



جامعة المستقبل  
AL MUSTAQBAL UNIVERSITY

كلية العلوم  
قسم الأدلة الجنائية

المحاضرة الثانية

The Structure and  
Functions of Proteins

المادة : علم الخلية  
المرحلة : الأولى  
اسم الاستاذ: م.م هويدا نزال حسين

---

# The Structure and Functions of Proteins

# The many functions of proteins

---

- Mechanoenzymes: myosin, actin
- Rhodopsin: allows vision
- Globins: transport oxygen
- Antibodies: immune system
- Enzymes: pepsin, renin, carboxypeptidase A
- Receptors: transmit messages through membranes
- Vitelogenin: molecular velcro
  - And hundreds of thousands more...

# Complex Chemistry Tutorial

---

- Molecules are made of atoms!
- There is a lot of hydrogen out there!
  - Atoms make a “preferred” number of *covalent* (strong) bonds
    - C – 4
    - N – 3
    - O, S – 2
- Atoms will generally “pick up” enough hydrogens to “*fill their valence capacity*” *in vivo*.
- Molecules also “prefer” to have a neutral charge

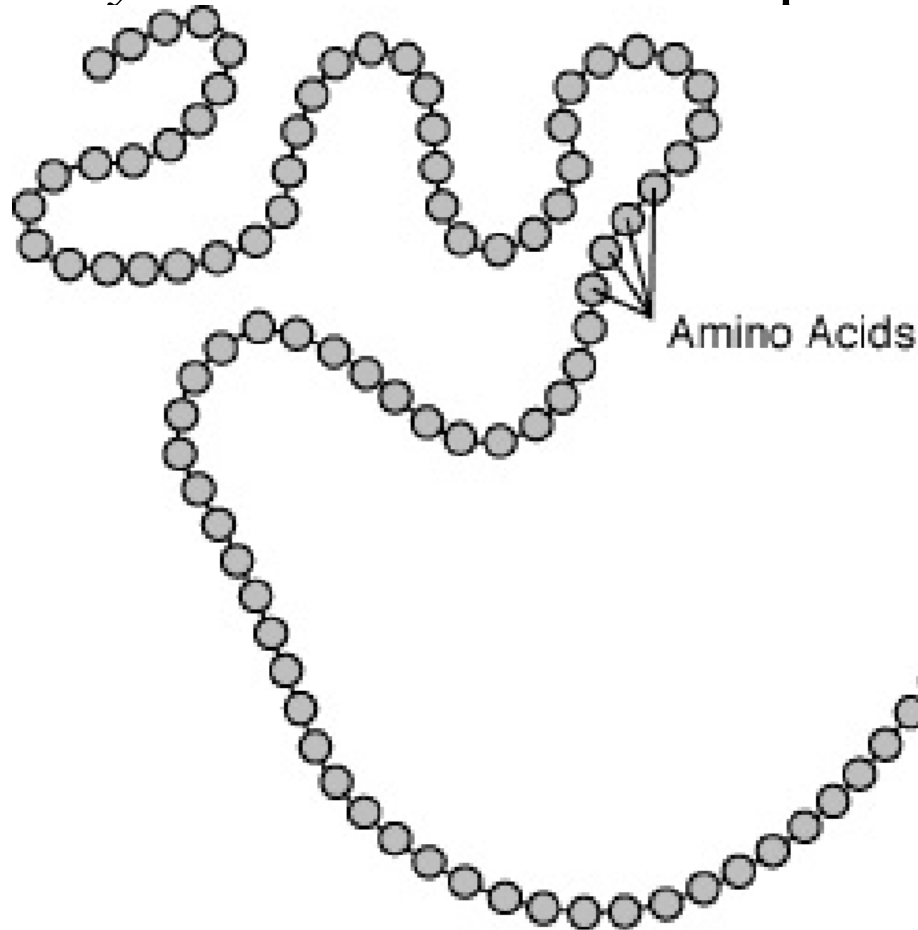
# Biochemistry

---

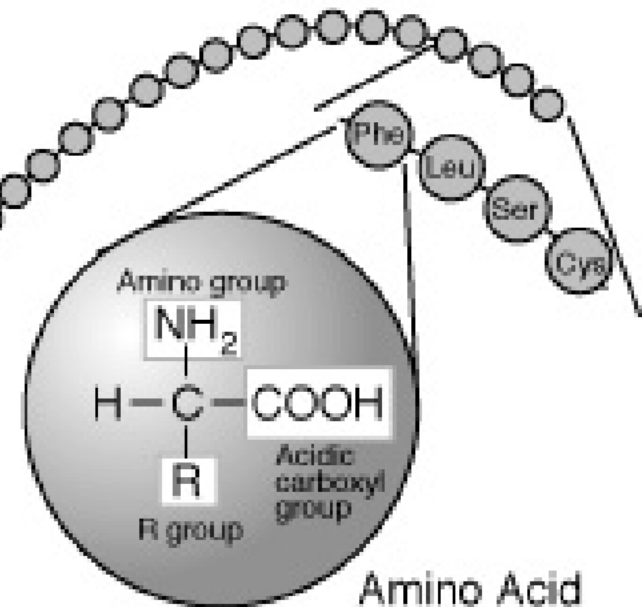
- In the context of a protein...
  - Oxygen tends to exhibit a slight negative charge
  - Nitrogen tends to exhibit a slight positive charge
  - Carbon tends to remain neutral/uncharged
- Atoms can “share” a hydrogen atom, each making “part” of a covalent bond with the hydrogen
  - Oxygen: H-Bond donor or acceptor
  - Nitrogen: H-Bond donor
  - Carbon: Neither

# Proteins are chains of amino acids

- *Polymer* – a molecule composed of repeating units



Primary protein structure  
is sequence of a chain of amino acids



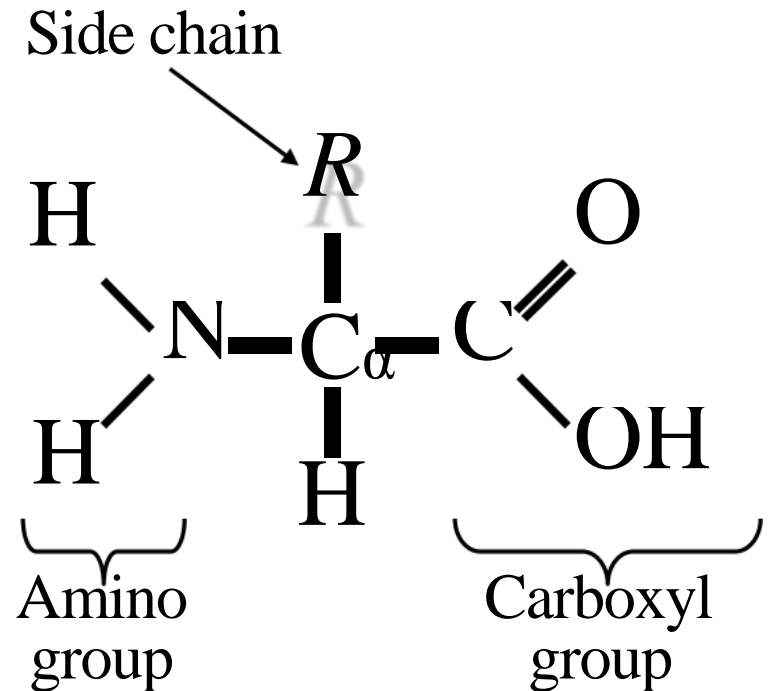
# Amino acid composition

---

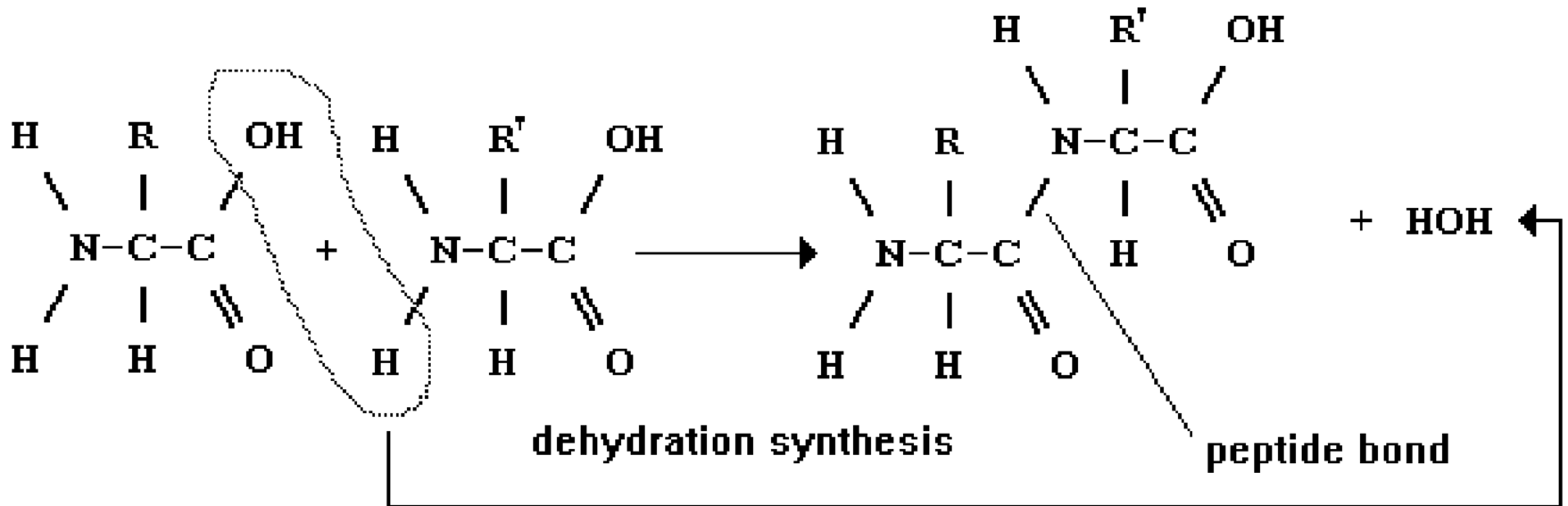
- Basic Amino Acid

Structure:

- The side chain, R, varies for each of the 20 amino acids



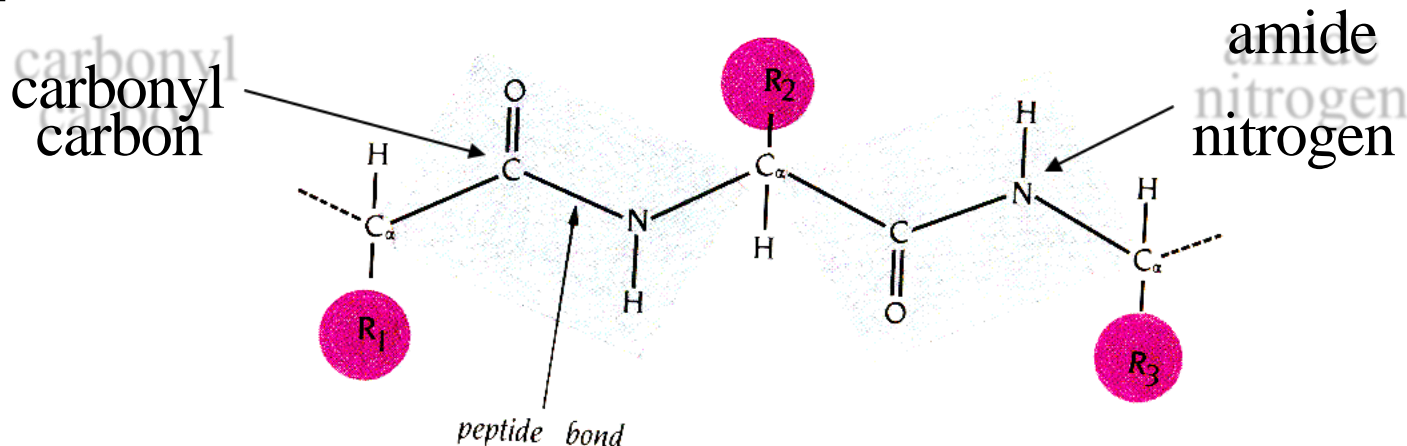
# The Peptide Bond



- Dehydration synthesis
- Repeating backbone:  $\text{N}-\text{C}_\alpha-\text{C}(=\text{O})-\text{N}-\text{C}_\alpha-\text{C}(=\text{O})$
- Convention – start at *amino terminus* and proceed to *carboxy terminus*

# Peptidyl polymers

- A few amino acids in a chain are called a *polypeptide*. A *protein* is usually composed of 50 to 400+ amino acids.
- Since part of the amino acid is lost during dehydration synthesis, we call the units of a protein *amino acid residues*.

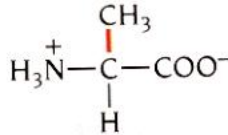


# Side chain properties

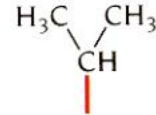
---

- Recall that the electronegativity of carbon is at about the middle of the scale for light elements
  - Carbon does not make hydrogen bonds with water easily – *hydrophobic*
  - O and N are generally more likely than C to h-bond to water – *hydrophilic*
- We group the amino acids into three general groups:
  - Hydrophobic
  - Charged (positive/basic & negative/acidic)
  - Polar

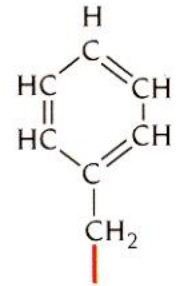
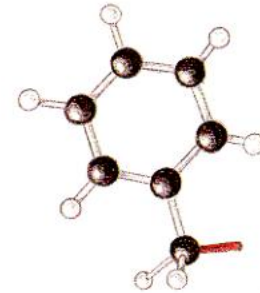
# The Hydrophobic Amino Acids



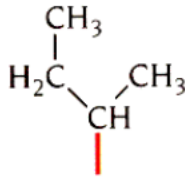
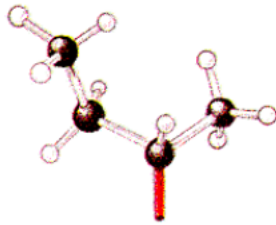
**A** Ala, Alanine



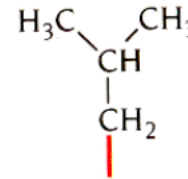
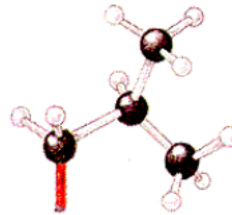
**V** Val, Valine



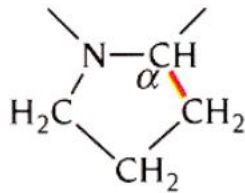
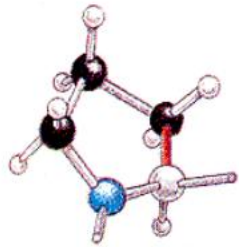
**F** Phe, Phenylalanine



**I** Ile, Isoleucine



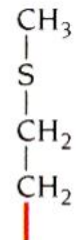
**L** Leu, Leucine



Proline severely  
limits allowable  
conformations!

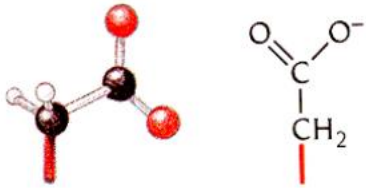
**P** Pro, Proline

Protein Structure and Function

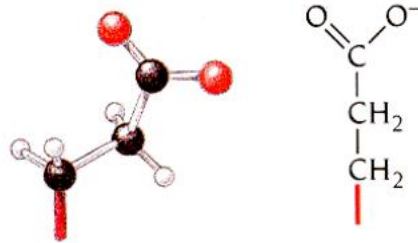


**M** Met, Methionine

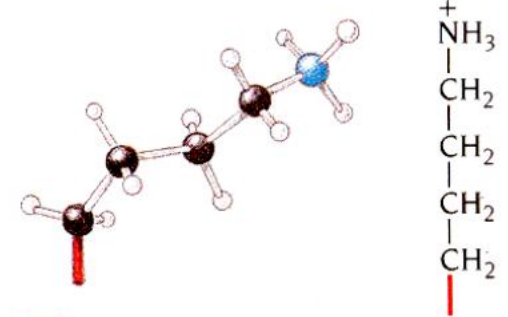
# The Charged Amino Acids



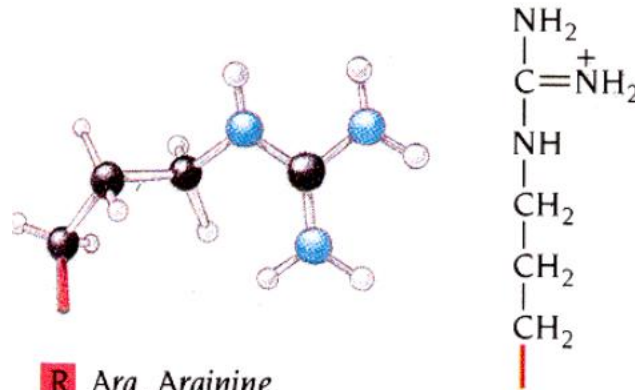
**D** Asp, Aspartic acid



**E** Glu, Glutamic acid

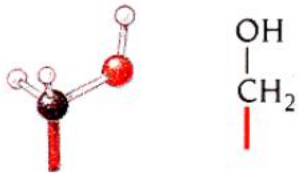


**K** Lys, Lysine

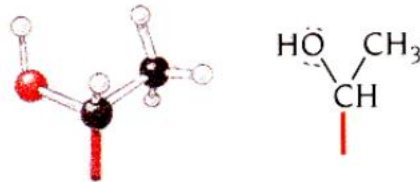


**R** Arg, Arginine

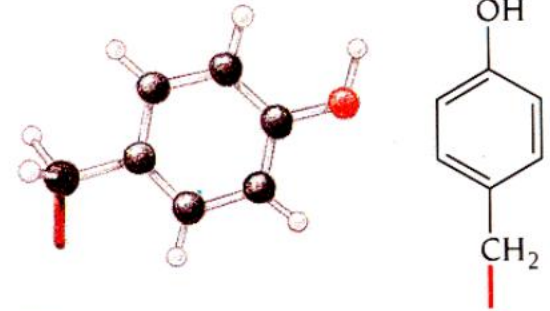
# The Polar Amino Acids



**S** Ser, Serine



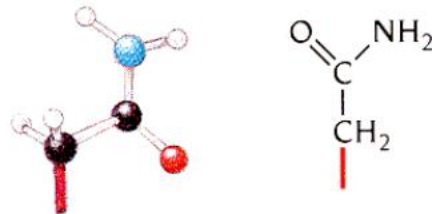
**T** Thr, Threonine



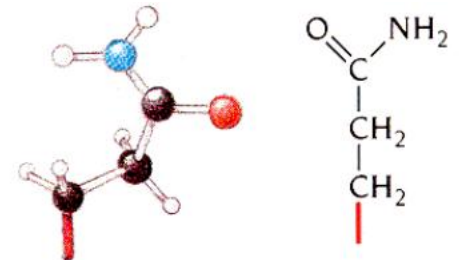
**Y** Tyr, Tyrosine



**C** Cys, Cysteine



**N** Asn, Asparagine

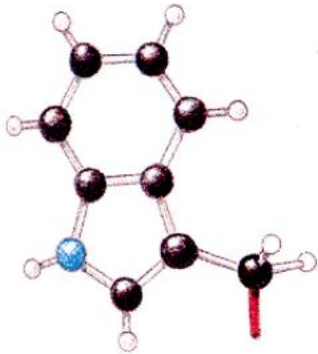
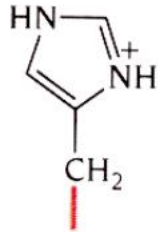


**Q** Gln, Glutamine

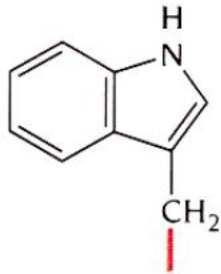
# More Polar Amino Acids



**H** His, Histidine



**W** Trp, Tryptophan

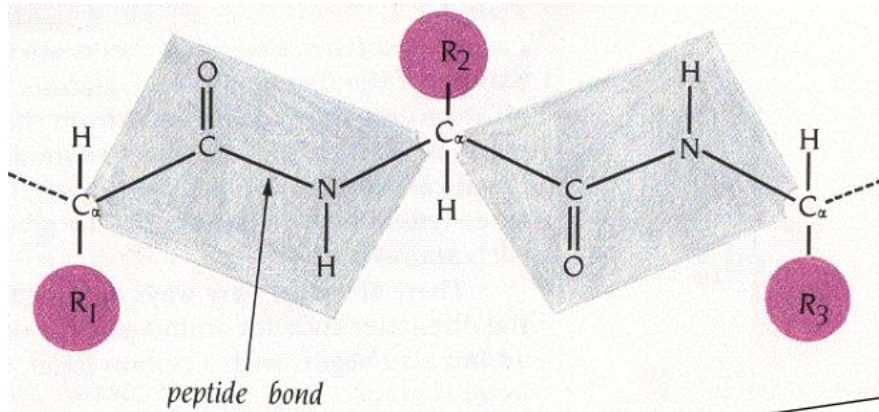


And then there's...



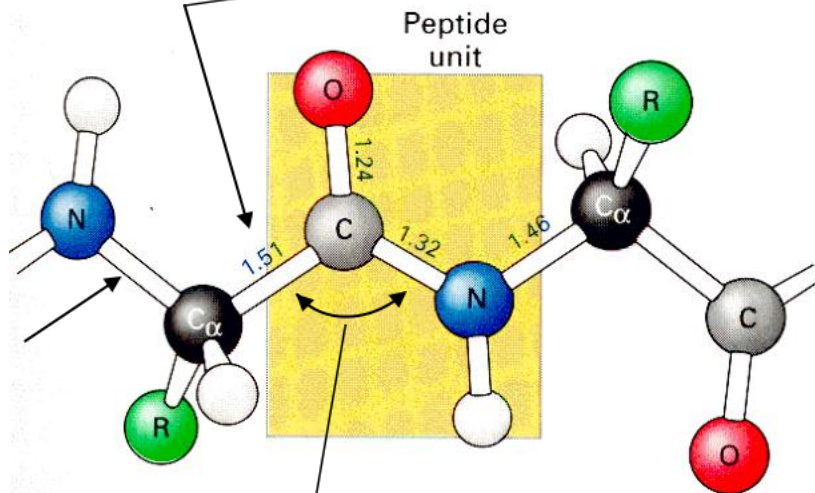
**G** Gly, Glycine

# Planarity of the peptide bond

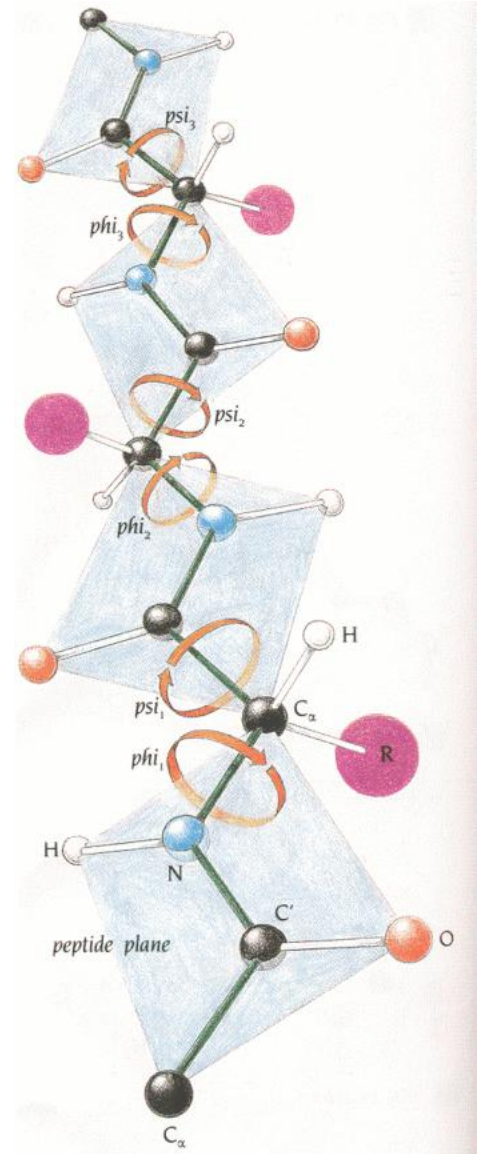


Psi ( $\psi$ ) – the angle of rotation about the  $C\alpha$ -C bond.

Phi ( $\phi$ ) – the angle of rotation about the N- $C\alpha$  bond.

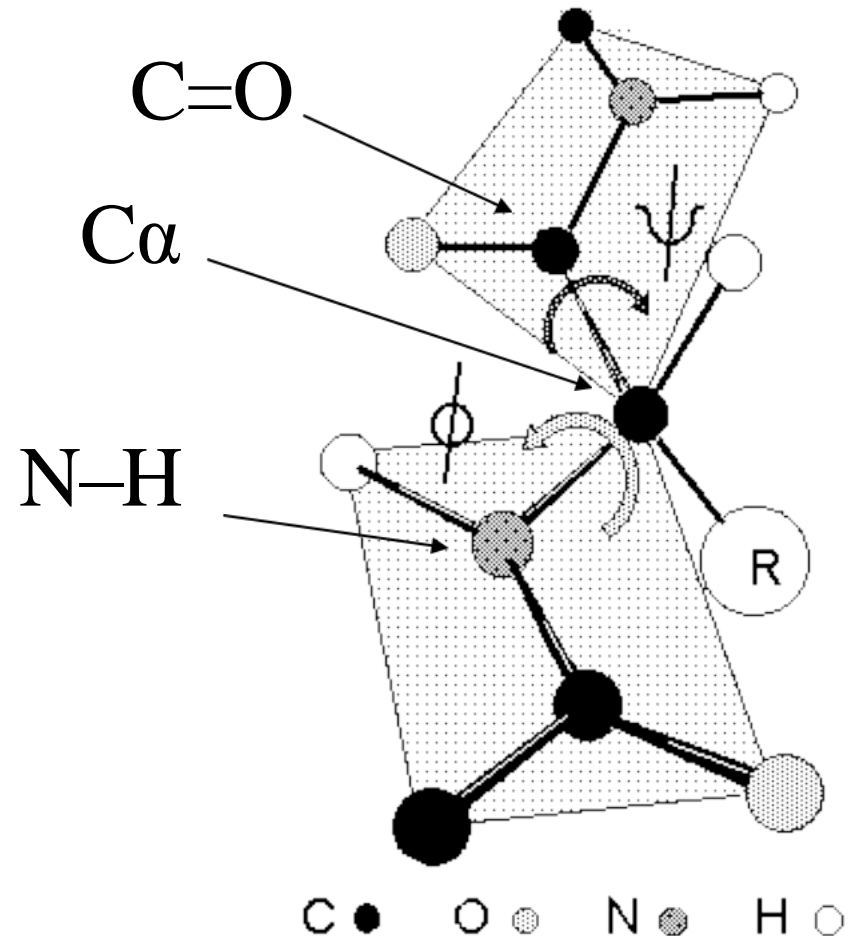


The planar bond angles and bond lengths are fixed.

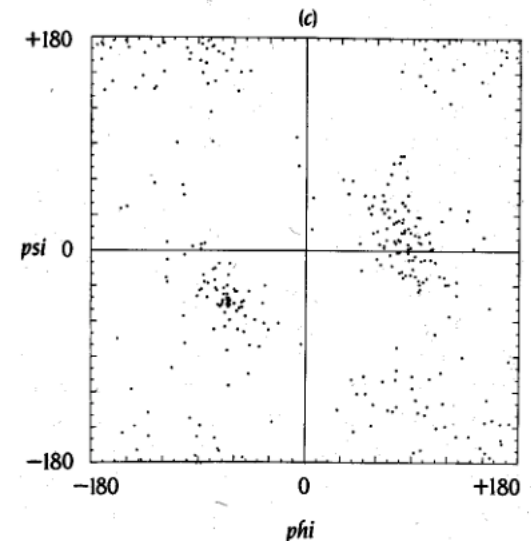
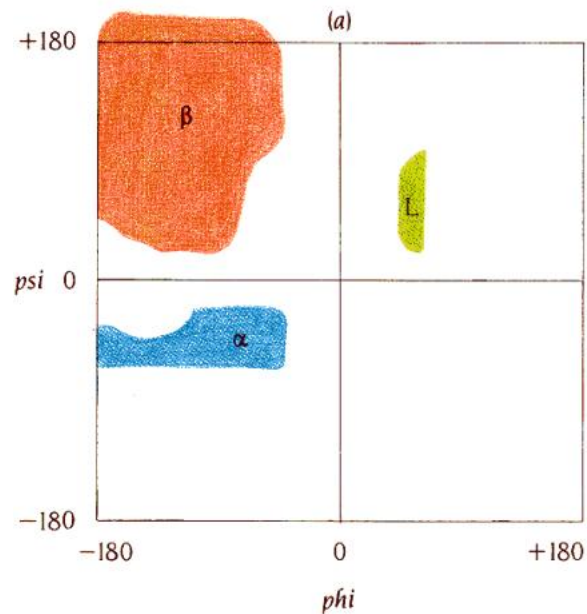
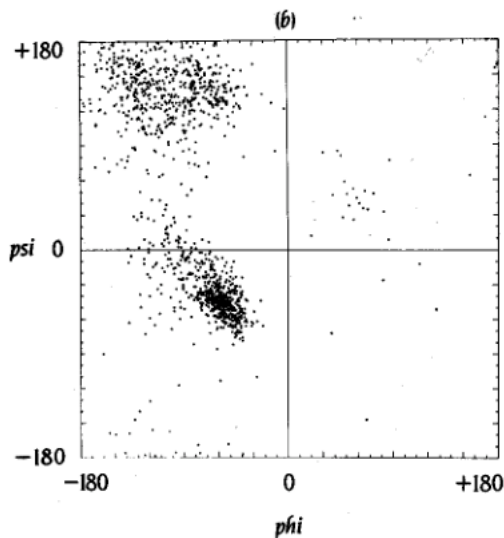


# Phi and psi

- $\phi = \psi = 180^\circ$  is extended conformation
- $\phi$  : C $\alpha$  to N-H
- $\psi$  : C=O to C $\alpha$



# The Ramachandran Plot



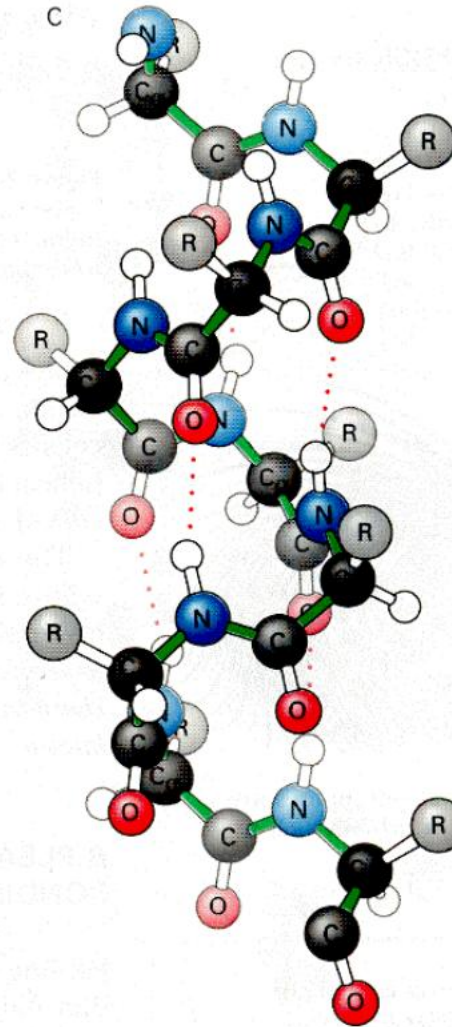
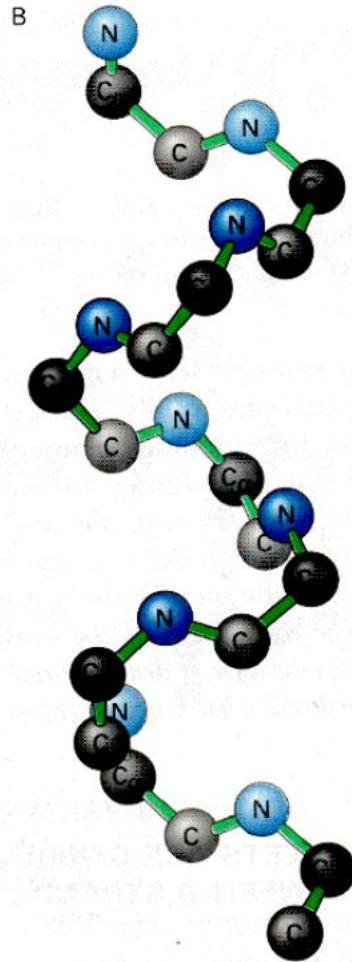
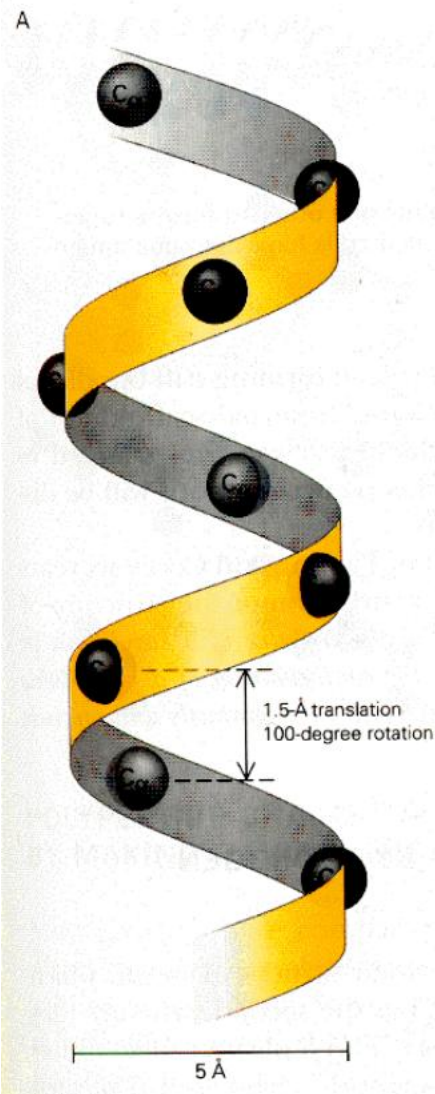
- G. N. Ramachandran – first calculations of *sterically* allowed regions of phi and psi
- Note the structural importance of glycine

# Primary & Secondary Structure

---

- Primary structure = the linear *sequence* of amino acids comprising a protein:  
**AGVGTVPMTAYGNDIQYYGQVT...**
- Secondary structure
  - Regular patterns of hydrogen bonding in proteins result in two patterns that emerge in nearly every protein structure known: the  $\alpha$ -*helix* and the  $\beta$ -*sheet*
  - The location of direction of these periodic, repeating structures is known as the *secondary structure* of the protein

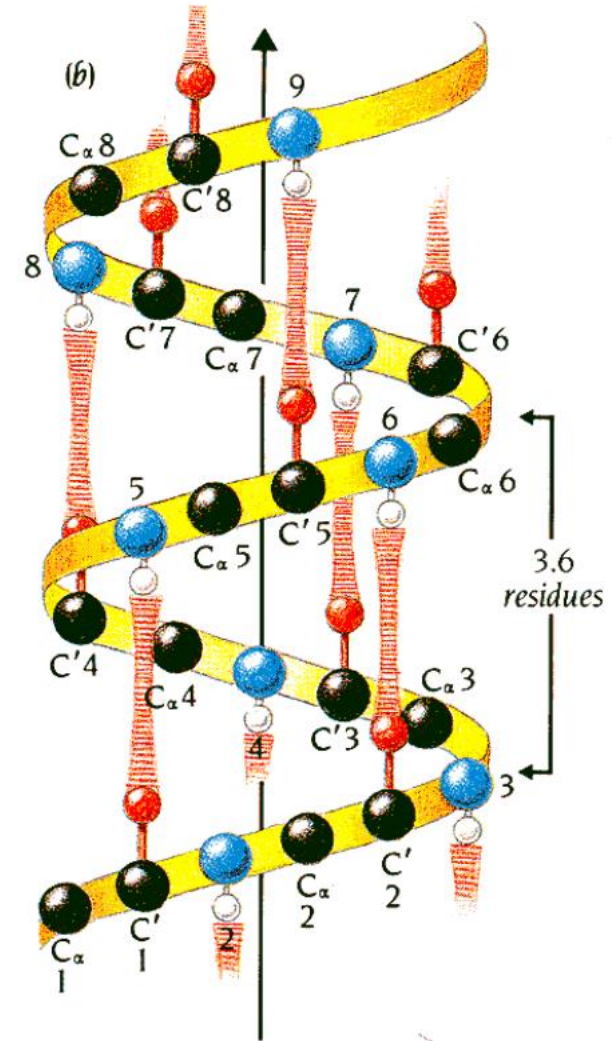
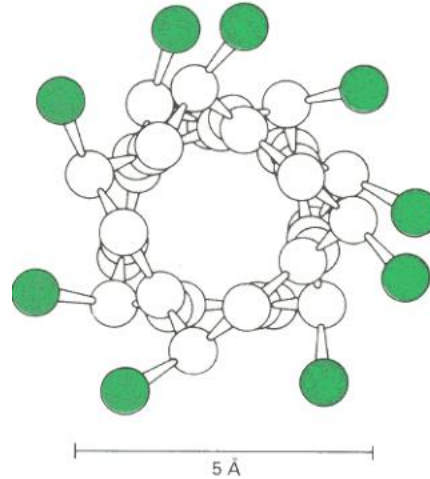
# The alpha helix



$$\begin{aligned}\phi &\approx \psi \\ &\approx -60^\circ\end{aligned}$$

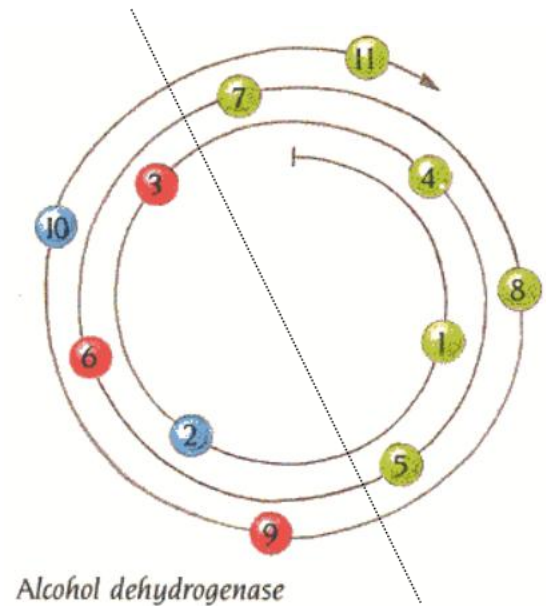
# Properties of the alpha helix

- $\phi \approx \psi \approx -60^\circ$
- Hydrogen bonds between C=O of residue  $n$ , and NH of residue  $n+4$
- 3.6 residues/turn
- 1.5 Å/residue rise
- $100^\circ$ /residue turn



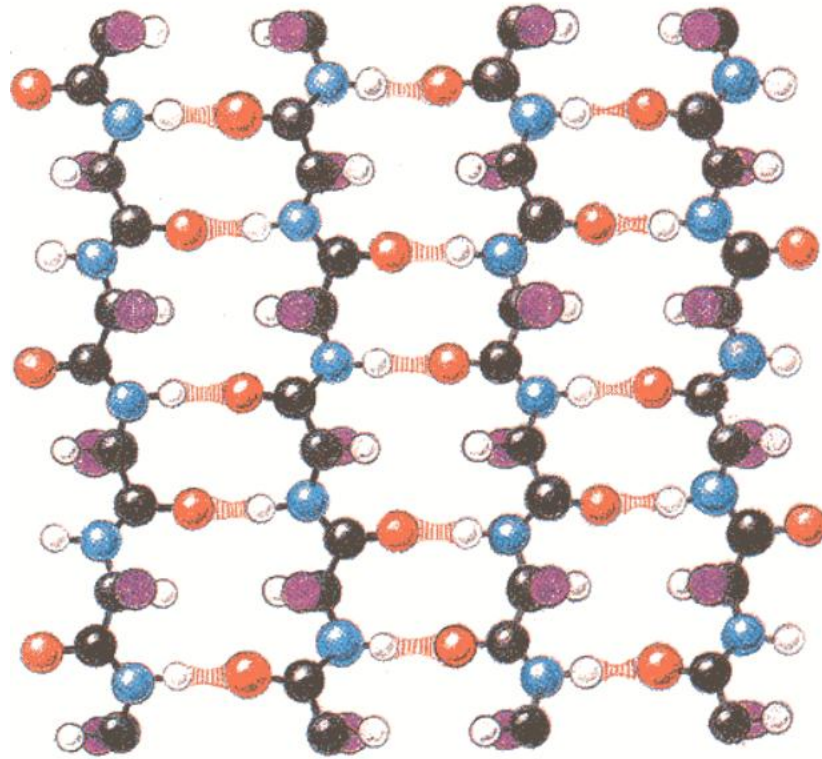
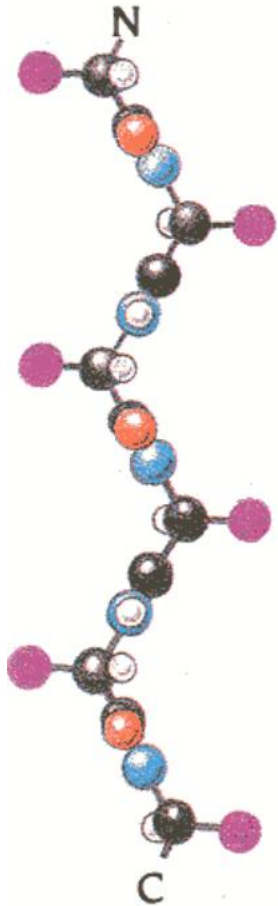
# Properties of $\alpha$ -helices

- 4 – 40+ residues in length
- Often *amphipathic* or “dual-natured”
  - Half hydrophobic and half hydrophilic
  - Mostly when surface-exposed
- If we examine many  $\alpha$ -helices, we find trends...
  - Helix formers: Ala, Glu, Leu, Met
  - Helix breakers: Pro, Gly, Tyr, Ser



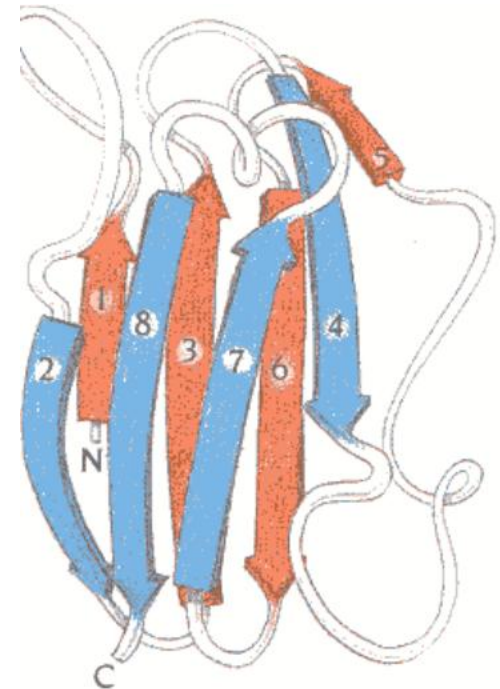
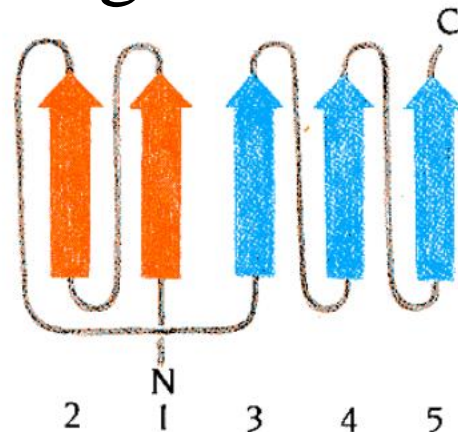
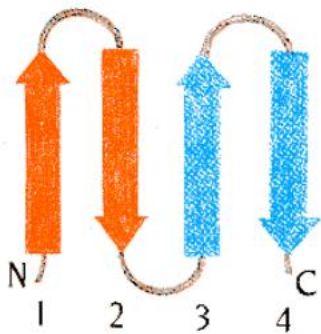
# The beta strand (& sheet)

$$\varphi \approx -135^\circ$$
$$\psi \approx +135^\circ$$



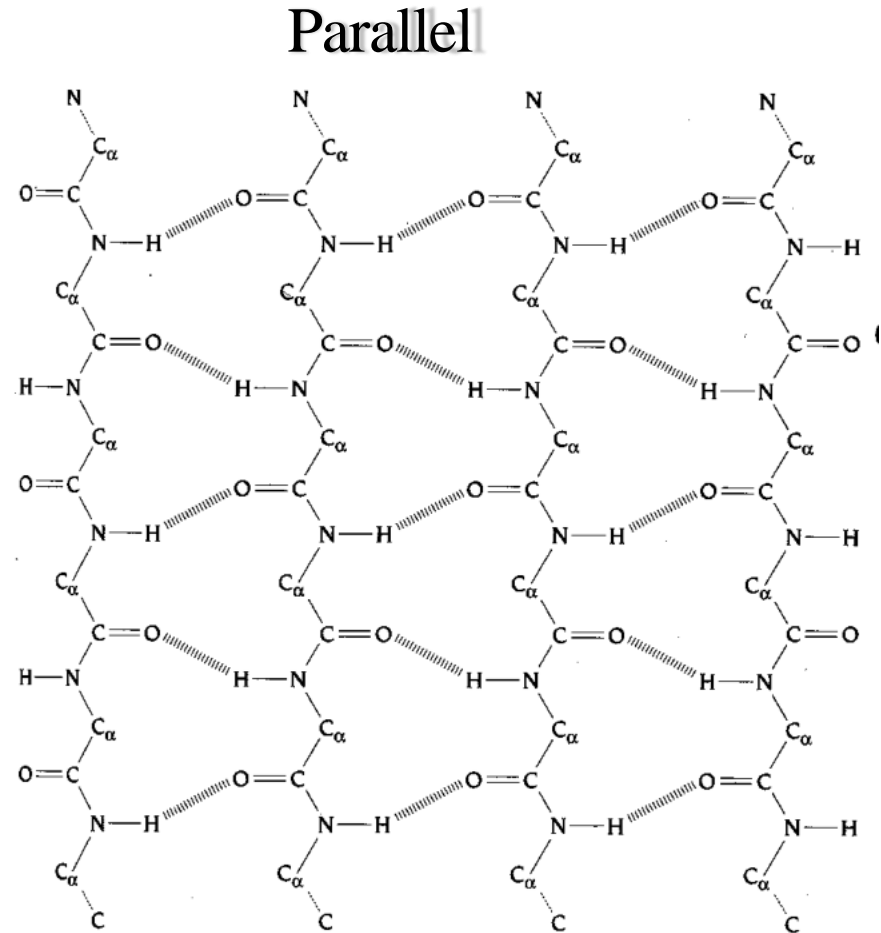
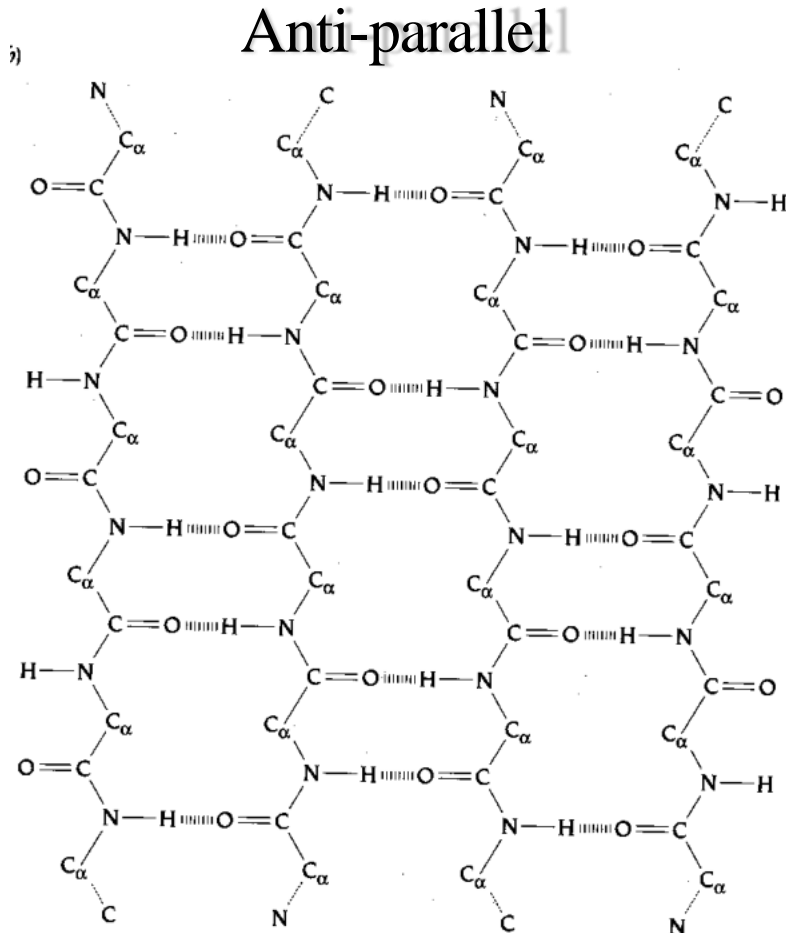
# Properties of beta sheets

- Formed of stretches of 5-10 residues in extended conformation
- *Pleated* – each C $\alpha$  a bit above or below the previous
- *Parallel/aniparallel*,  
contiguous/non-contiguous



# Parallel and anti-parallel $\beta$ -sheets

- Anti-parallel is slightly energetically favored



# Turns and Loops

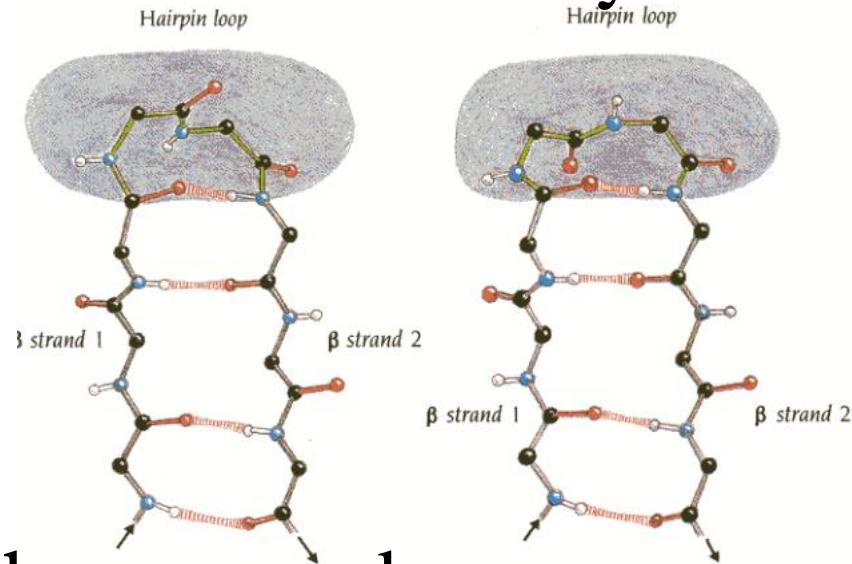
- Secondary structure elements are connected by regions of *turns* and *loops*

- Turns – short regions of non- $\alpha$ , non- $\beta$  conformation

- Loops – larger stretches with no secondary structure. Often disordered.

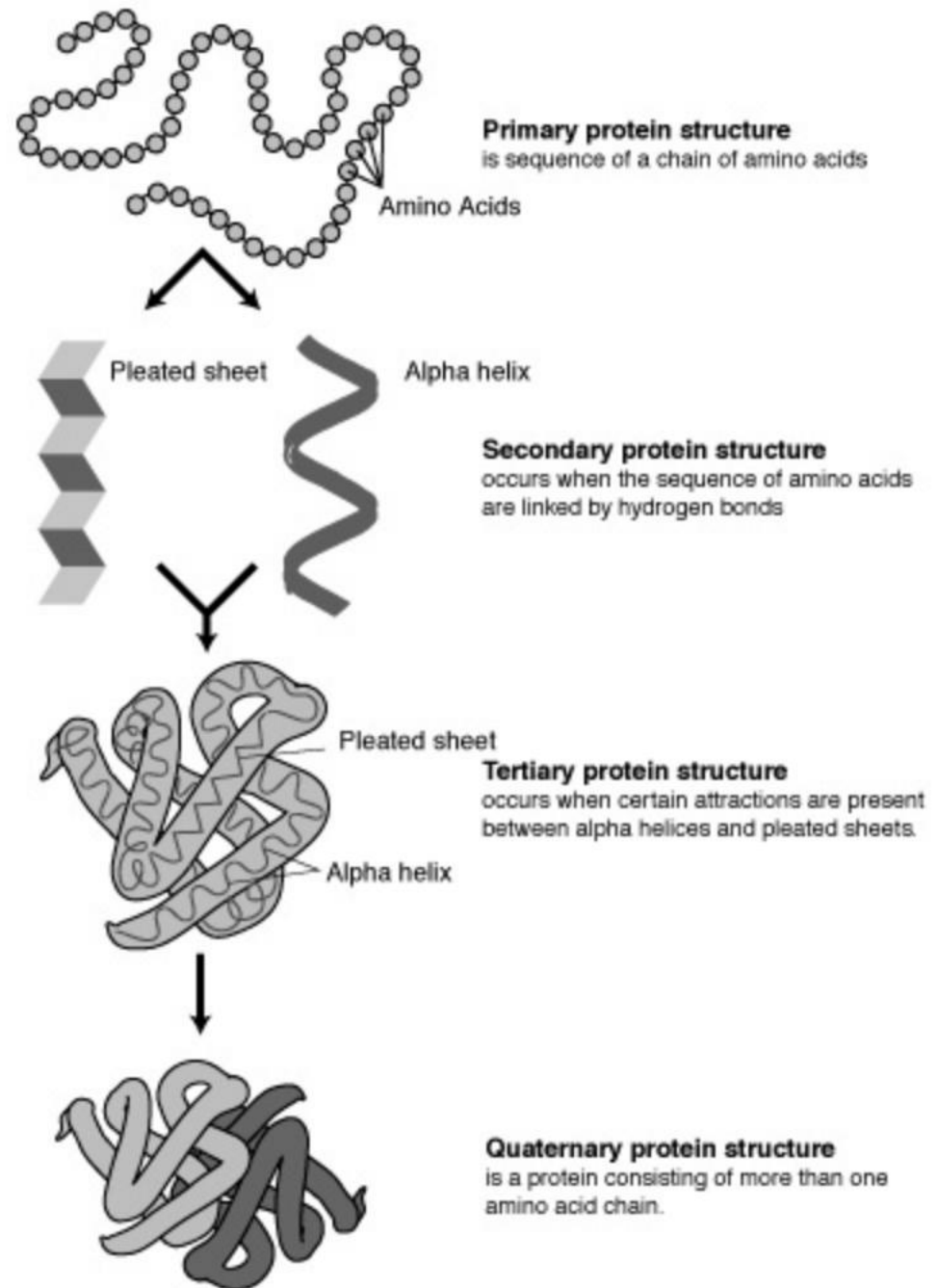
- “Random coil”

- Sequences vary much more than secondary structure regions

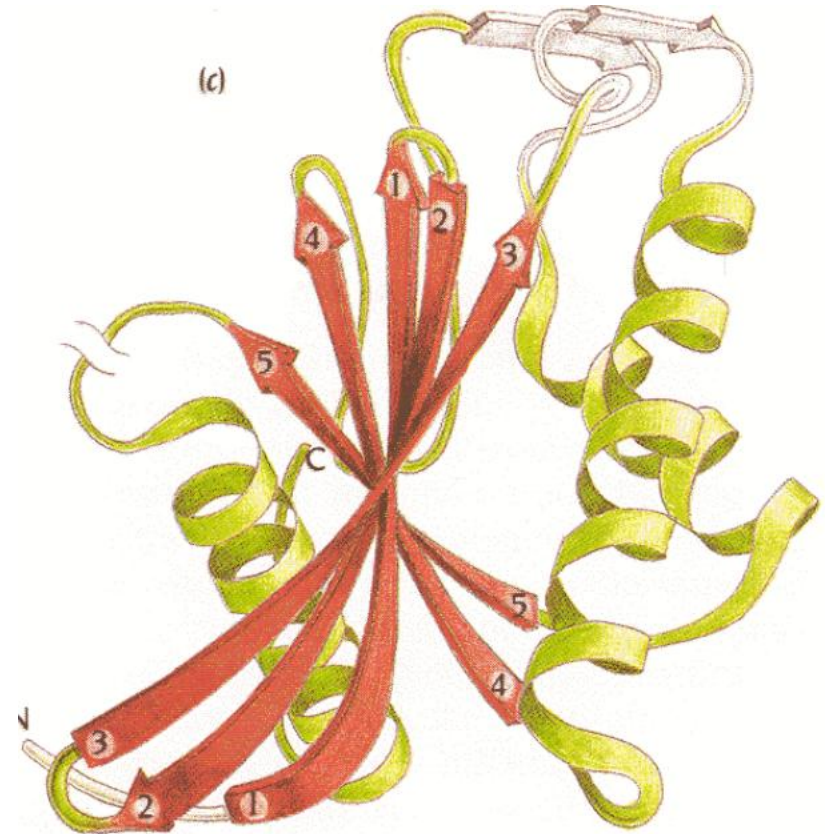
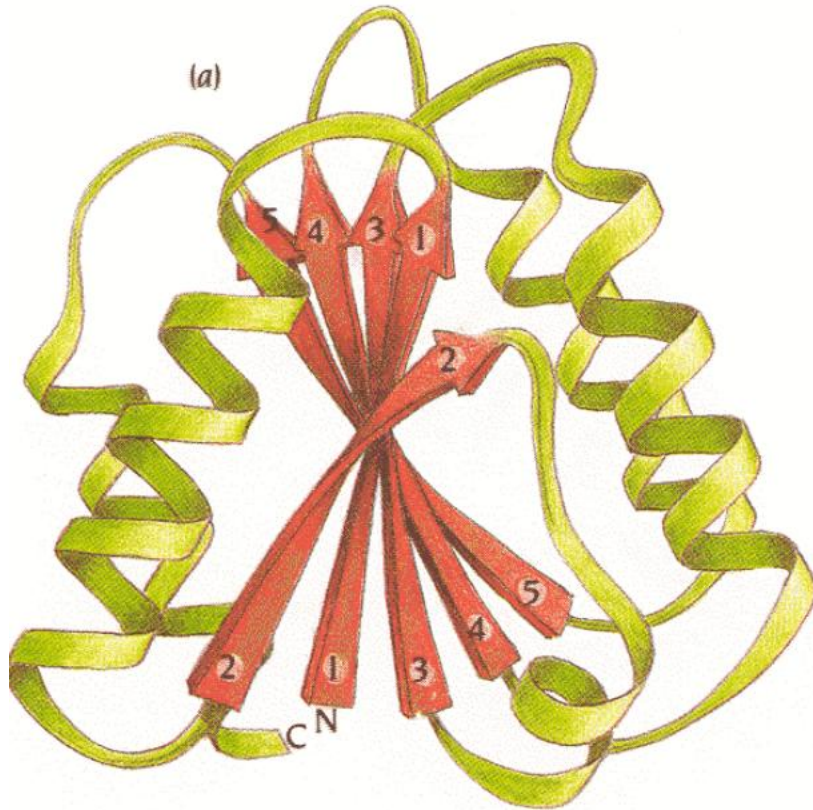


# Levels of Protein Structure

- Secondary structure elements combine to form tertiary structure
- Quaternary structure occurs in multienzyme complexes
  - Many proteins are active only as homodimers, homotetramers, etc.



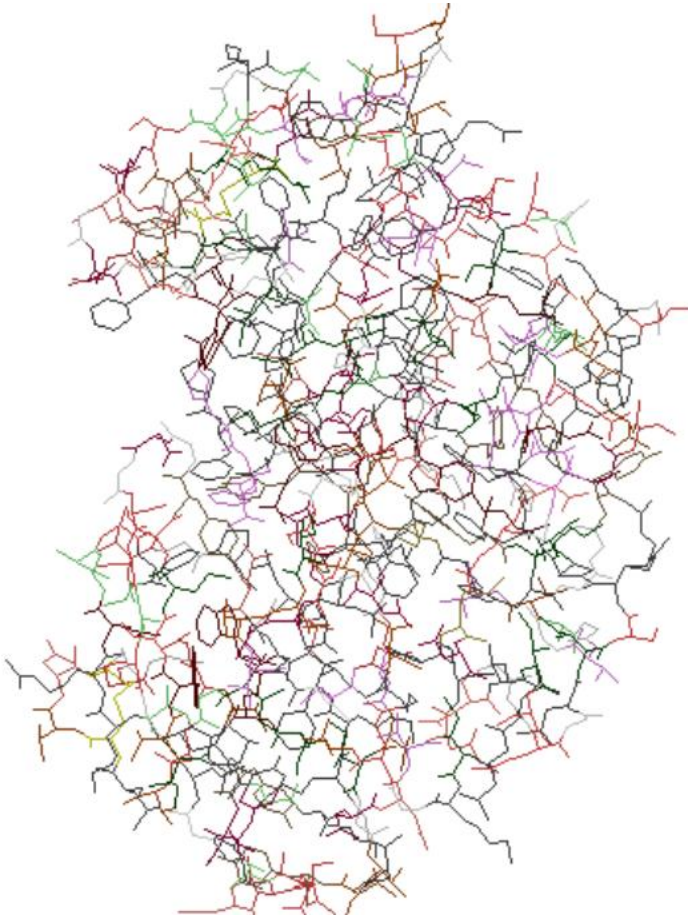
# Protein Structure Examples



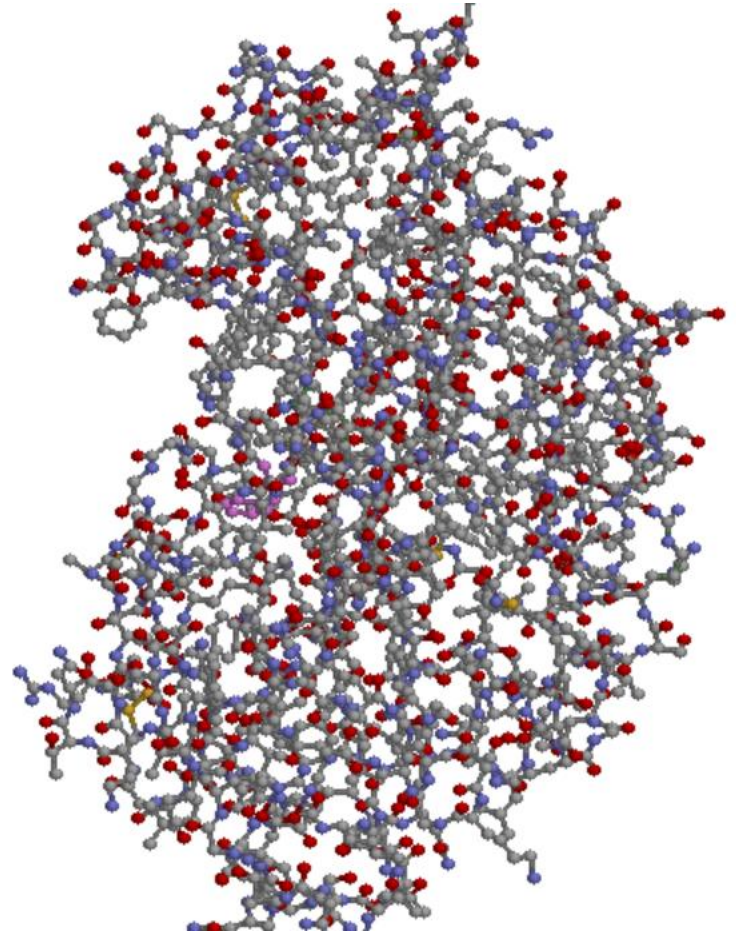
# Views of a protein

---

Wireframe



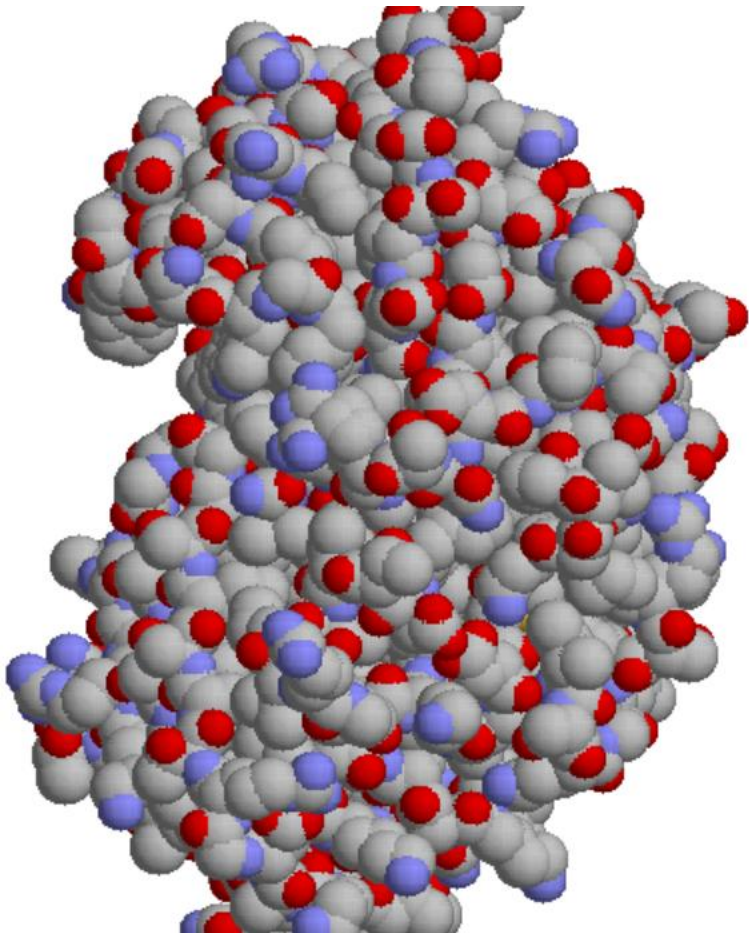
Ball and stick



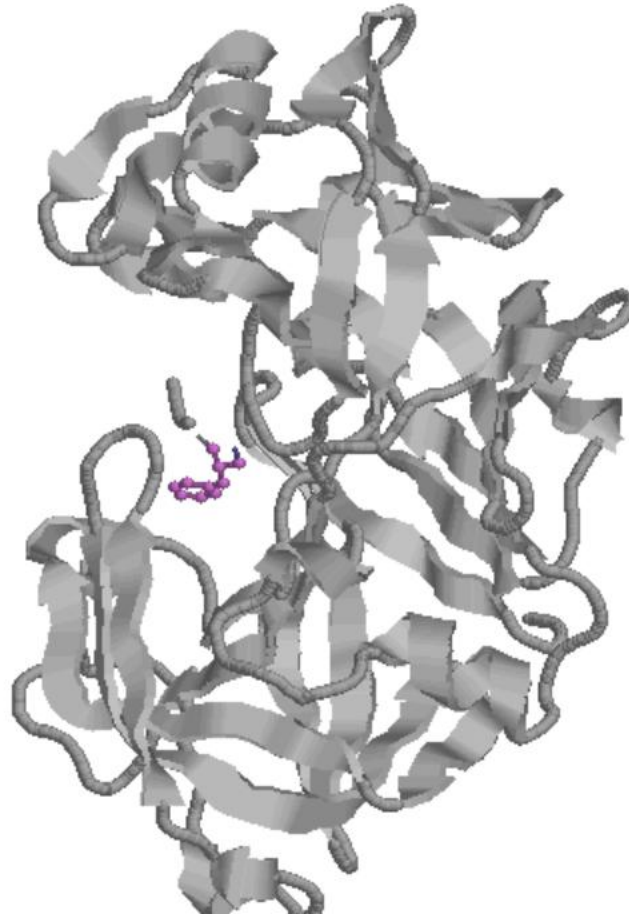
# Views of a protein

---

Spacefill



Cartoon



CPK colors

Carbon =  
green, black,  
or grey

Nitrogen =  
blue

Oxygen = red

Sulfur =  
yellow

Hydrogen =  
white