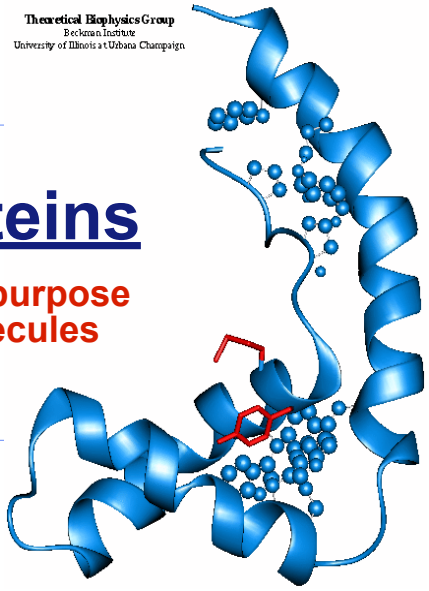
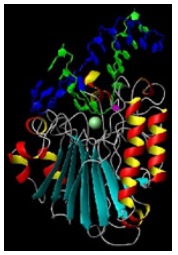


Proteins

Multi-purpose molecules

Proteins

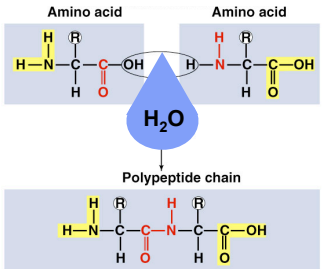


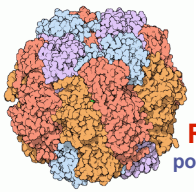
Most structurally & functionally diverse group

- Proteins are involved functionally in almost everything:
  - Enzymatic proteins - Speed up chemical reactions
    - Pepsin, DNA polymerase
  - Structural Proteins - Support
    - Keratin, collagen
  - Transport Proteins - Transporation & Carrying
    - Hemoglobin, aquaporin
  - Signaling Proteins - Send signals to coordinate activities
    - Insulin, adrenalin
  - Receptor Proteins - Respond to external stimuli
  - Defense Proteins - Disease Protection
    - Antibodies
  - Contractile & Motor Proteins - Movement
    - Actin & myosin
  - Storage Proteins - Storing amino acids
    - Ovalbumin, casein

Proteins

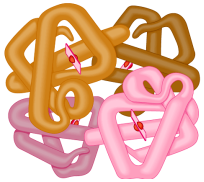
- Structure
  - monomers = amino acids
    - 20 different amino acids
  - polymer = polypeptide
    - Proteins consist of one or more polypeptide chains folded & bonded together
    - Can be very large macromolecules
    - Have complex 3-D shapes

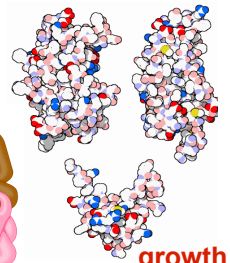




Hemoglobin - 4 polypeptide chains

Rubisco - 16 polypeptide chains

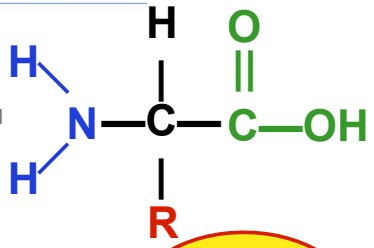


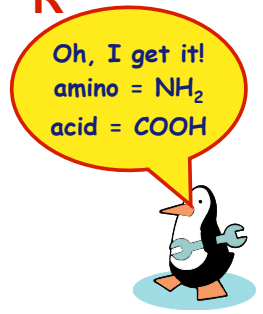


growth hormones

Amino acids

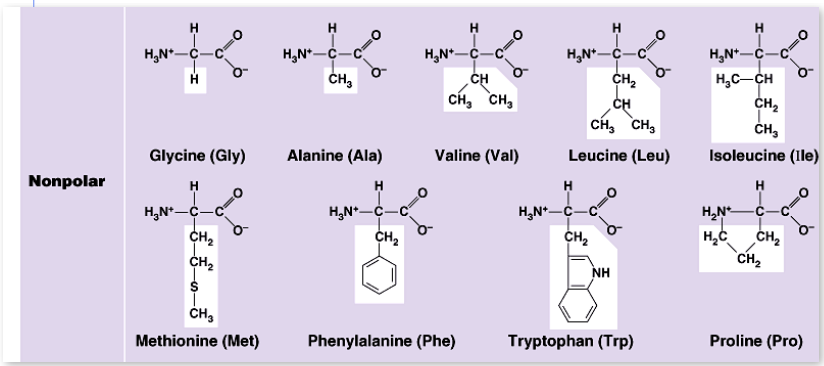
- Structure
  - central α carbon
    - Only glycine has no asymmetrical carbon since its R group is an H.
  - amino group
  - carboxyl group (acid)
  - R group (side chain)
    - variable group
    - different for each amino acid
    - confers unique chemical properties to each amino acid
      - Each becomes like a different letters of an alphabet
      - With 20 letters you can make many words (proteins)





Effect of different R groups.

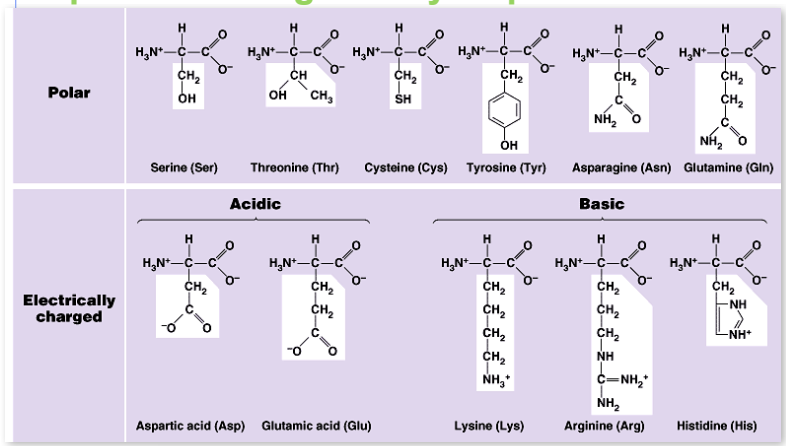
- nonpolar & hydrophobic side chains



Why are these nonpolar & hydrophobic?

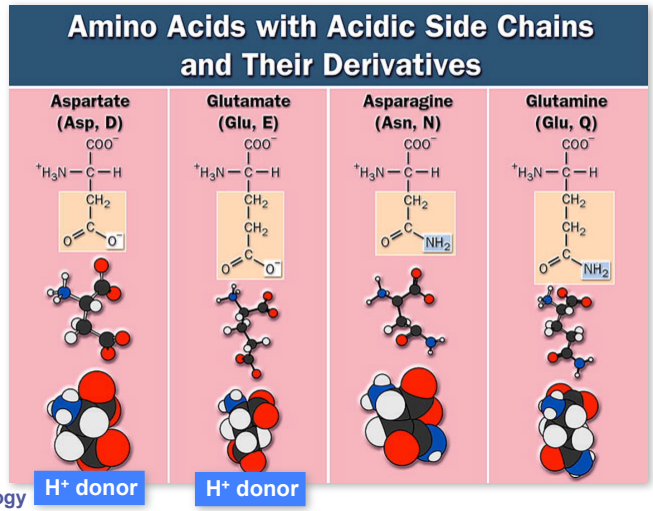
Effect of different R groups

- polar or charged & hydrophilic

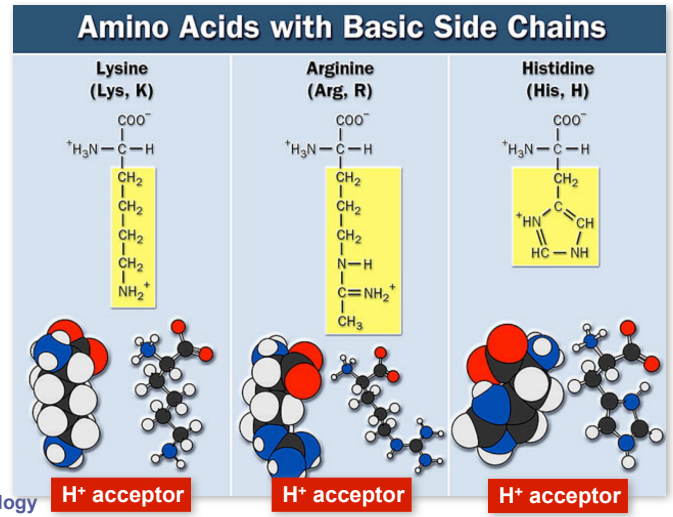


Why are these polar or charged & hydrophilic?

Ionizing in cellular waters - side chains that gain a full negative charge

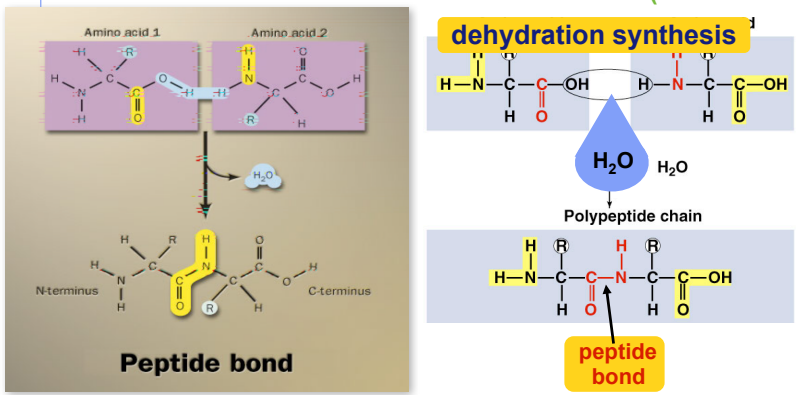


Ionizing in cellular waters - side chains that gain a full positive charge



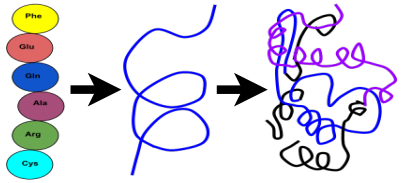
Building proteins involves building polymers of amino acids called polypeptides

- **Peptide bonds**
  - covalent bond between NH_2 (amine) of one amino acid & COOH (carboxyl) of another
  - Creates a C–N bond between monomers (amino acids)

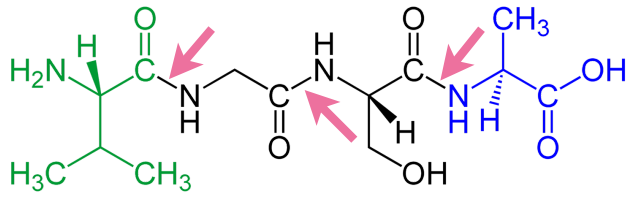


Sample polypeptide

- **Proteins are made up of ONE or MORE polypeptides**
  - Polypeptides fold up into 3D shapes.
  - One of more folded up polypeptides may come together to form a final functional protein



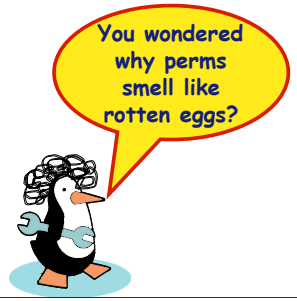
- Where are the peptide bonds in this sample polypeptide?

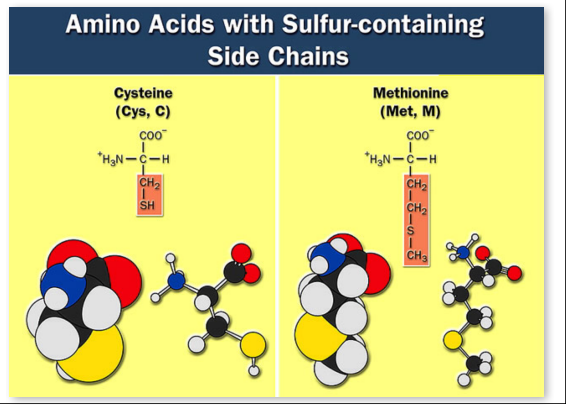


Sulfur containing R groups of amino acids

- Can form **disulfide bridges**
  - covalent cross links betweens sulfhydryl functional groups
  - stabilizes 3-D structures of folded up chains of amino acids

R-S – S-R

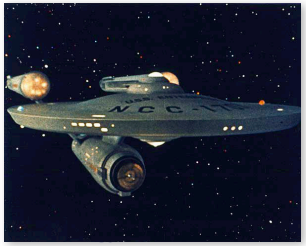


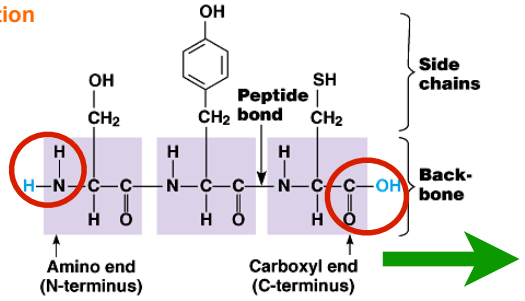


Building proteins

- **Polypeptide chains have direction**
  - **N-terminus** = NH_2 end
  - **C-terminus** = COOH end
  - repeated sequence (N-C-C) is the polypeptide backbone
    - polypeptides grow in only one direction

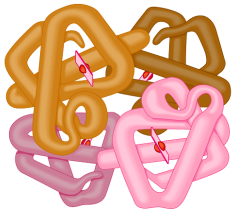
Polypeptides 'grow' in one direction: From the N to the C terminal.



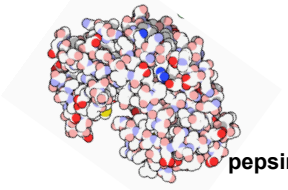


Protein structure & function

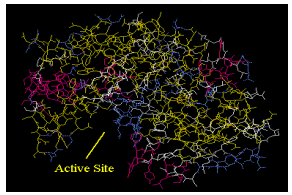
- Function depends on structure
  - 3-D structure
    - twisted, folded, coiled into unique shape

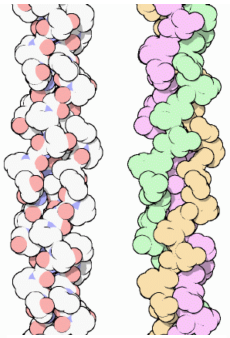


hemoglobin



pepsin

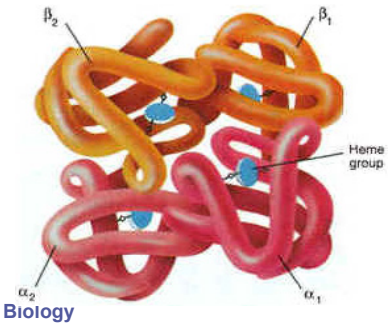


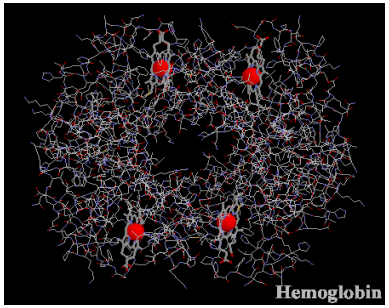


collagen

Form fits function

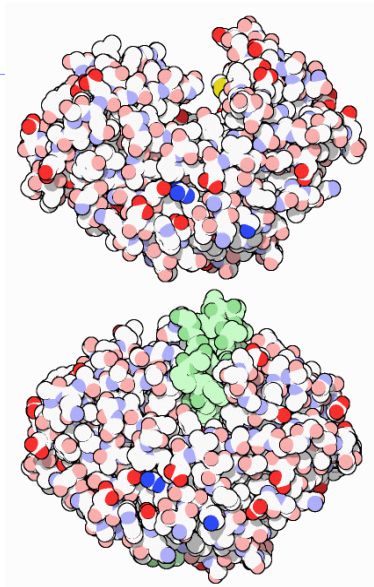
- Hemoglobin is the protein found in red blood cells.
- It is composed of four polypeptide chains, two alpha chains and two beta chains, each with a ring-like 'heme' group (of Cs and Ns) containing an iron atom at its center.
- Oxygen binds reversibly to these iron atoms and is transported through blood through an ion-induced dipole intermolecular force.





Form fits function

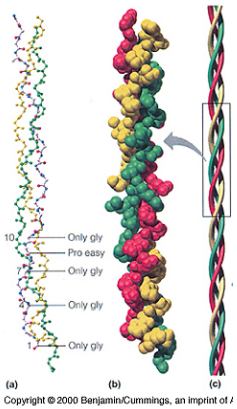
- Pepsin is the first in a series of enzymes in our digestive system that digest proteins.
- In the stomach, protein chains bind in the deep active site groove of pepsin, seen in the upper illustration and are broken into smaller pieces.
  - Then, a variety of proteases and peptidases in the intestine finish the job.
- The small fragments--amino acids and dipeptides--are then absorbed by cells for use as metabolic fuel or construction of new proteins.



Form fits function

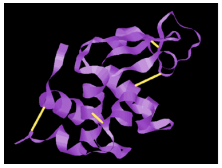
The most plentiful protein in bodies.

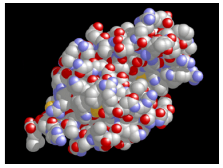
- About 1/4 of all of the protein in your body is collagen.
- Collagen is a major structural protein, forming molecular cables that strengthen the tendons and vast, resilient sheets that support the skin and internal organs. Bones and teeth are made by adding mineral crystals to collagen.
- Collagen provides structure to our bodies, protecting and supporting the softer tissues and connecting them with the skeleton.



Primary (1°) structure of Proteins

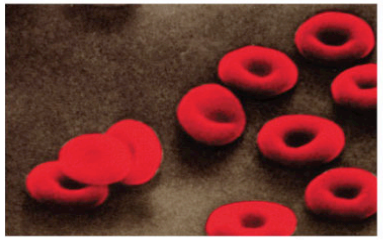
- Order of amino acids in chain
  - amino acid sequence determined by the genes (DNA)
  - slight change in amino acid sequence can affect protein's structure & its function
    - even just one amino acid change can make all the difference!

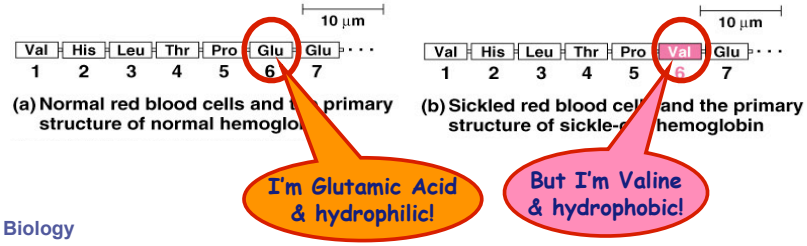




lysozyme: enzyme in tears & mucus that kills bacteria

Sickle cell anemia





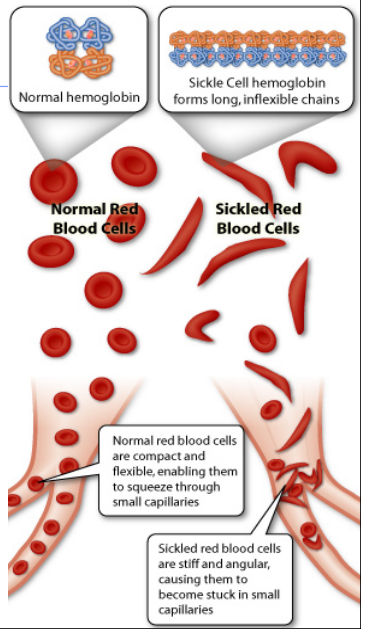
Sickle cell anemia

Non-polar Val is now stuck facing the aqueous solution but does not interact with polar water molecules unlike polar Glu.

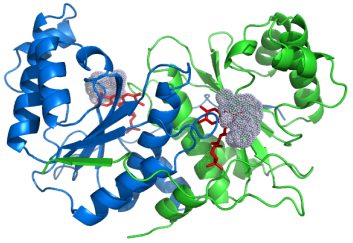
The non-polar Valines from adjacent polypeptide chains will stick together, excluded from water.

Instead do being separate proteins inside the red blood cell, hemoglobins now stick together forming crystal-like chains that can carry O_2 less efficiently & distort the outer shape of the cell.

Sickle shaped cells can form clots in the circulatory system.



Secondary (2°) structure of Proteins



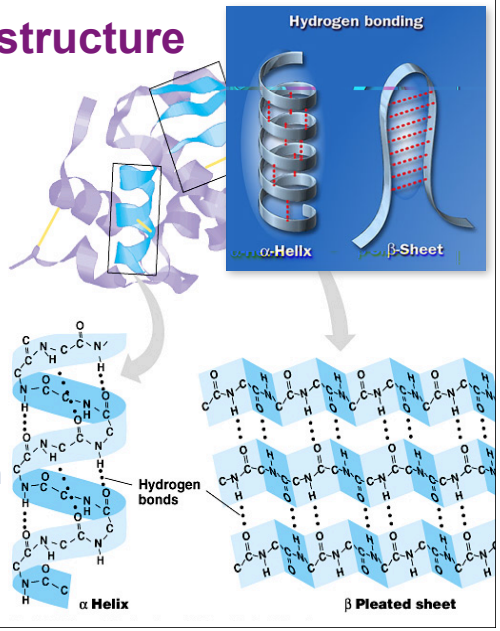
"Local folding"
- folding along short sections of polypeptide backbone
- interactions between adjacent amino acids
  - Caused by Hydrogen Bonding between the partially charged H of the backbone amino acid's amino group and partially negative O of the backbone amino acid's carboxyl group
    - weak bonds between polypeptide backbone (not a.a. side chains!)
- Hydrogen bonding forms sections of 3-D structures
  - α-helixes
  - β-pleated sheets
- One polypeptide can have both in different regions

Secondary (2°) structure

3-D structures

- α-helix
  - Coils with H-bonds between every forth a.a.
- β-pleated sheet
  - Two or more regions of polypeptide chain lying side by side with H-bonds between backbone

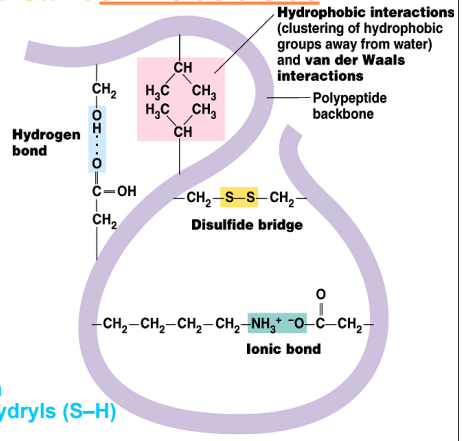
- One polypeptide can have both in different regions



Tertiary (3°) structure

"Whole molecule folding"

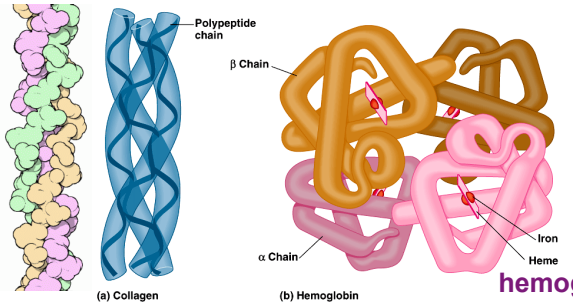
- interactions between distant amino acid side chains!
  - hydrophobic interactions
    - cytoplasm is water-based
    - non-polar amino acids cluster together away from water due to hydrophobic exclusion, Experiencing London Dispersion Forces
  - H bonds & ionic bonds
  - Disulfide bridges
    - covalent bonds between sulfurs in R group sulfhydryls (S–H)
    - anchors 3-D shape



Quaternary (4°) structure

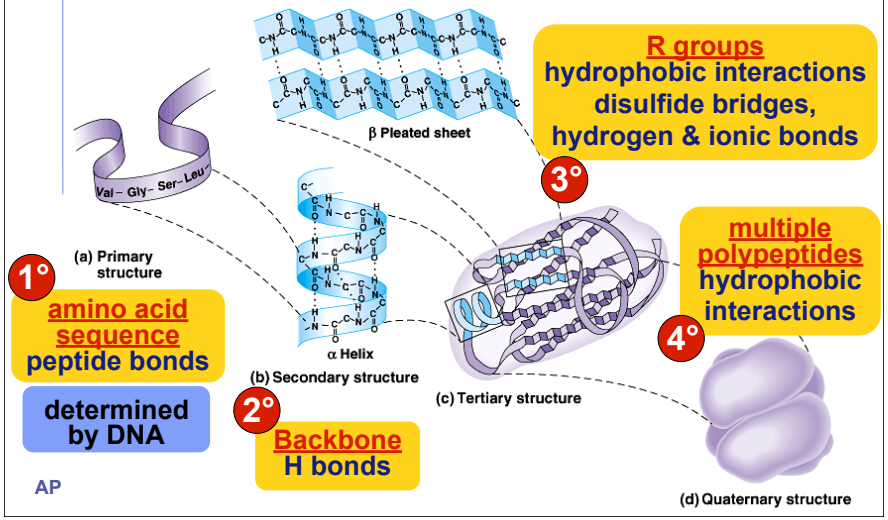
- More than one polypeptide chain bonded together
- Proteins can be made up of more than one polypeptide chain
  - For these, the protein is not functional until all polypeptides are assembled
    - hydrophobic interactions & van der Waals Interactions help hold polypeptides together

collagen = skin & tendons



hemoglobin

Protein structure (review)



1° amino acid sequence peptide bonds

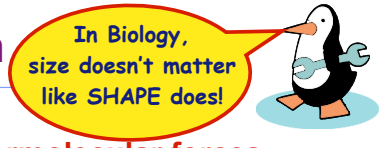
determined by DNA

2° Backbone H bonds

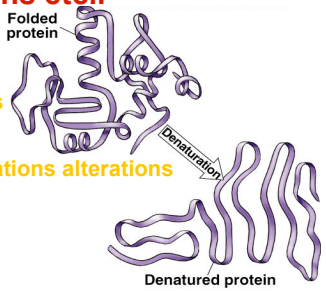
3° R groups hydrophobic interactions disulfide bridges, hydrogen & ionic bonds

4° multiple polypeptides hydrophobic interactions

Protein denaturation

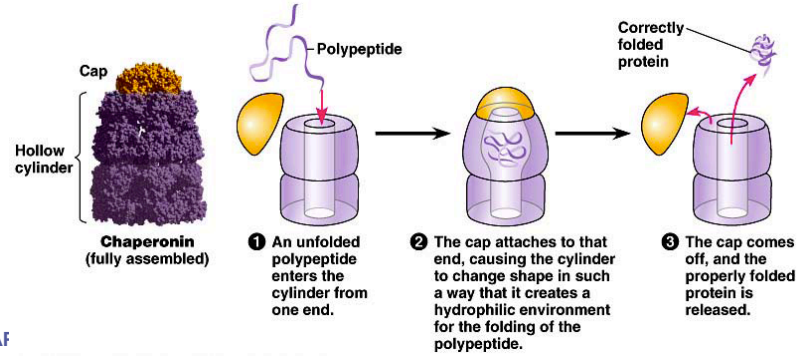


- Unfolding a protein
  - conditions that disrupt intermolecular forces like Hydrogen bonds, ionic attractions, dipole-ion and dipole-dipole attractions etc..
    1. temperature increases
    2. pH changes
       - proton concentrations alterations
    3. Salinity changes
       - positive & negative ion concentrations alterations
  - alter 2° & 3° structure
    - alter 3-D shape
  - destroys functionality
    - some proteins can return to their functional shape after denaturation under proper conditions, but many cannot.



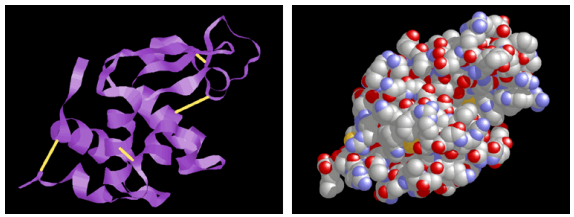
Chaperonin proteins

- Guide protein folding
  - provide shelter for folding polypeptides
  - keep the new protein segregated from cytoplasmic influences



Protein models

- Protein structure visualized by
  - X-ray crystallography
  - extrapolating from amino acid sequence
  - computer modeling



lysozyme

admire
Let's build those Proteins!