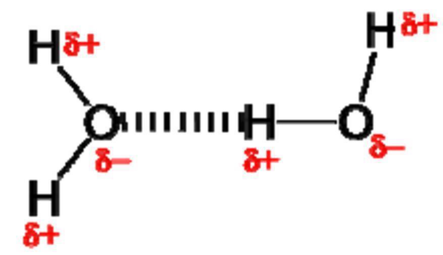
Crack the DAT

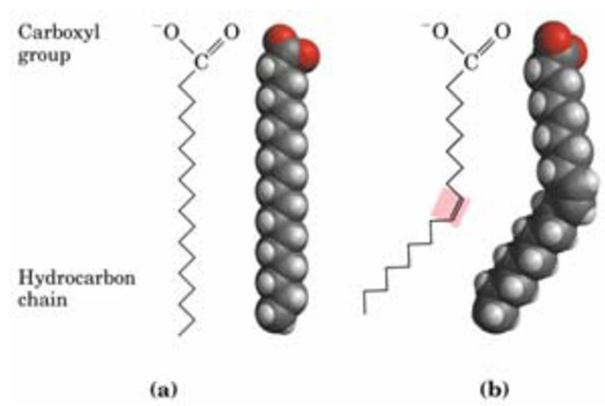
Crack Notes [Biology 1]
Molecular Biology & Cellular Respiration

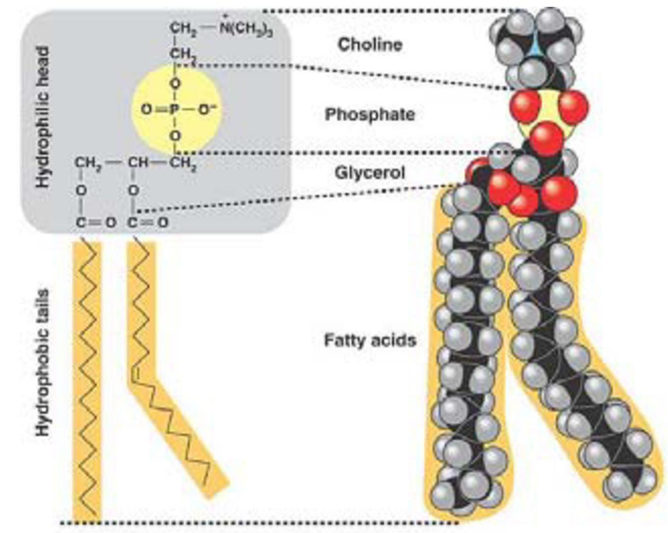
Water



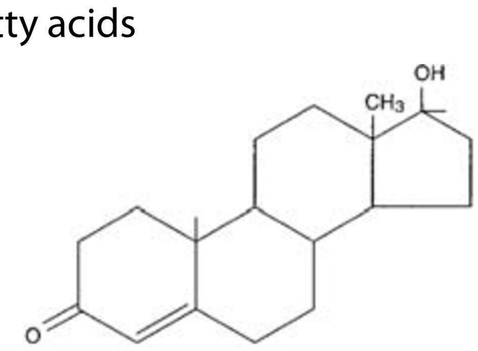
- *Hydrogen bonding*: polar H-O bonds cause partial negative O, partial positive H
- *Hydrophilic*: attracted to water; includes polar molecules/ions
- *Hydrophobic*: not attracted to water; pushed aside in aqueous environments
- *Hydrolysis*: adding water to a bond to break it (R-O-R → R-OH + HO-R)
- *Dehydration synthesis*: removing water to form a bond (R-OH + HO-R → R-O-R)

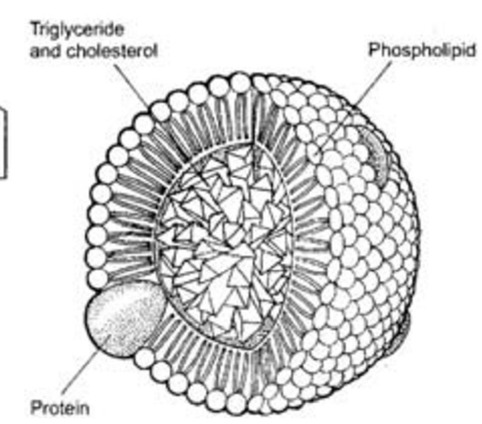
Lipids





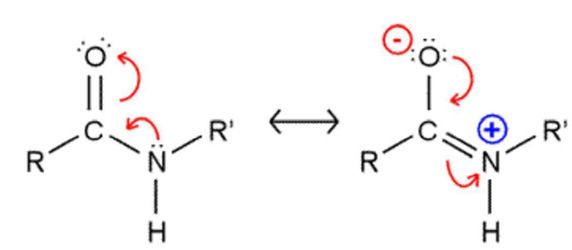
- <u>Functions:</u>
  - Store energy
  - Component of membranes
  - Thermal insulation/padding
  - Endocrine + local hormones
  - Vitamins
- <u>Types:</u>
  - *Fatty acids*: saturated (single bonds; higher density/energy; solid fats) vs. unsaturated (double bonds; kinks cause lower density; oils)
  - *Triacylglycerols/triglycerides*: glycerol (3 carbon + 3 OH groups) + 3 fatty acids
  - *Phospholipids*: glycerol + 2 fatty acids + phosphate group
  - *Steroids*: 4-ringed structures
  - *Lipoproteins*: lipid + proteins; have polar/nonpolar regions





Proteins

- <u>Globular proteins</u>
  - Enzymes
  - Hormones (second messenger system)
  - Membrane pumps i.e. Na^+/K^+-ATPase
  - Channels
  - Receptors i.e. receptor tyrosine kinases, G-protein coupled receptors
  - Transport/storage i.e. albumin (carrier for hydrophobic molecules, ions, drugs "taxi"), ferritin (stores iron), casein (stores amino acids)
  - Osmotic regulators i.e. albumin again
  - Immune system i.e. antibodies/immunoglobulins
- <u>Structural proteins</u>: add strength/elasticity to connective tissue i.e. collagen/elastin; maintain cell shape/size i.e. actin/tubulin; motor proteins i.e. myosin/kinesin/dynein



- Peptide bond: dehydration synthesis; carboxyl group reacts with amino group (amide). Limited rotation due to resonance structure

- <u>Amino acids</u>
  - 10 essential: cannot be synthesized by body
  - *Basic*: HAL 9000 - histidine arginine lysine
  - *Acidic*: aspartic acid glutamic acid
  - *Nonpolar*: I saw Lucy methodically probe and feel Alan, then Val tripped Glycine - isoleucine leucine methionine proline phenylalanine alanine valine tryptophan glycine
  - *Polar*: serine threonine cysteine tyrosine asparagine glutamine

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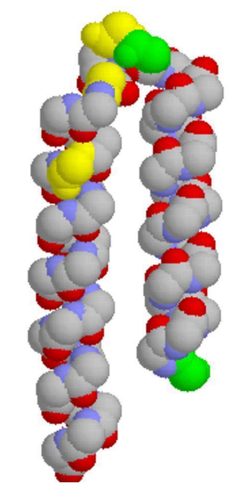
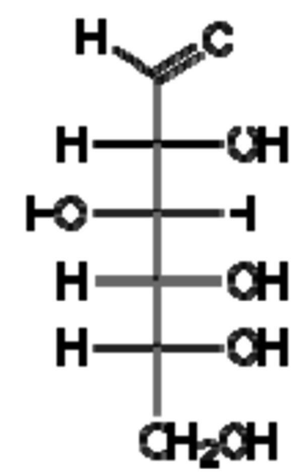
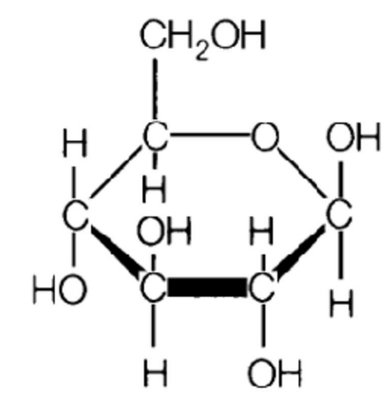


- Protein structure
  1. *Primary structure*: amino acid sequence
  2. *Secondary structure*: alpha helices, beta pleated sheets
  3. *Tertiary structure*: disulfide bonds, ionic bonds, hydrogen bonds, van der Waals forces, hydrophobic interactions
  4. *Quaternary structure*: multiple polypeptide chains, forces same as tertiary
  - Proline is a helix breaker, causes hairpins (green in figure to right)
  - *Denaturation*: increasing temperature; increasing/decreasing pH



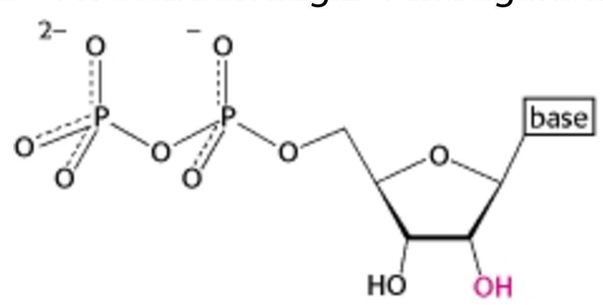


Carbohydrates

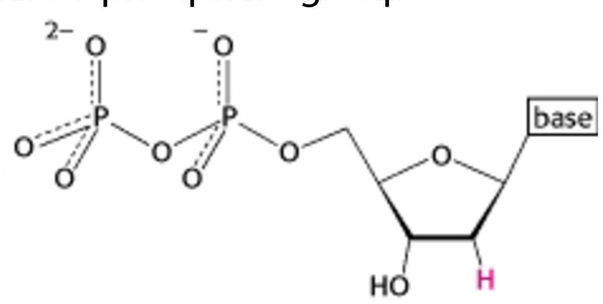
- Carbon and water, empirical formula $C(H_2O)$
- Glucose
  - Molecular formula $C_6H_{12}O_6$
  - Forms rings in solution due to nucleophilic addition
  - Has two ring forms (anomers) - alpha and beta; beta points up
  - Absorbed into blood against concentration gradient by sodium cotransport (active transport)
- *Glycogen*: branched polymer of glucose, 1,4 alpha linkages, energy storage, only in animals
- Liver converts all carbs to glucose including glycogen when necessary
- *Starch*: branched or unbranched polymer of glucose, 1,4 alpha linkages, only in plants
- *Cellulose*: unbranched polymer of glucose, 1,4 beta linkages, only in plants (we can't digest)

Nucleotides

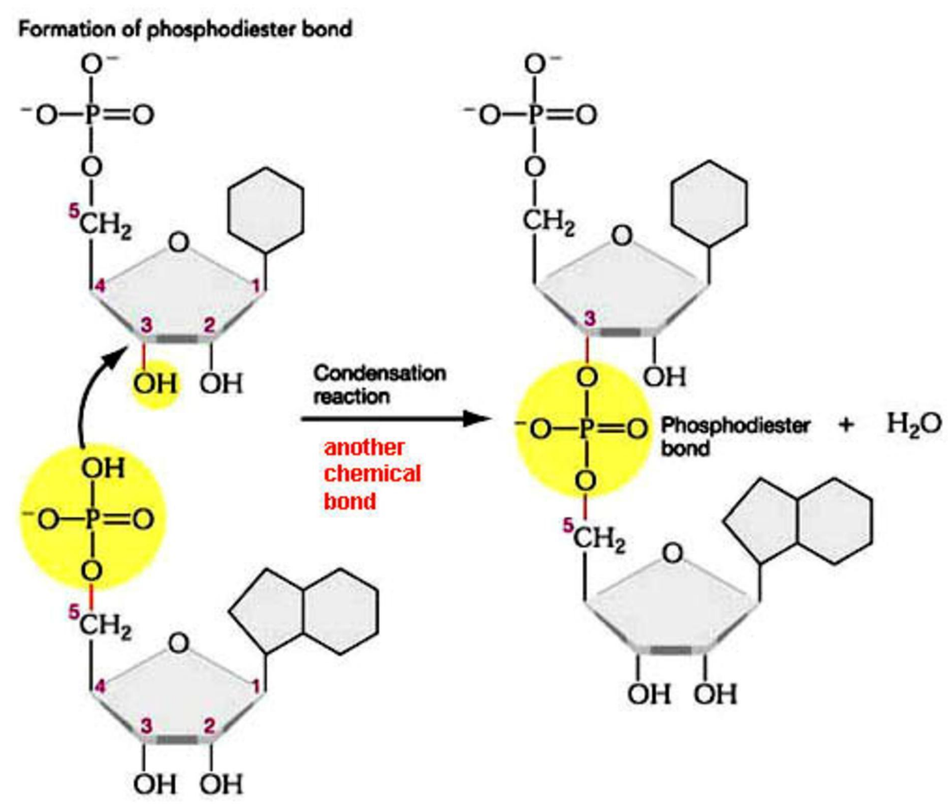
- Five carbon sugar + nitrogenous base + phosphate group



Ribonucleotide



Deoxyribonucleotide



- Adenine, guanine, cytosine, thymine (DNA), and uracil (RNA)
- *Phosphodiester bonds* to form strands
- DNA has A=T, G≡C, RNA has A=U, G≡C
- Strands go from 5'->3' (phosphate end to OH end)
- DNA has double helix (*antiparallel*), RNA may or may not
- A-T has 2 hydrogen bonds, C-G has 3 hydrogen bonds (more C-G = more resistant to denaturation = higher melting point)
- Other nucleotides: ATP (energy), cyclic AMP (2nd messenger), $NADH/FADH_2$ (high energy e^- carriers)

Minerals

- Dissolved inorganic ions
- Create electrochemical gradients to assist transport (Na, K, Cl), provide strength (Ca, P), act as cofactors (Zn, Fe, Cu, Se, Mn)

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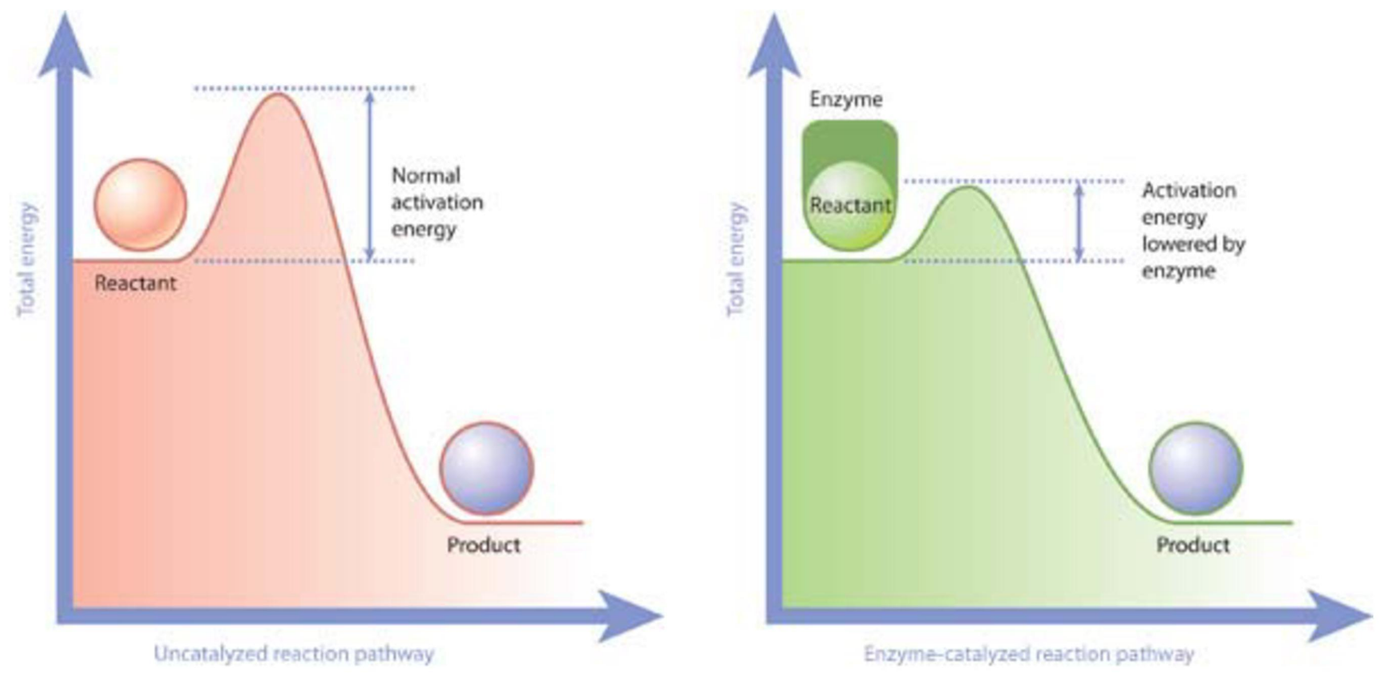
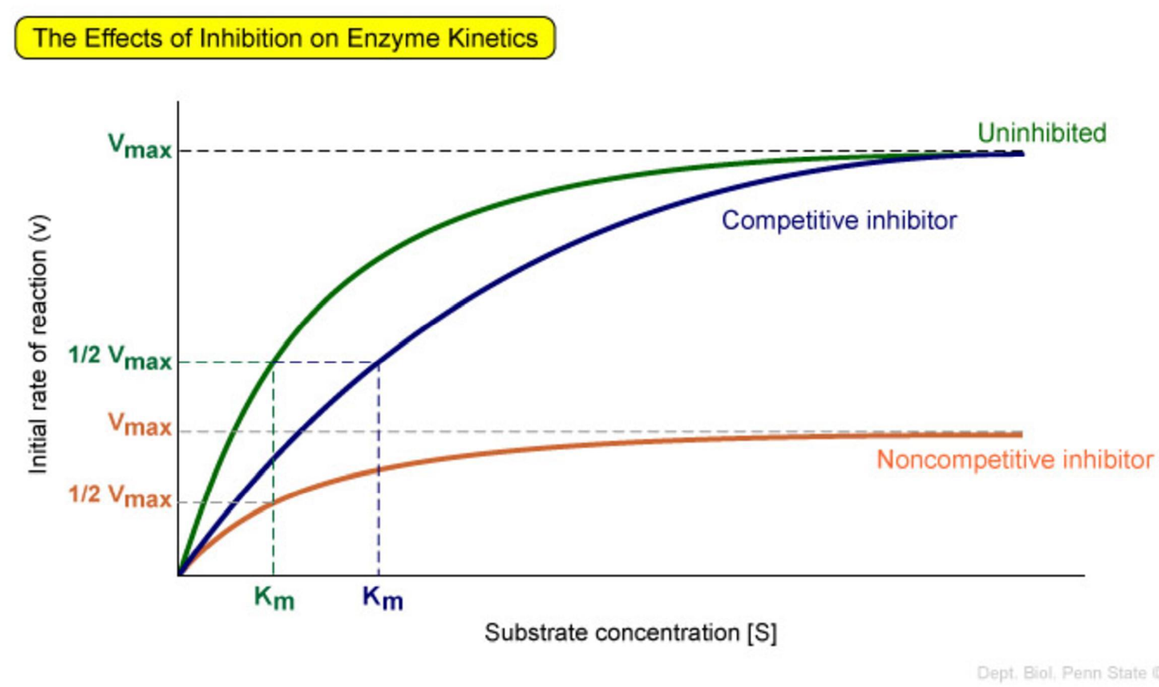
Enzymes

- Typically globular proteins, sometimes nucleic acids
- End in -ase, stuff before -ase is usually the substrate
  - *Kinase*: enyzme that phosphorylates something
  - *Phosphatase*: enzyme that dephosphorylates something
- Terms
  - *Catalyst* - lowers activation energy, doesn't alter equilibrium, not consumed in reaction
  - *Substrate* - what enzyme acts on
  - *Active site* - where substrate binds (noncovalently)
  - *Enzyme specificity* - only works on one substrate or small group of substrates
  - *Lock and key* - enzyme = lock, substrate = key
  - *Induced fit* - enzyme/substrate change shape after binding to facilitate reaction
  - *Saturation kinetics*: reaction rate increases sharply, then levels off to saturation
- V_{max} is maximum reaction rate, K_m is measure of affinity (higher K_m = lower affinity)
- Temperature, pH affect enzyme function
- Cofactors
  - *Cofactor*: non-protein compound
    - Can be organic (vitamins, ATP, heme) or inorganic (Mg^{2+}, Cu^{+}, Mn^{2+})
    - *Coenzyme*: loosely bound
    - *Prosthetic group*: covalently bound to enzyme
  - *Cosubstrate*: binds reversibly to enzyme, flip flops between two forms (ATP)
  - *Vitamins*: essential coenzymes (can't be produced by body)
- Inhibition
  - *Irreversible inhibition*: agent covalently bonds to enzyme, disables it
  - *Competitive inhibition*: agent competes with substrate in active site; can increase reaction rate by adding more substrate - increases K_m but doesn't change V_{max}
  - *Noncompetitive inhibition*: agent binds noncovalently to another location on enzyme; can't increase reaction rate by adding more substrate - lowers V_{max} but doesn't change K_m
- Regulation
  - *Zymogen/proenzyme*: original inactive form of enzyme, something in environment must change it by cleaving peptide bonds to activate it (i.e. pepsinogen → pepsin, fibrinogen → fibrin)
  - *Allosteric interactions*: enzyme conformation changed by binding of inhibitor or activator; doesn't usually follow typical kinetics.
  - *Cooperativity*: in an allosteric enzyme, first substrate binding can help other substrates to bind
  - *Negative feedback*: products downstream in metabolic process shut off enzymes early on
  - *Positive feedback*: products downstream activate enzyme early on





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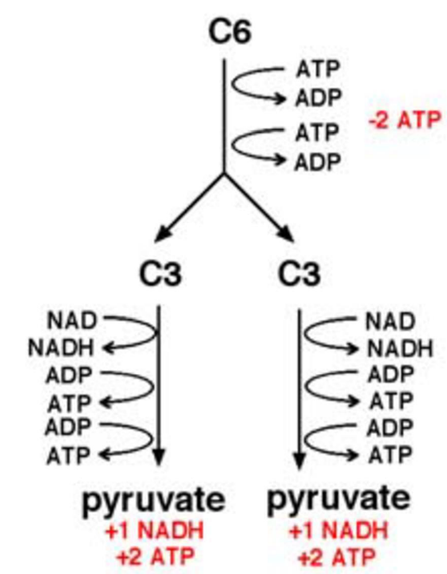
Cellular metabolism

- Steps:
  a. Macromolecules broken down
  b. Parts oxidized to metabolites to form ATP/NADH/$FADH_2$
  c. Citric acid cycle/oxidative phosphorylation if possible (respiration)
- Glycolysis
  - Occurs in the cytosol
  - 6-carbon glucose broken down to two 3-carbon pyruvates
  - 4 ATP + 2 NADH created, 2 ATP used to phosphorylate glucose = 2 net ATP, 2 NADH
  - ATP created via *substrate-level phosphorylation*



- Anaerobic respiration
  - Doesn't need oxygen
  - Need to convert NADH back to NAD^+ after glycolysis
    - *Ethanol fermentation*: converts pyruvate to ethanol (yeast)
    - *Lactic acid fermentation*: converts pyruvate to lactic acid (human muscle cells)
  - *Obligate anaerobe*: organism that is poisoned by oxygen
  - *Facultative anaerobe*: organism that can do either aerobic & anaerobic respiration
- Aerobic respiration
  - Occurs in mitochondrial matrix
  - Pyruvate converted to acetyl CoA within matrix releasing CO_2
  - *Krebs cycle*: Acetyl CoA (2C) + oxaloacetate (4C) -> -> -> -> oxaloacetate + 2 CO_2 + 1 ATP + 3 NADH + 2 $FADH_2$
  - Note glucose = 2 pyruvate = 2 acetyl CoA = 2 turns of Krebs = 2 ATP + 6 NADH + 4 $FADH_2$
  - Followed by electron transport chain
  - Total output of aerobic respiration: 36 ATP
  - Chemical formula: Glucose + O_2 -> CO_2 + H_2O

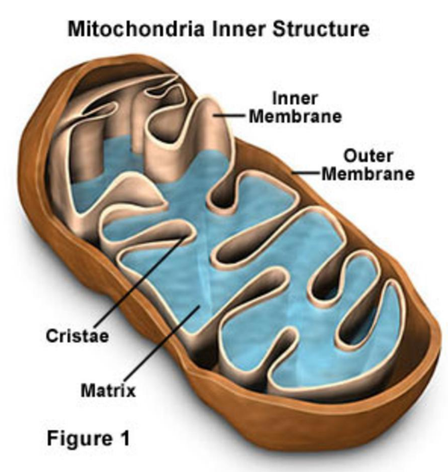
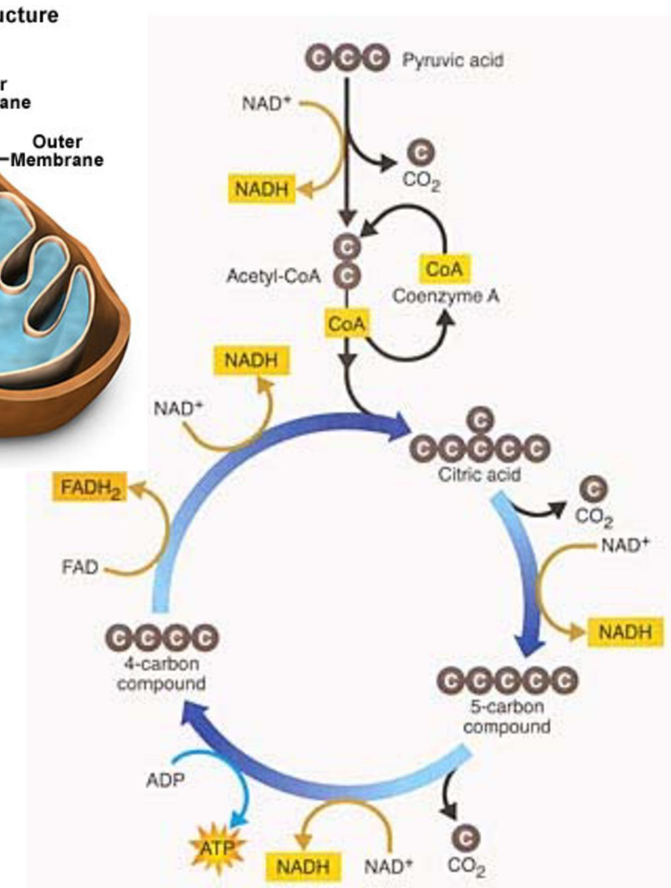
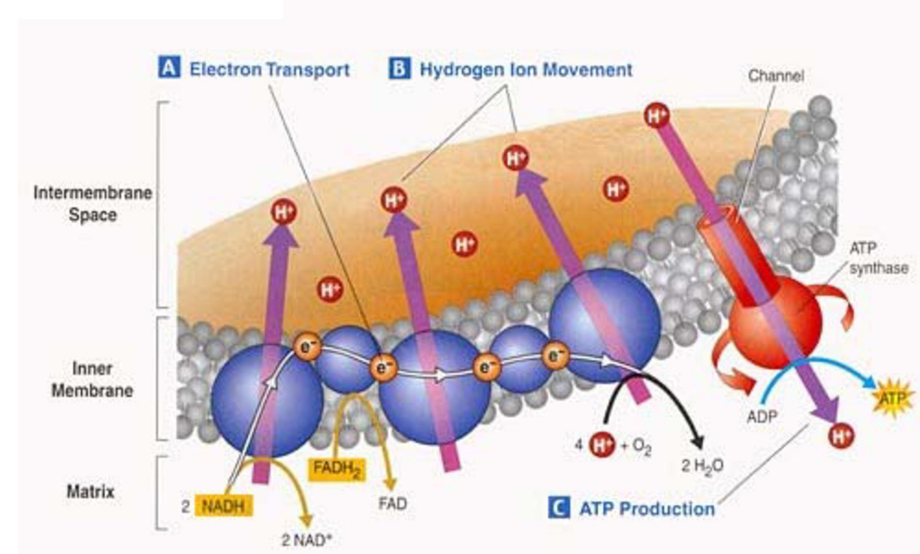


Figure 1



- Electron transport chain
  1. NADH/$FADH_2$ donate high energy electrons to (are oxidized by) series of proteins on inner mitochondrial membrane
  2. H^+ pumped into intermembrane space
  3. H^+ diffuses back into matrix through ATP synthase to create ATP (*oxidative phosphorylation*)
  - Produces 3 ATP per NADH (except NADH produced in glycolysis which is 2 ATP), 2 ATP per $FADH_2$
- Other molecules
  - Fatty acids are converted to acyl CoA (long chain), then chopped up in mitochondrial matrix into acetyl CoA releasing NADH and $FADH_2$
  - Amino acids deaminated in liver, can enter Krebs cycle as acetyl CoA or at other stages