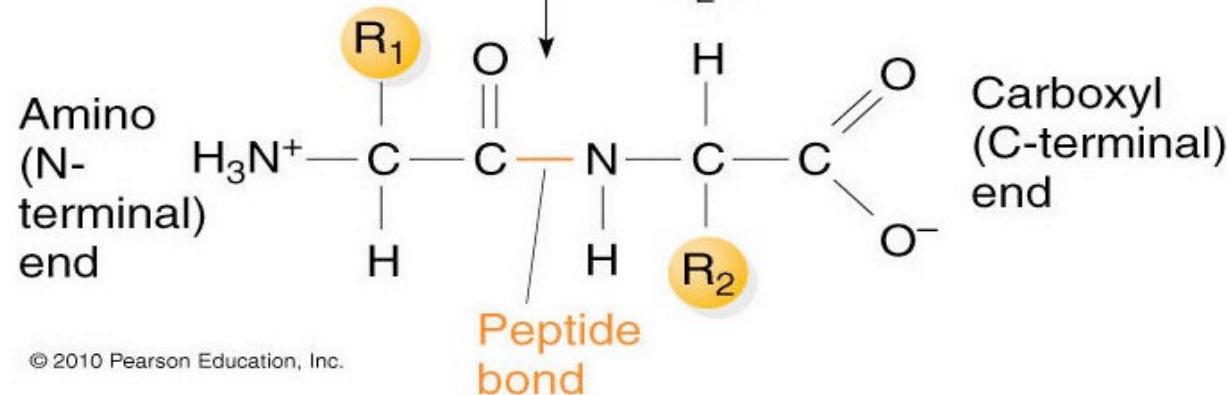
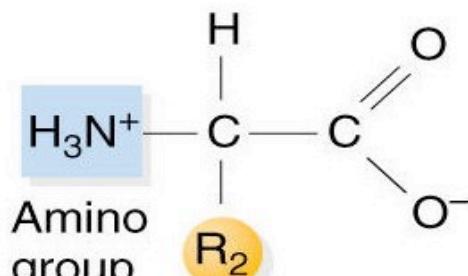
- peptide bond → covalent bond that forms between the carboxyl group (-COOH) of one amino acid and the amino group (-NH₂) of another
 - occurs through a condensation reaction → releases a molecule of H₂O

When amino acids link together

amino acid 1

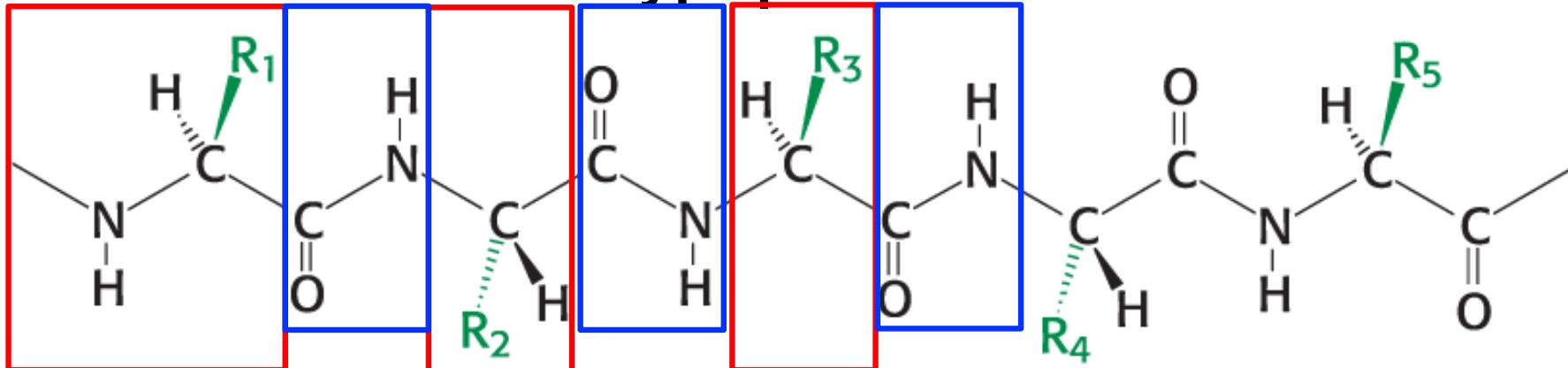


amino acid 2



- The **peptide bond** is also called an **amide bond**.
- Each amino acid in a protein is called a **residue**.

Polypeptide Chain



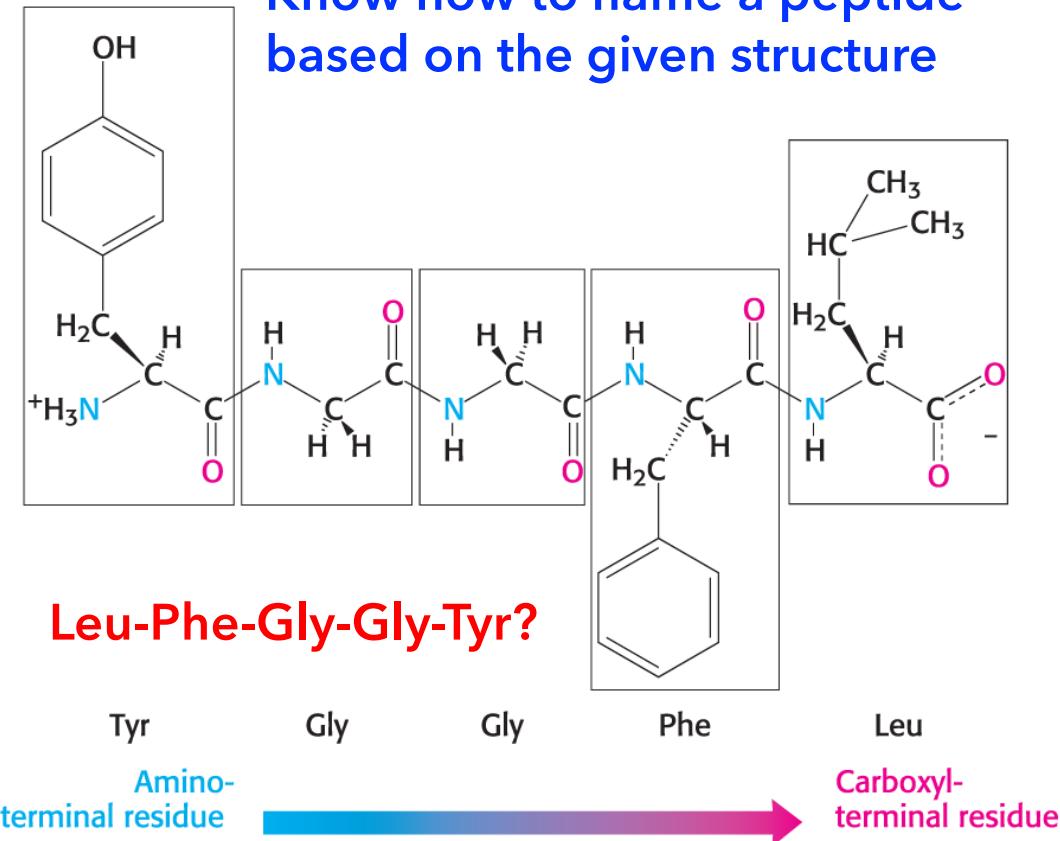
- **polypeptide chain:** a series of amino acids joined by peptide bonds
- main chain or backbone (black) and variable side chains (green)
- **From the polypeptide chain, you can name the peptide...**

Key Features

1. **Strong and Stable:** Provides structural integrity to proteins.
2. **Planar Structure:** Limits rotation, contributing to protein folding.
3. **Backbone of Proteins:** Found in all proteins and polypeptides.

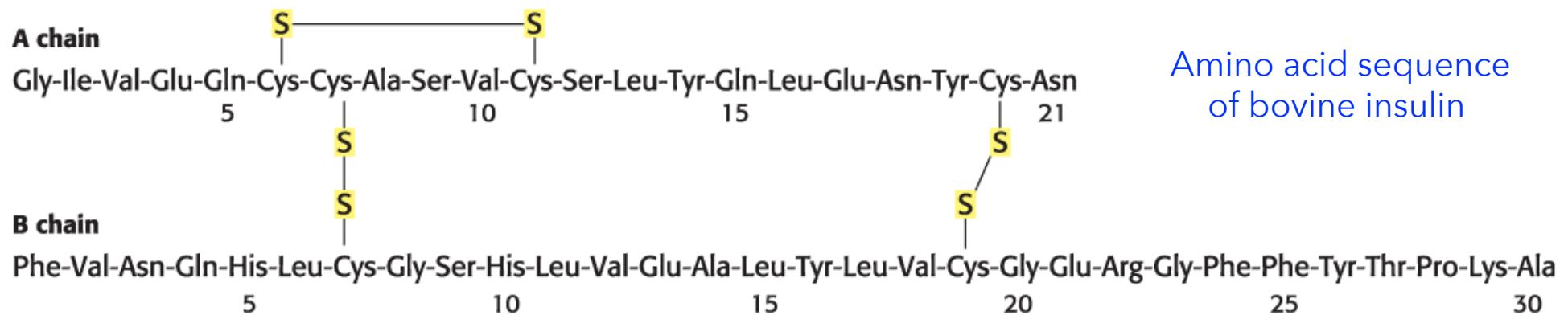
Amino acid sequences have direction

Know how to name a peptide based on the given structure



- A polypeptide bond has directionality.
- amino terminal end → start of the polypeptide chain
- carboxyl terminal end → end of the polypeptide chain
- primary structure is always written from the N-terminal to the C-terminal (left to right)
- Most proteins consist of 50 to 2000 amino acid residues.

Proteins have unique amino acid sequence specified by genes



- Kudos to Frederick Sanger (1953) for determining the very first protein sequence → later developed the Sanger DNA sequencing technique (commercially available)
- Amino acid sequence → 3D structures of proteins, function, understand abnormal protein functioning/diseases, evolutionary history (molecular paleontology)

Disulfide bridges

- In some proteins, the polypeptide chain can be cross-linked by **disulfide bonds**.
- Disulfide bonds form by the oxidation of two cysteines → cystine.
- an oxidation process (so you need a reducing agent to separate disulfide bridges)

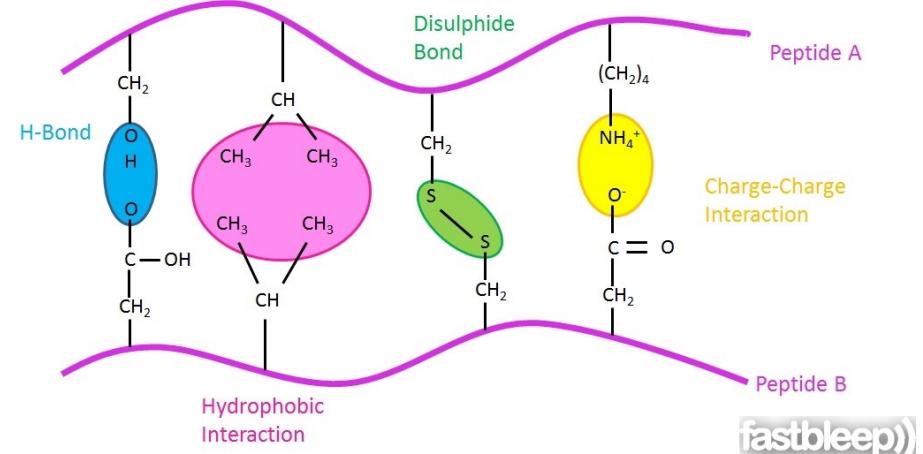
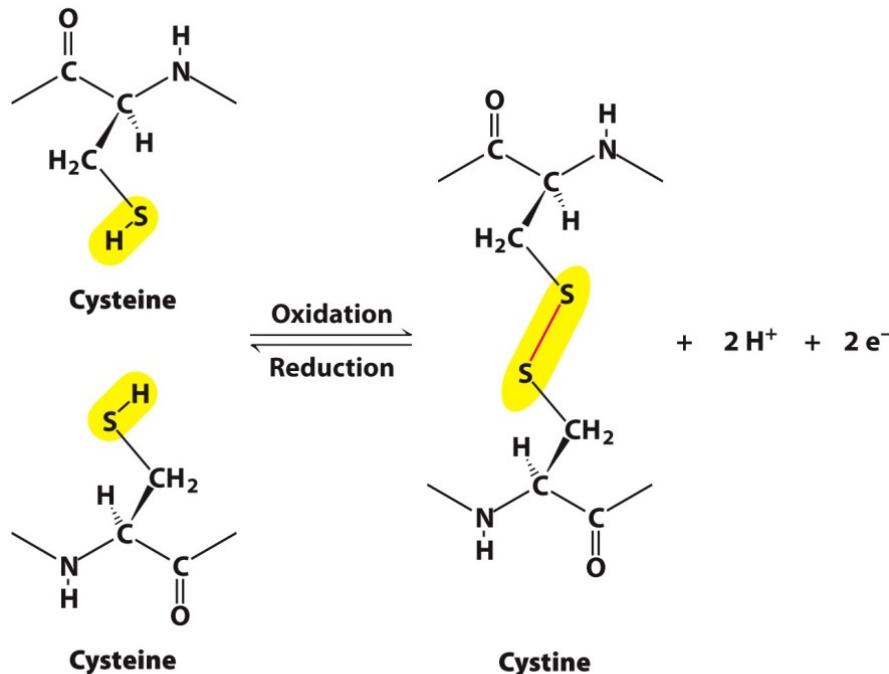
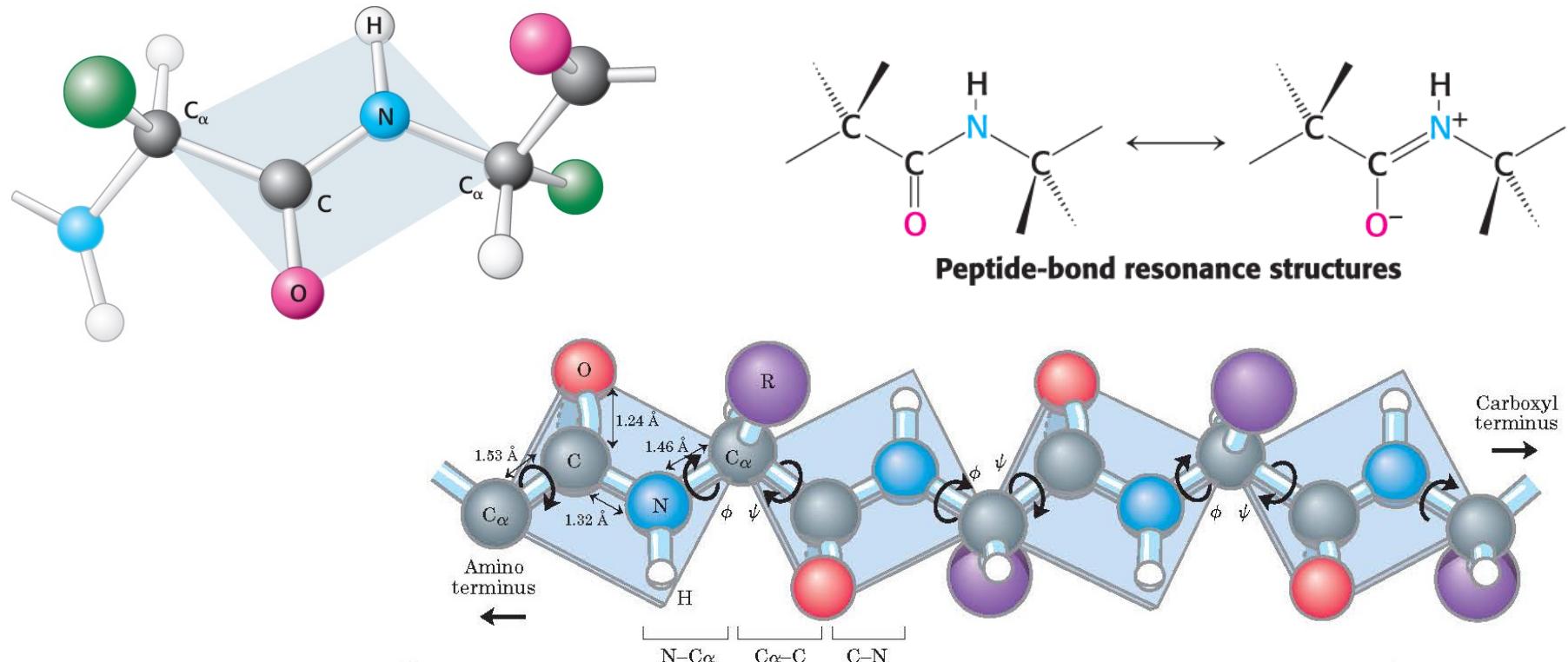


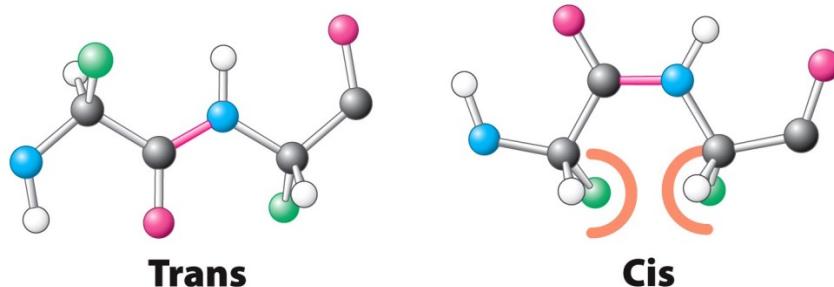
Figure 4.4
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Properties of the Peptide Bond

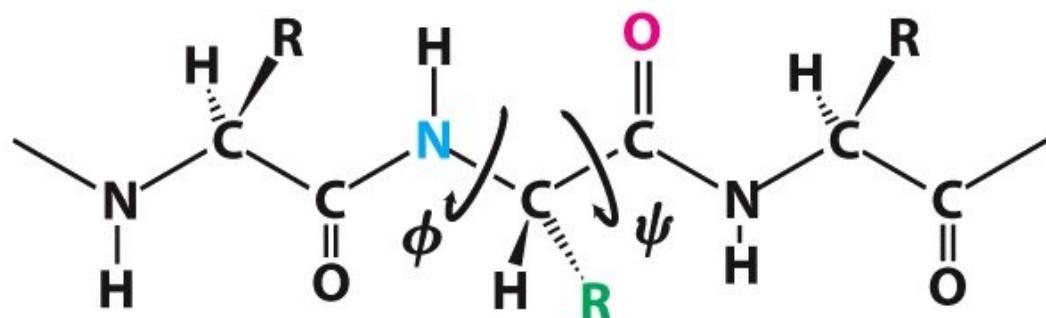
- The peptide bond is essentially **planar**. Six atoms (C_{α} , C, O, N, H, and C_{α}) lie in a plane.
- The peptide bond has partial double-bond character because of resonance \rightarrow rotation about the bond is prohibited \rightarrow constrains the conformation of the backbone



Polypeptide Chains Are Flexible Yet Conformationally Restricted



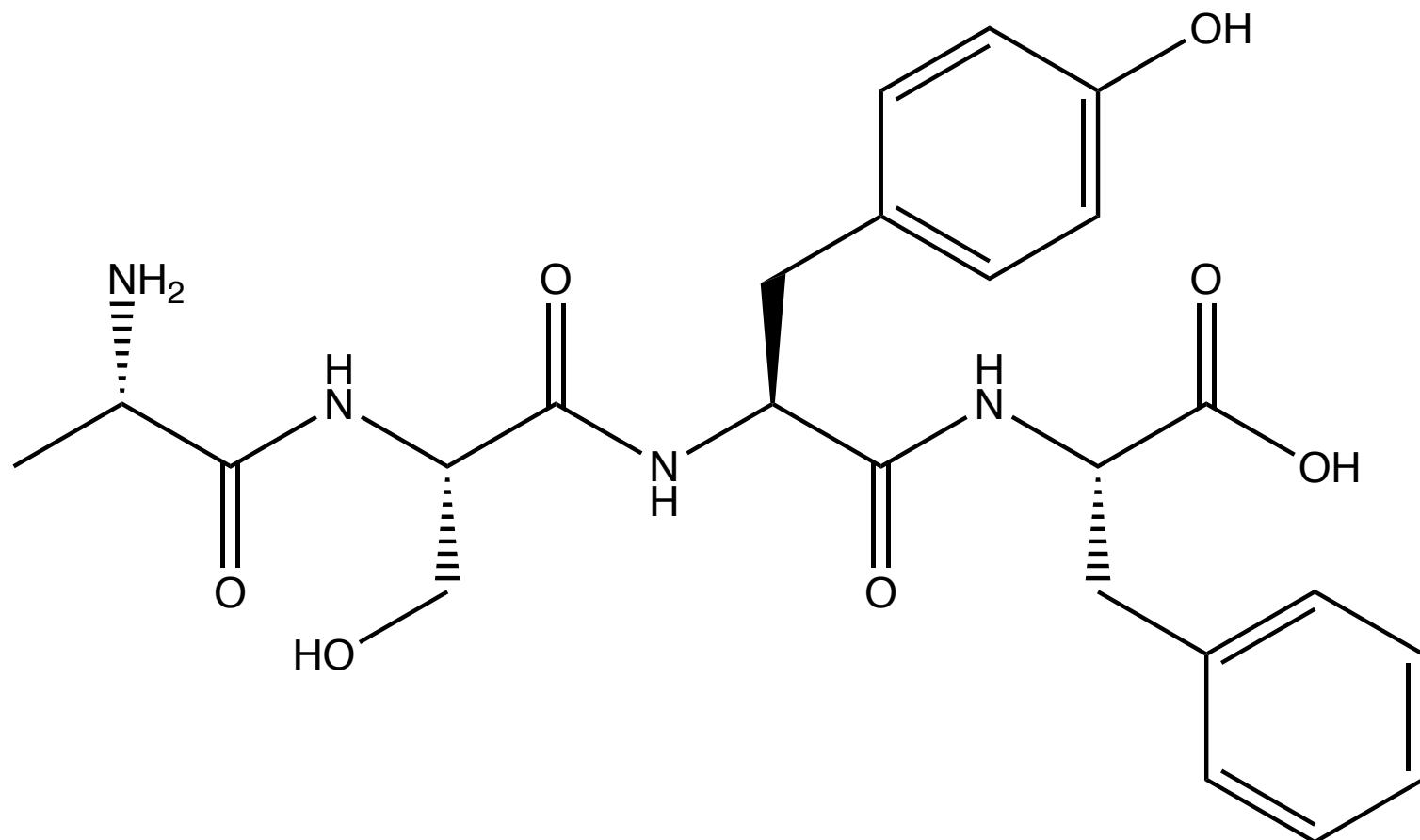
- Most peptide bonds are in the trans configuration so as to minimize steric clashes between neighboring R groups.



- Rotation is permitted about the N-C_α bond (the phi (ϕ) bond) and about C_α-carbonyl bond (the psi (ψ) bond.)
- The rotation about the ϕ and ψ bonds, called the torsion angle, determines the path of the polypeptide chain. Not all torsion angles are permitted (Ramachandran Plot)

- Freedom of rotation allows proteins to fold in many different ways.

Quick Quiz 1: Name the following peptide and circle its peptide bonds.



Hierarchy of protein structure

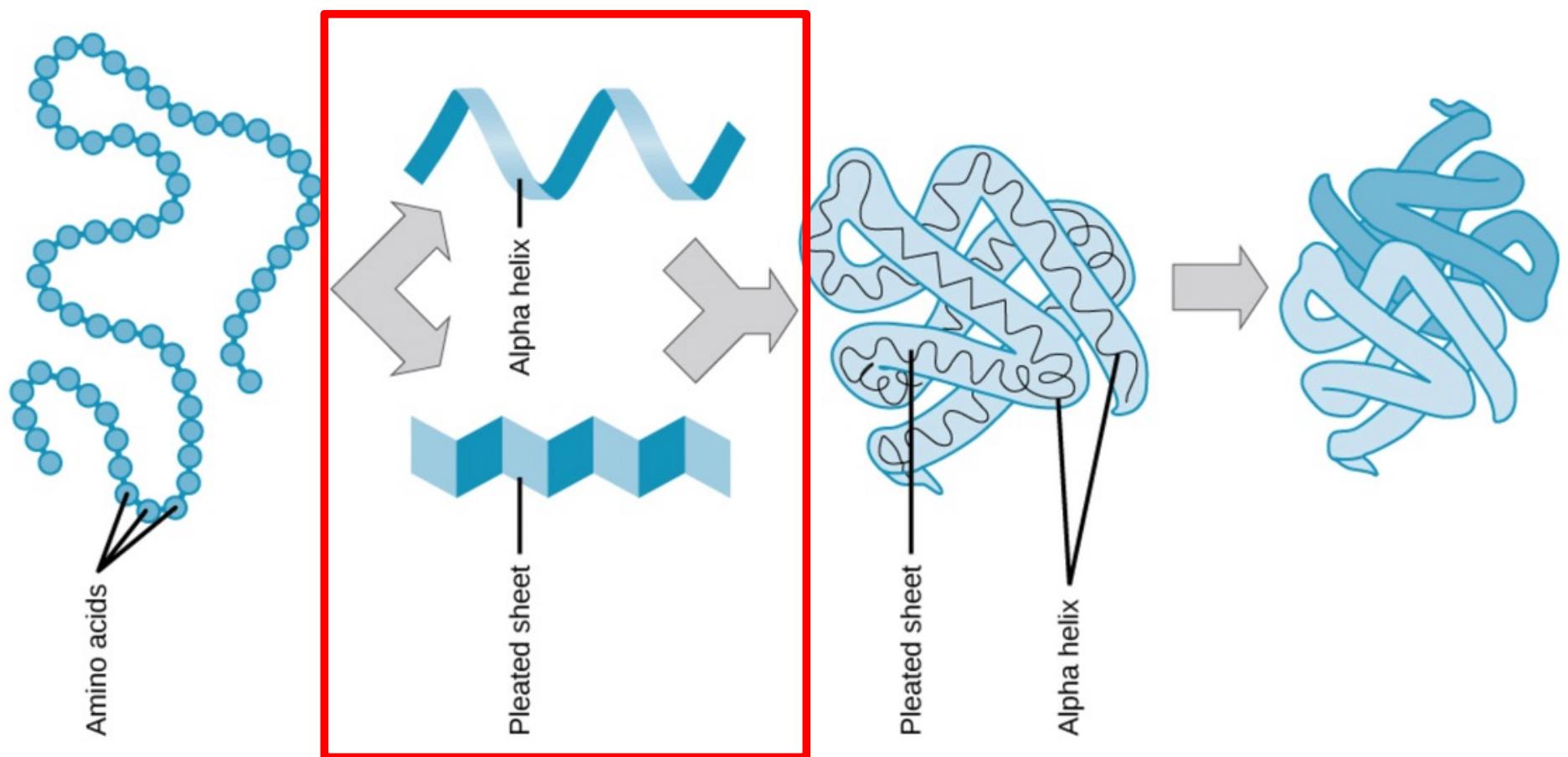
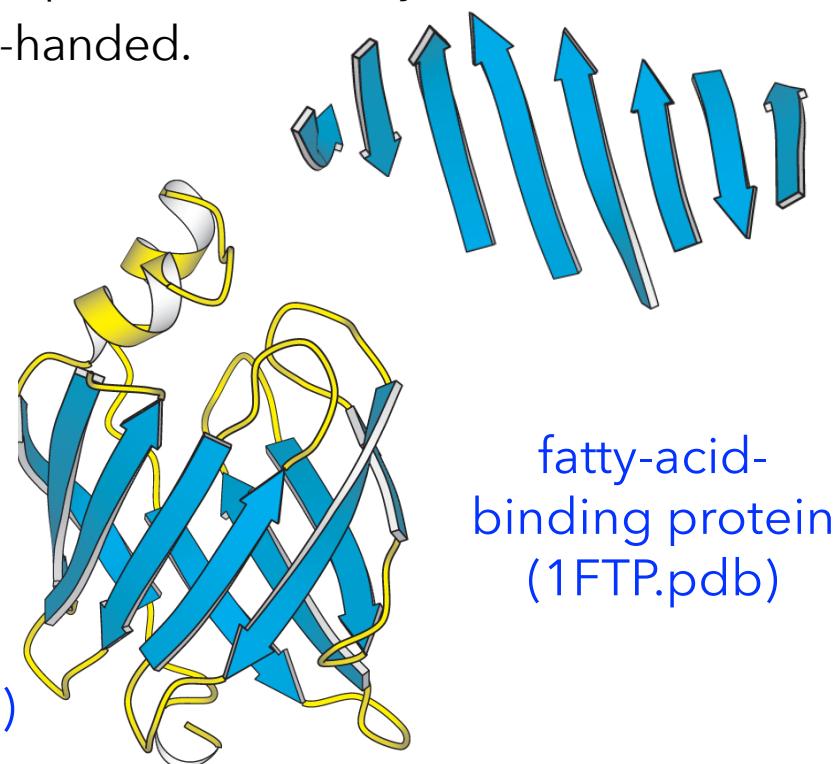
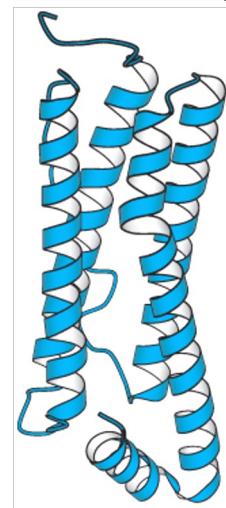
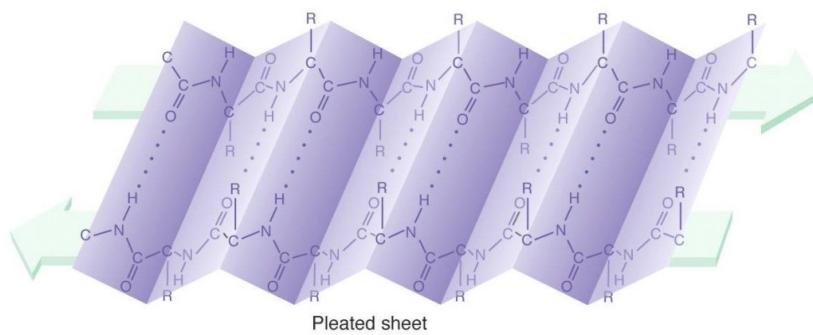
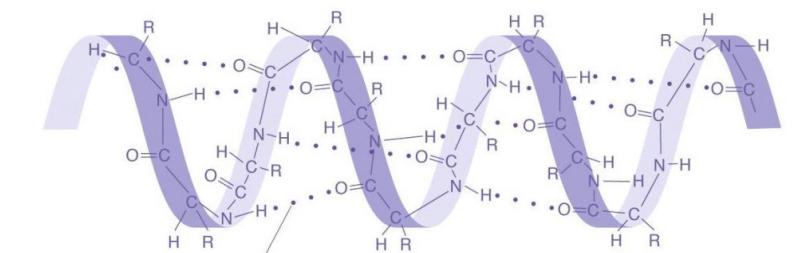


Image by Dillon Daudert

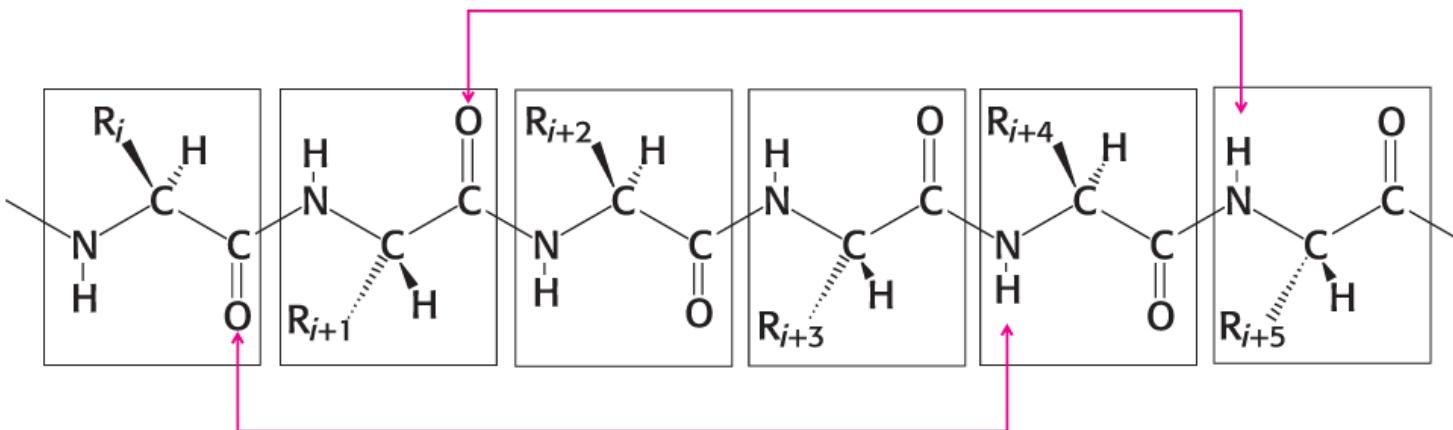
Polypeptide chains can fold into regular structure

- Secondary structure is the 3D structure formed by H-bonds between peptide NH and CO groups of amino acids that are near one another in the primary structure.
- The α -helix, β -sheets and turns are prominent examples of secondary structure.
- Essentially all α helices found in proteins are right-handed.

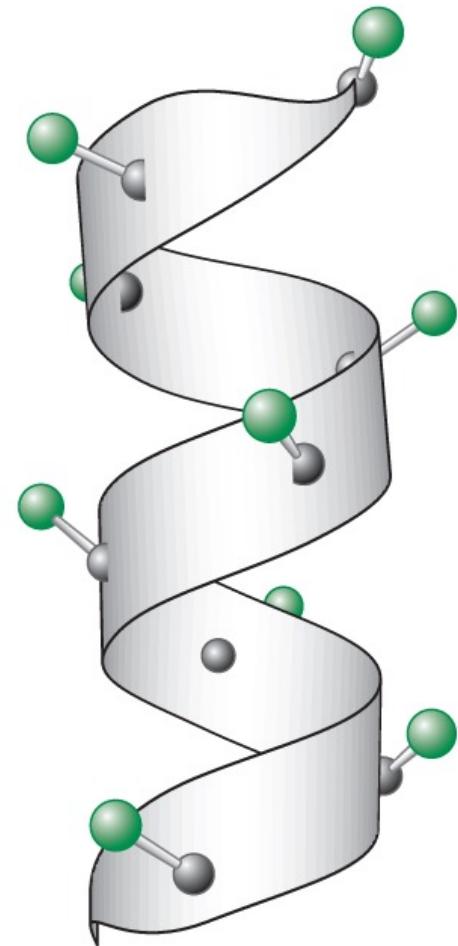


H-bonding in Alpha Helix

- In the α -helix, CO group of residue i forms an H-bond with the NH group of residue $i+4$
- The α -helix is a tightly coiled rod-like structure, with the R groups (green spheres) bristling out from the axis of the helix.
- All of the backbone CO and NH groups form hydrogen bonds except those at the end of the helix.



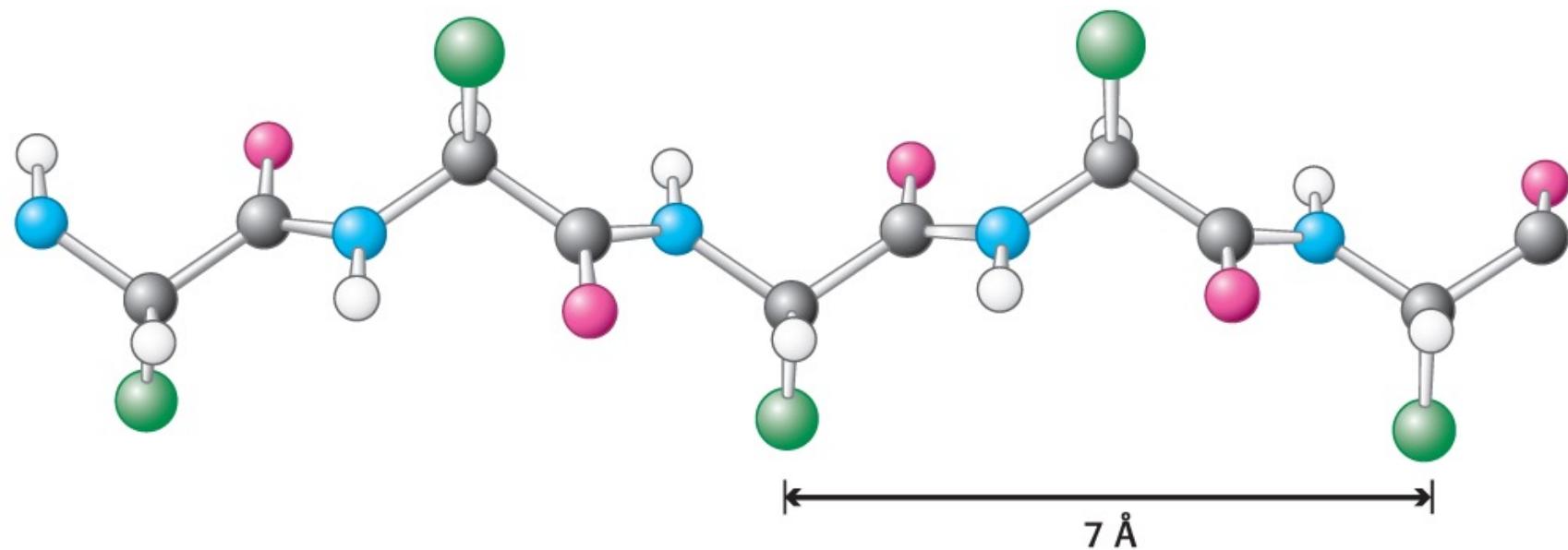
Which amino acids are considered as helix disruptors?



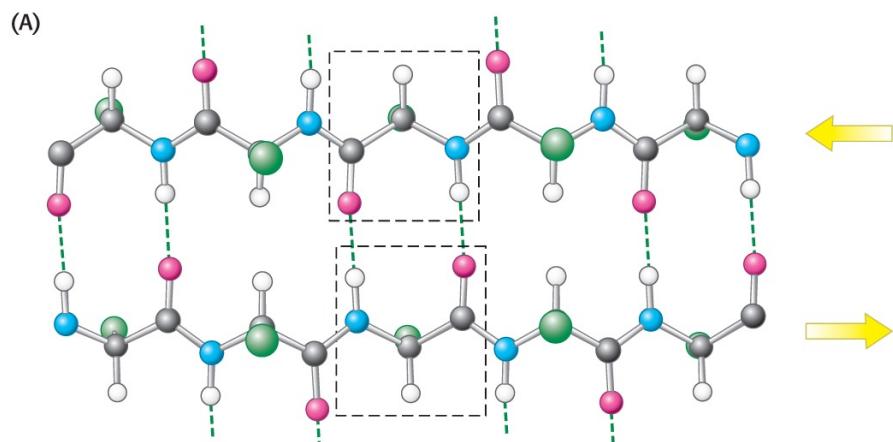
3.6 amino acid residues
per turn of helix

Hydrogen Bonds in β Sheets

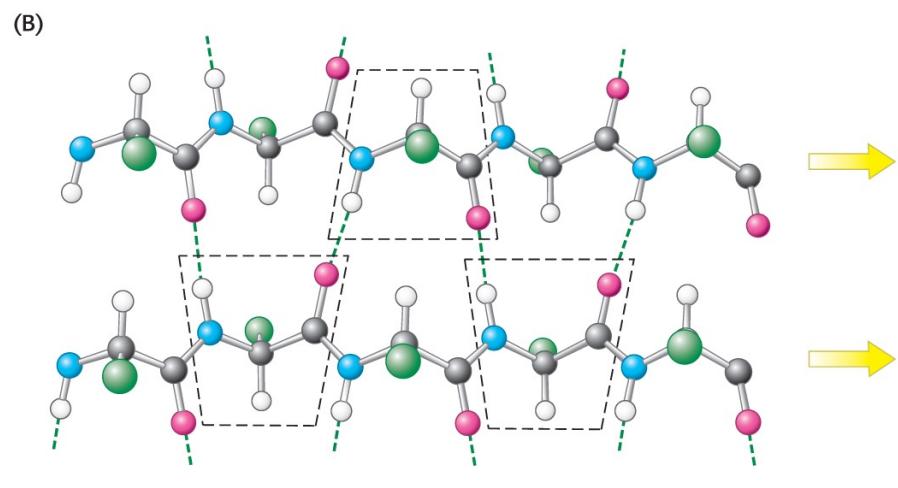
- Beta sheets are formed by adjacent β -strands.
- In contrast to an α -helix, the polypeptide in a β -strand is fully extended.
- The side chains (green spheres) of adjacent amino acids point in opposite directions.



Hydrogen Bonds in β Sheets



Antiparallel β sheet



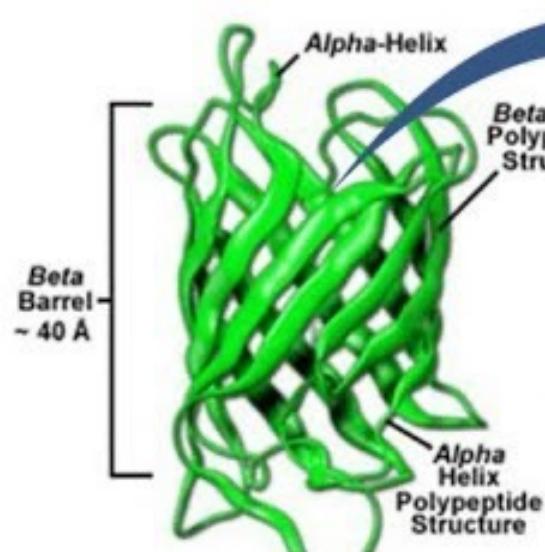
Parallel β sheet

- Hydrogen bonds link the strands in a β -sheet.
- H-bonds between NH and CO groups on adjacent strands stabilize the structure.
- The strands of a β -sheet may be parallel, antiparallel, or mixed.
- β -sheets may be flat or adopt a twisted conformation.

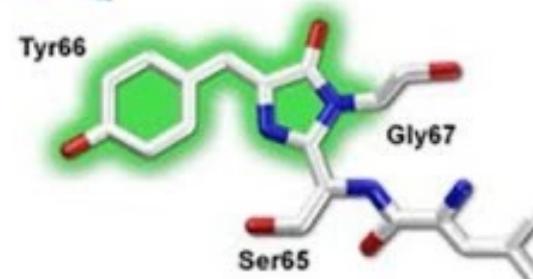
GFP (Green Fluorescence protein)

- A unique protein that emits green color in blue/UV light
- Produced by jellyfish *Aequorea victoria*

238 amino acids



Structure of GFP



Chromophore

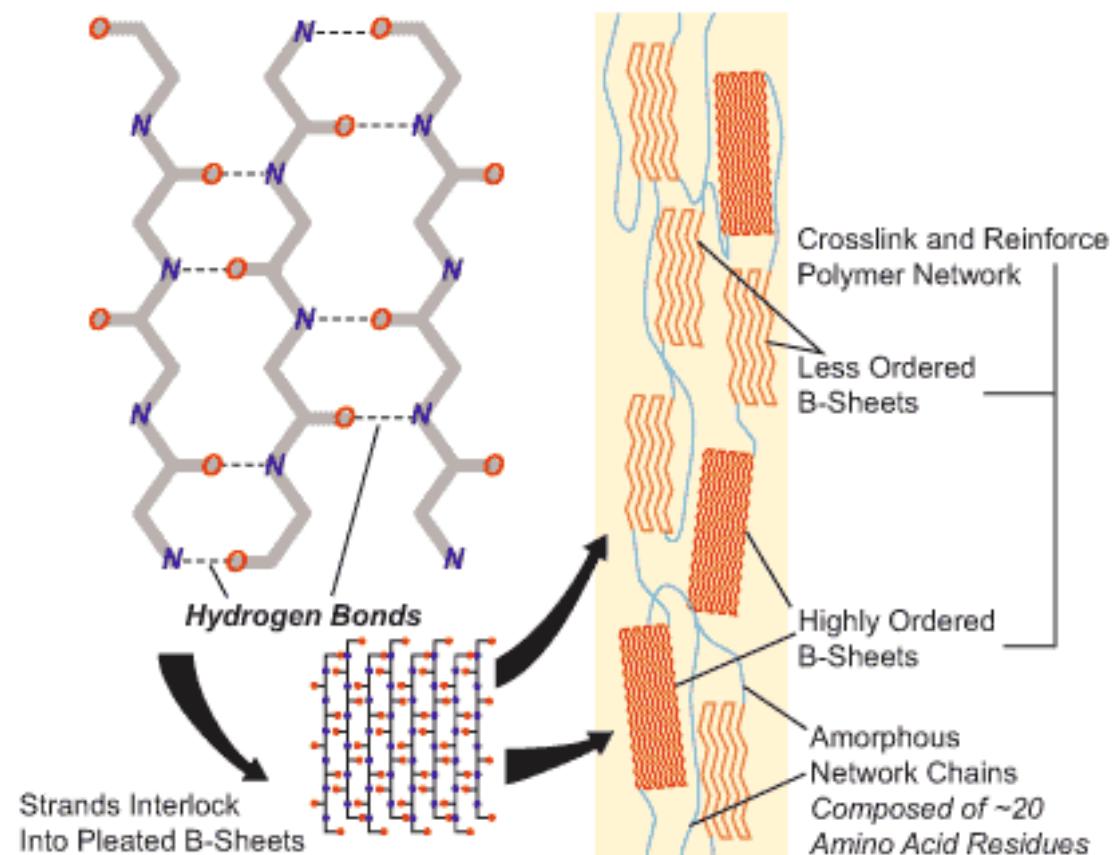
[GFP in PDB](#)

<https://zeiss-campus.magnet.fsu.edu/articles/probes/fpintroducti on.html>

Helix-Sheet Composites in Spider Silk



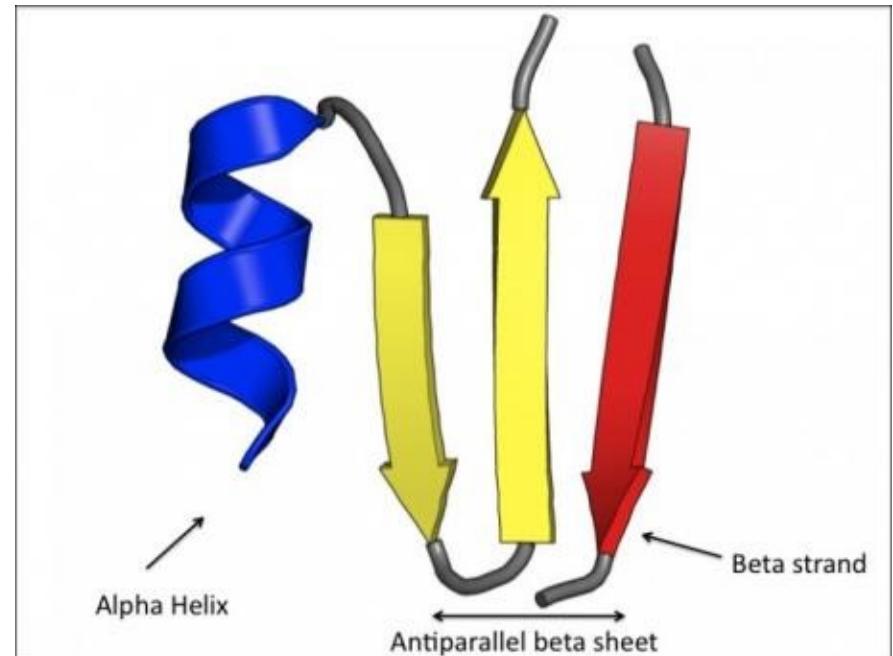
Smithsonian Magazine



Quick Quiz 2

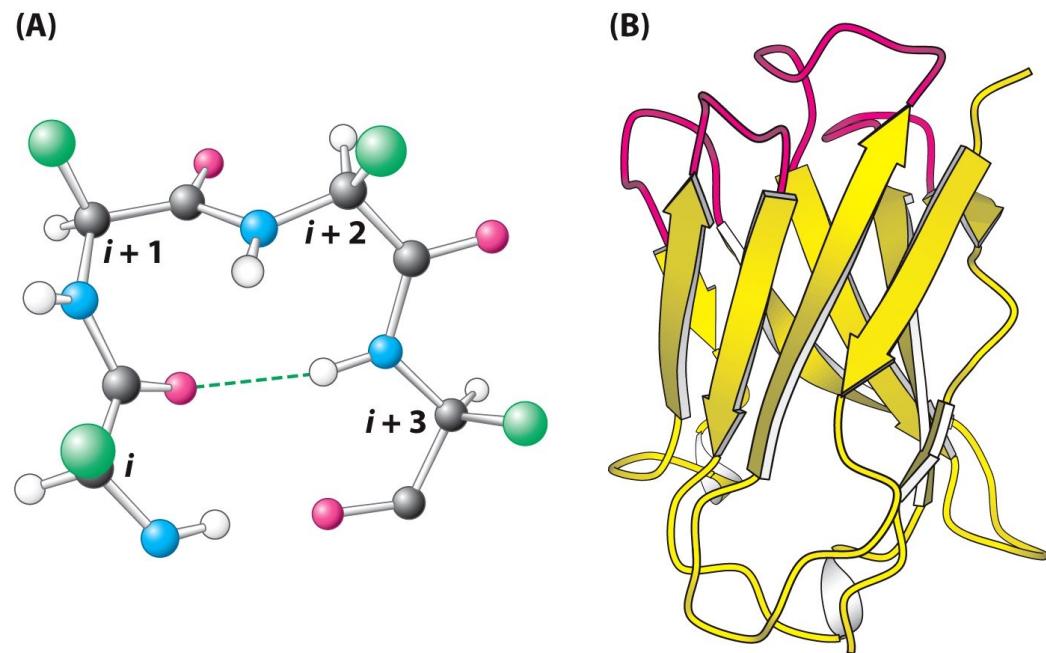
What maintains the secondary structure of a protein?

- A. hydrogen bonds
- B. disulfide bonds
- C. peptide bonds
- D. ionic bonds
- E. phosphodiester bonds



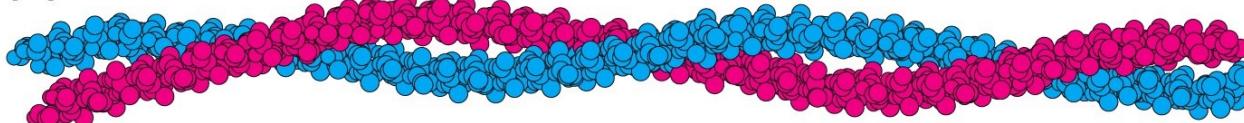
Polypeptide Chains Can Change Direction

- Most polypeptide chains require reversals in order to make a turn. *Reverse turns* and *loops* are protein structural elements responsible for reversals.
- **The structure of a reverse turn.** (A) The CO group of residue i of the polypeptide chain is hydrogen bonded to the NH group of residue $i + 3$ to stabilize the turn. (B) A part of an antibody molecule has surface loops (shown in red).

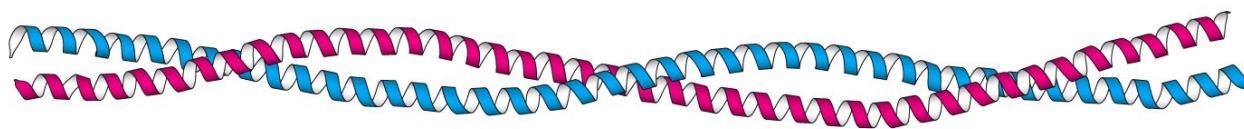


Fibrous Proteins Provide Structural Support for Cells and Tissues

(A)



(B)

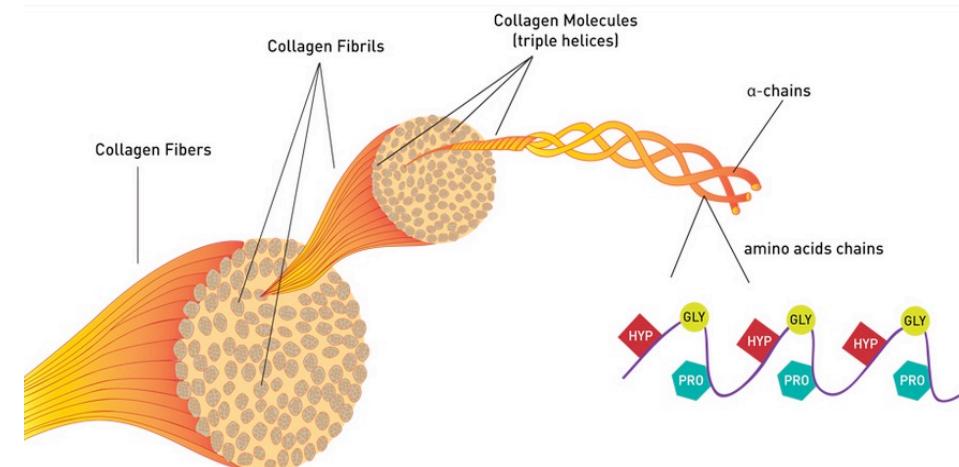


α -helical coiled coil:
two helices forming
a superhelix

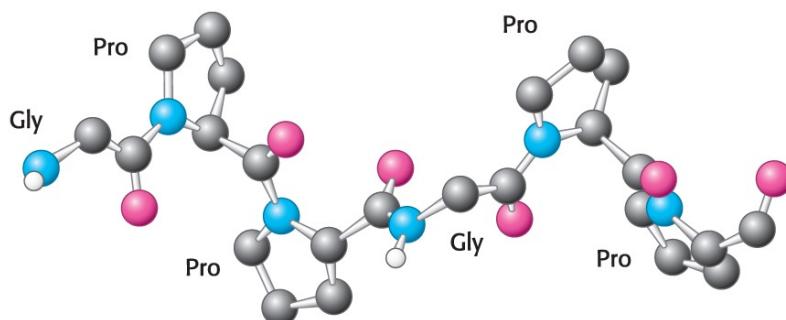
- α -Keratin, a structural protein found in wool and hair, is composed of two right-handed α -helices intertwined to form a left-handed superhelix called a **coiled-coil**.
- The helices interact with ionic bonds or van der Waals interactions.
- Other members of the family include some cytoskeleton proteins and muscle proteins.

Fibrous Proteins Provide Structural Support for Cells and Tissues

- Collagen is the main fibrous component of skin, bone, tendon, cartilage, and teeth.
- has three different α -helical polypeptide chains, each nearly 1000 residues long.
- Helices are stabilized by steric repulsion of the pyrrolidine rings of the proline residues.



<http://bayareapelleve.com/pelleve/collagen/>



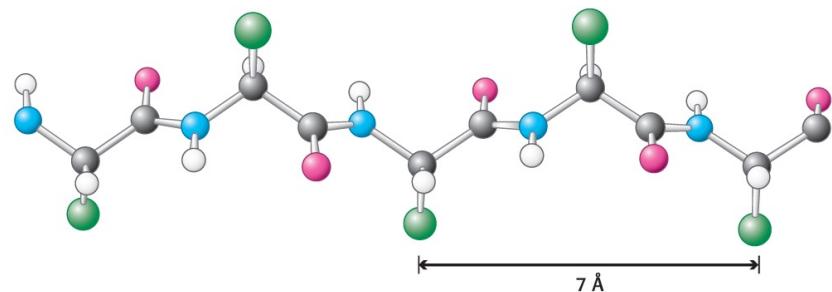
Partial amino acid sequence of a collagen chain

13	-Gly-Pro-Met-Gly-Pro-Ser-Gly-Pro-Arg-
22	-Gly-Leu-Hyp-Gly-Pro-Hyp-Gly-Ala-Hyp-
31	-Gly-Pro-Gln-Gly-Phe-Gln-Gly-Pro-Hyp-
40	-Gly-Glu-Hyp-Gly-Glu-Hyp-Gly-Ala-Ser-
49	-Gly-Pro-Met-Gly-Pro-Arg-Gly-Pro-Hyp-
58	-Gly-Pro-Hyp-Gly-Lys-Asn-Gly-Asp-Asp-

Quick Quiz 3

Which of the following statements is true?

- A. Alpha helices are stabilized by hydrogen bonding between polypeptide strands.
- B. Beta sheets can be right-handed or left-handed.
- C. In a beta sheet, side chains are found on only one side of the sheet.
- D. Proline is preferred in alpha helices because the cyclic side chain allows for a tighter turn along the helix axis.
- E. Beta sheets can be parallel or antiparallel.



Hierarchy of protein structure

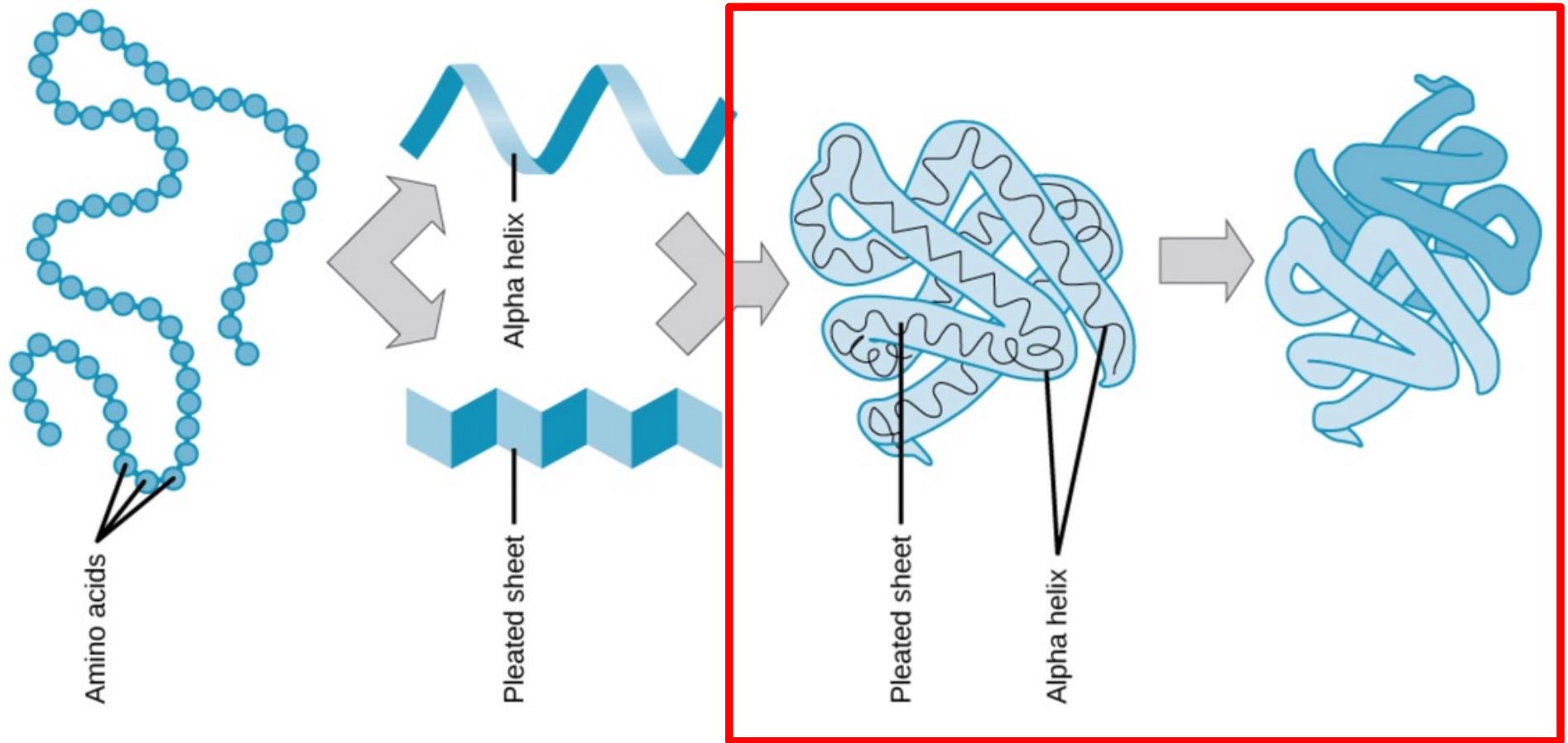
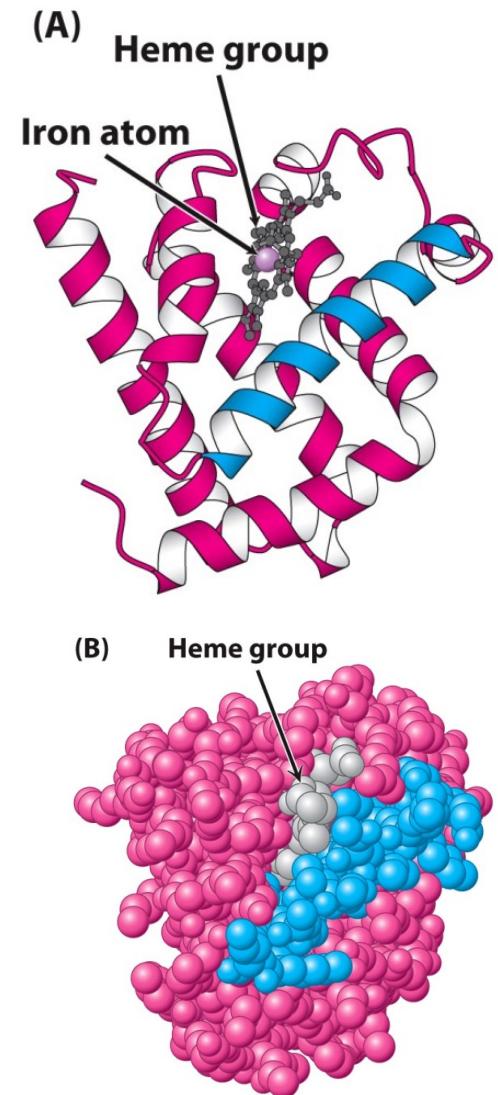


Image by Dillon Daudert

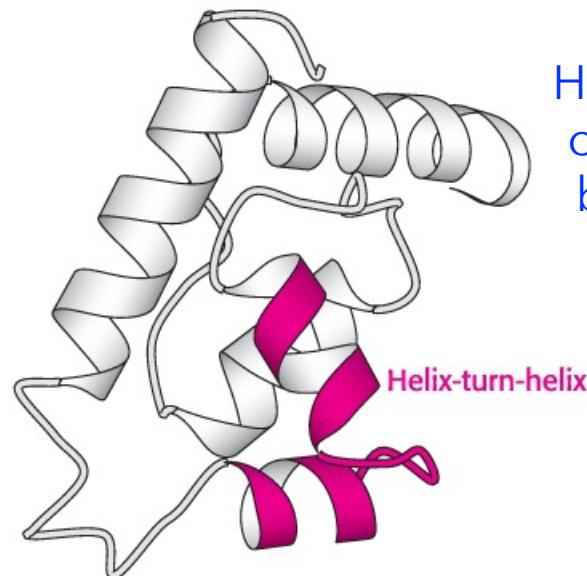
Tertiary Structure

- Tertiary structure refers to the spatial arrangement of amino acids that are far apart in the primary structure
- **Globular proteins**, such as myoglobin, form complicated three-dimensional structures.
- Globular proteins are very compact. There is little or no empty space in the interior of globular proteins.
- The interior of globular proteins consists mainly of hydrophobic amino acids.
- The exterior of globular proteins consists of charged and polar amino acids.

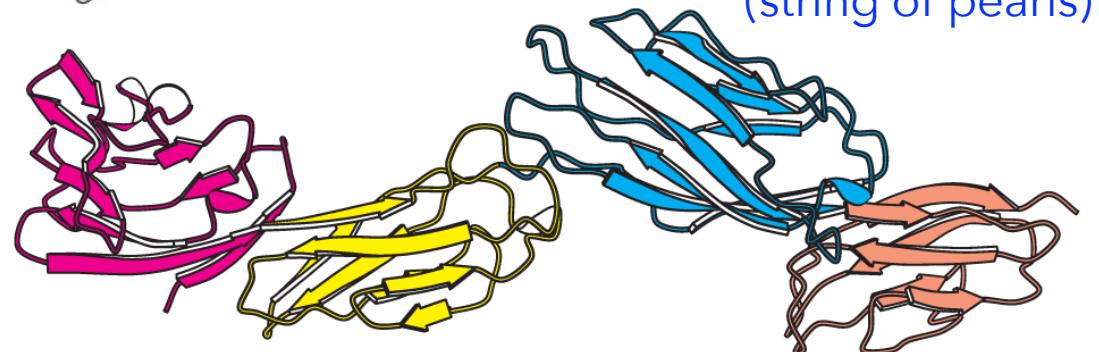


The Tertiary Structure of Many Proteins Can Be Divided into Structural and Functional Units

- Motifs, or super secondary structure, are combinations of secondary structure that are found in many proteins.
- Some proteins have two or more similar or identical compact structures called domains.
- Different proteins may have domains in common but different overall tertiary structure.

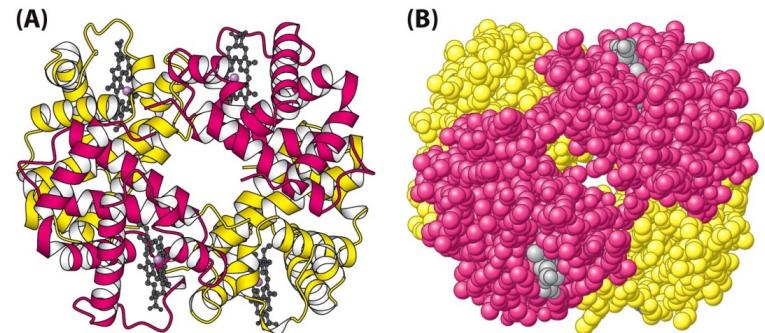


Helix-turn-helix are common in DNA-binding proteins

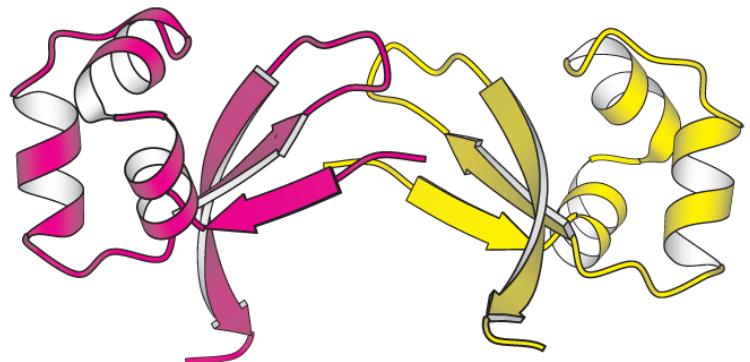


Multiple polypeptide chains can assemble into a single protein

- Many proteins are composed of multiple polypeptide chains called **subunits**. Such proteins are said to display **quaternary structure**.
- Quaternary structure can be as simple as two identical polypeptide chains or as complex as dozens of different polypeptide chains.
- Mostly stabilized by weak bonds (H-bonds, ionic, van de Waals)

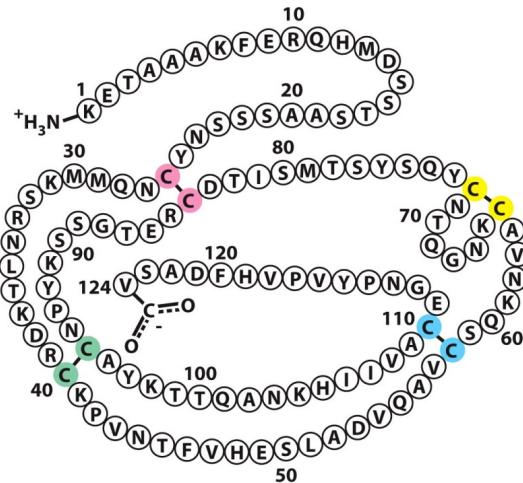


Hemoglobin has 4 subunits



Cro protein (bacteriophage):
dimer of identical subunits

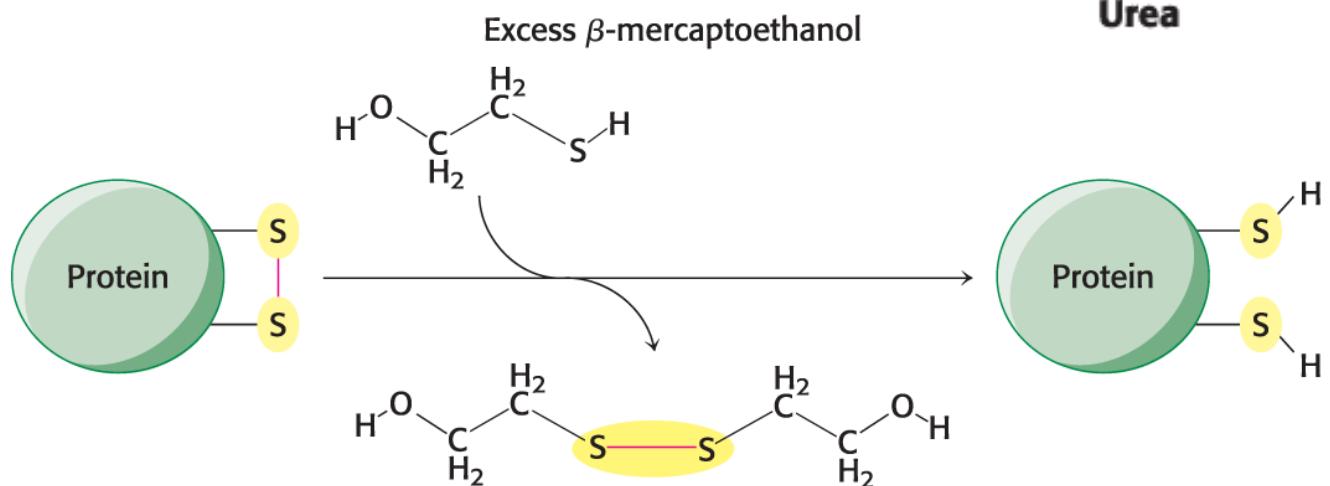
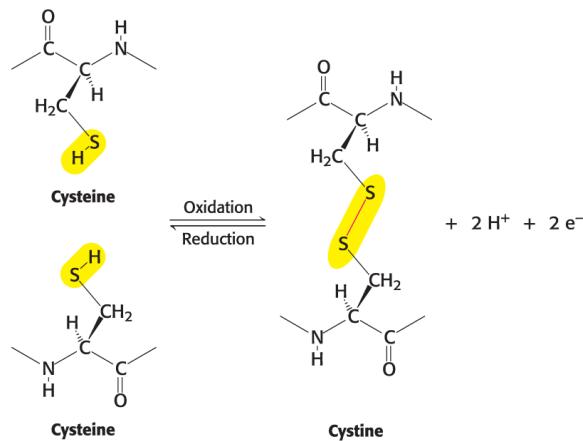
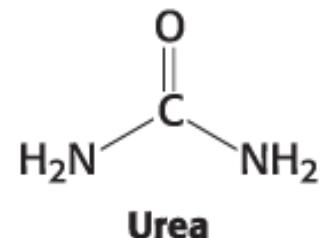
Sequence specifies conformation



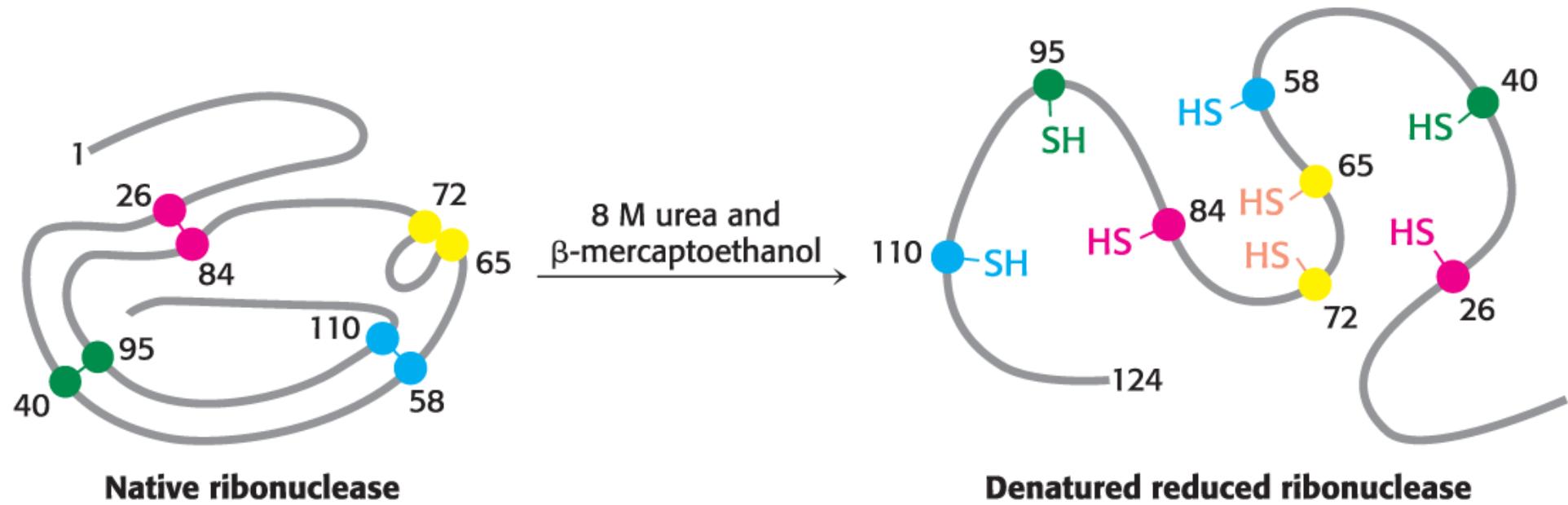
Amino acid sequence of the protein
Ribonuclease (digests RNA)

Colors (pink, green, blue, yellow) show
locations of disulfide bonds/bridges

Experiment:
+ urea
+ β -mercaptoethanol



Sequence specifies conformation... and determines function

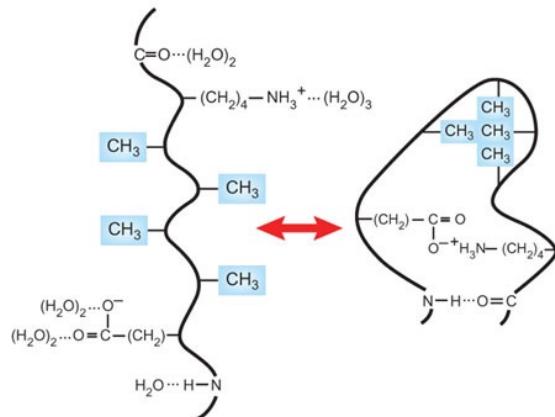


- Christian Anfinsen in 1950s placed the enzyme ribonuclease (degrades RNA) in a solution of urea and β -mercaptoethanol. Urea destroyed all noncovalent bonds, while the β -mercaptoethanol destroyed the disulfide bonds. The enzyme displayed no enzymatic activity and existed only as a random coil. The ribonuclease was **denatured**.

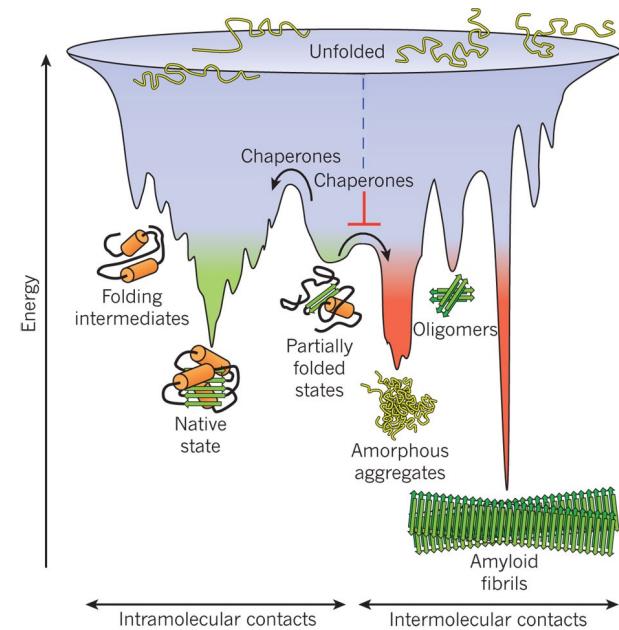
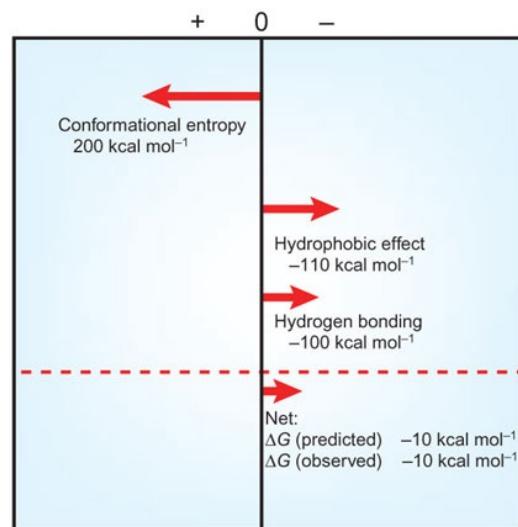
Protein Stabilization Forces

- The largest force governing protein structure is the hydrophobic effect.
- Hydrogen bonding by itself is not a major determinant of protein stability.
- Cross-links help stabilize proteins.
- All the information required for a protein to fold is contained in its amino acid sequence.

a



b



Quick Quiz 4

When a protein is converted in a randomly coiled peptide without its normal activity, it is said to be _____.

- A. oxidized
- B. degraded
- C. denatured
- D. dimerized
- E. None of the above

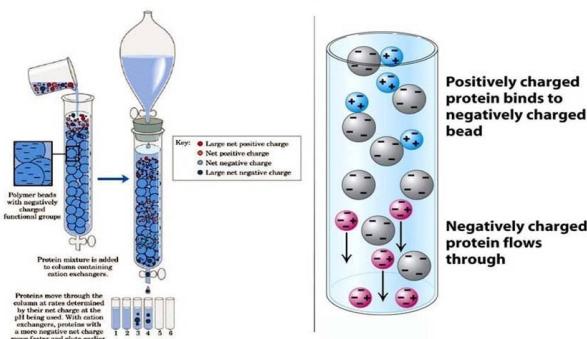
Tools and Techniques: Analyzing Protein Structure

Different tools and techniques could be used to analyze protein structure:

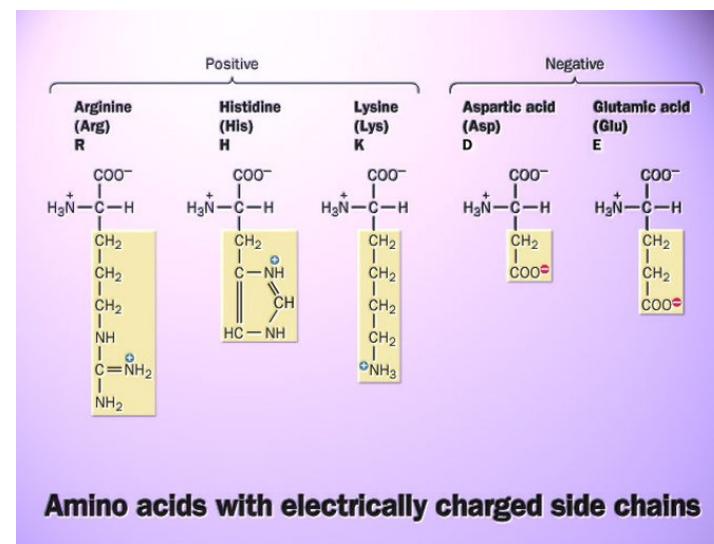
A. Chromatography (size-exclusion, ion exchange, HPLC, etc.)

Proteins or other solutes pass through the column at different rates, depending of how they can interact with stationary phase.

Ion Exchange Chromatography Principle

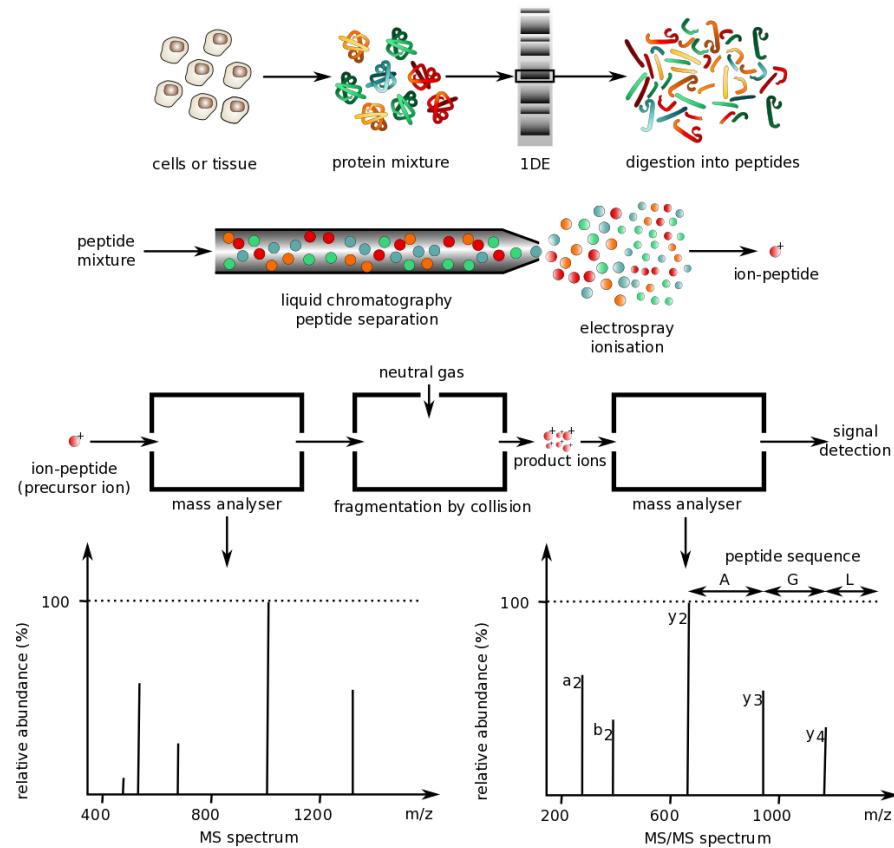


www.technologyinscience.blogspot.com



Tools and Techniques: Analyzing Protein Structure

B. Mass spectrometry reveals amino acid sequences.



Protein Misfolding

- Amyloidoses are diseases that result from the formation of protein aggregates, called amyloid fibrils or plaques.
- Alzheimer disease is an example of an amyloidosis.
- Some infectious neurological diseases are caused by infectious proteins called prions. Prions exist in two states, one α -helix rich (PrP) and the other β -sheet rich (PrP^{SC}).
- PrP^{SC} forms aggregates that disrupt cell function.

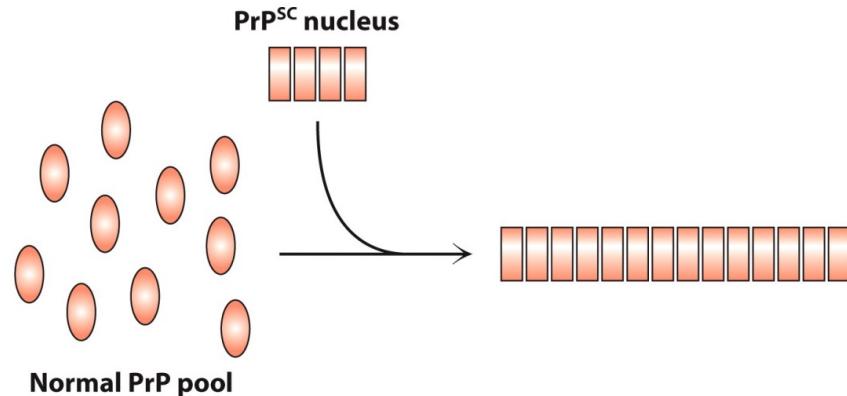
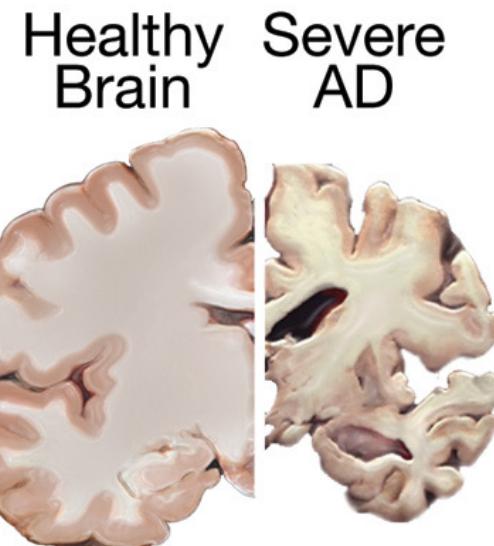


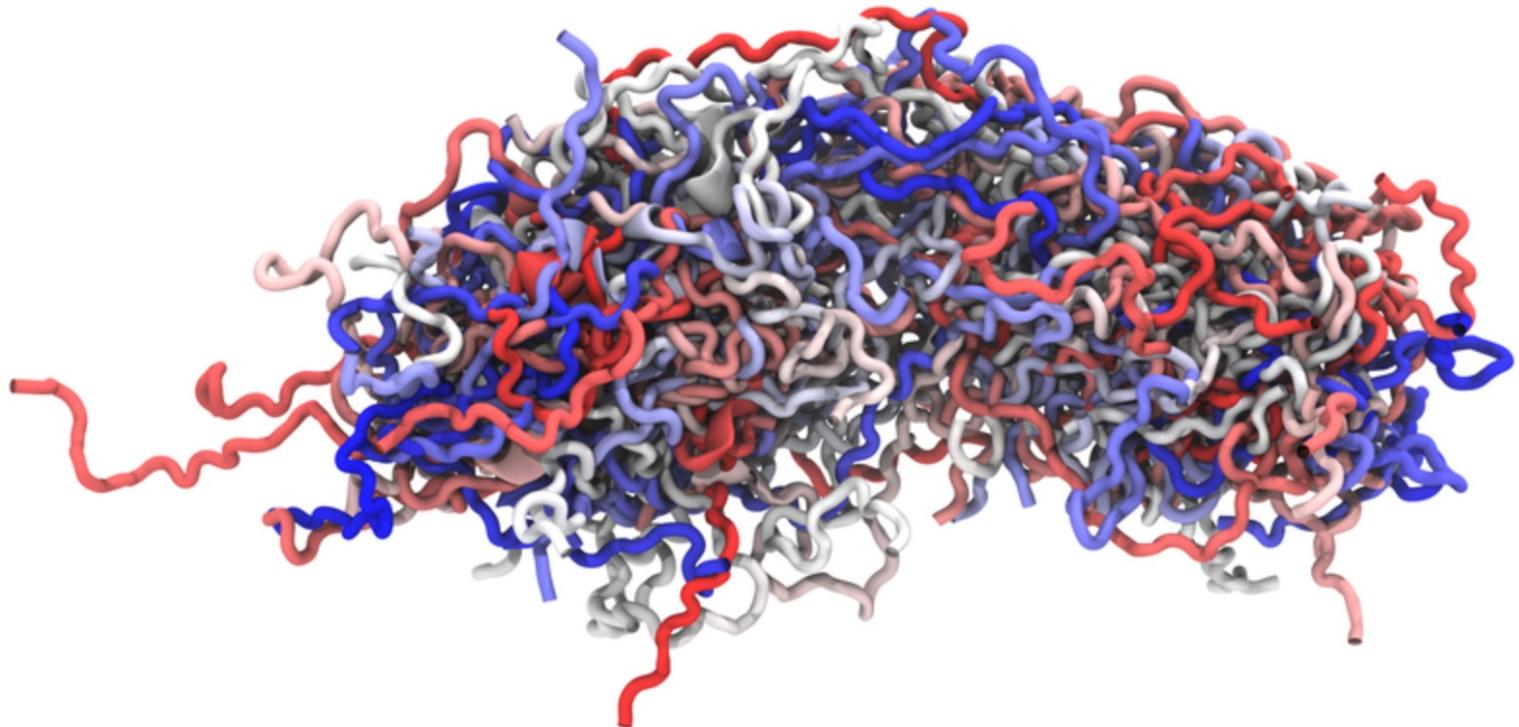
Figure 4.38
Biochemistry: A Short Course, Second Edition
© 2013 W. H. Freeman and Company



Rauscher Lab

Our lab works on problems in computational biophysics with a focus on intrinsically disordered proteins (IDPs). We are located at the Mississauga campus of the University of Toronto.

There are currently openings in the group for graduate and undergraduate students. If you are interested, please send an email including your CV/resume and transcript to sarah.rauscher@utoronto.ca.



The Grdinaru Lab

Single-Molecule Biophysics Research



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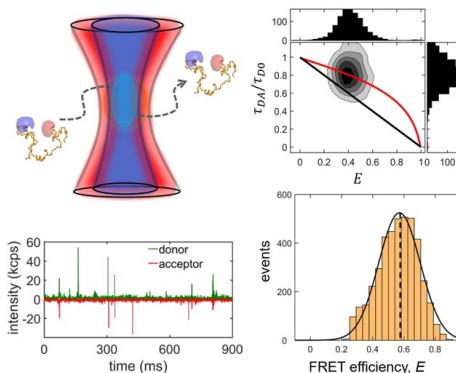
Intrinsically Disordered Proteins (IDPs): Conformational Dynamics and Interactions

G Protein Coupled Receptors (GPCRs): Implications of Dynamics and Oligomerization for Cellular Signalling

Ensemble Descriptions of Disordered Proteins: Integrating Experiments and Computations

Intrinsically Disordered Proteins (IDPs): Conformational Dynamics and Interactions

Unlike the funnel-shaped landscape of globular proteins, IDPs have a rather shallow but rugged energy landscape, with many local minima separated by small barriers. They interact, often tightly and specifically, with several partners in so-called "hubs", but the physics of this process (kinetics, energetics, molecular forces) is underdetermined. Around 65% of the signaling and 75% of the cancer-associated proteins are predicted to have disordered regions, thus implying an important role for IDPs in mediating regulatory interactions in biological processes.



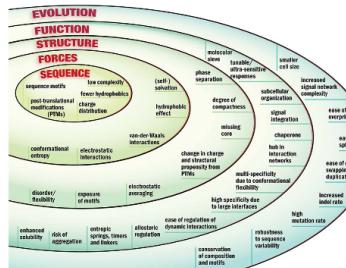
We study two IDP systems: Sic1, a kinase inhibitor in the yeast the cell cycle, and 4E-BP2, a translation inhibitor involved in regulating synaptic plasticity. Sic1 forms a dynamic "fuzzy" complex with the WD40 domain of the Cdc4 protein, where the binding affinity shows an intriguing non-linear dependence on the number of phosphate groups on Sic1. 4E-BP2 acts like a regulatory switch: in the non-phosphorylated state is disordered and bound to the initiation factor eIF4E, whereas in the phosphorylated state it partially folds and detaches, allowing another protein to dock on eIF4E and initiate translation. We use single-molecule fluorescence spectroscopy to study these two IDP complexes, to understand how "binding without folding" occurs in biology.

G Protein Coupled Receptors (GPCRs): Implications of Dynamics and Oligomerization for Cellular Signalling

Lab of Dr. Julie D. Forman-Kay

Molecular Medicine Program
SickKids Research Institute

Roles of protein dynamics, disorder and large-scale association in biological function



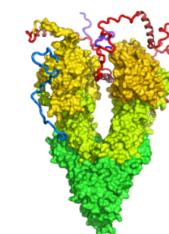
protein activation.

Intrinsically disordered proteins are critical for mediating regulatory protein interactions. However, structural studies of these highly dynamic proteins lag far behind studies of folded proteins. The major focus of my lab has been to provide insights into how dynamic properties of proteins are related to biological function and methodological tools to enable better understanding of dynamic and disordered states. We work on a number of projects of relevance to cystic fibrosis, cancer and neurobiology. My group has a strong interest in CFTR, the cystic fibrosis transmembrane conductance regulator, particularly its cytoplasmic domains including the disordered regulatory R region. Effects of phosphorylation and other post-translational modification on structural and binding properties of this and other disordered regions are a significant interest. Most recently my lab has started to explore the phase separation of disordered proteins in cellular organization and plasma membrane

Dynamic Complexes

Disordered proteins often bind targets in highly dynamic complexes. We demonstrated that the disordered Sic1 cyclin dependent kinase inhibitor binds to the Cdc4 component of an SCF ubiquitin ligase complex in a dynamic complex with multiple phosphorylation sites of Sic1 exchanging on and off of the Cdc4 binding site [Mittag et al (2008), PNAS; Tang et al (2012), PNAS; Csizmok et al (2017), Nat Commun] and have calculated models of the free Sic1 and its dynamic complex with Cdc4, shedding insight into the ultrasensitive ubiquitination of Sic1 within the SCF ligase [Mittag et al (2010), Structure]. We characterized Abp SH3 domain complexes involved in actin organization and correlated the degree of engagement within the dynamic complexes with functional data [Stollar et al (2009), J Biol Chem; Stollar et al (2012), PLoS One]. We demonstrated a dynamic interaction of 4E-BP2 that is key for translational regulation [Lukhele et al (2013), Structure].

Importantly, we showed that phosphorylation induces folding of 40 residues of 4E-BP2 to a 4E-binding-incompatible state [Bah et al (2015), Nature], the first time significant folding of an IDP due to post-translational modification has been reported. We have also characterized the phase separation of the

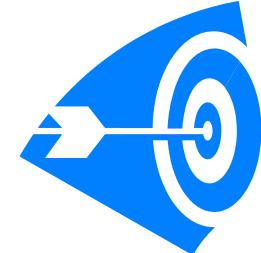


Think → Pair → Share

1. Discuss which features of the amino acids make them particularly useful for generating many protein structures.
2. For an amino acid such as alanine, the major species in solution at pH 7 is the zwitterionic form. Assume a pKa value of 8 for the amino group and a pKa value of 3 for the carboxylic acid.

Estimate the ratio of the concentration of the neutral amino acid species (with the carboxylic acid protonated and the amino group neutral) to that of the zwitterionic species at pH 7.

Assigned Problems



Chapter	Tymochko, Berg, Stryer, Biochemistry, 2 nd Edition,	Chapter	Tymochko, Berg, Stryer, Biochemistry, 2 nd Edition,
3	1, 3, 4, 6, 7, 11, 15	4	2, 3, 6, 7, 9, 15, 16, 18, 21, 24, 26, 32, 33
Chapter	Tymochko, Berg, Stryer, Biochemistry, 3 rd and 4 th Edition, respectively	Chapter	Tymochko, Berg, Stryer, Biochemistry, 3 rd and 4 th Edition, respectively
3	1, 4, 5, 7, 8, 12, 17	4	2, 3, 6, 7, 10, 16, 17, 19, 22, 25, 26, 34, 35
3	5, 8, 9, 11, 12, 16, 21	4	6, 7, 10, 11, 14, 20, 21, 23, 26, 29, 30, 38, 39