Questions 1-10: True or False? Answer A if the following statement is True or B if the following statement is False

1. Proteins fold by random search than by progressive stabilization of intermediates.
2. Two proteins with significantly different sequences can have the same backbone structure, if their hydrophobicity patterns are alike.
3. Active sites of enzymes are usually clefts or crevices.
4. Transition-state analogs are potent inhibitors of enzymes.
5. The second law of thermodynamics states that the total energy of the system and its surroundings is a constant.
6. Lysozyme is a protease that hydrolyzes the glycosidic bond between C1 of NAM and C4 of NAG.
7. Esterification of aspartate 52 of lysozyme leads to a total loss of catalytic activity.
8. Carboxypeptidase A is a serine protease.
9. T-cell receptors are antibody-like proteins consisting of two Tα and one Tβ chains.
10. IgG is the principal antibody in the serum.

Questions 11-50: Select the correct answer

11. Which of the following is not a property of the molten globule?
   a. It is compact
   b. It has a hydrophobic core
   c. It contains secondary-structure elements
   d. It has a defined three-dimensional structure
   e. It is more flexible than the native protein

12. Ramachadran plots
   a. display the secondary structure of a polypeptide
   b. predict the folding motifs of a polypeptide
   c. are the most reliable method to predict the 3D structure of proteins
   d. display the conformation of the molten globule of a polypeptide
e. display allowed conformations of the main chain of a polypeptide

13. Which of the following is not a property of protein disulfide isomerase (PDI)
   a. PDI accelerates cis-trans isomerization of X-proline bonds
   b. PDI is a protein folding catalyst
   c. PDI accelerates disulfide interchange in kinetically trapped folding intermediates
   d. PDI contains two Cys-Gly-His-Cys sequences
   e. The thiols of PDI are highly reactive at physiologic pH

14. The first step in protein structure prediction is to
   a. ask whether the sequence of a new protein is similar to one whose the 3D structure is already known
   b. determine the quaternary structure of your protein
   c. remove parts of the new protein to determine their role in the folding process
   d. perform pulsed-label NMR studies
   e. construct the Ramandrandran plot of the new polypeptide

15. Which of the following answers completes the sentence correctly? A Ramachandran plot
   a. Predicts α-helical structures from given amino acid sequences
   b. Shows the x-ray diffraction pattern of a protein
   c. Represents the sterically allowed conformations of a polypeptide backbone
   d. Gives the frequency of occurrence of amino acids in β sheet structures
   e. Predicts the tertiary structure of a polypeptide chain
16. Which of the following is not a property of the HIV protease?
   a. It is an aspartic protease
   b. It is a homodimer of 99-residue subunits
   c. It is inhibited by drugs ritonavir and saquinavir
   d. It belongs to the same protease family with pepsin
   e. It specifically cleaves the peptide bond Pro-Pro

17. Which of the following is a mechanism for the regulation of the catalytic activity of enzymes?
   a. The covalent modification of tryptophan residues
   b. The binding of regulatory proteins
   c. The binding of regulatory peptides via disulfide bonds
   d. The proteolytic cleavage of an inactive substrate precursor
   e. The change of the 3D conformation of the substrate

18. The inhibition of bacterial cell wall synthesis by penicillin is a classic example of a medically significant inhibition of an enzymatic reaction. Which of the following statements about the inhibition of glycopeptide transpeptidase by penicillin is true?
   a. The inhibition is noncompetitive
   b. Penicillin binds irreversibly to an allosteric site of the enzyme
   c. Penicillin resembles acyl-D-Ala-D-Ala, one of the substrates of the transpeptidase
   d. Penicillin inhibits bacterial cell wall synthesis by incorrectly cross-linking the peptides of the proteoglycan
   e. The penicilloyl-enzyme intermediate may be dissociated by high concentration of D-alanine

19. Which of the following statements about the different types of enzyme inhibition is correct?
a. Competitive inhibition is seen when the substrate and the inhibitor compete for the active site on the enzyme
b. Noncompetitive inhibitors often bind to the enzyme irreversibly
c. Competitive inhibition is seen when a substrate competes with an enzyme for binding to an inhibitor protein
d. Noncompetitive inhibition of an enzyme can be overcome by adding large amount of substrate
e. Competitive inhibitors are usually different in chemical structure to the substrate of the inhibited enzyme

20. The chemical structure shown below corresponds to

![Chemical Structure]

a. Penicillin  
b. Proline  
c. PDI  
d. D-Ala-D-Ala  
e. Porphyrin

21. Which of the following is not a general property of enzymes?
   a. Enzymes are almost exclusively proteins  
   b. Enzymes have great catalytic power  
   c. Enzymes bind substrates specifically
d. The catalytic activity of enzymes can be regulated

e. Enzymes use only hydrophobic interactions in binding substrates

22. Which of the following amino acid pairs are most likely to be found in the bridging right turn of a β-bend?
   a. Pro and Gly
   b. Gly and His
   c. His and Ser
   d. Ser and Thr
   e. Pro and Ser

23. Which statement is not true about a transition state analog?
   a. It is usually a distorted or strained molecule
   b. It fits better in the active site than the substrate
   c. It can be used as a hapten to produce catalytic antibodies
   d. It is a potent inhibitor of the enzyme
   e. It can provide insight into the catalytic mechanism

24. Serine proteases catalyze peptide cleavage via a covalent intermediate linked to which of the following amino acids?
   a. Histidine
   b. Aspartic acid
   c. Lysine
   d. Serine
   e. None of the above

25. Which of the following is a catalytic amino acid residue of lysozyme?
   a. serine 57
   b. tryptophan 62
   c. histidine 24
d. lysine 74
e. glutamic acid 35

26. Which site would you expect chymotrypsin to cleave the following peptide?

\[
\text{Lys-Gly-Phe-Thr-Tyr-Pro-Asn-Trp}
\]

\[
\text{a b c d e}
\]

27. The structure shown below corresponds to

\[
\begin{align*}
\text{H}_3\text{C} & \quad \text{CH}_2\text{OH} \\
\text{H} & \quad \text{H} \\
\text{O} & \quad \text{H} \\
\text{H} & \quad \text{H} \\
\text{H} & \quad \text{N-H} \\
\text{N} & \quad \text{O=C} \\
\text{CH}_3 & \quad \text{CH}_3
\end{align*}
\]

a. N-acetylmuramate
b. N-acetylglucosamine
c. NAG
d. Chitin
e. Lysozyme

28. Which of the following enzymes can be irreversibly inactivated with diisopropylphosphofluoridate (DIPF)?

a. lysozyme
b. trypsin
c. pepsin
d. carboxypeptidase A
e. tyrosine kinase

29. Suppose that hexa-NAG is synthesized so that the glycosidic oxygen between its D and E sugar residues is labeled with $^{18}$O. Where will this isotope appear in the products formed by hydrolysis with lysozyme?
   a. in the C-1 hydroxyl of tetra-NAG
   b. in the C-4 hydroxyl of di-NAG
   c. in the H$_2$O released from the reaction
   d. in the C-6 hydroxyl of the C sugar
   e. in the C-5 hydroxyl of the A sugar

30. The main type of interactions between lysozyme and tri-NAG are
   a. electrostatic bonds
   b. hydrogen bonds and van der Waals interactions
   c. van der Waals interactions
   d. covalent bonds
   e. hydrogen and covalent bonds

31. Which of the following statements about monoclonal antibodies is not correct?
   a. monoclonal antibodies that bind nearly any antigen can be produced
   b. monoclonal antibodies are useful for qualifying specific proteins in human blood
   c. monoclonal antibodies can be produced in large amounts by growing many mice, each of which has been immunized with the same antigen
d. immobilized monoclonal antibodies can be used to purify scarce proteins by affinity chromatography

e. fluorescent-labeled monoclonal antibodies can be used in conjunction with fluorescence-activated cell sorting to isolate cells having a given cell-surface antigen

32. Which of the following statements about IgG structure is correct?
   a. Each of the two antigen-combining sites on an IgG molecule can bind to a structurally distinct epitope.
   b. Both interchain and intrachain disulfide bonds stabilize IgG structure
   c. Both the K and L chains of IgG contain domains with similar structures
   d. The Fc unit of IgG binds to a complement-pathway component to initiate the lysis of an infected cell
   e. The hypervariable regions of the L chain are the sole determinants for the binding of the IgG to the specific antigen

33. Which of the following statements about carboxypeptidase A is not correct?
   a. The binding of substrate is accompanied by many changes in the structure of enzyme
   b. The zinc ion at the active site markedly increases the reactivity of the bound water molecule
   c. The enzyme contains regions of alpha-helix (38 %) and of beta-pleated sheet (17 %)
   d. The enzyme is a single polypeptide chain of 307 amino acid residues
   e. Substrate binding is accompanied by a 12 Å movement of the phenolic hydroxyl group of serine 248.
34. Which of the following is not a property of the human immunodeficiency virus (HIV)?
   a. it is retrovirus
   b. it contains a bilayer membrane with two kinds of glycoproteins
   c. it interacts with the CD4 coreceptor of helper cells through the gp120 glycoprotein
   d. it impairs and destroys the host cell by affecting its permeability and interfering with the expression of host-cell mRNA transcripts and recognition of peptide-class II MHC complexes on target cells
   e. it injects its RNA into the cell and releases the coat into the medium surrounding the cell

35. Which of the following is not a protease inhibitor?
   a. sarin
   b. DIPF
   c. parathion
   d. malathion
   e. acetylcholine

36. Which of the following is not a method of regulating enzyme activity in vivo?
   a. altering protein folding equilibria
   b. proteolytic control
   c. feedback inhibition
   d. regulatory protein interaction
   e. covalent modification

37. What type(s) of interactions are likely to be formed between an antibody and its antigen?
a. ionic bonds
b. hydrogen bonds
c. van der Waals interactions
d. none of the above
e. all of the above

38. Which of the following statements regarding simple Michaelis-Menten enzyme kinetics are correct?
   a. $K_m$ is the dissociation constant of the enzyme-substrate complex
   b. $K_m$ is the concentration of substrate required to convert half the total enzyme into the enzyme-substrate complex
   c. $K_m$ is expressed in terms of a reaction velocity (e.g., mol s$^{-1}$)
   d. The maximal velocity $V_{max}$ is related to the minimal number of substrate molecules that can be “turned over” in unit time by a molecule of enzyme
   e. $K_m$ is the concentration of substrate required to convert half the total enzyme into the enzyme-substrate complex

39. Which of the following statements is true? Enzyme catalysis of a chemical reaction
   a. decreases $\Delta G'$ so that the reaction can proceed spontaneously
   b. increases the energy of the transition state
   c. increases the forward and reverse reaction rates
   d. decreases the entropy of the reaction
   e. does not change $\Delta G^0$, but it changes the ratio of products to reactants
40. What happens if you add more substrate to an enzyme-catalyzed reaction already operating at $V_{\text{max}}$?
   a. $K_M$ will decrease
   b. No change
   c. Observed rate will be faster
   d. $K_{\text{cat}}$ will increase
   e. Observed rate will be slower

41. Pepsin cleaves IgG molecules on the carboxyl-terminal side of the interchain disulfide bonds between heavy chains. How many physical pieces would result from the cleavage of IgG by pepsin?
   a. two
   b. three
   c. four
   d. five
   e. eight

42. You conduct polyacrylamide gel electrophoresis of a monoclonal antibody preparation, previously treated with $\beta$-mercaptoethanol. How many protein bands would you expect to appear on the gel?
   a. one
   b. two
   c. three
   d. four
   e. six

43. The three illustrations shown below (I, II, and III) correspond to simplified representations of the substrate-binding sites of three different proteases. What are those three proteases?
44. Each amino acid in a run of several amino acid residues in a polypeptide chain has \( \phi \) values of approximately \(-140\) and \( \varphi \) values of approximately \(+147\). This run of amino acids is separated from another run of amino acids with similar values for \( \phi \) and \( \varphi \) by amino acid residue X with a \( \phi \) value of \(+100\) and a \( \varphi \) value of \(-40\). What kind of structure is formed by the two runs?

a. The two runs are likely \( \alpha \) helices
b. The two runs are likely parallel \( \beta \) sheets
c. The two runs are likely antiparallel \( \beta \) sheet
d. The two runs are likely hairpin turns
e. The first run is likely an \( \alpha \) helix and the second a \( \beta \) sheet
Ramachandran plot showing allowed values of \( \phi \) and \( \psi \) for L-alanine residues (green regions). Additional conformations are accessible to glycine (yellow regions) because it has a very small side chain.

45. Predict the relative rates of hydrolysis by lysozyme of these three oligosaccharides (G stands for N-acetylglucosamine residue and M for N-acetylmuramic acid):

oligosaccharide I: M-M-M-M-M-M
oligosaccharide II: M-G-M-G-M-G
oligosaccharide III: G-M-G-M-G-M

a. III faster than II, II faster than I
b. II faster than III, III faster than I
c. I faster than II, II faster than III
d. III faster than II, I is not hydrolyzed
e. The rates for all three oligosaccharides will be similar
46. The enzyme hexokinase catalyzes the following reaction:

\[
glucose + ATP \rightleftharpoons glucose \text{ 6-phosphate} + ADP
\]

For this reaction, \(\Delta G^0 = -4.0 \text{ kcal/mol}\). Calculate the change in free energy \(\Delta G'\) for this reaction under typical intracellular conditions using the following concentrations: glucose, 55 mM; ATP, 5.0 mM; ADP, 1.0 mM; and glucose 6-phosphate, 0.1 mM. Assume that the temperature is 25'C.

a. 8.7 kcal/mol  
b. 5.5 kcal/mol  
c. -1.3 kcal/mol  
d. -8.7 kcal/mol  
e. -15.0 kcal/mol

47. What is the ratio of [S] to \(K_M\) when the velocity of an enzyme-catalyzed reaction is 80% of \(V_{max}\)?

a. 1  
b. 2  
c. 4  
d. 8  
e. 12

48. Calculate the value of \(K_{eq}^{'eq}\) if \(\Delta G^0 = -1\) kcal/mol. Assume that the temperature is 25'C.

a. 10 kcal/mol  
b. 5.4  
c. 8  
d. 5.4 kcal/mol  
e. 1 M
49. The hydrolysis of glucose 6-phosphate to give glucose and phosphate has a \( \Delta G^0' = -3.3 \text{ kcal/mol} \). The reaction takes place at 25°C. Initially the concentration of glucose 6-phosphate is \( 10^{-5} \text{ M} \), that of glucose is \( 10^{-1} \text{ M} \), and that of phosphate is \( 10^{-1} \text{ M} \). What is the equilibrium constant of the reaction?

a. 297  
b. 103  
c. 217  
d. 21  
e. 267

50. The free-energy difference between folded and unfolded states of a typical 100-residue protein is 10 kcal/mol. What would be the ratio between folded and unfolded states at 25°C?

a. \( 10.5 \times 10^5 \)  
b. \( 2.25 \times 10^7 \)  
c. 2  
d. 10  
e. \( 3.4 \times 10^3 \)