MCB 150

Proteins, Part 1

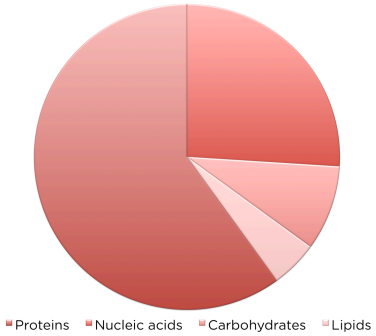
Today's Learning Catalytics Session ID is:
65931785

Announcements:

- Exam I is Thursday, February 8, from 7:00–9:00 PM
  - Check Canvas or your TA for room assignments
  - Additional practice questions should be available by tomorrow
  - Fill out Conflict Exam Request Form by Monday at 5:00 PM

Our Final Macromolecule: Proteins

- We are the product of our proteins and protein activity
  - The study of proteins and protein activity: Proteomics
- Proteins account for most of the dry weight in the cell



Proteins are involved in nearly all categories of cellular function:

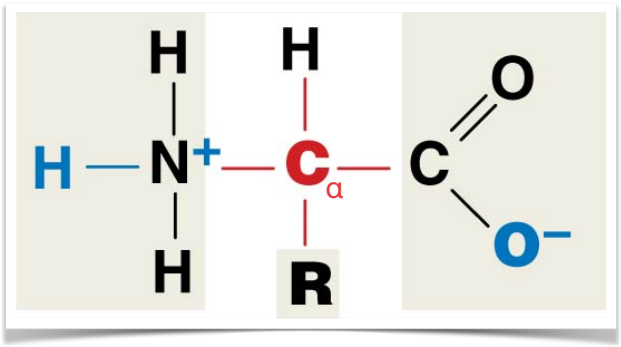
- Movement (Actin/Myosin)
- Defense (Antibodies)
- Structure (Keratin)
- Transport (Hemoglobin)
- Signaling (Glucagon)
- Catalysis/Regulation/Metabolism

Most of our (useful) genetic information instructs the cell how to build proteins or regulates that process

Amino Acids are the monomers of Proteins

- Basic structure of an amino acid (ionized form):

Amino (or N) Terminus

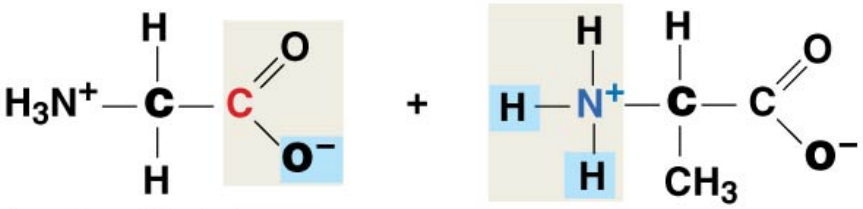


Carboxyl (or C) Terminus

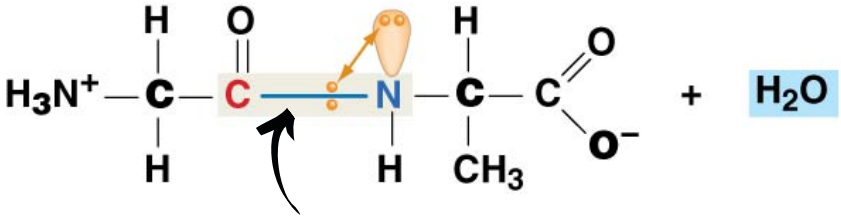
Side Chain, or R-Group

The R group—the only part that differs—is what makes one amino acid different from another

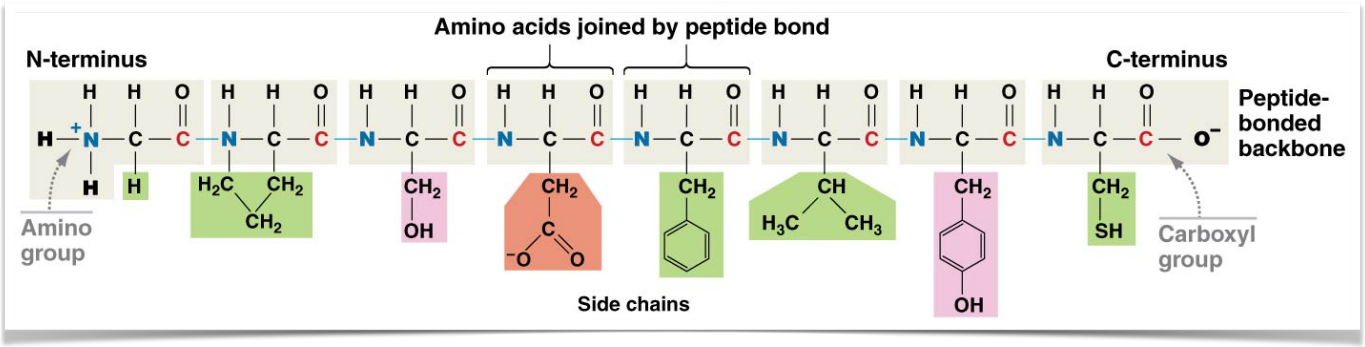
Peptide bond formation:



Condensation/ Dehydration



Peptide bond



During protein synthesis, ribosomes link amino acids by constructing covalent PEPTIDE BONDS that join the NH_2 (or $NH3^+$) group of the incoming amino acid to the COOH (or COO^-) group of what was already there, in the N→C direction.

Some common (and familiar) terminology:

- Two amino acids = DIPEPTIDE
- A few amino acids = OLIGOPEPTIDE
- A long chain of amino acids = POLYPEPTIDE
- A polypeptide with a purpose = PROTEIN

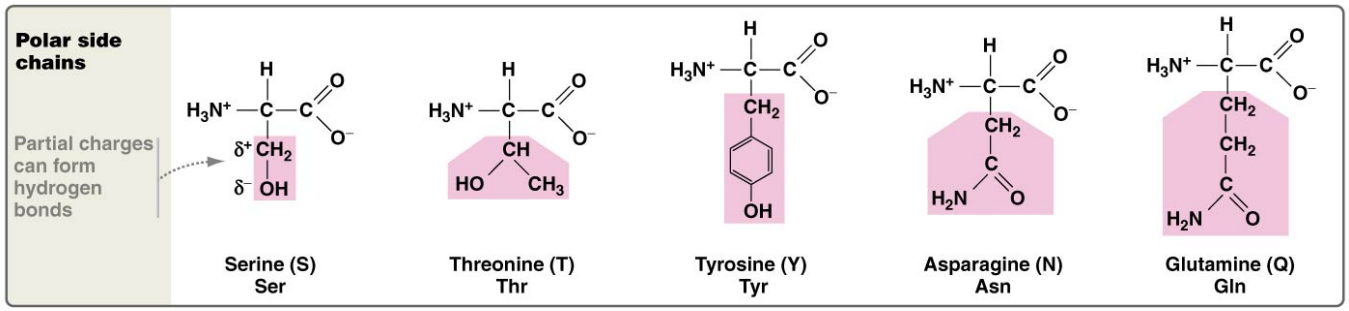
20 different amino acids commonly found in proteins

- differ only in R groups, which confer distinct properties to that amino acid
- large number of amino acids makes possible a huge number of different amino acid sequences
  - 20^2 (=400) possibilities for dipeptides
  - 20^3 (=8,000) possibilities for tripeptides
  - 20^5 (=3,200,000) possibilities for pentapeptides
  - most proteins are >100 amino acids!!

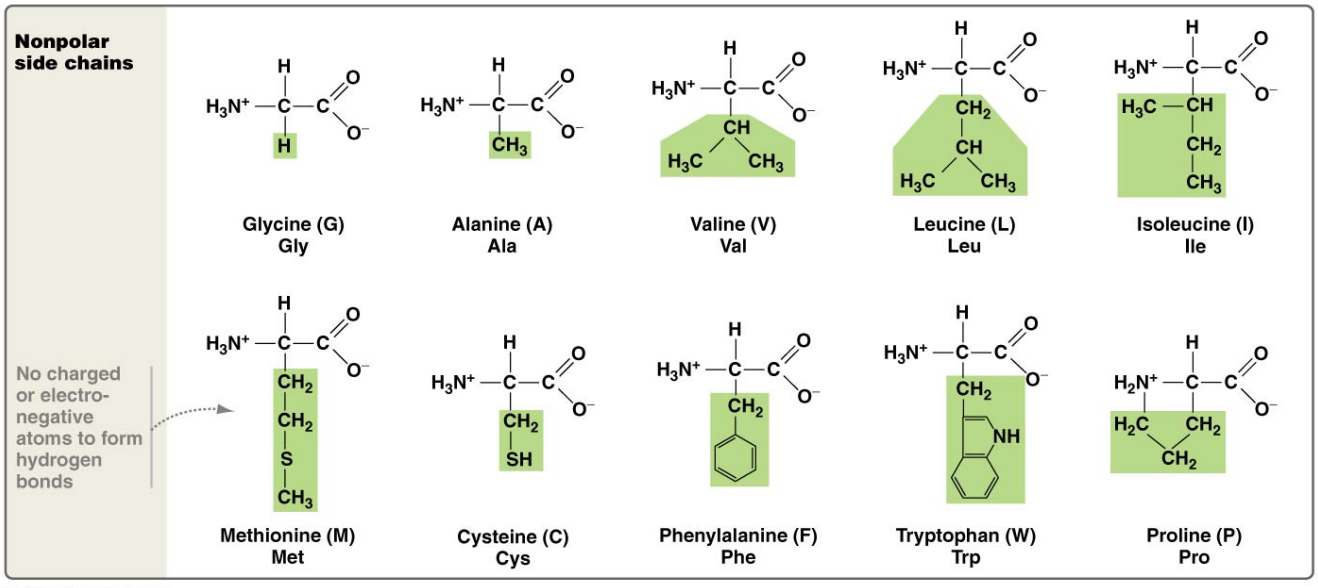
Amino acid R-groups (4 classes based on charge):

- Uncharged, but polar
- Uncharged and non-polar (hydrophobic)
- Positively-charged (basic)
- Negatively-charged (acidic)

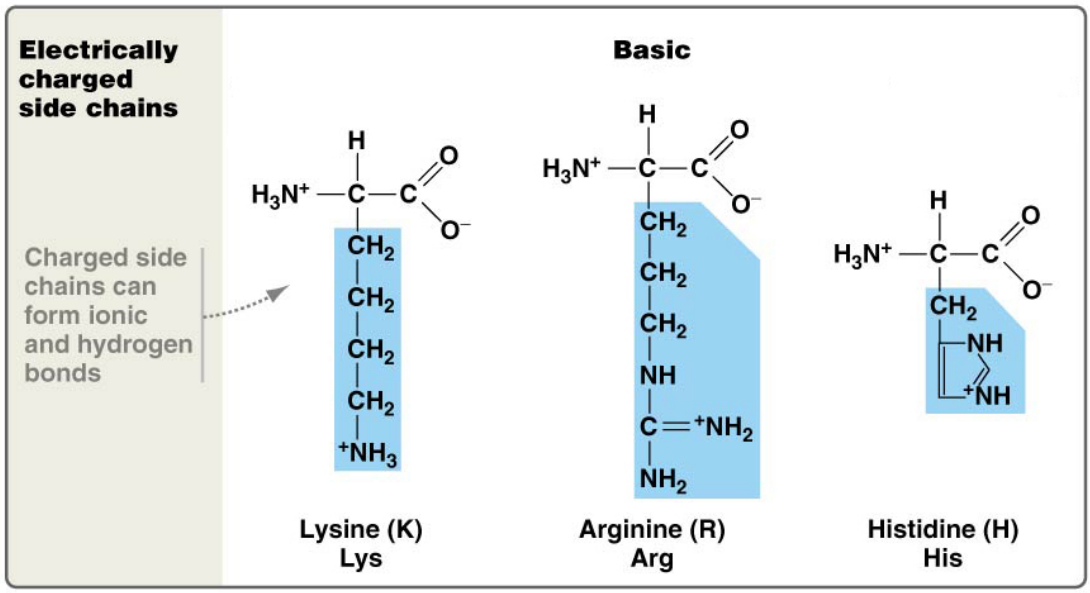
Polar amino acids:



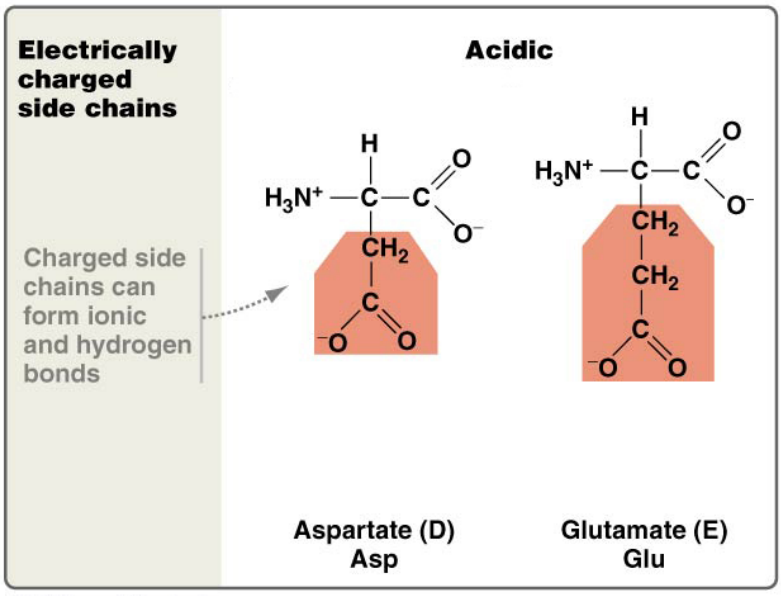
Nonpolar (hydrophobic) amino acids:



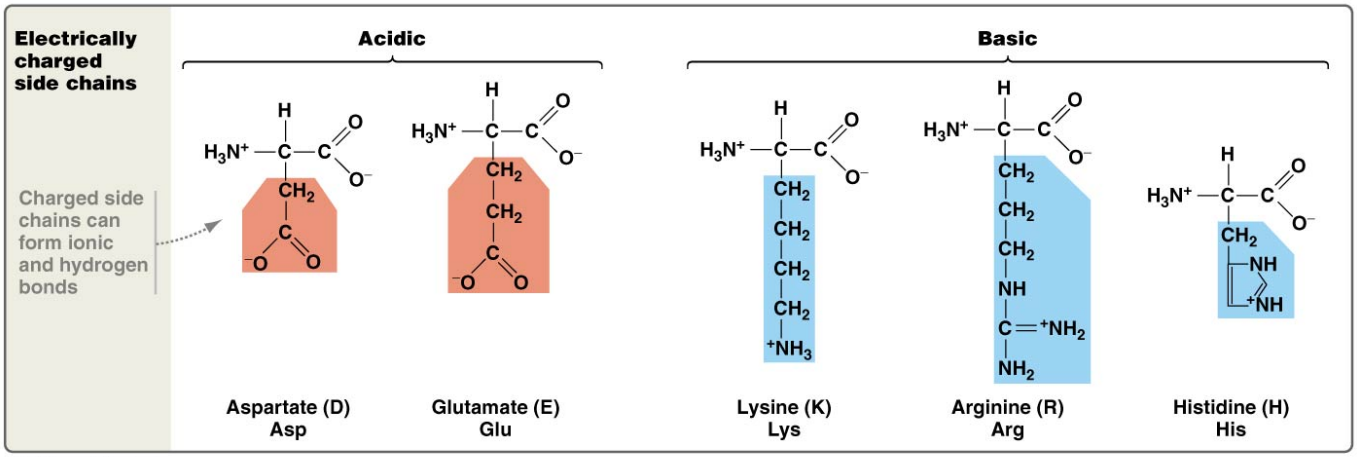
Basic (positively-charged) amino acids:



Acidic (negatively-charged) amino acids:



Charged amino acids:



Proteins exist in a virtually infinite number of 3-dimensional conformations

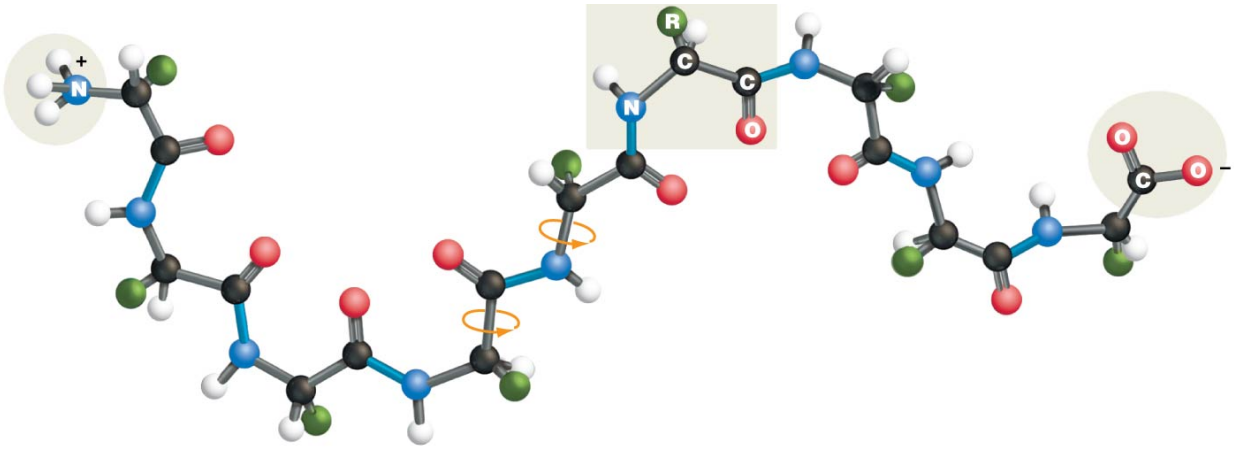
- That conformation is critical to the functioning of each protein
- The consequence of folding improperly is usually very significant
  - Alzheimer's, CF, Parkinson's, Mad Cow –– all caused by errors in protein folding → accumulation of toxic insoluble "gunk" (e.g. "plaques" in Alzheimer's)

To describe how linear protein chains fold into their 3-D conformations, protein structure is organized into 4 different categories:

- 1° (pronounced 'primary')
- 2° (pronounced 'secondary')
- 3° (pronounced 'tertiary')
- 4° (pronounced 'quaternary')

Primary structure (1°, or primary sequence):

- Linear sequence of amino acids from N → C ("beads on a string")
- All proteins have a UNIQUE primary structure

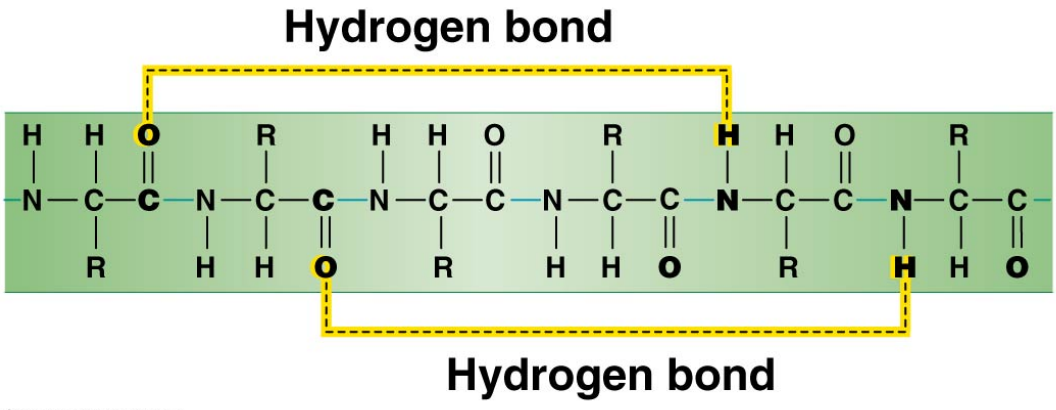


Secondary Structure (2°):

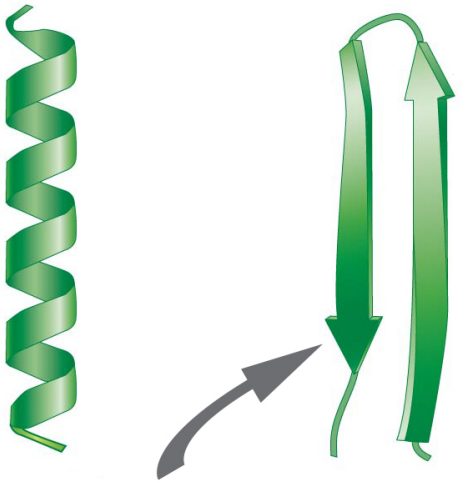
- First level of folding
- Stabilized by (relatively weak) hydrogen bonds between peptide linkages
  - Peptide backbone is polar (N-H is partially +, C=O is partially –)
- Independent of R groups, so found in most proteins
- α-helix and β-pleated sheet are 2 major types

Secondary Structure (2°):

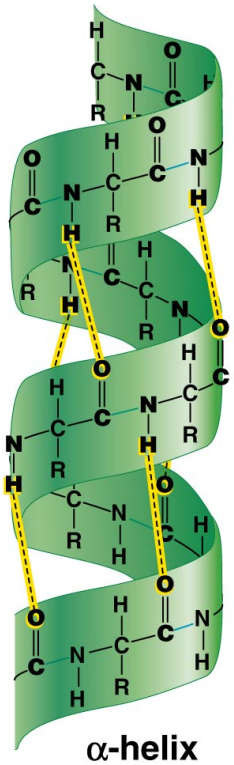
(a) Hydrogen bonds can form between nearby amino and carbonyl groups on the same polypeptide chain.



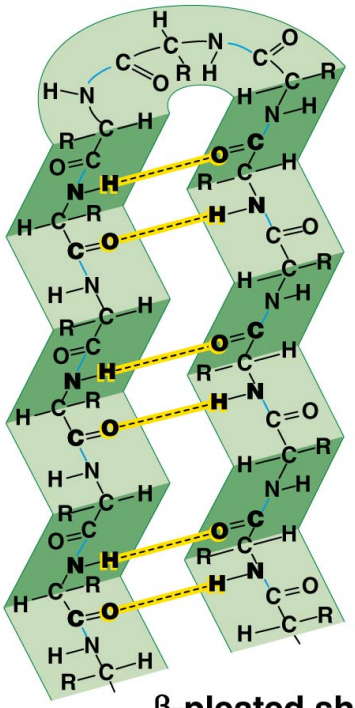
Secondary Structure (2°):



Arrowheads point toward the C-terminus of the primary structure



α-helix



β-pleated sheet