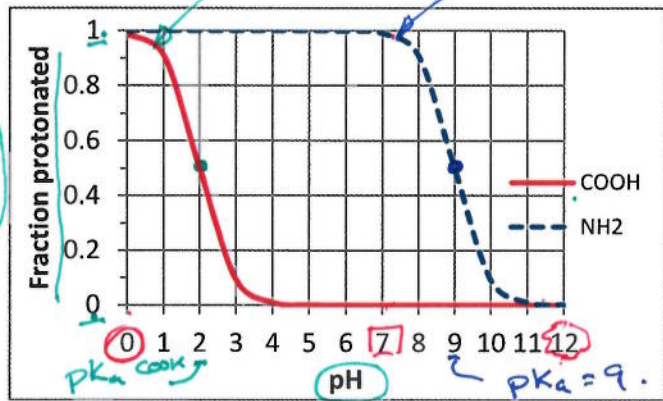
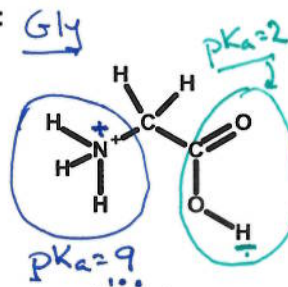


- i) Homework
- ii) Blackboard quiz.

Lecture 6: Amino acids & Introduction to Protein Structure.

Pre-lecture Example:

- a) Draw the correct form of glycine at pH=0, pH=7 and pH=12. The pKa of the carboxylate group is 2, and the amino group is 9.
- b) At what pH is it more likely for glycine to go through a membrane?



Solution:

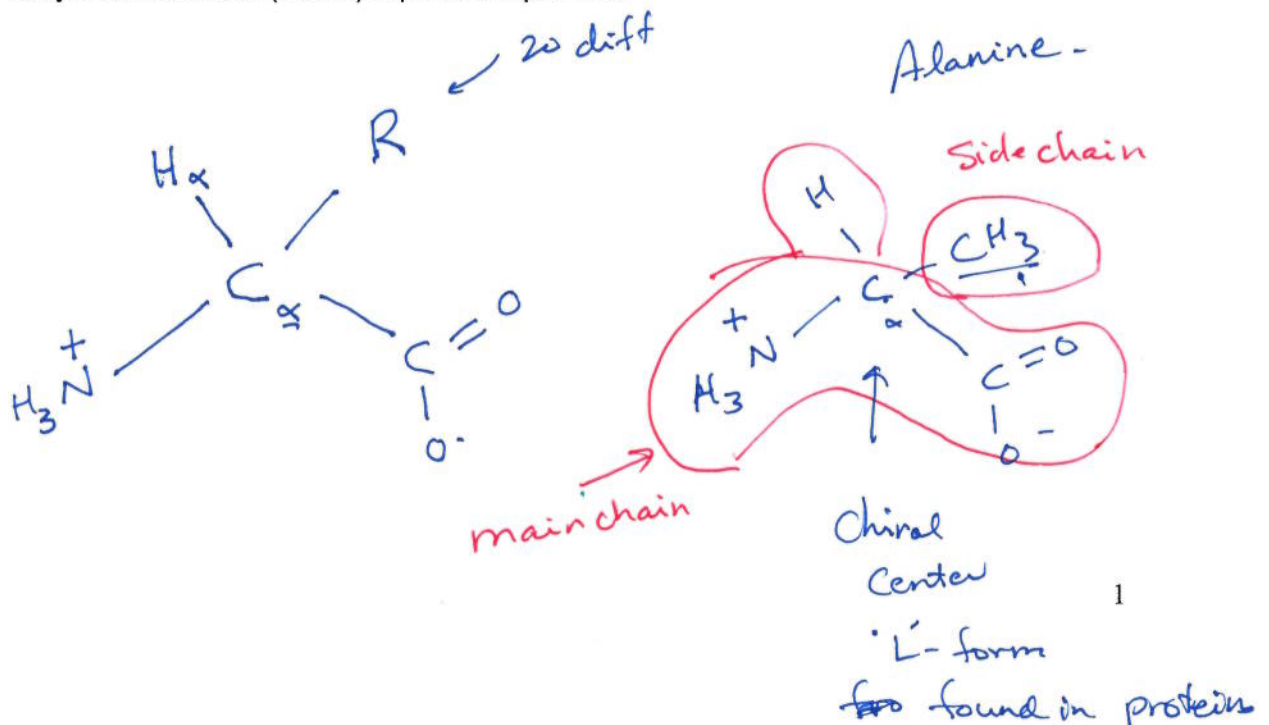
- 1) Sketch the curves for fraction protonated versus pH for both the carboxylate (red, solid) and the amino (blue, dotted), using their respective pKa values.
- 2) Draw the structure based on the fraction protonated at each pH.

pH = 0	pH = 7	pH = 12
Both the carboxylate and amino are fully protonated at low pH (high [H ⁺])	The amino is still full protonated, but the carboxylate is fully deprotonated.	Both groups are fully deprotonated at high pH (low [H ⁺]).

- 3) Only neutral molecules can go through the membrane, glycine cannot go through a membrane at any pH value – it is always charged.

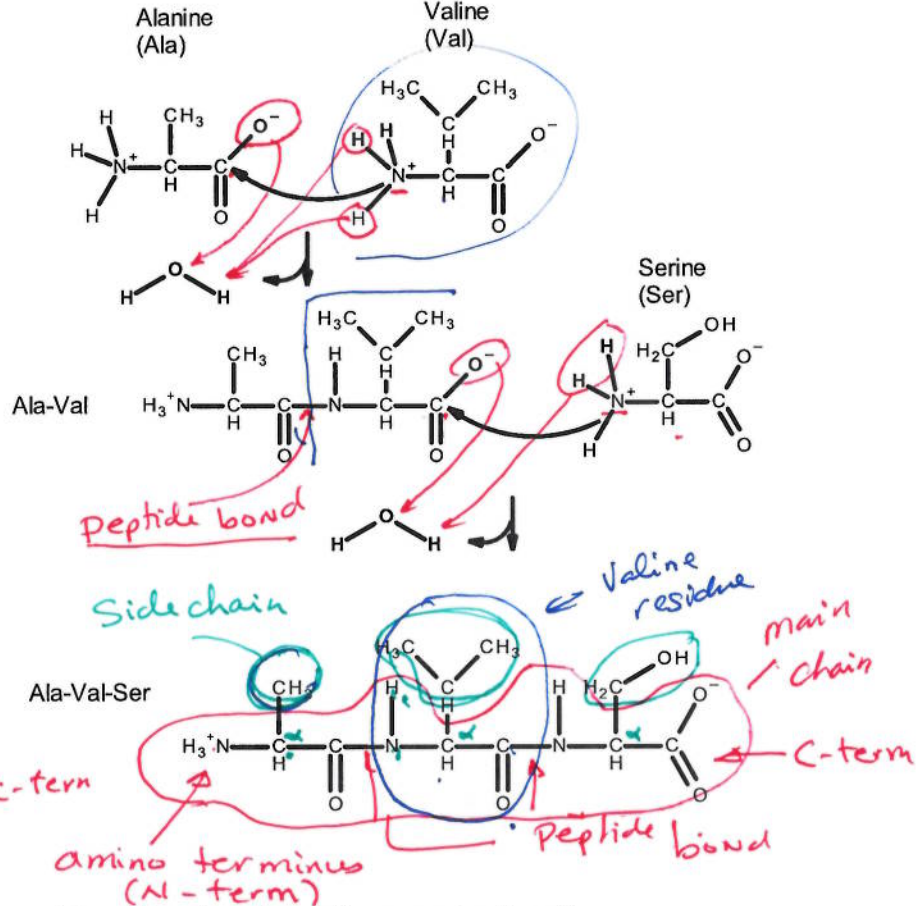
Amino Acids (Chapter 6)

- An amino group attached to a central carbon (α-carbon).
- A carboxylic acid group attached to the α-carbon.
- The amino group, α-carbon, and carboxylic acid will become the “mainchain” of a protein.
- One of twenty different “sidechains” attached to the α-carbon.
- The α-carbon is chiral in all but one amino acid because four different groups are attached to the α-carbon.
- Only one enantiomer (L-form) is present in proteins.



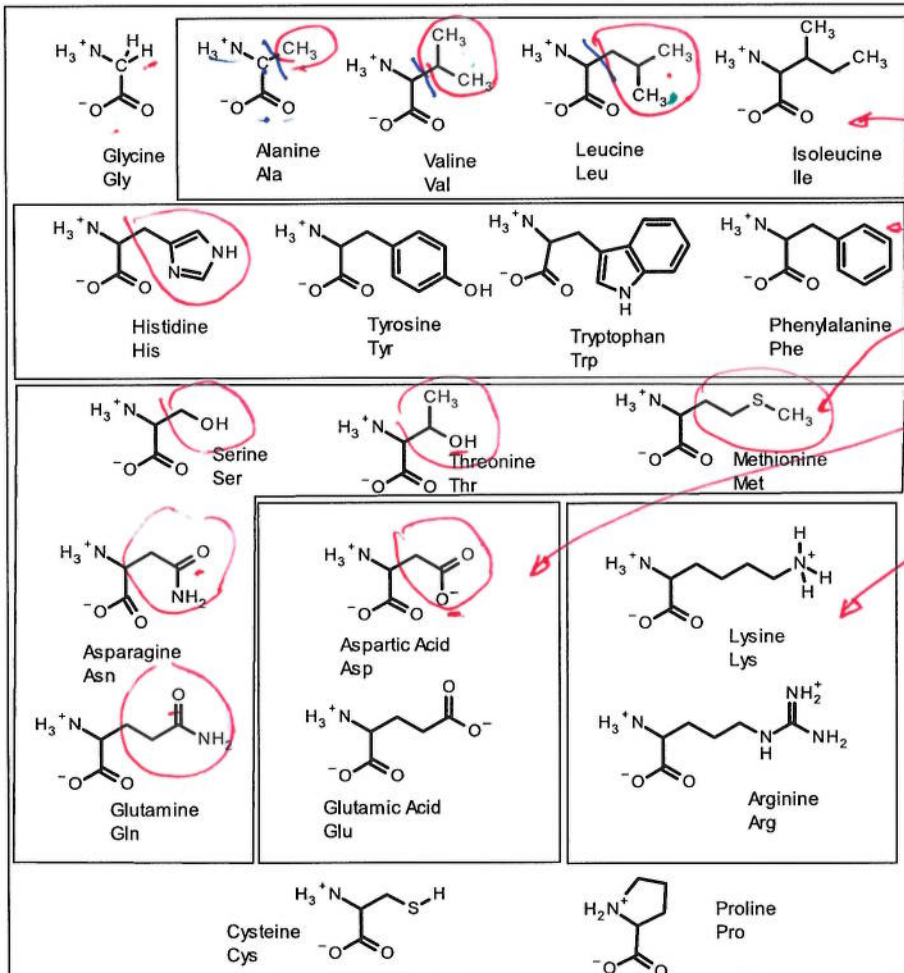
Protein Structure

- Amino acids are linked together in linear chains to form proteins.
- The **peptide bond** is formed when two amino acids are linked, releasing a water molecule (**condensation reaction**).
- When incorporated into a protein, an amino acid is called a **residue** ("amino acid residue").
- Sequence is written starting from the amino terminus to the carboxy-terminus.
- The residue number also begins at the amino terminus: 1-2-3. In this example valine is the second residue.



Name
 N-Term Ala-Val-Ser C-term
 ① ② ③

Twenty common amino acids found in proteins (You do not need to memorize these).



Glycine: side chain is -H, neither polar or non-polar.

Non-polar, non-aromatic (Ala, Val, Leu, Ile)

Aromatic, polar (His) to non-polar (Phe)

Polar sidechain (Ser, Thr, Met, Asn, Gln)

Acidic side chain, these groups ionize at pH=7, giving them a negative charge (Asp, Glu).

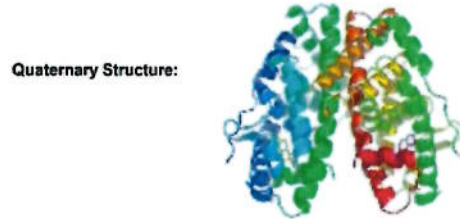
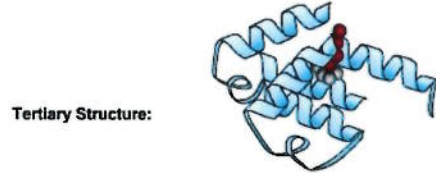
Basic side chains, these groups are protonated at pH=7, giving them a positive charge (Lys, Arg).

Two special amino acids: Cys – forms crosslinks in proteins.

Pro – its sidechain forms a covalent bond with the nitrogen.

Protein Structural Hierarchy:

1. **Primary structure (1°):** The amino acid sequence, written from the amino to the carboxy termini.
2. **Secondary structure (2°):** Configuration of mainchain atoms only.
3. **Tertiary structure (3°):** Entire 3-D structure of one chain, both mainchain and sidechain.
4. **Quaternary structure (4°):** Association of subunits. Subunits can be the same (homo) or different (hetero).

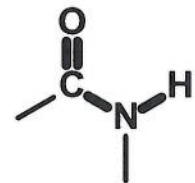
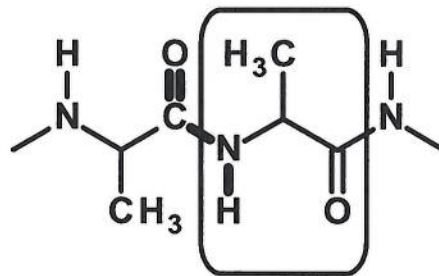


Secondary Structure:

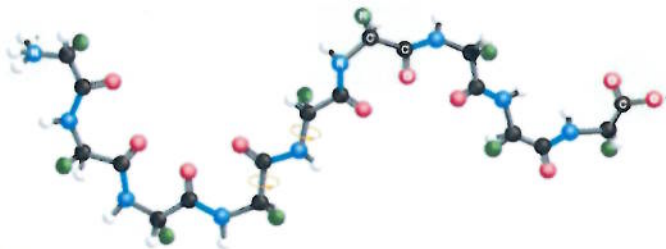
Peptide bond:

- i. It cannot rotate (partial double bond).
- ii. The carbon is planar because it is bound to three atoms.
- iii. The nitrogen is also planar, so all four atoms (O, C, N, H) lie in a plane.
- iv. The C=O can accept a hydrogen bond
- v. The N-H can donate a hydrogen bond, but cannot accept one since it is involved in a partial double bond.
- vi. Trans form is more stable than cis.

N-C_α & C_α-CO – are single bonds and are freely rotatable, giving the unfolded polypeptide chain considerable flexibility.



- The large number of possible conformations stabilizes the unfolded state of proteins because disorder is favored.



Although the mainchain atoms can assume many different conformations, there are two **hydrogen bonded structures** that are stable. The hydrogen bonds are between main chain atoms, the C=O accepts a hydrogen bond from an N-H.

α-Helix Structures

Dimensions, geometry, & H-bonds
 3.6 residues/turn
 5.4 Å/turn

H-bonds || to helix axis.
 Sidechains point outwards
 Right handed twist.

