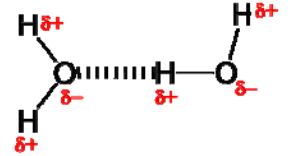


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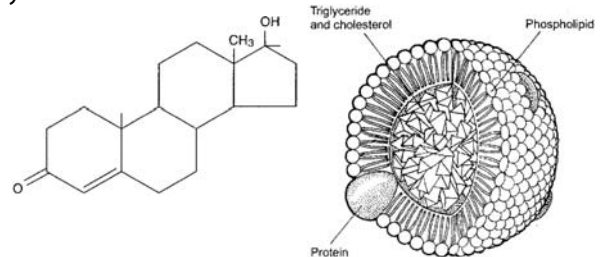
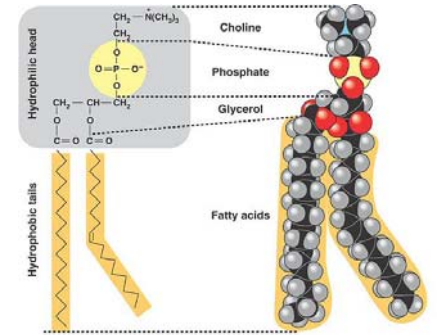
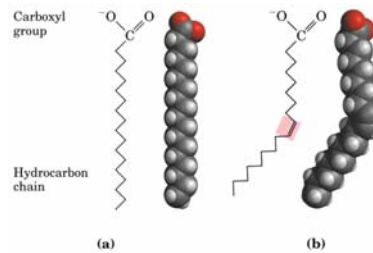
Water

- *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 ($R-O-R \rightarrow R-OH + HO-R$)
- *Dehydration synthesis*: removing water to form a bond ($R-OH + HO-R \rightarrow R-O-R$)



Lipids

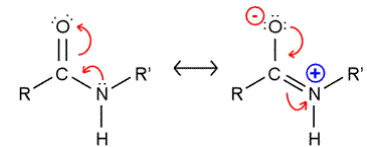
- Functions:
 - Store energy
 - Component of membranes
 - Thermal insulation/padding
 - Endocrine + local hormones
 - Vitamins
- Types:
 - *Fatty acids*: saturated (single bonds; higher density/energy; solid fats) vs. unsaturated (double bonds; kinks cause lower density; oils)
 - *Triacylglycerols/triglycerides*: 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



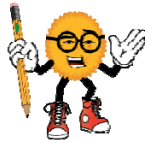
Proteins

- Globular proteins
 - 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
- Structural proteins: 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



- Amino acids
 - 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

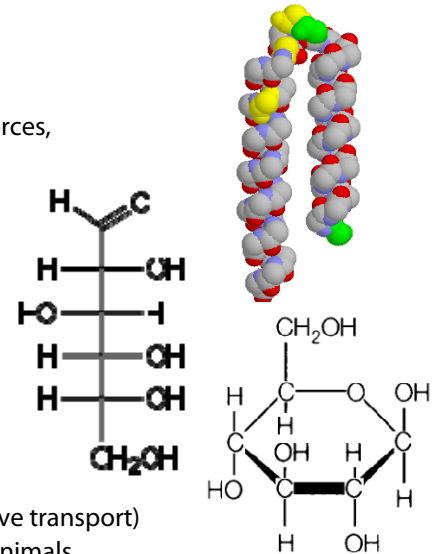


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Protein structure

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
 - o Proline is a helix breaker, causes hairpins (green in figure to right)
 - o *Denaturation*: increasing temperature; increasing/decreasing pH

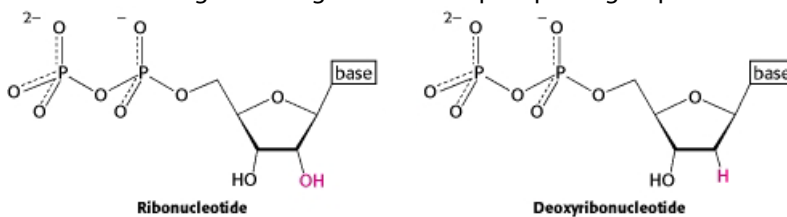


Carbohydrates

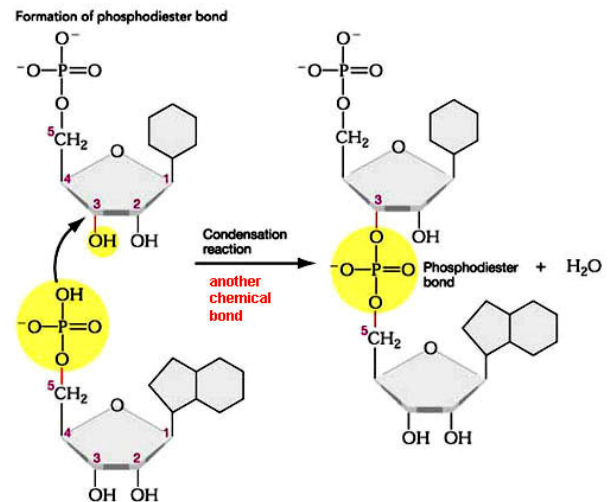
- Carbon and water, empirical formula $C(H_2O)$
- Glucose
 - o Molecular formula $C_6H_{12}O_6$
 - o Forms rings in solution due to nucleophilic addition
 - o Has two ring forms (anomers) - alpha and beta; beta points up
 - o Absorbed into blood against concentration gradient by sodium cotransport (active 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

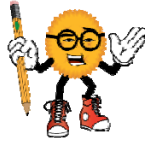


- Adenine, guanine, cytosine, thymine (DNA), and uracil (RNA)
- *Phosphodiester bonds* to form strands
- DNA has A=T, G≡C, RNA has A=U, G≡C
- Strands go from 5'→3' (phosphate end to OH end)
- DNA has double helix (*antiparallel*), RNA may or may not
- A-T has 2 hydrogen bonds, C-G has 3 hydrogen bonds (more C-G = more resistant to denaturation = higher melting point)
- Other nucleotides: ATP (energy), cyclic AMP (2nd messenger), NADH/FADH₂ (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)

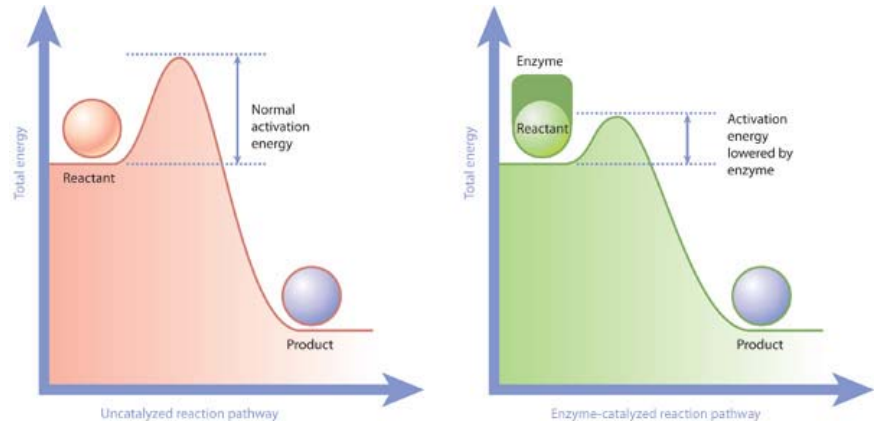


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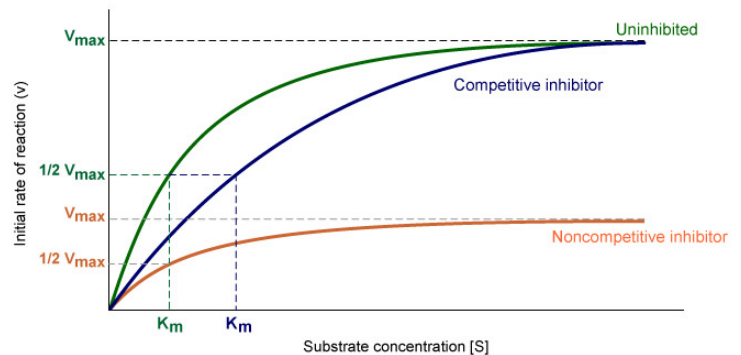
Enzymes

- Typically globular proteins, sometimes nucleic acids
- End in -ase, stuff before -ase is usually the substrate
 - *Kinase*: enzyme 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)

The Effects of Inhibition on Enzyme Kinetics



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- 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:**
 - Macromolecules broken down
 - Parts oxidized to metabolites to form ATP/NADH/FADH₂
 - Citric acid cycle/oxidative phosphorylation if possible (respiration)
- **Glycolysis**
 - Occurs in the cytosol
 - 6-carbon glucose broken down to two 2-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 CO₂
 - *Krebs cycle*: Acetyl CoA (2C) + oxaloacetate (4C) → → → → oxaloacetate + 2 CO₂ + 1 ATP + 3 NADH + 2 FADH₂
 - Note glucose = 2 pyruvate = 2 acetyl CoA = 2 turns of Krebs = 2 ATP + 6 NADH + 4 FADH₂
 - Followed by electron transport chain
 - Total output of aerobic respiration: 36 ATP
 - Chemical formula: Glucose + O₂ → CO₂ + H₂O
- **Electron transport chain**
 - NADH/FADH₂ donate high energy electrons to (are oxidized by) series of proteins on inner mitochondrial membrane
 - H⁺ pumped into intermembrane space
 - 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 FADH₂
- **Other molecules**
 - Fatty acids are converted to acyl CoA (long chain), then chopped up in mitochondrial matrix into acetyl CoA releasing NADH and FADH₂
 - Amino acids deaminated in liver, can enter Krebs cycle as acetyl CoA or at other stages

