GENERAL PROPERTIES & TYPES OF CELLS

*Cell Theory

1. All living organisms composed of cells
2. All cells originate from other cells
3. Cells are the fundamental unit of life

*_Defining_ Features of a Cell

1. Plasma membrane
2. Uses metabolism to convert energy for cellular function
3. Contains DNA for self-replication (encodes for protein, RNA)

*Eukaryotes VS Prokaryotes

- Eukaryotes have true nucleus, nuclear membrane, membrane-bound organelles, mitochondria & chloroplasts (endosymbionts)
- Prokaryotes have nucleoid, circular DNA, no internal organelles, smaller than eukaryotes
- Both can be unicellular *and* multicellular
- Both have ribosomes

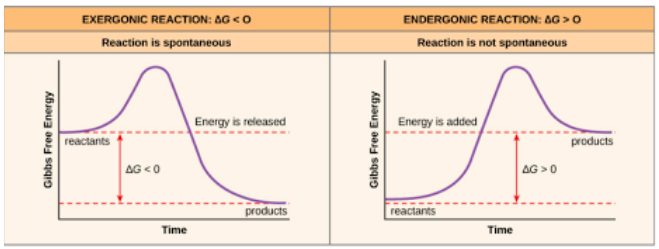
*Domains on Tree of Life

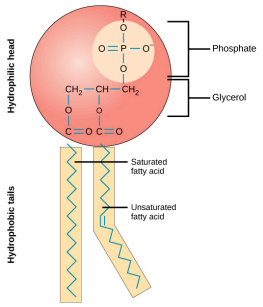
1. Bacteria
2. Archaea
3. Eukarya
   - All organisms evolved from Last Universal Common Ancestor
   - Prokaryotes arose 3.5-4 billion years ago, eukaryotes 2 billion years ago
   - Eukaryotes evolved from Archaea

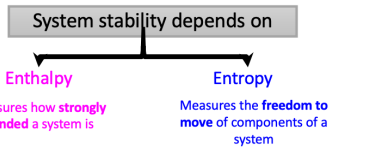
*Endosymbiotic Theory

- mitochondria & chloroplasts free-living cells engulfed by early eukaryotes
  - Have circular DNA similar to prokaryotes
  - Mitochondria similar to bacteria
  - DNA sequences more like bacteria

CHEMISTRY & THERMODYNAMICS



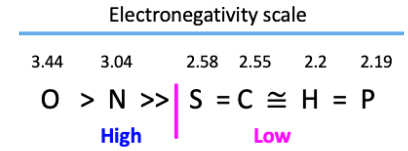


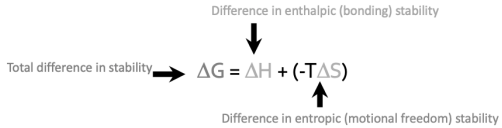


Polar Bonds form when atoms are electronegative:
- O-H
- N-H
- S-H(weaker)
- C-O
- O-P

Non-polar bonds form between less electronegative atoms:
- C-H

Bond type: Covalent vs. Non-covalent types	
Covalent	
Non-covalent	Ionic (two charged atoms interacting)
	Ion – Permanent Dipole (I-PD)
	Permanent dipole – Permanent dipole (PD-PD)
	Permanent dipole – Induced dipole (PD-ID) Ion – Induced Dipole (I-ID)
	Included dipole – nduced dipole (ID-ID)

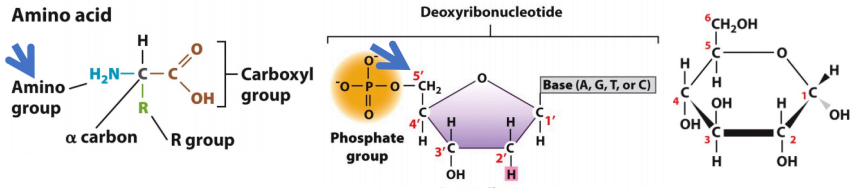


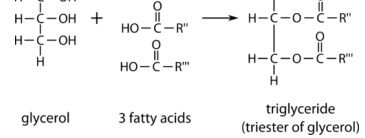


INTRO TO MACROMOLECULES

- monomers linked by covalent bonds
- 3D structure depends on non-covalent *interactions* b/w R groups
- chemical polarity: electronegativity & dipoles
- directionality: 2 chemically distinct ends
- functional groups: impart chemical characteristics that determine how a molecule interacts w/ surroundings

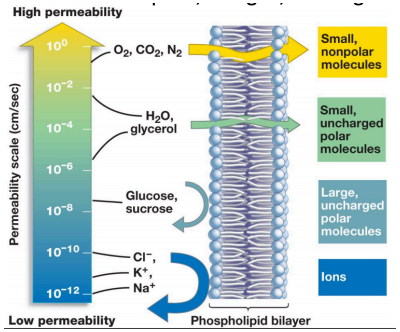
Macromolecule	Monomer	Covalent Bond/Linkage
Protein	Amino Acid	Peptide
Nucleic Acid (DNA/RNA)	Nucleotide	Phosphodiester
Carbohydrates	Monosaccharide	Glycosidic
Lipids	Fatty Acid	Ester

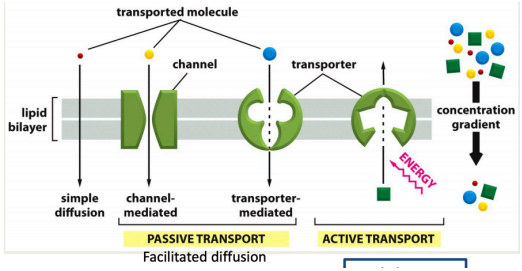




LIPIDS

- Fluid Mosaic Model: membranes composed of phospholipids & proteins
- Liposome: purified lipids w/ small heads, double tails (artificial)
- Bilayer: mixed lipids with small heads, double tails
- Micelle: bulky heads, single tails
- Single sheet
- Hydrophobic groups exposed to water, constrains water molecules
- Hydrophobic groups cluster together, the water is free to be in a more disordered state (energetically favoured); increased entropy of water

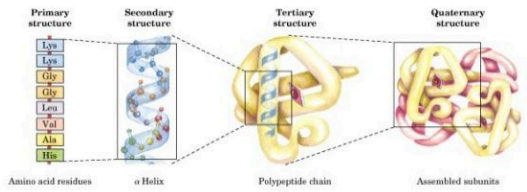




TRANSPORTERS
- diffusion: random movement of molecules from an area of high [ ] to low [ ]; facilitated uses channel or transporters
- osmosis: movement of a solvent from an area of high [solute] to low [solute]
-active transport: against concentration gradient, needs ATP & protein transporter
-secondary active transport: electrochemical gradient & co-transports solute down its concentration gradient as another solute is transported up its concentration gradient (ex. pump H-ion to create electrochemical gradient)

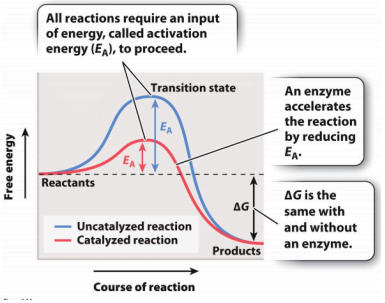
PROTEINS
1. Primary structure- sequence of amino acids
   - determine structure & function, non-covalent int.
   - N to C direction
   - same backbone, diff. R groups
2. Secondary structure-alpha helix (H-bond ALONG backbone) & beta sheets (H-bond b/w peptide backbone)
   - stabilized by H-bond backbone, NOT R groups
3. Tertiary structure- three-dimensional folded structure
   - determined by non-covalent int. b/w R groups
   - FINAL FOLDED STRUCTURE
   - stabilized by side-chain interactions
4. Quaternary structure- different polypeptide chains interact

- hydrophobic side chains: gly, ala, val, leu, Ile, met, phe, trip, pro
- hydrophilic, non-charged: ser, thr, cys, tyr, asn, gin
- charged, hydrophilic: asp, glu, lys, arg, his



*Protein Denaturation

- lose tertiary structure, unfold, denature
- disruption of covalent int.



ENZYMES
- active sites in tertiary structure
- catalysts

1. Binding of substrates in the active site of enzymes trigger a conformation change (shape change)
2. Helps the enzyme to make the transition state more stable
3. The reaction is catalyzed, producing products
4. Products are released

- transition state: highly unstable, lots of free energy, existing chemical bonds break, new ones form