Test I October 3rd 2005 BIOG300

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1. The three-dimensional structure of macromolecules is formed and maintained primarily through noncovalent interactions. Which one of the following is *not* considered a noncovalent interaction?

1. **carbon-carbon bonds**
2. hydrogen bonds
3. hydrophobic interactions
4. ionic interactions
5. van der Waals interactions

2. What functional groups are present on this molecule?

![F03002](data:None;base64,)

1. ether and aldehyde
2. **hydroxyl and aldehyde**
3. hydroxyl and carboxylic acid
4. hydroxyl and ester
5. hydroxyl and ketone

3. Stereoisomers that are nonsuperimposable mirror images of each other are known as:

1. anomers.
2. cis-trans isomers.
3. diastereoisomers.
4. **enantiomers.**
5. geometric isomers.

4. If heat energy is absorbed by the system during a chemical reaction, the reaction is said to be:

1. at equilibrium.
2. endergonic.
3. **endothermic.**
4. exergonic.
5. exothermic.

5. The major carrier of chemical energy in all cells is:

1. acetyl triphosphate.
2. adenosine monophosphate.
3. **adenosine triphosphate.**
4. cytosine tetraphosphate.
5. uridine diphosphate.

6. Energy requiring metabolic pathways that yield complex molecules from simpler precursors are:

1. amphibolic.
2. **anabolic.**
3. autotrophic.
4. catabolic.
5. heterotrophic.

7. The three-dimensional structure of a protein is determined primarily by:

1. electrostatic guidance from nucleic acid structure.
2. how many amino acids are in the protein.
3. hydrophobic interaction with lipids that provide a folding framework.
4. modification during interactions with ribosomes.
5. **the sequence of amino acids in the protein.**

8. Which of these statements about hydrogen bonds is *not* true?

1. Hydrogen bonds account for the anomalously high boiling point of water.
2. In liquid water, the average water molecule forms hydrogen bonds with three to four other water molecules.
3. Individual hydrogen bonds are much weaker than covalent bonds.
4. **Individual hydrogen bonds in liquid water exist for many seconds and sometimes for minutes.**
5. The strength of a hydrogen bond depends on the linearity of the three atoms involved in the bond.

9. Hydrophobic interactions make important energetic contributions to:

1. binding of a hormone to its receptor protein.
2. enzyme-substrate interactions.
3. membrane structure.
4. three-dimensional folding of a polypeptide chain.
5. **all of the above are true.**

10. Which of the following is true about the properties of aqueous solutions?

1. A pH change from 5.0 to 6.0 reflects an increase in the hydroxide ion concentration ([OH-]) of 20%.
2. A pH change from 8.0 to 6.0 reflects a decrease in the proton concentration ([H+]) by a factor of 100.
3. Charged molecules are generally insoluble in water.
4. **Hydrogen bonds form readily in aqueous solutions.**
5. The pH can be calculated by adding 7 to the value of the pOH.

11. The pH of a sample of blood is 7.4, while gastric juice is pH 1.4. The blood sample has:

1. 0.189 times the [H+] as the gastric juice.
2. 5.29 times lower [H+] than the gastric juice.
3. 6 times lower [H+] than the gastric juice.
4. 6,000 times lower [H+] than the gastric juice.
5. **a million times lower [H+] than the gastric juice.**

12. Phosphoric acid is tribasic, with p*K*a’s of 2.14, 6.86, and 12.4. The ionic form that predominates at pH 3.2 is:

1. H3PO4.
2. **H2PO4–.**
3. HPO42–.
4. PO43–.
5. none of the above.

13. Three buffers are made by combining a 1 M solution of acetic acid with a 1 M solution of sodium acetate in the ratios shown below.

##### 1 M acetic acid 1 M sodium acetate

Buffer 1: 10 mL 90 mL

Buffer 2: 50 mL 50 mL

Buffer 3: 90 mL 10 mL

Which of these statements is true of the resulting buffers?

1. pH of buffer 1 < pH of buffer 2 < pH of buffer 3
2. pH of buffer 1 = pH of buffer 2 = pH of buffer 3
3. **pH of buffer 1 > pH of buffer 2 > pH of buffer 3**
4. The problem cannot be solved without knowing the value of p*K*a.
5. None of the above.

14. The chirality of an amino acid results from the fact that its  carbon:

1. has no net charge.
2. is a carboxylic acid.
3. **is bonded to four different chemical groups.**
4. is in the l absolute configuration in naturally occurring proteins.
5. is symmetric.

15. Of the 20 standard amino acids, only \_\_\_\_\_\_\_\_\_\_\_ is not optically active. The reason is that its side chain \_\_\_\_\_\_\_\_\_\_\_.

1. alanine; is a simple methyl group
2. **glycine; is a hydrogen atom**
3. glycine; is unbranched
4. lysine; contains only nitrogen
5. proline; forms a covalent bond with the amino group

16. Which of the following statements about *cystine* is correct?

1. **Cystine forms when the —CH2—SH R group is oxidized to form a —CH2—S—S—CH2— disulfide bridge between two cysteines.**
2. Cystine is an example of a nonstandard amino acid, derived by linking two standard amino acids.
3. Cystine is formed by the oxidation of the carboxylic acid group on cysteine.
4. Cystine is formed through a peptide linkage between two cysteines.
5. Two cystines are released when a —CH2—S—S—CH2— disulfide bridge is reduced to —CH2—SH.

17. Amino acids are ampholytes because they can function as either a(n):

1. **acid or a base.**
2. neutral molecule or an ion.
3. polar or a nonpolar molecule.
4. standard or a nonstandard monomer in proteins.
5. transparent or a light-absorbing compound.

18. Titration of valine by a strong base, for example NaOH, reveals two p*K*’s. The titration reaction occurring at p*K*2 (p*K*2 = 9.62) is:

A) —COOH + OH  —COO + H2O.

B) —COOH + —NH2   —COO + —NH2+.

C) —COO + —NH2+   —COOH + —NH2.

D)  **—NH3+ + OH  —NH2 + H2O.**

E) —NH2 + OH  —NH + H2O.

19. At the isoelectric pH of a tetrapeptide:

1. only the amino and carboxyl termini contribute charge.
2. the amino and carboxyl termini are not charged.
3. **the total net charge is zero.**
4. there are four ionic charges.
5. two internal amino acids of the tetrapeptide cannot have ionizable R groups.

20. Which of the following is correct with respect to the amino acid composition of proteins?

1. Larger proteins have a more uniform distribution of amino acids than smaller proteins.
2. Proteins contain at least one each of the 20 different standard amino acids.
3. **Proteins with different functions usually differ significantly in their amino acid composition.**
4. Proteins with the same molecular weight have the same amino acid composition.
5. The average molecular weight of an amino acid in a protein increases with the size of the protein.

21. In a mixture of the five proteins listed below, which should elute second in size-exclusion (gel- filtration) chromatography?

1. cytochrome *c* *M*r = 13,000
2. **immunoglobulin G *M*r = 145,000**
3. ribonuclease A *M*r = 13,700
4. RNA polymerase *M*r = 450,000
5. serum albumin *M*r = 68,500

22. By adding SDS (sodium dodecyl sulfate) during the electrophoresis of proteins, it is possible to:

1. determine a protein’s isoelectric point.
2. determine an enzyme’s specific activity.
3. determine the amino acid composition of the protein.
4. preserve a protein’s native structure and biological activity.
5. **separate proteins exclusively on the basis of molecular weight.**

23. The first step in two-dimensional gel electrophoresis generates a series of protein bands by isoelectric focusing. In a second step, a strip of this gel is turned 90 degrees, placed on another gel containing SDS, and electric current is again applied. In this second step:

1. **proteins with similar isoelectric points become further separated according to their molecular weights.**
2. the individual bands become stained so that the isoelectric focus pattern can be visualized.
3. the individual bands become visualized by interacting with protein-specific antibodies in the second gel.
4. the individual bands undergo a second, more intense isoelectric focusing.
5. the proteins in the bands separate more completely because the second electric current is in the opposite polarity to the first current.

24. The term *specific* *activity* differs from the term *activity* in that specific activity:

1. is measured only under optimal conditions.
2. **is the activity (enzyme units) in a milligram of protein.**
3. is the activity (enzyme units) of a specific protein.
4. refers only to a purified protein.
5. refers to proteins other than enzymes.

25. The functional differences, as well as differences in three-dimensional structures, between two different enzymes from *E.* *coli* result directly from their different:

1. affinities for ATP.
2. **amino acid sequences.**
3. roles in DNA metabolism.
4. roles in the metabolism of *E.* *coli*.
5. secondary structures.

26. A nonapeptide was determined to have the following amino acid composition: (Lys)2, (Gly) 2, (Phe) 2, His, Leu, Met. The native peptide was incubated with 1-fluoro-2,4-dinitrobenzene (FDNB) and then hydrolyzed; 2,4-dinitrophenylhistidine was identified by HPLC. When the native peptide was exposed to cyanogen bromide (CNBr), an octapeptide and free glycine were recovered. Incubation of the native peptide with trypsin gave a pentapeptide, a tripeptide, and free Lys. 2,4-Dinitrophenyl-histidine was recovered from the pentapeptide, and 2,4-dinitrophenylphenylalanine was recovered from the tripeptide. Digestion with the enzyme pepsin produced a dipeptide, a tripeptide, and a tetrapeptide. The tetrapeptide was composed of (Lys) 2, Phe, and Gly. The native sequence was determined to be: (Pepsin cleaves at (N) Phe, Trp, Tyr)

1. Gly–Phe–Lys–Lys–Gly–Leu–Met–Phe–His.
2. His–Leu–Gly–Lys–Lys–Phe–Phe–Gly–Met.
3. **His–Leu–Phe–Gly–Lys–Lys–Phe–Met–Gly.**
4. His–Phe–Leu–Gly–Lys–Lys–Phe–Met–Gly.
5. Met–Leu–Phe–Lys–Phe–Gly–Gly–Lys–His.

27. The term “proteome” has been used to describe:

1. regions (domains) within proteins.
2. regularities in protein structures.
3. **the complement of proteins encoded by an organism’s DNA.**
4. the structure of a protein-synthesizing ribosome.
5. the tertiary structure of a protein.

28. All of the following are considered “weak” interactions in proteins, *except:*

1. hydrogen bonds.
2. hydrophobic interactions.
3. ionic bonds.
4. **peptide bonds.**
5. van der Waals forces.

29. In the diagram below, the plane drawn behind the peptide bond indicates the:

![F06006](data:None;base64,)

1. **absence of rotation around the C—N bond because of its partial double-bond character.**
2. plane of rotation around the C—N bond.
3. region of steric hindrance determined by the large C=O group.
4. region of the peptide bond that contributes to a Ramachandran plot.
5. theoretical space between –180 and +180 degrees that can be occupied by the  and  angles in the peptide bond.

30. Which of the following best represents the backbone arrangement of two peptide bonds?

1. C—N—C—C—C—N—C—C
2. C—N—C—C—N—C
3. C—N—C—C—C—N
4. **C—C—N—C—C—N**
5. C—C—C—N—C—C—C

31. Which of the following pairs of bonds within a peptide backbone show free rotation around both bonds?

1. **C—C and N—C**
2. C=O and N—C
3. C=O and N—C
4. N—C and C—C
5. N—C and N—C

32. In an  helix, the R groups on the amino acid residues:

1. alternate between the outside and the inside of the helix.
2. **are found on the outside of the helix spiral.**
3. cause only right-handed helices to form.
4. generate the hydrogen bonds that form the helix.
5. stack within the interior of the helix.

33. Amino acid residues commonly found in the middle of  turn are:

1. Ala and Gly.
2. hydrophobic.
3. **Pro and Gly.**
4. those with ionized R-groups.
5. two Cys.

34. Proteins often have regions that show specific, coherent patterns of folding or function. These regions are called:

1. **domains.**
2. oligomers.
3. peptides.
4. sites.
5. subunits.

35. Which of the following is *not* known to be involved in the process of *assisted* folding of proteins?

1. Chaperonins
2. Disulfide interchange
3. Heat shock proteins
4. **Peptide bond hydrolysis**
5. Peptide bond isomerization

36. The interactions of ligands with proteins:

1. are relatively nonspecific.
2. are relatively rare in biological systems.
3. are usually irreversible.
4. **are usually transient.**
5. usually result in the inactivation of the proteins.

37. When oxygen binds to a heme-containing protein, the two open coordination bonds of Fe2+ are occupied by:

1. one O atom and one amino acid atom.
2. **one O2 molecule and one amino acid atom.**
3. one O2 molecule and one heme atom.
4. two O atoms.
5. two O2 molecules.

38. In the binding of oxygen to **myoglobin**, the relationship between the concentration of oxygen and the fraction of binding sites occupied can best be described as:

1. **hyperbolic.**
2. linear with a negative slope.
3. linear with a positive slope.
4. random.
5. sigmoidal.

**\*Hemoglobin is sigmoidal.**

39. An allosteric interaction between a ligand and a protein is one in which:

1. binding of a molecule to a binding site affects binding of additional molecules to the same site.
2. **binding of a molecule to a binding site affects binding properties of another site on the protein.**
3. binding of the ligand to the protein is covalent.
4. multiple molecules of the same ligand can bind to the same binding site.
5. two different ligands can bind to the same binding site.

40. In hemoglobin, the transition from T state to R state (low to high affinity) is triggered by:

1. Fe2+ binding.
2. heme binding.
3. **oxygen binding.**
4. subunit association.
5. subunit dissociation.

41. Which of the following is ***not correct*** concerning **2,3-bisphosphoglycerate (BPG)?**

1. It binds at a distance from the heme groups of hemoglobin.
2. It binds with lower affinity to fetal hemoglobin than to adult hemoglobin.
3. **It increases the affinity of hemoglobin for oxygen.**
4. It is an allosteric modulator.
5. It is normally found associated with the hemoglobin extracted from red blood cells.

42. The fundamental cause of sickle-cell disease is a change in the structure of:

1. blood.
2. capillaries.
3. **hemoglobin.**
4. red cells.
5. the heart.

43. One of the enzymes involved in glycolysis, aldolase, requires Zn2+ for catalysis. Under conditions of zinc deficiency, when the enzyme may lack zinc, it would be referred to as the:

1. **apoenzyme.**
2. coenzyme.
3. holoenzyme.
4. prosthetic group.
5. substrate.

44. Enzymes are potent catalysts because they:

1. are consumed in the reactions they catalyze.
2. are very specific and can prevent the conversion of products back to substrates.
3. drive reactions to completion while other catalysts drive reactions to equilibrium.
4. increase the equilibrium constants for the reactions they catalyze.
5. **lower the activation energy for the reactions they catalyze.**

45. The role of an enzyme in an enzyme-catalyzed reaction is to:

1. bind a transition state intermediate, such that it cannot be converted back to substrate.
2. ensure that all of the substrate is converted to product.
3. ensure that the product is more stable than the substrate.
4. **increase the rate at which substrate is converted into product.**
5. make the free-energy change for the reaction more favorable.

46. Compare the two reaction coordinate diagrams below and select the answer that correctly describes their relationship. In each case, the single intermediate is the ES complex.

![](data:None;base64,)

1. **(a) describes a strict “lock and key” model, whereas (b) describes a transition-state complementarity model.**
2. The activation energy for the *catalyzed* reaction is #5 in (a) and is #7 in (b).
3. The activation energy for the *uncatalyzed* reaction is given by #5 + #6 in (a) and by #7 + #4 in (b).
4. The contribution of binding energy is given by #5 in (a) and by #7 in (b).
5. The ES complex is given by #2 in (a) and #3 in (b).

46. Which of the following statements about a plot of *V*0 vs. [S] for an enzyme that follows Michaelis-Menten kinetics is *false*?

1. As [S] increases, the initial velocity of reaction *V*0 also increases.
2. **At very high [S], the velocity curve becomes a horizontal line that intersects the y-axis at *K*m.**
3. *K*m is the [S] at which *V*0 = 1/2 *V*max.
4. The shape of the curve is a hyperbola.
5. The y-axis is a rate term with units of m/min.

47. The double-reciprocal transformation of the Michaelis-Menten equation, also called the Lineweaver-Burk plot, is given by

1/*V*0 = *K*m /(*V*max[S]) + 1/*V*max.

To determine *K*m from a double-reciprocal plot, you would:

1. **multiply the reciprocal of the x-axis intercept by 1.**
2. multiply the reciprocal of the y-axis intercept by 1.
3. take the reciprocal of the x-axis intercept.
4. take the reciprocal of the y-axis intercept.
5. take the x-axis intercept where *V*0 = 1/2 *V*max.

48. In a plot of l/*V* against 1/[S] for an enzyme-catalyzed reaction, the presence of a competitive inhibitor will alter the:

1. curvature of the plot.
2. **intercept on the l/[S] axis.**
3. intercept on the l/*V* axis.
4. p*K* of the plot.
5. *V*max.

49. In competitive inhibition, an inhibitor:

1. binds at several different sites on an enzyme.
2. binds covalently to the enzyme.
3. binds *only* to the ES complex.
4. **binds reversibly at the active site.**
5. lowers the characteristic *V*max of the enzyme.

50. A small molecule that *decreases* the activity of an enzyme by binding to a site other than the catalytic site is termed a(n):

1. **allosteric inhibitor.**
2. alternative inhibitor.
3. competitive inhibitor.
4. stereospecific agent.
5. transition-state analog.