

AP* BIOLOGY

BIOCHEMISTRY

Biochemistry

Objective

To review the student on the concepts and processes necessary to successfully answer questions over biochemistry excluding enzymes. Enzymes receive a more thorough treatment in a separate session

Standards

Photosynthesis is addressed in the topic outline of the College Board AP Biology Course Description Guide as described below.

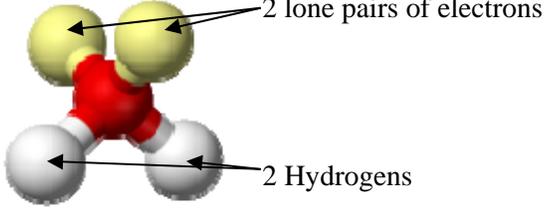
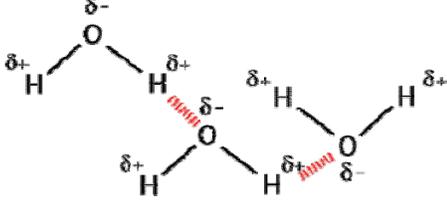
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|--------------------------------|
| I. Molecules & Cells |
| A. Chemistry of Life |
| Water |
| Organic molecules in organisms |
| Free energy changes |
| Enzymes |

AP Biology Exam Connections

Biochemistry is tested every year on the multiple choice and also make appearances on the free response section of the exam. As with many AP Biology free response, these topics are often intertwined with other topics. It is not common to see an entire biochemistry free response. Biochemistry questions usually seem to permeate questions about membranes and transpiration. The College Board seems to be especially fond of the four levels of protein structure on the free response portion of the test. The list below identifies free response questions that have been previously asked over these topics. These questions are available from the College Board and can be downloaded free of charge from AP Central <http://apcentral.collegeboard.com>.

Biochemistry

Atoms & Bonding Review	
Atoms	Bonding
<p>→Matter is made up of atoms</p> <p>→Atoms are made up of p^+, n, and e^-</p> <p>→Terms to know: elements, atomic number, and atomic mass</p> <p>→Atomic structure determines chemical characteristics.</p> <ul style="list-style-type: none"> ▪ isotopes (ex. C^{12}, C^{13}, C^{14}) ▪ valence electrons: outer most shell of e^- ▪ orbitals: clouds where electrons tend to be found ▪ energy levels: distance of e^- measured from the nucleus 	<p>→Ionic bonds: transferring of electrons</p> <p>→Covalent bonds: sharing of electrons</p> <ul style="list-style-type: none"> ▪ single, double, triple bonds ▪ may not share equally (polarity) <p>→Hydrogen bonds: Occur in polar molecules in which a hydrogen atom is covalently bonded to a very electronegative element, specifically N, O, or F. Hydrogen bonds are technically an intermolecular force, not a bond.</p>
<p>Summary→ The nucleus consists of protons and neutrons. Electrons are found in general areas with general shapes. These areas are called electron clouds. In addition, electron energy can be measured as a distance from the nucleus. Energy levels and electron orbitals overlap. It is therefore possible that two electrons be at different energy levels while occupying the same orbital. The valence electrons are most significant as they are involved in bonding.</p>	

Water	
	
<p>→Due to the two lone pairs of electrons (represented as the two on top in the picture), the molecular shape of water is bent.</p> <p>→Though oxygen and hydrogen are bonded covalently, oxygen is <i>highly electronegative</i> in comparison to hydrogen. This unequal sharing of electrons results in water molecules being <u>polar</u> with slight negative and slight positive charges as displayed top, right.</p> <p>→Hydrogen bonds: This polarity results in hydrogen bonding between H_2O molecules.</p> <p>→Nearly all other characteristics of liquid water can be explained based on the information above.</p> <ul style="list-style-type: none"> ▪ Cohesion and surface tension: water “sticks to itself” due to H bonding ▪ Adhesion: water sticks to other substances so long as H bonds are a possibility. ▪ Capillary action: such as water traveling up a straw is due to adhesion (water is sticking to the sides) and cohesion (water pulls up more water molecules as it moves up the side). ▪ High specific heat & high heat of vaporization: Remember that temperature is a measure of kinetic energy. Even though individual H bonds are considered weak, a water molecule must break free from many H bonds when increasing in temperature or changing phase to water vapor. ▪ Universal solvent: Due to the polarity of water molecules, they are “good dissolvers” of all things polar. <p>→Ice floats: Due to the crystalline structure of ice, it is less dense than water.</p>	

Biological significance

→Due to the high specific heat of water, much energy is needed to raise the temperature of water. During the heat of day, a body can sweat to cool off. A little bit of sweat will result in the absorbance of a great amount of heat. When heat exits the body, the body is cooling. If water did not have a high specific heat, more water would be needed to cool the body increasing the likelihood of dehydration. For the same reasons, bodies of water would experience greater temperature swings from midnight to midday were it not for the high specific heat of water. It may be more challenging for organisms to maintain homeostasis in this environment.

→Ironically, floating ice acts as an insulator to the water underneath. Lakes are less likely to freeze completely due to the fact that ice floats.

→This list is not all inclusive (surface tension: water striders,etc.).

Carbon & Biomolecule Synthesis

Carbon & Bonding

→Remember that the name ending denotes the type of covalent bond (single: -ane, double: ene, triple: yne)

→Carbon bonding is naturally covalent NOT ionic.

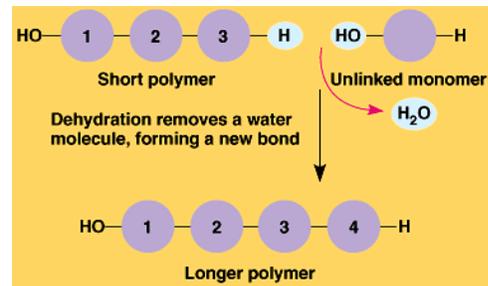
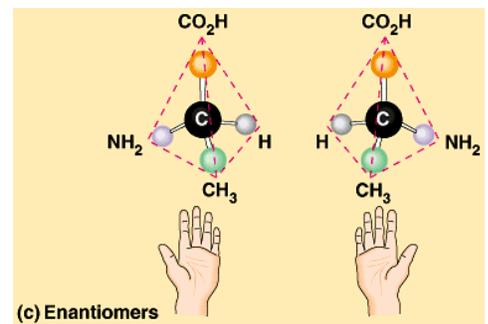
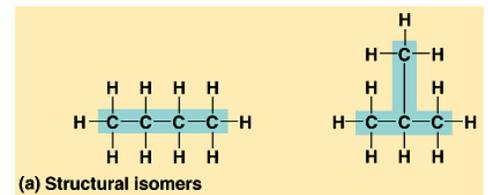
→Carbon has 4 valence electrons resulting in 4 bonds (tetravalent). Recall that shape is important in biomolecules. Because C has 4 bonding sites and can bond with itself, essentially endless chains and shapes can be created. These shapes are important in enzymes, protein channels, etc.

→Functional groups: Be able to identify

- Hydroxyl (-OH)
- Sulfhydryl (-SH)
- Carboxyl (-COOH or -COO⁻)
- Amino (-NH₂ or NH₃⁺)
- Phosphate (-PO₄)
- Methyl (-CH₃)

→Isomers: An isomer is a rearrangement of a molecule's components. The same number and kind of each atom is involved, but they are rearranged.

- Structural isomer- relocation of atoms
- Stereoisomer (enantiomer)- mirror image.
 - The importance is that arrangement and shape matters: L- amino acids are biologically available, R- are not.



Building of macromolecules

→Metabolism is the elegant interplay of catabolic (breaking down) and anabolic (building up) reactions.

→Polymers are made up of smaller units called monomers

→Dehydration synthesis removes an -H from one monomer and an -OH from another to form a bond ($H+OH \rightarrow H_2O$). This bond is called a glycosidic bond in carbohydrates.

→Hydrolysis is the “catabolic reverse” of dehydration synthesis. Water is split, H and OH are added, bonds of the polymer are broken.

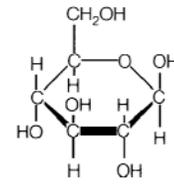
Carbohydrates

→Carbohydrates have an empirical formula of CH_2O unless they are polysaccharides. For polysaccharides subtract an H_2O for each bond.
 Example: A polymer of 6 glucose molecules would have 5 bonds created by dehydration synthesis. $\text{C}_{30}\text{H}_{60}\text{O}_{30} - 5 \text{H}_2\text{O} = \text{C}_{30}\text{H}_{50}\text{O}_{25}$
 →Carbohydrates typically have an -ose ending (glucose, fructose, lactose...)

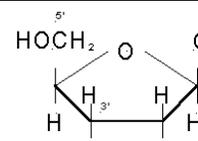
→Functions of carbohydrates

- Energy source (stored in the C-H bonds): Glucose, glycogen
- Structural: cellulose
- Cell recognition: glycoproteins

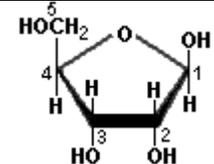
→Carbohydrates may be monosaccharides (glucose, fructose), disaccharides (sucrose, lactose), or polysaccharides (starch, cellulose, glycogen)



Glucose



Deoxyribose



Ribose

→Students are often asked to identify molecular structures on the exam. Students should be able to identify ribose, deoxyribose, and glucose. Note: Ribose has an -OH group at the 2' carbon, while **Deoxyribose** has an -H.

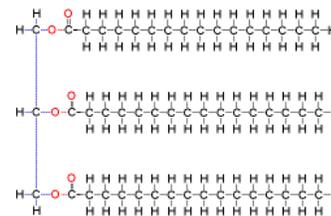
Lipids

→Energy is contained in the C-H bonds of lipids
 →Lipids are hydrophobic.
 →Common example: triglyceride (glycerol molecule with 3 fatty acid tails)
 →Cholesterol is a lipid. While cholesterol is more likely to participate in arterial blockage, cholesterol is needed in membranes for fluidity control and also acts as the precursor to steroid hormones.

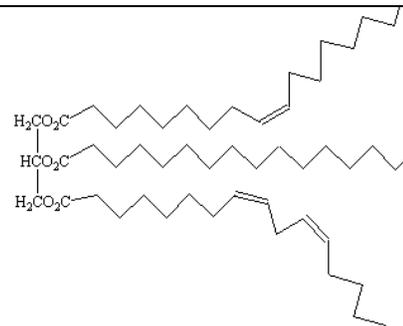
Bonding

→**Saturated fats:** Triglycerides with only single C-C bonds are called saturated. They are “saturated” with the maximum amount of hydrogen. Because the fatty acid tails are straight and uniform it is possible to pack many saturated fats into a small area making a solid. Saturated fats therefore tend to be solid at room temperature. Sticky, hydrophobic fats are still quite sticky when absorbed into the water-based bloodstream. It is thought that these fats are more likely to stick to artery walls; because of this, saturated fats are/were often referred to as “bad” fats.

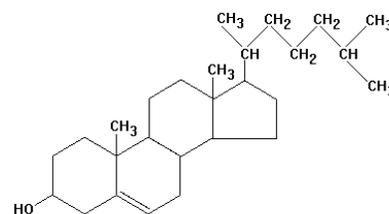
→**Unsaturated fats:** Triglycerides with C=C bonds are not completely saturated with hydrogen (for every C=C two hydrogens must be removed). These are called unsaturated fats. When C=C bonds are introduced, “kinks” are more likely to occur (esp. cis formation). This shape results in the inability of the lipids to pack together closely and because of this, unsaturated fats tend to be liquid at room temperature.



Saturated fat



Unsaturated fat



Cholesterol

→Students are often asked to identify molecular structures on the exam. Students should be able to identify the glycerol molecule a saturated and unsaturated triglyceride, and cholesterol

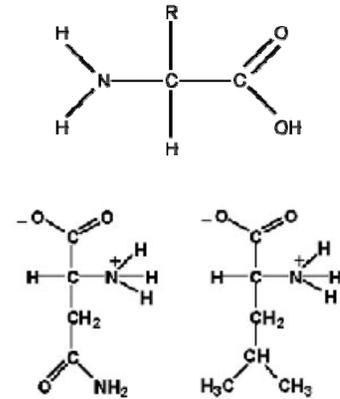
Proteins

Diversity of Structure & Function

- globular (enzymes, receptors, channels, etc.)
- fibrous (collagen, keratin, actin & myosin, etc.)
- peptides (signals)
- “-ase” ending denotes an enzyme, non-enzyme proteins often end with “-in”

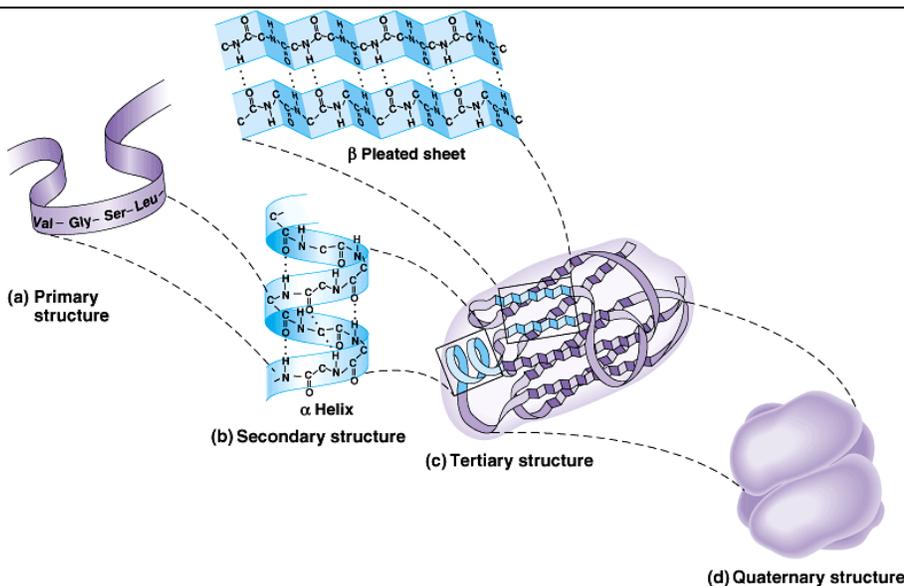
Amino Acids

- Note that each amino acid contains an **amino** group and a **carboxylic acid** (carboxyl). These two groups may gain and lose hydrogen depending on pH of the surrounding environment. The amino group may be $-NH_3^+$ or NH_2 . The carboxyl group may be $-COOH$ or $-COO^-$
- Amino acids are the building blocks of proteins. Each amino “R” group = diff. properties = versatility...small, large, polar, nonpolar, charged, etc.
- Amino acids linked via peptide bonds through dehydration synthesis.
- Hydrophobic / hydrophilic interactions shape proteins based on the R groups involved.
- In addition, chaperonin proteins can also sequester amino acid chains to allow proper folding.



Proteins: Levels of Protein Structure

- Primary structure is the order of the amino acids (coded for by DNA/RNA)
- Secondary structure is the interaction of primary structure with itself forming hydrogen bonds within the same chain of amino acids.
 - Alpha helix
 - Beta pleated sheet
- Tertiary structure is the interaction of secondary structures with other secondary structures within the same chain of amino acids. Disulfide bridges between cysteines are common for added strength & stability.
- Quaternary structure is the introduction of additional amino acid chains. Essentially the tertiary structures of one polymer of amino acids interacting with another (hemoglobin is the most commonly cited example).

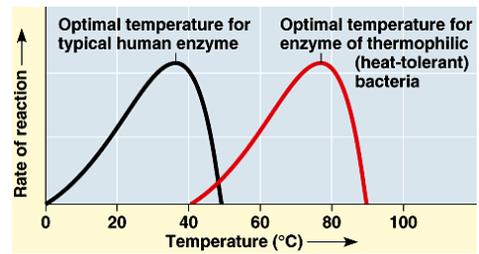
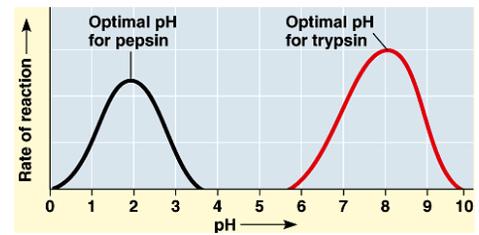


Proteins: Shape & Denaturation

→ Be it the active site of an enzyme or the long rod-like shape of myosin, shape is of paramount importance to proteins. Shape is determined based on the sequence of amino acids. One change in an amino acid can have a drastic effect (sickle cell anemia, cystic fibrosis, etc.)

→ Denaturation is when the shape of a protein irreversibly changes.

- pH- A high concentration of H^+ ions will certainly interfere with negatively charged “R” groups. Once this occurs the most stable form/shape of the protein may be different from what was originally intended. Low pH may also denature a protein.
- Ion concentration- High concentrations of a specific ion may denature enzymes through a scenario similar to pH.
- High temperature- High temperature results in a shift in protein shape to a form that is more stable at that temperature. Low temperature does not typically denature a protein, enzyme activity at low temperature decreases due to decreased molecular collisions.



Summary → Proteins have a “window of life” in which they function properly. They are able to maintain shape as long as the pH, ion concentrations, and temperature are not at extremes. Protein shape is due to the levels of protein structure which begin with amino acid sequences coded for by DNA. In short genetic diseases can be explained by the following flow chart: A change in the genetic code → possible change in the amino acid sequence (“possible” due to redundancy of the genetic code) → change in shape of the protein → likely useless protein.

→ Students are often asked to ID the structure of an amino. Students may also be asked to identify the carboxyl and amino groups within the structure.

Nucleic Acids

→DNA is a polymer the monomer of which is the nucleotide. A nucleotide consists of a phosphate, deoxyribose, and a nitrogenous base(A,T,G,C). RNA is similar with differences being: single stranded, U instead of T, ribose instead of deoxyribose.

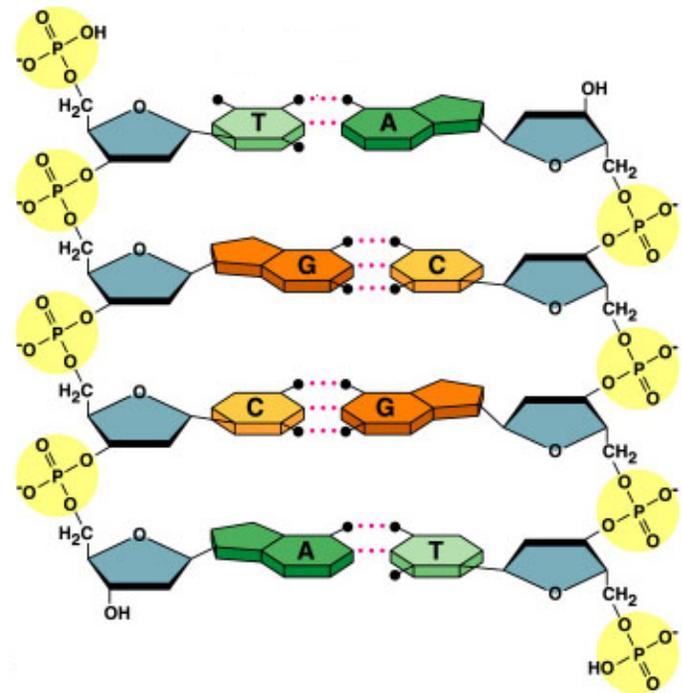
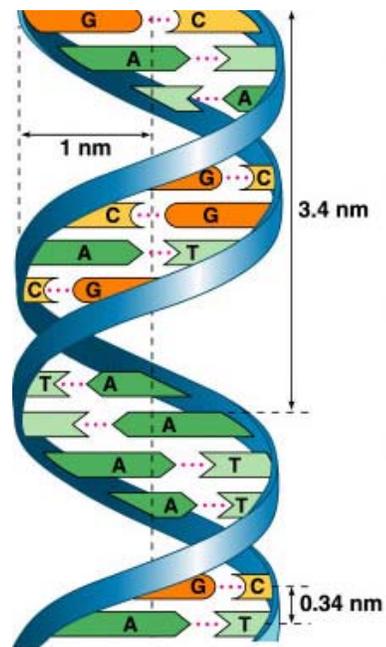
→Notation of sugar 5' and 3' - Students should be able to point out the 5' and 3' and realize that this is a man made mechanism equivalent to giving a molecule a right side up/upside down nomenclature

→Adenine is complementary to Thymine; Guanine is complementary to Cytosine.
 Note that the A and G are both “double ring structures” and that T and C are “single ring structures.” A and G are referred to as purines. T & C are pyrimidines.
 (Mnemonic: Purines = a,g...Pure as gold). Due to size constraints of the DNA backbone, a purine (big) must combine with a pyrimidine (small) in order to fit. Why can't A:C?...Note that there are three sites for H bonds on G & C and only two on A & T. The only possible combination that due to size and bonding is A:T and G:C.

→DNA is stable. The charged DNA backbone (thanks to phosphate) and polar sugars will be stable in the water based fluid in the nucleus, the hydrophobic bases are shielded internally from H₂O. This is of course reminiscent of the phospholipid bilayer.

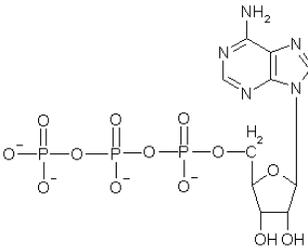
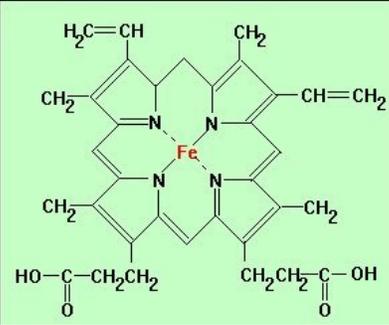
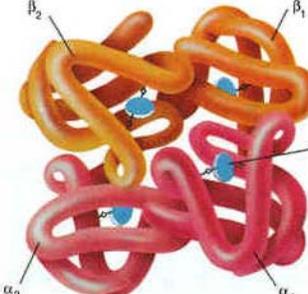
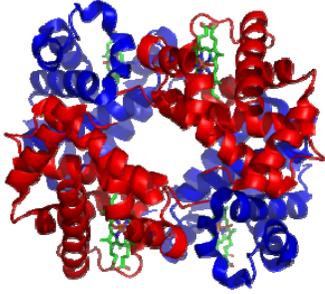
→The sugar phosphate backbone is joined via a phosphodiester bond. The joining of this backbone is accomplished via dehydration synthesis.

→DNA has a major groove and a minor groove. Note the difference in groove when looking up at the pic vertically. The significance of the major groove comes later during transcription as transcription factors are thought to “scan” the major grooves before unzipping DNA



→In the past, students have been asked to identify the “anatomy” of DNA. Students should be able to identify a: purine, pyrimidine, deoxyribose, phosphate group, phosphodiester bond, covalent bond, hydrogen bond, and 5' and 3' carbons on deoxyribose.

Summary of “Molecules that you absolutely must be able to identify”

Summary of “Molecules and functional groups that you absolutely must be able to identify”	
<p>Functional groups</p> <ul style="list-style-type: none"> ▪ Hydroxyl (-OH) ▪ Sulfhydryl (-SH) ▪ Carboxyl (-COOH or -COO⁻) ▪ Amino (-NH₂ or NH₃⁺) ▪ Phosphate (-PO₄) ▪ Methyl (-CH₃) <p>Common Molecules</p> <ul style="list-style-type: none"> ▪ Ribose ▪ Deoxyribose ▪ Glucose ▪ Polymers of glucose may be starch, chitin, glycogen, etc. depending on bonding arrangement. No need to be able to decipher between them. ▪ Glycerol ▪ Saturated fat ▪ Unsaturated fat ▪ Cholesterol ▪ ATP ▪ DNA components <ul style="list-style-type: none"> ▪ Purine ▪ Pyrimidine ▪ Deoxyribose (including 5' and 3' carbon notation) ▪ Phosphate ▪ Bonds (hydrogen, phosphodiester, covalent) ▪ Amino acid structure ▪ Hemoglobin 	<p>Structures NOT represented previously in this packet</p> <div style="display: flex; justify-content: space-around; align-items: flex-start;"> <div style="text-align: center;">  <p>ATP</p> </div> <div style="text-align: center;">  <p>Hemoglobin</p> </div> </div> <div style="display: flex; justify-content: space-around; align-items: center; margin-top: 20px;"> <div style="text-align: center;">  <p>Hemoglobin (another view)</p> </div> <div style="text-align: center;">  <p>Hemoglobin (another view)</p> </div> </div>