1. The formation of a peptide bond between two amino acids is an example of a(n) ______________ reaction.  
   A) cleavage  
   B) condensation  
   C) group transfer  
   D) isomerization  
   E) oxidation reduction

2. Which of the following statements about cystine is correct?  
   A) Cystine forms when the —CH₂—SH R group is oxidized to form a —CH₂—S—S—CH₂— disulfide bridge between two cysteines.  
   B) Cystine is an example of a nonstandard amino acid, derived by linking two standard amino acids.  
   C) Cystine is formed by the oxidation of the carboxylic acid group on cysteine.  
   D) Cystine is formed through a peptide linkage between two cysteines.  
   E) Two cystines are released when a —CH₂—S—S—CH₂— disulfide bridge is reduced to —CH₂—SH.

3. At the isoelectric pH of a tetrapeptide:  
   A) only the amino and carboxyl termini contribute charge.  
   B) the amino and carboxyl termini are not charged.  
   C) the total net charge is zero.  
   D) there are four ionic charges.  
   E) two internal amino acids of the tetrapeptide cannot have ionizable R groups.

4. Which of the following is correct with respect to the amino acid composition of proteins?  
   A) Larger proteins have a more uniform distribution of amino acids than smaller proteins.  
   B) Proteins contain at least one each of the 20 different standard amino acids.  
   C) Proteins with different functions usually differ significantly in their amino acid composition.  
   D) Proteins with the same molecular weight have the same amino acid composition.  
   E) The average molecular weight of an amino acid in a protein increases with the size of the protein.

5. The average molecular weight of the 20 standard amino acids is 138, but biochemists use 110 when estimating the number of amino acids in a protein of known molecular weight. Why?  
   A) The number 110 is based on the fact that the average molecular weight of a protein is 110,000 with an average of 1,000 amino acids.  
   B) The number 110 reflects the higher proportion of small amino acids in proteins, as well as the loss of water when the peptide bond forms.  
   C) The number 110 reflects the number of amino acids found in the typical small protein, and only small proteins have their molecular weight estimated this way.  
   D) The number 110 takes into account the relatively small size of nonstandard amino acids.  
   E) The number 138 represents the molecular weight of conjugated amino acids.

6. Which of the following refers to particularly stable arrangements of amino acid residues in a protein that give rise to recurring patterns?  
   A) Primary structure  
   B) Secondary structure  
   C) Tertiary structure  
   D) Quaternary structure  
   E) None of the above
7. 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:

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

8. 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) (Sanger Method) and then hydrolyzed; 2,4-dinitrophenylhistidine was identified by HPLC. Incubation of the native peptide with trypsin (Cleavage points at Lys, Arg) gave a pentapeptide, a tripeptide, and free Lys. 2,4-Dinitrophenylhistidine was recovered from the pentapeptide, and 2,4-dinitrophenylphenylalanine was recovered from the tripeptides (Sanger Method). Digestion with the enzyme pepsin (Cleavage points at Phe,Trp, Tyr) 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:


9. Compare the following sequences taken from four different proteins, and select the answer that best characterizes their relationships.

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>DVEKGKKIDMKCS</td>
<td>HTVEKGKHKKTGPNLH</td>
<td>GLFGRKTGQAPGYSYT</td>
</tr>
<tr>
<td>2</td>
<td>DVQRALKIDNLNGQ</td>
<td>HTVEKGAKHTAPNVH</td>
<td>GLADRIAYQAKATNEE</td>
</tr>
<tr>
<td>3</td>
<td>LVTRPLYIFNGQ</td>
<td>HTLEKAAKHKTGPNLH</td>
<td>ALKSSKDLMFTVINDD</td>
</tr>
<tr>
<td>4</td>
<td>FFMMNEDALVARSSN</td>
<td>HQFAASSIHKNAPQFH</td>
<td>NLKDSKTYLKKPVSET</td>
</tr>
</tbody>
</table>

A) Based only on sequences in column B, protein 4 reveals the greatest evolutionary divergence.
B) Comparing proteins 1 and 2 in column A reveals that these two proteins have diverged the most throughout evolution.
C) Protein 4 is the protein that shows the greatest overall homology to protein 1.
D) Proteins 2 and 3 show a greater evolutionary distance than proteins 1 and 4.
E) The portions of amino acid sequence shown suggest that these proteins are completely unrelated.

10. 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?

A) carbon-carbon bonds
B) hydrogen bonds
C) hydrophobic interactions
D) ionic interactions
E) van der Waals interactions
11. A polypeptide is hydrolyzed, and it is determined that there are 3 Lys residues and 2 Arg residues (as well as other residues). How many peptide fragments can be expected when the native polypeptide is incubated with the proteolytic enzyme Trypsin?
A) Five peptide fragments
B) Six peptide fragments
C) Five peptide fragments if the carboxy-terminal residue is Lys or Arg and six peptide fragments if it is not.
D) Six peptide fragments if the carboxy-terminal residue is Lys or Arg and five peptide fragments if it is not.
E) The number of peptide fragments cannot be determined from the information given

12. In an aqueous solution, protein conformation is determined by two major factors. One is the formation of the maximum number of hydrogen bonds. The other is the:
A) formation of the maximum number of hydrophilic interactions.
B) maximization of ionic interactions.
C) minimization of entropy by the formation of a water solvent shell around the protein.
D) placement of hydrophobic amino acid residues within the interior of the protein.
E) placement of polar amino acid residues around the exterior of the protein.

13. Which of the following best represents the backbone arrangement of two peptide bonds?
A) C—N—C—C—N
B) C—N—C—N—C
C) C—N—C—C—N
D) C—N—C—C—N—C
E) C—C—N—C—C—C

14. A D-amino acid would interrupt an α helix made of L-amino acids. Another naturally occurring hindrance to the formation of an α helix is the presence of:
A) a negatively charged Arg residue.
B) a nonpolar residue near the carboxyl terminus.
C) a positively charged Lys residue.
D) a Pro residue.
E) two Ala residues side by side.

15. The three-dimensional conformation of a protein may be strongly influenced by amino acid residues that are very far apart in sequence. This relationship is in contrast to secondary structure, where the amino acid residues involved are:
A) always side by side.
B) generally near each other in sequence.
C) invariably restricted to about 7 of the 20 standard amino acids.
D) often on different polypeptide strands.
E) usually near the polypeptide chain’s amino terminus or carboxyl terminus.

16. A sequence of amino acids in a certain protein is found to be -Ser-Gly-Pro-Gly-. The sequence is most probably part of a(n):
A) antiparallel β sheet.
B) parallel β sheet.
C) α helix.
D) α sheet.
E) β turn.
17. Proteins are classified within families or superfamilies based on similarities in:
   A) evolutionary origin.
   B) physico-chemical properties.
   C) structure and/or function.
   D) subcellular location.

18. Which of the following statements concerning the process of spontaneous folding of proteins is false?
   A) It may be an essentially random process.
   B) It may be defective in some human diseases.
   C) It may involve a gradually decreasing range of conformational species.
   D) It may involve progression from a high state of entropy to a low state of entropy.
   E) It may involve initial formation of local secondary structure.

For questions 19-23 complete the numbered statements using one of the following lettered terms:

   A. α-helix
   B. β-pleated sheet
   C. random coil
   D. all of the above
   E. none of the above

19. is present only in proteins that have a quaternary structure
20. structure is broken at proline residues
21. is produced by procedures that denature proteins
22. is formed by hydrogen bonding between the peptide bonds on adjacent chains
23. is maintained by hydrogen bonds parallel to the axis of the protein

24. Which of the following is least likely to result in protein denaturation?
   A) Altering net charge by changing pH
   B) Changing the salt concentration
   C) Disruption of weak interactions by boiling
   D) Exposure to detergents
   E) Mixing with organic solvents such as acetone

25. The interactions of ligands with proteins:
   A) are relatively nonspecific.
   B) are relatively rare in biological systems.
   C) are usually irreversible.
   D) are usually transient.
   E) usually result in the inactivation of the proteins

26. 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:
   A) hyperbolic.
   B) linear with a negative slope.
   C) linear with a positive slope.
   D) random.
   E) Sigmoidal
27. An allosteric interaction between a ligand and a protein is one in which:
   A) binding of a molecule to a binding site affects binding of additional molecules to the same site.
   B) binding of a molecule to a binding site affects binding properties of another site on the protein.
   C) binding of the ligand to the protein is covalent.
   D) multiple molecules of the same ligand can bind to the same binding site.
   E) two different ligands can bind to the same binding site

28. In hemoglobin, the transition from T state to R state (low to high affinity) is triggered by:
   A) Fe\(^{2+}\) binding.
   B) heme binding.
   C) oxygen binding.
   D) subunit association.
   E) subunit dissociation

29. The fundamental cause of sickle-cell disease is a change in the structure of:
   A) blood.
   B) capillaries.
   C) hemoglobin.
   D) red cells.
   E) the heart.

30. The substitution of a single amino acid residue in a protein due to a mutation in the DNA may have the following consequence(s):
   A) no change in protein conformation
   B) a major change in protein conformation
   C) defective folding of the protein resulting in disease
   D) any of the above
   E) none of the above

31. Kuru, Bovine spongiform encephalopathy (BSE), variant Creutzfeldt-Jakob disease (vCJ) are all examples of:
   A) genetically based diseases
   B) diseases involving defective and infectious protein
   C) diseases caused by mutations in the genome
   D) diseases that are spread by animals not humans
   E) diseases that cannot be prevented

32. The Bohr effect describes which one the following:
   A) an increased affinity of hemoglobin for oxygen at a lower pH
   B) an increased affinity of hemoglobin for oxygen at a higher partial pressure of oxygen
   C) an decreased affinity of hemoglobin for oxygen at a higher partial pressure of oxygen
   D) a decreased affinity of hemoglobin for oxygen at a lower pH
   E) a decreased affinity of hemoglobin for oxygen at a higher pH

33. Enzymes are potent catalysts because they:
   A) are consumed in the reactions they catalyze.
   B) are very specific and can prevent the conversion of products back to substrates.
   C) drive reactions to completion while other catalysts drive reactions to equilibrium.
   D) increase the equilibrium constants for the reactions they catalyze.
   E) lower the activation energy for the reactions they catalyze
34. The role of an enzyme in an enzyme-catalyzed reaction is to:
   A) bind a transition state intermediate, such that it cannot be converted back to substrate.
   B) ensure that all of the substrate is converted to product.
   C) ensure that the product is more stable than the substrate.
   D) increase the rate at which substrate is converted into product.
   E) make the free-energy change for the reaction more favorable.

35. One of the enzymes involved in glycolysis, aldolase, requires Zn$^{2+}$ for catalysis. Under conditions when the enzyme may have zinc, it would be referred to as the:
   A) apoenzyme.
   B) coenzyme.
   C) holoenzyme.
   D) prosthetic group.
   E) substrate.

36. Which one of the following is not among the six internationally accepted classes of enzymes?
   A) Hydrolases
   B) Ligases
   C) Oxidoreductases
   D) Polymerases
   E) Transferases

37. Which of the following statements about a plot of $V_0$ vs. [S] for an enzyme that follows Michaelis-Menten kinetics is false?
   A) As [S] increases, the initial velocity of reaction $V_0$ also increases.
   B) At very high [S], the velocity curve becomes a horizontal line that intersects the horizontal y-axis at $K_m$.
   C) $K_m$ is the [S] at which $V_0 = 1/2 V_{max}$.
   D) The shape of the curve is a hyperbola.
   E) The horizontal y-axis is a rate term with units of $\mu$m/min

38. The optimal complementation in terms of mutual shape or fit between an enzyme and substrate occurs:
   A) before they interact
   B) following the catalytic conversion of substrate to product
   C) before they are inhibited by feedback inhibition
   D) during the transition state
   E) throughout the enzymatic process

39. The following data were obtained in a study of an enzyme known to follow Michaelis-Menten kinetics:

<table>
<thead>
<tr>
<th>$V_0$ (µmol/min)</th>
<th>Substrate added (mmol/L)</th>
</tr>
</thead>
<tbody>
<tr>
<td>217</td>
<td>0.8</td>
</tr>
<tr>
<td>325</td>
<td>2</td>
</tr>
<tr>
<td>433</td>
<td>4</td>
</tr>
<tr>
<td>488</td>
<td>6</td>
</tr>
<tr>
<td>647</td>
<td>1,000</td>
</tr>
</tbody>
</table>

The $K_m$ for this enzyme is approximately:
   A) 1 mM.
   B) 1,000 mM.
   C) 2 mM.
   D) 4 mM.
   E) 6 mM.
40. In competitive inhibition, an inhibitor:

A) binds at several different sites on an enzyme.
B) binds covalently to the enzyme.
C) binds only to the ES complex.
D) binds reversibly at the active site.
E) lowers the characteristic $V_{\text{max}}$ of the enzyme.

41. $V_{\text{max}}$ for an enzyme-catalyzed reaction:

A) generally increases when pH increases.
B) increases in the presence of a competitive inhibitor.
C) is limited only by the amount of substrate supplied.
D) is twice the rate observed when the concentration of substrate is equal to the $K_m$.
E) is unchanged in the presence of a uncompetitive inhibitor.

42. Which of the following statements about allosteric control of enzymatic activity is false?

A) Allosteric effectors give rise to sigmoidal $V_0$ vs. [S] kinetic plots.
B) Allosteric proteins are generally composed of several subunits.
C) An effector may either inhibit or activate an enzyme.
D) Binding of the effector changes the conformation of the enzyme molecule.
E) Heterotropic allosteric effectors compete with substrate for binding sites.

43. Allosteric enzymes:

A) are regulated primarily by covalent modification.
B) usually catalyze several different reactions within a metabolic pathway.
C) usually have more than one polypeptide chain.
D) usually have only one active site.
E) usually show strict Michaelis-Menten kinetics.

44. A metabolic pathway proceeds according to the scheme, $R \rightarrow S \rightarrow T \rightarrow U \rightarrow V \rightarrow W$. A regulatory enzyme, X, catalyzes the first reaction in the pathway. Which of the following is most likely correct for this pathway?

A) Either metabolite U or V is likely to be a positive modulator, increasing the activity of X.
B) The first product S, is probably the primary negative modulator of X, leading to feedback inhibition.
C) The last product, W, is likely to be a negative modulator of X, leading to feedback inhibition.
D) The last product, W, is likely to be a positive modulator, increasing the activity of X.
E) The last reaction will be catalyzed by a second regulatory enzyme.

45. How is trypsinogen converted to trypsin?

A) A protein kinase-catalyzed phosphorylation converts trypsinogen to trypsin.
B) An increase in Ca$^{2+}$ concentration promotes the conversion.
C) Proteolysis of trypsinogen forms trypsin.
D) Trypsinogen dimers bind an allosteric modulator, cAMP, causing dissociation into active trypsin monomers.
E) Two inactive trypsinogen dimers pair to form an active trypsin tetramer