

P R E F A C E

The principal purpose of writing this book **“GATE Life Science Topic Wise Solved Exam Questions”** is to cater the needs of the candidates aspiring for GATE Life Science examinations. It is observed that all the aspirants of GATE Life Science exam are in confusion and dilemma, as student do not know what to prepare and to what extent. The latest trend of GATE exam is randomized computer based multiple choice, multiple select and numerical answer type questions. For student it becomes very difficult to find out the topic from which question has been asked and in its absence students fails to develop any strategy for the exam.

It is imperative for every GATE life Science exam aspirant to understand the concepts and the pattern of exam. Through this book an effort has been made for aspirants to target GATE Life Science exam with full confidence. For sure success, a student should approach this exam with a strategy and planning in his/her mind. To help students, we have compiled this book in user-friendly and well-structured manner. Last 26 Year GATE exam question are sorted in 6 sections and sections are further divided into total 48 chapter as per GATE syllabus. This fine shorting of questions will help the student to understand the important topic of the subject, which is most frequent in examinations. Every section starts with the table showing questions asked during different years of GATE Life Science exam. The students will also be able to understand a change in trend of the questions over time. This will help them to understand the important topics of the subject and to prepare for exam in systemic planned way, which will enhance their selection chances. The quality of the question asked in GATE exams is always as par with other examinations. Practice of these questions will also help the students who are preparing for GATE BT, CSIR NET, ICMR, DBT, SET and other exams in Life Science or related streams.

A word or suggestion from your side may add another feather to the cap in the compilation of questions in this book. The author looks forward to the comments, suggestions and criticism from the students. Constructive suggestions and feedback from users would be highly appreciated, gratefully acknowledged and suitably incorporated.

ACKNOWLEDGEMENT

Compiling this book **“GATE Life Science - Topic Wise Solved Exam Questions”** has been a satisfying and happy journey for us. All the sections and chapters have taken a final shape after endless inputs of time and effort. Though many teachers assisted us in compiling this book, we, first of all, would like to thank all our students, who have helped motivated to bring such book.

We would like to specially mention the effort made by Mr. Radheshyam Choudhary, Director IFAS Publications, who extended immense support in myriad ways for bringing out the book in its present form.

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And finally our humble greetings to all who put their significant efforts and are unmentioned.

CUT – OFF

YEAR ↓	GEN	OBC-NCL/EWS	SC/ST/PwD
2025	31.3	28.1	20.8
2024	29.3	26.3	19.5
2023	32.9	29.6	21.9
2022	33.9	30.5	22.5
2021	36	32.4	24
2020	31.7	28.5	21.1
2019	36.7	33	24.5
2018	29.9	26.9	19.9

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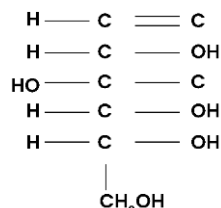
**NUMBER OF QUESTION ASKED IN GATE - XL LIFE SCIENCE
(2000 to 2025)**

Biochemistry	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
1 ORGANIZATION OF LIFE (Biomolecules)	5	5	2	5	-	2	6	2	5	1	2	2	3	3	2	3	3	-	4	5	4	6	1	5	6	2
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Previous Year Exam Questions

[GATE 2000]

1. How many asymmetric carbon atoms are present in the compound whose structure is as follows?



- (A) 1 (B) 2
(C) 3 (D) 4

[GATE 2000, Answer writing type]

2. Early experiments on the problem of protein folding suggested that the native three-dimensional structure of a protein was an automatic consequence of its primary structure. Cite an experimental evidence that shows that this is the case.

[GATE 2000]

3. Match the entries in Column I with Column II and write matching pairs in the answer book.

Column I	Column II
P. Van der Waals bonds	1. Spatial arrangement of amino acids that are near each other in the linear sequence
Q. γ -Globulins	2. Glycosylation inhibitor
R. Tertiary structure	3. Cooperativity of oxygen binding
S. Hill-coefficient (η_H)	4. Involves polarizable atoms
T. Tunicamycin	5. Immune protection

- (A) P-3; Q-1; R-4; S-2; T-5
(B) P-5; Q-3; R-1; S-2; T-4
(C) P-4; Q-5; R-1; S-3; T-2
(D) P-3; Q-1; R-2; S-4; T-3

[GATE 2000]

4. Histones have very high percentage of arginine and lysine residues (15%-30%). For this class of proteins which of the following reagents would be a suitable choice for generating peptides in the determination of the amino acid sequence of the protein?

- (A) Cyanogen bromide
(B) Thermolysin
(C) Trypsin
(D) N-bromosuccinimide

[GATE 2000]

5. The properties of water include

- (A) The ability to form hydrophobic bonds with itself.
(B) A disordered structure in the liquid state.
(C) A low dielectric constant.
(D) Being a dipole, with the negative end at the oxygen atom.

[GATE 2001]

6. Gangliosides contain
(A) a ceramide structure.
(B) glucose or galactose.
(C) sialic acid.
(D) all of the above.

[GATE 2001]

7. The active site amino acid residue that could be involved in a reaction catalyzed by an enzyme with a pH optimum of 4 would be
(A) arginine (B) cysteine
(C) serine (D) glutamate

[GATE 2001, Answer writing type]

8. Give correct answers to the following:
(A) Which of the following amino acids are likely to have their side chains on the inside of globular proteins in solution?
(B) What is the coenzyme form of vitamin B6? Name the reactions in which this coenzyme is involved.
(C) In preparation of mitochondria, oxidation of fatty acids is carried out in the presence of CoA, O_2 , ADP and PO_4 .
(i) How many molecules of ATP will be produced per two carbon fragments converted to CO_2 ?
(ii) What will this number be if amytal is added to the preparation?
(D) Northern analysis of nuclear RNA and cytoplasmic RNA from the liver when probed with aldolase genomic clone showed that the nuclear RNA specific to aldolase had a molecular weight higher than that of cytoplasmic RNA. Explain why?

[GATE 2001]

9. The length of a helical section of a polypeptide chain of 20 residues would be
(A) 30 Å (B) 20 Å
(C) 5.4 Å (D) 3.6 Å

[GATE 2001]

10. Which of the following types of interactions is mainly responsible for the aggregation of proteins in dilute solutions?
- (A) Hydrogen bonds
(B) Hydrophobic interactions
(C) Disulfide bonds
(D) Peptide bonds

[GATE 2002]

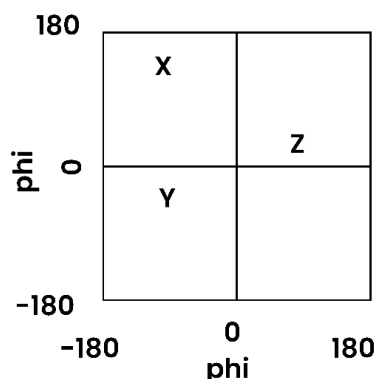
11. Which of the following has a quaternary structure?
- (A) α -Chymotrypsin (B) Hemoglobin
(C) Insulin (D) Myoglobin

[GATE 2002]

12. Which of the following statements is correct in the case of chaperone proteins?
- (A) These do not prevent aggregation.
(B) They cleave incorrect S-S bonds.
(C) They act on fully synthesized polypeptides.
(D) They are involved in the transport of proteins across mitochondria and endoplasmic reticulum.

[GATE 2003]

13. In the following Ramachandran diagram, which type of secondary structure does the regions marked X, Y and Z represent?



- (A) X: Right-handed α -helix; Y: Left-handed α -helix; Z: β -sheet
(B) X: Left-handed α -helix; Y: Right-handed α -helix; Z: β -sheet
(C) X: β -sheets, Y: Right-handed α -helix, Z: Left-handed α -helix
(D) X: β -sheet; Y: Left-handed α -helix; Z: Right-handed α -helix

[GATE 2003]

14. Of the following peptide sequences, which one is the digestive enzyme trypsin most likely to cleave?
- (A) ---Val- Lys- Pro- Met ---
(B) ---Arg- Val- Phe- Tyr ---
(C) ---Trp- Asp- Gln- Pro ---
(D) ---Glu- Gly- Trp- Gly ---

[GATE 2003]

15. Which one of the following statements about protein secondary structure is correct?
- (A) An α -helix is primarily stabilized by ionic interactions between the side chains of the amino acids.
(B) β -sheets exist only in antiparallel form.
(C) β -turns often contain proline.
(D) An α -helix can be composed of more than one polypeptide chain.

[GATE 2003]

16. Choose the correct common sequence motif of Zn finger proteins from the following choices. X stands for any amino acid.
- (A) X_3 -Cys- X_{2-4} -Cys- X_{1-2} -His- X_{3-4} -His- X_4
(B) X_3 -Cys-Cys- X_{2-4} -His-His- X_4
(C) X_3 -Cys-Cys-His-His- X_4
(D) X_V -Cys- H_{2-4} , 4-His- X_{1-2} -His- X_{3-4} -Cys- X_4

[GATE 2003]

17. Which amino acid residue is most likely to be found in the interior of a water-soluble globular protein?
- (A) Ser (B) Arg
(C) Val (D) Asp

[GATE 2005]

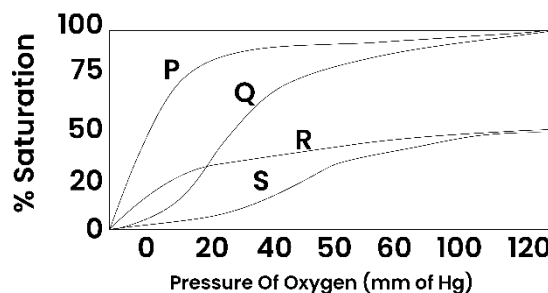
18. Which pair of amino acid residues can interact in the interior of a protein only through van der Waals forces?
- (A) Arg, Thr (B) Ser, Thr
(C) Glu, His (D) Val, Leu

[GATE 2005]

19. For a double stranded DNA, which one of the following base-ratios will always be equal to 1?
- (A) $(A+T)/(G+C)$ (B) $(A+G)/(C+T)$
(C) C/T (D) A/G

Statement for Linked Answer Questions 20 and 21:

The figure shows the oxygen binding curves: for hemoglobin (Hb) and myoglobin (Mb)



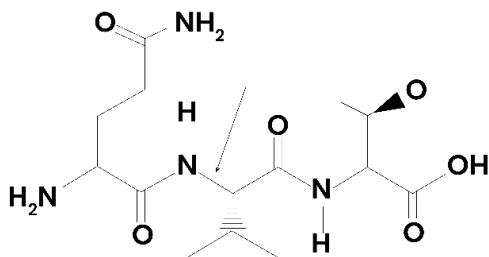
[GATE 2006]

20. Identify the correct curves for Hb and Mb
- (A) P: Mb; Q: Hb (B) Q: Mb; P: Hb
(C) R: Mb; S: Hb (D) S: Mb; R: Hb

[GATE 2006]

21. Sick cell anemia arises due to the formation of a hydrophobic patch in one of the proteins shown in the above curves. This is due to the replacement of
- Glu 6 by Val 6 in the β -subunit of P.
 - Glu 6 by Val 6 in the β -subunit of Q.
 - Glu 6 by Val 6 in the β -subunit of R.
 - Glu 6 by Val 6 in the β -subunit of S.

Statement for Linked Answer Questions 22 and 23:



[GATE 2006]

22. The dihedral angle indicated by an arrow in the tripeptide structure corresponds to the
- psi angle.
 - phi angle.
 - chi angle.
 - omega angle.
23. The amino acid sequence of the above tripeptide is
- Glutamine - valine - threonine
 - Asparagine - valine - serine
 - Glutamine - leucine - threonine
 - Asparagine - valine - threonine

[GATE 2006]

24. Which one of the following cannot be considered as a weak interaction?
- Van der Waals forces
 - Peptide bonds
 - Hydrogen bonds
 - Ionic interaction

[GATE 2006]

25. Which one of the following statements refers to glycogen, and which one refers to cellulose?
- P. Branched molecule containing $\beta(1\rightarrow4)$ glycosidic bond
 - Q. Straight chain molecule containing $\beta(1\rightarrow4)$ glycosidic bond
 - R. Branched molecule containing $\alpha(1\rightarrow6)$ glycosidic bond
 - S. Straight chain molecule containing $\alpha(1\rightarrow6)$ glycosidic bond
- P: Glycogen; S: Cellulose
 - Q: Glycogen; R: Cellulose
 - R: Glycogen; Q: Cellulose
 - S: Glycogen; P: Cellulose

[GATE 2007]

26. How does hemoglobin carry carbon dioxide generated in tissues back to the lungs?

- By coordination with heme
- By forming N-terminal carbamate
- By forming C-terminal carbamate
- By linking to the epsilon-amino group of lysine

[GATE 2007]

27. The maximum number of hydrogen bonds that a molecule of water can form is
- 1
 - 2
 - 3
 - 4

[GATE 2008]

28. Equal volumes of two buffers of pH 4 and pH 6 of identical ionic strengths are mixed. The resultant pH is
- close to 4
 - close to 5
 - close to 6
 - exactly 5

[GATE 2008]

29. Match the transition state or chemical entity of each enzyme that is responsible for their catalytic function.

Column I

Column II

P. Ribonuclease

1. Oxyanion

Q. Lysozyme

2. Pentacovalent

R. Chymotrypsin

phosphorus

S. Carboxypeptidase

3. Carbonium ion

4. Mixed anhydride

(A) P-3; Q-2; R-4; S-1

(B) P-2; Q-3; R-1; S-4

(C) P-2; Q-1; R-3; S-4

(D) P-4; Q-3; R-2; S-1

Statement for Linked Answer Questions 30 and 31:

Nearly 46% of 45S pre-rRNA is unstable. The remaining portion of it forms mature 5.8S, 18S and 28S rRNA having lengths 160 bases, 1.9 kb and 5.1 kb, respectively. The content of pre rRNA per human genome is 7.8×10^{-15} g.

[GATE 2008]

30. The molecular weight of 45S pre-rRNA is

(A) 2×10^6 (B) 4.5×10^5 (C) 4.5×10^6 (D) 3.9×10^7

[GATE 2008]

31. The number of pre-rRNA genes per genome is approximately.

(A) 10

(B) 100

(C) 1000

(D) 10,000

[GATE 2008]

32. Match the polysaccharides in Column I with their constituent monosaccharide in Column II

Column I

Column II

P. Chitin

1. D-Glucose

Q. Hemicellulose

2. N-Acetyl glucosamine

R. Glycogen

3. D-Xylose

4. D-Galactose

(A) P-1; Q-3; R-4

(B) P-2; Q-4; R-1

(C) P-4; Q-2; R-3

(D) P-2; Q-3; R-1

[GATE 2009]

33. The advantage of hemoglobin having a high histidine content is
 (A) Histidine binds to oxygen
 (B) Histidine carries oxygen to the tissues
 (C) Histidine imparts buffering capacity to hemoglobin
 (D) 'R' group of histidine has low pKa.

[GATE 2010]

34. Chymotrypsin and lysozyme are involved respectively in.
 P. Removal of successive carboxyl terminal residues.
 Q. Hydrolytic cleavage of peptide bond.
 R. Cleavage of glycosidic C-O bond.
 S. Oxygen transport in blood.
 (A) P, O (B) Q, R
 (C) Q, S (D) R, S

[GATE 2010]

35. The rise per residue of α -helix is about 1.5 Å. A protein spans 4 nm bilayer 7 times through its transmembrane α -helical domain. Approximately, how many amino acid residues constitute the transmembrane domain of the protein?
 (A) 105 (B) 450
 (C) 30 (D) 190

[GATE 2011]

36. The polarity of water molecule is due to.
 (A) Its tetrahedral structure
 (B) Bonding electrons being attracted more to oxygen
 (C) Bonding electrons being attracted more to hydrogen
 (D) Its weak electrolytic property

[GATE 2011]

37. Collagen, α -keratin and tropomyosin have common structural features. They are
 P) Disulphide bridges to neighbouring proteins.
 Q) Repeating sequences of amino acids
 R) A high β -sheet content
 S) Super-helical coiling
 (A) P, Q (B) Q, R
 (C) Q, S (D) P, R

[GATE 2012]

38. Which one of the following pairs of amino-acids in the protein has high propensity to take up the α -helix conformation?
 (A) Gly-Asp (B) Pro-His
 (C) Gly-Pro (D) Ala-Arg

[GATE 2012]

39. Which one of the following closely defines 'Molten Globule' state of protein?

- (A) State with high degree of secondary structures and loss of tertiary structure
 (B) State with complete loss of secondary structure
 (C) Completely unfolded state
 (D) Loss of quaternary structure

[GATE 2012]

40. Which one of the following amino-acids has highest fluorescence quantum yield (ϕ) in aqueous solution?
 (A) Tyrosine (B) Tryptophan
 (C) Phenylalanine (D) Histidine

[GATE 2013]

41. Which one of the following amino acids has a higher propensity for *cis* peptide bond formation?
 (A) Histidine (B) Cysteine
 (C) Glycine (D) Proline

[GATE 2013]

42. The length of an α -helix composed of 36 amino acid residues is.
 (A) 10 Å (B) 54 Å
 (C) 27 Å (D) 360 Å

[GATE 2013]

43. Which one of the following amino acid residues is specifically recognised by chymotrypsin during peptide bond cleavage?
 (A) Phe (B) Leu
 (C) Val (D) Asp

[GATE 2014]

44. Which one of the following proteases does **NOT** cleave on the carboxyl side of any Arginine residue in a protein?
 (A) Trypsin (B) Proteinase K
 (C) Thrombin (D) Chymotrypsin

[GATE 2014]

45. Choose the option with two reducing sugars.
 (A) Lactose and Maltose
 (B) Trehalose and Sucrose
 (C) Maltose and Trehalose
 (D) Lactose and Sucrose

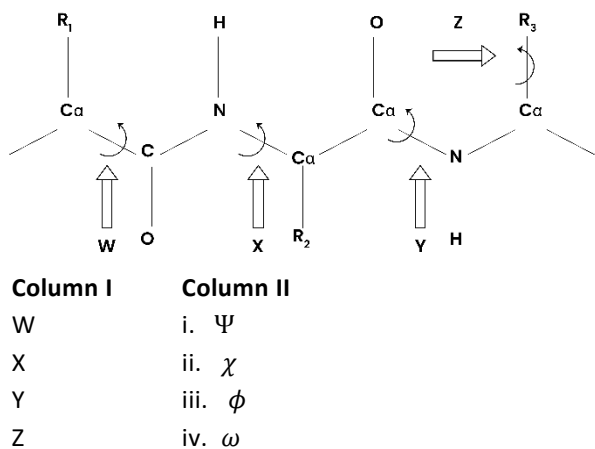
[GATE 2015]

46. Which one of the following amino acid substitutions is likely to cause the largest change in protein conformation?
 (A) Phe $\rightarrow$ Ile (B) Ser $\rightarrow$ Thr
 (C) Gln $\rightarrow$ Tyr (D) Glu $\rightarrow$ Val

[GATE 2015]

47. Which one of the following does NOT constitute the lipid moiety in lipid-linked membrane proteins?
 (A) Palmitic acid (B) Stearic acid
 (C) Farnesyl groups (D) Myristic acid

48.



Which of the following identifies the correctly matched pairs?

- (A) W-iii, X-i; Y-iv; Z-ii
(B) W-i; X-iii, Y-iv; Z-ii
(C) W-i; X-iii; Y-ii; Z-iv
(D) W-iii; X-i; Y-ii; Z-iv

[GATE 2016]

49. Hydrolysis of a peptide involves cleavage of the bond between the atoms

- (A) N and C_{α}
(B) C and O
(C) C_{α} and C
(D) N and C

[GATE 2016]

50. Amino acid residues predominantly involved in protein-DNA interactions are

- (A) alanines
(B) negatively charged
(C) prolines
(D) positively charged

[GATE 2016]

51. Cellulose serves as a structural polymer whereas starch does not. This is because cellulose contains

- (A) $\beta 1 \rightarrow 4$ linked glucose monomers and inter-chain hydrogen bonds
(B) $\beta 1 \rightarrow 4$ linked glucose monomers and intra-chain hydrogen bonds
(C) $\alpha 1 \rightarrow 4$ linked glucose monomers and inter-chain hydrogen bonds
(D) $\alpha 1 \rightarrow 4$ linked glucose monomers and intra-chain hydrogen bonds

[GATE 2018]

52. To which one of the following classes of enzymes does chymotrypsin belong?

- (A) Oxidoreductase
(B) Hydrolase
(C) Transferase
(D) Isomerase

[GATE 2018]

53. Which one of the following conformations of glucose is most stable?

- (A) Boat
(B) Half Chair
(C) Chair
(D) Planar

[GATE 2018]

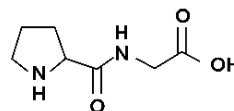
54. Which one of the following amino acids is responsible for the intrinsic fluorescence of proteins?

- (A) Pro
(B) Met
(C) His
(D) Trp

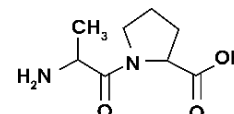
[GATE 2019]

55. The dipeptide with least rotational barrier in the peptide bond is

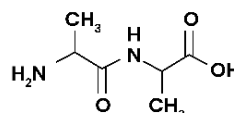
A)



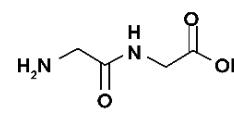
B)



C)



D)



[GATE 2019]

56. Which one of the following is an incorrect biomolecule-modification pair?

- (A) Lipid – Palmitoylation
(B) DNA and Protein – Methylation
(C) Protein - Glycosylation
(D) RNA – Polyadenylation

[GATE 2019]

57. The crystal structure of a peptide has an ordered structural repeat of amino acids with a distance of ~ 6.5 Å between the alternate C_{α} atoms. Which one of the following pair of dihedral angles (Φ and Ψ) accurately represents the peptide structure?

- (A) $\phi \approx -60^\circ, \Psi \approx -50^\circ$
(B) $\phi \approx -120^\circ, \Psi \approx -50^\circ$
(C) $\phi \approx -60^\circ, \Psi \approx +120^\circ$
(D) $\phi \approx -120^\circ, \Psi \approx +120^\circ$

[GATE 2020]

58. The reaction involved in the direct conversion of L-phenylalanine to L-tyrosine is

- (A) Reduction
(B) Transamination
(C) Decarboxylation
(D) Hydroxylation

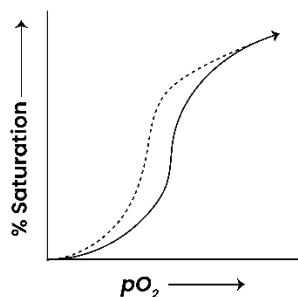
[GATE 2020]

59. The correct combination of glycosidic linkages present in glycogen is

- (A) $\alpha 1 \rightarrow 6$ and $\beta 1 \rightarrow 4$
(B) $\alpha 1 \rightarrow 4$ and $\alpha 1 \rightarrow 6$
(C) $\alpha 1 \rightarrow 6$ and $\beta 1 \rightarrow 6$
(D) $\alpha 1 \rightarrow 4$ and $\beta 1 \rightarrow 6$

[GATE 2021]

60. In the plot given below, the solid line represents oxygen binding to hemoglobin under physiological conditions. The broken line represents the condition(s) of



- (A) Loss of cooperativity
(B) High pH
(C) High CO₂ concentration
(D) Increase in 2, 3- Bisphosphoglycerate concentration

[GATE 2021]

61. Which of the following lipids is non-ionic?

- (A) Sphingomyelin (B) Lecithin
(C) Phosphatidyl inositol (D) Galactocerebroside

[GATE 2021]

62. A molecule that forms a donor-acceptor energy transfer pair with the dansyl group is _____

- (A) Aspartate (B) Histidine
(C) Tryptophan (D) Lysine

[GATE 2021]

63. Which one of the following molecules (~1mg/mL) do NOT absorb at 280 nm in an aqueous solution of pH 7.00 at room temperature?

- (A) Adenosine triphosphate
(B) Tyrosine
(C) Phenylalanine
(D) Poly deoxy-Guanylate (poly dG)

[GATE 2021]

64. Considering the open chain forms, which of the following pair(s) represent/s an epimer?

- (A) D-glucose and D-fructose
(B) D-glucose and D-mannose
(C) D-mannose and D-fructose
(D) D-galactose and D-glucose

[GATE 2021]

65. pKa value of the guanidinium group of Arginine is _____

- (A) 4.30 (B) 12.50
(C) 7.40 (D) 9.20

[GATE 2022]

66. Which of the following carbohydrates has/have a $\beta 1 \rightarrow 4$ glycosidic linkage?

- (A) Maltose (B) Cellulose
(C) Chitin (D) Lactose

[GATE 2023]

67. Which one of the following amino acids has more than two acid-base groups?

- (A) Alanine (B) Leucine
(C) Phenylalanine (D) Tyrosine

[GATE 2023]

68. Four statements about lipids are given below as options. Choose the statement(s) which is/are CORRECT.

- (A) Cholesterol is amphipathic
(B) Self-assembly of phospholipids in water is due to hydrophobic effect
(C) The temperature at which the gel phase changes to liquid crystalline phase increases with an increase in the degree of unsaturation of fatty acyl tails
(D) The choline head group of lipids is positively charged

[GATE 2024]

69. Which one of the following pairs of amino acids is NOT incorporated in a polypeptide chain?

- (A) 4-Hydroxyproline and γ -carboxyglutamate
(B) γ -Carboxyglutamate and desmosine
(C) Ornithine and citrulline
(D) 4-Hydroxyproline and 5-hydroxylysine

[GATE 2024]

70. Metabolic intermediates provide the backbone for the synthesis of amino acids. Match the metabolic intermediates listed in **Column I** with their corresponding amino acids given in **Column II**.

Column I	Column II
P. α -Ketoglutarate	i. Histidine
Q. Ribose 5- phosphate	ii. Glutamate
R. 3-Phosphoglycerate	iii. Aspartate
S. Phosphoenolpyruvate	iv. Phenylalanine
	v. Serine

Code:

- (A) P-ii; Q-i; R-v; S-iv (B) P-iii; Q-ii; R-i; S-v
(C) P-iv; Q-iii; R-ii; S-v (D) P-ii; Q-i; R-iv; S-v

[GATE 2025]

71. Zinc is essential for the function of

- (A) carboxypeptidase A.
(B) chlorophyll a.
(C) myoglobin.
(D) vitamin B12.

[GATE 2025]

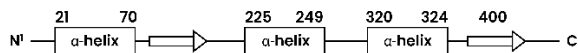
72. Which of the following is/are heteropolysaccharide(s)?

- (A) Chondroitin-4-sulfate
(B) Chitin
(C) Cellulose
(D) Heparin

NAT

[GATE 2018]

1. The secondary structure topology diagram of 400 amino acid long "Protein-X" is depicted in the figure. The start and end amino acid residue numbers of each α -helix are marked. The percentage (correct to integer number) of residues forming α -helix is ____.



[GATE 2019]

2. The electrostatic interaction energy between a positively charged atom A and negatively charged atom B separated by 3 Å in water is -6 kJ/mol. Considering the relative permittivity of water to be 80, the electrostatic interaction energy in kJ/mol (rounded off to one decimal place) between atoms A and B in vacuum is ____.

[GATE 2019]

3. The C-terminal carboxyl group and the N-terminal amino group in amino acids have a dissociation constant (pK_a) of 2.2 and 9.2, respectively. The pK_a of side chain carboxyl group in glutamic acid is 4.2 and side chain amino group in lysine is 10.2. The difference in isoelectric point (pI) of lysine and glutamic acid (rounded off to two decimal places) is ____.

[GATE 2020]

4. Considering that the three pK_a s of histidine are $pK_1=1.8$, $pK_2=9.2$ and $pK_R=6.0$, its isoelectric point will be ____ (rounded off to one decimal place).

[GATE 2020]

5. The second pK_a of phosphoric acid is 6.8. The ratio of Na_2HPO_4 to NaH_2PO_4 required to obtain a buffer of pH 7.0 is ____ (rounded off to two decimal places).

[GATE 2023]

6. A protein has seven cysteine residues. The maximum number of disulfide bonds of different combinations that can possibly be formed by these seven cysteine residues is ____ (in integer).

[GATE 2023]

7. A lyophilized sample of 20 nanomoles of an oligonucleotide is dissolved in water and the volume of the solution is made up to 200 μ L. The concentration (in μ M) of the oligonucleotide in this solution is ____ (in integer).

[GATE 2023]

8. A 100 ml solution of pH 10 was well-mixed with a 100 ml solution of pH 4. The pH of the resultant 200 ml solution is ____ (rounded off to two decimal places).

[GATE 2024]

9. A newly identified viral protein contains one long α -helix spanning 60 amino acid residues. The number of main chain H-bonds formed in this helix is _____. (Answer in integer)

[GATE 2024]

10. In a lactic acid solution at pH 4.8, the concentrations of lactic acid and lactate are 0.01 M and 0.087 M, respectively. The calculated pK_a of lactic acid is _____. (Round off to one decimal place)

[GATE 2024]

11. If a 10 mM solution of a biomolecule in a cuvette of path length 10 mm absorbs 90% of the incident light at 280 nm, the molar extinction coefficient of the biomolecule at this wavelength is _____ $M^{-1}cm^{-1}$. (Round off to two decimal places)

[GATE 2024]

12. A 5250 base-pair long plasmid with 10 negative supercoils would have a linking number of _____, considering 10.5 base pairs per turn for B DNA. (Answer in integer)

ANSWER KEY									
1	2	3	4	5	6	7	8	9	10
D	-	C	C	D	D	D	-	A	B
11	12	13	14	15	16	17	18	19	20
B	D	C	B	C	A	C	D	B	A
21	22	23	24	25	26	27	28	29	30
B	B	A	D	C	B	D	A	B	C
31	32	33	34	35	36	37	38	39	40
C	D	C	B	D	B	C	D	A	B
41	42	43	44	45	46	47	48	49	50
D	B	A	D	A	D	B	B	D	D
51	52	53	54	55	56	57	58	59	60
A	B	C	D	B	A	D	D	B	B
61	62	63	64	65	66	67	68	69	70
D	C	C	B, D	B	B,C,D	D	A,B,D	C	A
71	72								
A	A, D								
NAT									
1	2	3	4	5	6	7	8	9	10
20 to 20	-480.1 to -479.9	6.49 to 6.51	7.5 to 7.7	1.58 to 1.60	48	100	4.29	56	3.93
11	12								
100	490								

:-EXPLANATION:-

1. **Topic:** Carbohydrates

Answer (D)

Explanation: Asymmetric carbon is one to which four different functional groups are attached. The given molecule is glucose with six carbon atoms and it has four asymmetric carbons.

2. **Explanation:** Christian Anfinsen and his colleagues performed an experiment in early 1960s to demonstrate the process of protein folding. The scientist isolated Ribonuclease A from bovine pancreas. Ribonuclease A is an enzyme which contains 124 amino acid residues and its molecular weight is 13,700Da. In the presence of urea and a reducing agent known as β -mercaptoethanol, ribonuclease A got denatured and its disulphide bonds got reduced. Then, the denaturing agent and β -mercaptoethanol was removed from the protein, and it was observed that the protein refolded into its native conformation with the formation of four correctly paired disulphide bonds. This experiment demonstrated that the primary structure of proteins

contain all the necessary information required to fold the protein into its three-dimensional form.

3. **Topic:** Protein

Answer (C)

Explanation: Van der Waals bonds are weak electrostatic force of interaction that occur in all types of molecules, both polar and non-polar. γ -globulins are proteins that forms antibodies and play role in immune protection. Tertiary structure of protein represents the three-dimensional conformation of protein. It is stabilized by various non-covalent bonds like hydrophobic interactions, salt bridges, hydrogen-bonds and van der Waals interactions and covalent intra-chain disulphide bonds. Hill-coefficient represents the degree of cooperativity during oxygen binding curve of hemoglobin. Tunicamycin is a drug which inhibits N-linked glycosylation of proteins.

4. **Topic:** Protein sequencing

Answer (C)

Explanation: Trypsin cleaves the peptide bond on the carboxyl side of lysine and arginine which is not followed by proline residue.

5. **Topic:** Water

Answer (D)

Explanation: Water is a polar molecule because its atoms share electrons unequally. The oxygen is more electronegative than hydrogen and therefore pulls shared pair of electron between H-O towards itself. Polarity of a molecule is measured with the help of dipole moment (μ). Net dipole moment of water is 1.84 debye(D).

6. **Topic:** Lipids

Answer (D)

Explanation: Gangliosides are sphingoglycolipids that contains ceramide (sphingosine covalently attached to fatty acid) and oligosaccharides having N-acetyl neuraminic acid (NAM). NAM is also known as sialic acid.

7. **Topic:** Amino acids

Answer (D)

Explanation: At pH=4, the amino acid that can exist as an active residue of active site of an enzyme should be polar and acidic in nature. Glutamate and aspartate are two acidic amino acids as they have carboxyl group in their side chains.

8. **Explanation:**

- (a) Val, Pro, Phe, Asp, Lys, Ile, His
- (b) Co-enzyme form of vitamin B6 is Pyridoxal phosphate. It participates during transamination reactions, α - and β - decarboxylation, aldol reactions and β - and γ -elimination reactions.
- (c)
- (i) During one cycle of β -oxidation one molecule of two carbon compound that is acetyl CoA is formed and 1 NADH and 1 FADH₂ are produced to give 4 ATP. Acetyl CoA formed, enter into TCA cycle to get converted to carbon dioxide and total 10 ATP are produced in this pathway (1 ATP, 1 FADH₂, and 3 NADH). Therefore, total 14 ATP are produced.
- (ii) Amytal inhibits complex 1 of electron transport chain and therefore, NADH will not be oxidised to generate ATP. Total 4 ATP will be produced from β -oxidation and TCA.
- (d) It is because the nuclear mRNA is in the pre-mRNA form which will undergo maturation process before moving to cytosol, due to which there will be decrease in the molecular weight of mature mRNA present in the cytosol.

9. **Topic:** secondary structure of proteins

Answer (A)

Explanation: In case of right-handed α -helix, the rise per amino acid residue is 1.5 Å. Accordingly, the length of α -helix formed by 20 amino acids = $20 \times 1.5 \text{ Å} = 30 \text{ Å}$

10. **Topic:** Protein folding and aggregation

Answer (B)

Explanation: The driving force behind protein aggregation is the reduction in free surface energy by the removal of hydrophobic residues from contact with the solvent.

11. **Topic:** Globular proteins

Answer (B)

Explanation: Hemoglobin is a globular, multimeric protein having quaternary structure. In adults, it is composed of two α -polypeptide chains and two β -polypeptide chains ($\alpha_2\beta_2$). It contains 4 hemes (each subunit has 1 heme) as prosthetic group.

12. **Topic:** Protein sorting

Answer (D)

Explanation: Molecular chaperones are protein folding modulators that help in proper folding of proteins. They bind to the incompletely folded or unfolded proteins so as to fold them correctly. They also play important role during signal transduction and protein trafficking mechanisms.

13. **Topic:** Ramachandran Plot

Answer (C)

Explanation: Many values of ψ and ϕ are not allowed because of steric hindrance between atoms of polypeptide backbone and side chains groups of amino acids. The permitted values of ψ and ϕ can be found out with the help of Ramachandran plot. Shaded portion of the plot indicate the permitted values of ψ and ϕ while unshaded region indicates the unallowed values.

14. **Topic:** Protein sequencing

Answer (B)

Explanation: Trypsin cleaves the peptide bond on the Carboxyl side of lysine and arginine which is not followed by proline residue. Therefore option (B) is correct.

15. **Topic:** Protein secondary structure

Answer (C)

Explanation: Glycine and proline are often found in β -turns. Glycine is present in the β -turns because it is smallest amino acid and contains hydrogen atom as side chain and therefore it is very flexible. The reason behind occurrence of proline in the β -turn is that its side chain has built in bent.

16. **Topic:** DNA-protein interactions

Answer (A)

Explanation: Zinc finger motif is characterized by coordination of one or more zinc ions. Several types of zinc finger motifs are present but most common is C₂-H₂ type in which two cysteine in one chain and two histidine in other one are coordinated to zinc ion. The motif contains a consensus sequence of approximately thirty amino acid residues and the sequence is mentioned in option (A).

17. **Topic:** Globular proteins

Answer (C)

Explanation: Valine is non-polar in nature and can form hydrophobic interactions. Therefore, it lies in the interior of globular proteins. External surface of globular proteins contain polar and charged amino acid residues (serine, arginine and aspartate) so that they can interact with the polar surrounding environment to increase the solubility of globular proteins.

18. **Topic:** Amino acids

Answer (D)

Explanation: valine and isoleucine are non-polar amino acids, therefore they interact with each other with help of van der Waals forces. Serine and threonine are polar amino acids and can form hydrogen bonding with neighboring residues. Glutamate is acidic while histidine is basic amino acid and these can interact with the help of ionic interactions.

19. **Topic:** Nucleic acids

Answer (B)

Explanation: According to Chargaff's rule:

In a double stranded DNA, the total number of purines (A, G) is always equal to the number of pyrimidines (C, T). Therefore, (A+G) = (C+T) or $\frac{(A+G)}{(C+T)} = 1$

20. **Topic:** Globular proteins

Answer (A)

Explanation: Oxygen binding curve of myoglobin is hyperbolic in nature (P) and that of hemoglobin is sigmoid in nature (Q).

21. **Topic:** Globular proteins

Answer (B)

Explanation: Sick-cell anemia is a molecular disease which occur due to point mutation in β -chain of hemoglobin. The 6th amino acid residue in β -chain is glutamate which is negatively charged at physiological pH. By point mutation, it is replaced by valine, which is non-polar in nature. Therefore, a hydrophobic patch is developed on the surface of hemoglobin and shape of RBC changes.

22. **Topic:** Peptide bond

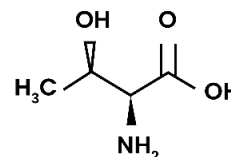
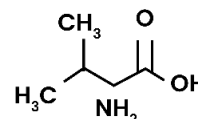
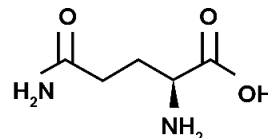
Answer (B)

Explanation: The angle around C _{α} -C bond is called psi angle (ψ) and the angle around N-C _{α} bond is called phi angle (ϕ).

23. **Topic:** Amino acids and Peptide bond

Answer (A)

Explanation: This tri-peptide is made up of glutamine, valine and threonine whose respective structures are given below:



24. **Topic:** Stabilising interactions

Answer (B)

Explanation: Peptide bonds are strong interactions because these are covalent in nature.

25. **Topic:** Carbohydrates

Answer (C)

Explanation: Glycogen is a highly branched polysaccharide made up of α -glucose. Linearly, glucose molecules are joined together by $\alpha(1,4)$ -glycosidic bond while branching occur by the virtue of $\alpha(1,6)$ -glycosidic bond. Cellulose is a linear polysaccharide and a component of plant cell wall. It is made up of β -glucose joined together by $\beta(1,4)$ -glycosidic bond.

26. **Topic:** Globular proteins

Answer (B)

Explanation: 70% of carbon-dioxide is transported through blood plasma as bicarbonate ion. Only 23% of carbon dioxide is transported by hemoglobin as carbamino hemoglobin. Carbon dioxide binds to unprotonated amino group of N-terminal amino acid residue of α - and β - chains.

27. **Topic:** Water

Answer (D)

Explanation: One water molecule can form maximum 4 hydrogen bonds with neighbouring water molecules. However, at room temperature

water only form 3.4 hydrogen bonds with other water molecules because its molecules are disordered and are in continuous motion. In ice, water molecules are properly organised and form 4 hydrogen bonds with each other.

28. **Topic:** pH and buffers

Answer (A)

Explanation: Let us assume there are 1 L volume of both buffers.

For buffer having pH=4:

$$\text{pH} = -\log [\text{H}^+]$$

$$\begin{aligned}\text{Therefore, } [\text{H}^+] &= 10^{-4} \text{ Molar} \\ &= 10^{-4} \text{ moles/L}\end{aligned}$$

For buffer having pH=6:

$$\text{pH} = -\log [\text{H}^+]$$

$$\begin{aligned}\text{Therefore, } [\text{H}^+] &= 10^{-6} \text{ Molar} \\ &= 10^{-6} \text{ moles/L}\end{aligned}$$

Adding two buffers together.

Total volume=2L

$$\text{Total concentration of } \text{H}^+ = 10^{-4} + 10^{-6} = \frac{1}{10000} +$$

$$\frac{1}{1000000} = \frac{101}{1000000} = 1.01 \times 10^{-4}$$

In 2L, there will be 1.01×10^{-4} moles

$$\begin{aligned}\text{In 1L, number of moles} &= \frac{1.01 \times 10^{-4}}{2} = 0.505 \times 10^{-4} \\ &\text{moles}\end{aligned}$$

$$\text{pH of resultant buffer} = -\log [\text{H}^+]$$

$$\begin{aligned}&= -\log (0.505 \times 10^{-4}) = -(\log 0.505 + \log 10^{-4}) \\ &= -(-0.2967 - 4) = 4.3\end{aligned}$$

29. **Topic:** Enzymes

Answer (B)

Explanation: Ribonuclease is an endonuclease that catalyzes the cleavage of RNA molecule and result in the formation of 2', 3'- cyclic phosphate intermediate. Lysozyme are hydrolytic enzymes that can cleave β -(1, 4)-glycosidic bond between N-acetylmuramic acid and N-acetylglucosamine of bacterial cell wall. They act through the formation of carbonium ion. In the esterolytic reaction of carboxypeptidase. A deacylation of the mixed anhydride intermediate is catalyzed by a metal-bound hydroxide group.

30. **Topic:** Nucleic acids

Answer (C)

Explanation: Unstable pre-rRNA= 46%, therefore remaining 54% is stable and it forms 5.8S, 18S and 28S rRNAs. Length of 5.8S rRNA is 160 bases and that of 18S and 28S are 1.9kb and 5.1kb, respectively. Total number of bases in pre-rRNA= $(0.16+1.9+5.1) \times 100/54$
 $= (7.16 \times 100)/54$
 $= 13.26 \text{ kb} = 13.26 \times 1000 \text{ bases}$

Average molecular weight of one molecule of ribonucleotide= 325 Da

The molecular weight of 45S pre-rRNA

$$= 325 \times 13.26 \times 1000 \text{ Da}$$

$$= 4309500 \text{ Da}$$

$$= 4.3 \times 10^6 \text{ Da}$$

31. **Topic:** Nucleic acids

Answer (C)

Explanation: Pre-rRNA content of human genome =

$$7.8 \times 10^{-15} \text{ g}$$

$$1 \text{ Dalton} = 1.67 \times 10^{-24} \text{ g}$$

$$\text{Therefore, } 7.8 \times 10^{-15} \text{ g}$$

$$= 7.8 \times 10^{-15} \text{ g} / 1.67 \times 10^{-24} \text{ g} = 4.73 \times 10^9 \text{ Da}$$

Number of genes

$$= 4.73 \times 10^9 \text{ Da} / 4.3 \times 10^6 \text{ Da} = 1000$$

32. **Topic:** Carbohydrates

Answer (D)

Explanation: Chitin is a polysaccharide which is made up of β (1, 4)-linked N-acetyl-glucosamine. It is found in the exoskeleton of insects and crustaceans. Hemicellulose are polysaccharides present in plant cell walls and include xyloglucans, xylans, mannans and others. Glycogen is a polysaccharide made up of β (1, 4)-linked D-glucose.

33. **Topic:** globular proteins

Answer (C)

Explanation: Histidine residues present in hemoglobin can undergo protonation and deprotonation upon change in pH and therefore imparts buffering capacity to it.

34. **Topic:** Enzymes

Answer (B)

Explanation: Chymotrypsin is a digestive enzyme which belongs to the class 'hydrolases'. It is a protease that cleaves on the C-terminus of peptide bond formed by aromatic amino acids. Lysozyme digest the bacterial cell wall made up of carbohydrates by breaking the glycosidic linkage.

35. **Topic:** Proteins secondary structure

Answer (D)

Explanation: Rise per amino acid residue of an α -helix= 1.5 Å

$$\text{Area spanned by protein} = 4 \text{ nm} = 4 \times 10^3 \text{ Å} = 40 \text{ Å}$$

$$\begin{aligned}\text{Total area spanned by protein in 7 times} &= 7 \times 40 \text{ Å} = 280 \text{ Å}\end{aligned}$$

$$\begin{aligned}\text{Number of amino acid residues} &= 280/1.5 = 187 \text{ which} \\ &\text{is approximately equals to 190}\end{aligned}$$

36. **Topic:** Water

Answer (B)

Explanation: Water is a polar molecule because its atoms share electrons unequally. The oxygen is

more electronegative than hydrogen and therefore pulls shared pair of electron between H-O towards itself. Polarity of a molecule is measured with the help of dipole moment (μ). Net dipole moment of water is 1.84 debye (D).

37. **Topic:** Proteins

Answer (C)

Explanation: Collagen has a triple helical coiled coil structure. It contains three amino acids: glycine, proline and hydroxyproline in abundance. These amino acids make up the characteristic repeating motif gly-pro-X. Keratin is a fibrous protein and there are two types of keratin proteins: α -keratins and β -keratins. α -keratin has predominantly helical conformation. Tropomyosin is made up of two α -helical chains arranged in coiled-coil form.

38. **Topic:** Proteins secondary structure

Answer (D)

Explanation: Certain amino acids like alanine, leucine, histidine, arginine, lysine, methionine, glutamate and glutamine are categorized as helix former while amino acid glycine and proline tend to destabilize the helical conformation of proteins.

39. **Topic:** Protein folding

Answer (A)

Explanation: Molten globule is an intermediate state that occurs when a protein undergoes transition from unfolded state to folded native state. It has most of the secondary structure of native state but it is less compact and lacks proper packing interactions.

40. **Topic:** Amino acids

Answer (B)

Explanation: The fluorescence quantum yield is the ratio of photons absorbed to photons emitted by fluorescence. Aromatic amino acids like tyrosine, tryptophan and phenylalanine act as intrinsic fluorophores of proteins. Tryptophan shows much stronger fluorescence and higher quantum yield than the other two aromatic amino acids and tryptophan shows four times more absorbance at 280nm as compared to tyrosine.

41. **Topic:** Peptide bond

Answer (D)

Explanation: Most amino acids form peptide bond in *trans* configuration but proline can occur in both *trans* and *cis* arrangement because in case of proline α -amino group is covalently linked to its side chain to form pyrrolidone ring and because of this ring structure, both *cis* and *trans* forms are equally stable.

42. **Topic:** secondary structure of proteins

Answer (B)

Explanation: In case of right-handed α -helix, the rise per amino acid residue is 1.5 Å. Accordingly, the length of α -helix formed by 36 amino acids = $36 \times 1.5 \text{ Å} = 54 \text{ Å}$

43. **Topic:** Protein sequencing

Answer (A)

Explanation: Chymotrypsin is a protease and it catalyzes the hydrolysis of peptide bond formed by aromatic amino acids (phenylalanine, tyrosine and tryptophan) at their carboxyl side.

44. **Topic:** Protein sequencing

Answer (D)

Explanation: Chymotrypsin is a protease that catalyzes the hydrolysis of peptide bond formed by aromatic amino acids at their carboxyl side.

45. **Topic:** Carbohydrates

Answer (A)

Explanation: Both sucrose and trehalose are non-reducing disaccharides because their monomeric carbohydrate units are joined together by the virtue of their anomeric ends. No anomeric ends are available in both sucrose and trehalose.

46. **Topic:** amino acids

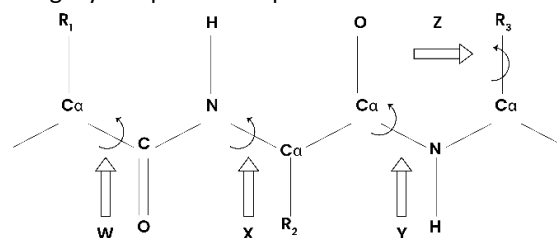
Answer (D)

Explanation: glutamate is a negatively charged amino acid while valine is aliphatic amino acid. Substitution of glutamate with valine will have an adverse effect on the overall structure of protein because both amino acids have different chemical nature and glutamate can participate in ionic interactions to stabilize the overall structure of proteins while valine cannot participate in ionic interactions.

47. **Topic:** Plasma membrane and membrane proteins

Answer (B)

Explanation: Membrane proteins that are covalently attached to lipid molecules are called lipid-linked proteins. Stearic acid does not constitute the lipid moiety in lipid-linked membrane proteins. Isoprenyl (farnesyl/geranyl/geranyl), myristoyl, palmitoyl act as lipid anchors. GPI-linked proteins also fall under the category of lipid-linked proteins.



Column I	Column II
W	i. Ψ
X	ii. χ
Y	iii. ϕ
Z	iv. ω

48. **Topic:** Peptide bond and proteins

Answer (B)

Explanation: The angle around C_{α} -C bond is called psi angle (ψ). The angle around N- C_{α} bond is called phi angle (ϕ). The angle around C-N bond is called omega (ω) and the angle around C_{α} -R is called chi angle (χ).

49. **Topic:** peptide bond

Answer (D)

Explanation: A peptide bond is the amide bond which is formed when the carboxyl group of one amino acid becomes linked to the amino group of another to form a peptide.

50. **Topic:** protein-DNA interactions

Answer (D)

Explanation: DNA is a negatively charged molecule due to the presence of phosphate group therefore it interacts with positively charged amino acid residues containing proteins with the help of electrostatic interactions.

51. **Topic:** carbohydrates

Answer (A)

Explanation: Cellulose is a structural polysaccharide made up of β -D- glucose joined together by $\beta 1 \rightarrow 4$ linkage. Several linear chains of cellulose are held together by inter-chain hydrogen bonds.

52. **Topic:** enzymes

Answer (B)

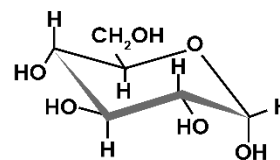
Explanation: There are six classes of enzymes which are oxidoreductases, transferases, hydrolases, lyases, isomerases, and ligases. Chymotrypsin is a hydrolase because it catalyzes the hydrolysis of peptide bond formed by aromatic amino acids.

53. **Topic:** carbohydrates

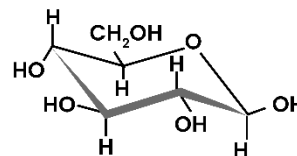
Answer (C)

Explanation: There can be either β -glucose or α -glucose anomeric form. For glucose, chair conformation is the most stable arrangement because all the substituents are equatorial. The chair conformation for α -glucose and β -glucose are shown below:

The Chair Form of α -D-Glucopyranose is



The Structure of β -D-glucopyranose is



54. **Topic:** amino acids

Answer (D)

Explanation: Aromatic amino acids: tryptophan, tyrosine and phenylalanine are responsible for intrinsic fluorescence of proteins.

55. **Topic:** Peptide bond

Answer (B)

Explanation: Rotation around peptide bond is not possible due to partial double bond character. Peptide bonds are in the *trans* conformation. However, *cis* forms can occur in peptide bonds that precede a proline residue. In such cases, the *cis* form occurs as the proline side-chain offers less of a hindrance.

56. **Topic:** Protein modification

Answer (A)

Explanation: Proteins undergo palmitoylation not lipids.

57. **Topic:** Proteins secondary structure

Answer (D)

Explanation: The distance between adjacent amino acid in case of β -sheet is $\sim 3.5\text{\AA}$ and hence between alternate amino acid would be $\sim 6.5\text{\AA}$ therefore the given structure represents β -sheet and the value of dihedral angles (Φ and Ψ) for parallel β sheet is -120 and 120 , respectively. Hence option (D) is correct.

58. **Topic:** amino acids metabolism

Answer (D)

Explanation: On the basis of structure, the difference between L-phenylalanine and L-tyrosine is the presence of hydroxyl group attached to the aromatic ring, in case of tyrosine. Hence, L-phenylalanine undergoes hydroxylation to get converted to L-tyrosine.

59. **Topic:** Carbohydrates

Answer (B)

Explanation: Glycogen is a polysaccharide made up of α -D-glucose. Glucose molecules are joined

linearly by α 1 $\rightarrow$ 4 bond while branching occur by the virtue of α 1 $\rightarrow$ 6 bond.

60. **Topic:** Globular proteins

Answer (B)

Explanation: The line has shifted towards left and it indicates the affinity of oxygen for hemoglobin has increased. Correct option is (B) and this is due to Bohr's effect. At high pH, the concentration of protons in the solution decreases due to which the side chain of histidine residue of β -globin chain of hemoglobin becomes deprotonated. Quaternary structure of deoxy-hemoglobin will be less stabilized due to decreased ionic interactions and hence the affinity of hemoglobin towards oxygen increases.

61. **Topic:** Lipids

Answer (D)

Explanation: galactocerebroside is made up of ceramide and galactose sugar. Ceramide is made up of sphingosine and a fatty acid attached to it via amide bond. Both galactose and ceramide are non-ionic in nature.

62. **Topic:** Amino acids

Answer (C)

Explanation: A donor-acceptor energy transfer pair must be able to absorb energy so that it can show fluorescence. Tryptophan act as intrinsic fluorophore and act as donor-acceptor energy transfer pair with dansyl group.

63. **Topic:** Amino acids

Answer (C)

Explanation: Phenylalanine show characteristic absorbance at 257.4 nm. Nucleotides and nucleic acids (adenosine triphosphate and poly dG) show characteristic maxima at 260 nm and at 280 nm, they absorb about half as much UV as compared to 260 nm.

64. **Topic:** carbohydrates

Answer (B & D)

Explanation: Epimers are diastereomers that contain more than one chiral center but differ from each other in the absolute configuration at only one chiral center. D-glucose and D-mannose differ from each other at C-2 position only, and D-glucose and D-galactose differ from each other at C-4 position only.

65. **Topic:** amino acids

Answer (B)

Explanation: Arginine is a basic amino acid, its pKa of guanidinium (pKR) value would be above 7, that is towards basic pH.

66. **Topic:** Bio molecules (Carbohydrate)

Answer (B, C, D)

Explanation: Cellulose, Chitin and Lactose is an example of sugars having β 1 $\rightarrow$ 4 glycosidic linkage. But maltose has α 1 $\rightarrow$ 4 glycosidic linkage.

67. **Topic:** Amino acid

Answer (D)

Explanation: Tyrosine

Amino acids contain at least two acid-base groups: the amino group (-NH₂) and the carboxyl group (-COOH). However, some amino acids, such as tyrosine, also contain additional acid-base groups. In the case of tyrosine, it has a phenolic hydroxyl group (-OH) that can also act as an acid or a base, depending on the pH of the environment. At low pH, the phenolic hydroxyl group can be protonated, while at high pH, it can lose a proton and become negatively charged. Therefore, tyrosine has a total of three acid-base groups: the amino group, the carboxyl group, and the phenolic hydroxyl group

68. **Topic:** Lipids

Answer (A), (B) and (D).

Explanation: (A) is true. Cholesterol is amphipathic. It is a steroid molecule that is mostly hydrophobic, with a small hydrophilic hydroxyl group. (B) is true. Self-assembly of phospholipids in water is due to hydrophobic effect, which is the tendency of hydrophobic tails to aggregate together to minimize their exposure to water. The hydrophilic head groups of the phospholipids interact with the surrounding water molecules, resulting in the formation of bilayer structures. (C) is false. The temperature at which the gel phase changes to liquid crystalline phase decreases with an increase in the degree of unsaturation of fatty acyl tails. This is because unsaturated fatty acyl chains introduce kinks in the acyl chain, making it more difficult for the chains to pack together in a tight, ordered structure. As the degree of unsaturation increases, the chains become more disordered, and the gel phase transition temperature decreases. (D) is true. The choline head group is a quaternary ammonium cation with a permanent positive charge, which is neutralized by an anionic group in the lipid molecule, such as phosphate in phosphatidylcholine.

69. **Topic:** Amino acid

Answer (C)

Explanation: Ornithine and citrulline are not incorporated into polypeptide chains during protein synthesis. They are amino acids involved in other metabolic pathways, such as the urea cycle, and are

not part of the standard set of amino acids used for protein synthesis.

70. **Topic:** Amino acid

Answer: (A)

Explanation:

P. α -Ketoglutarate is a precursor for glutamate.

Q. Ribose 5-phosphate is involved in the pentose phosphate pathway and contributes to the synthesis of histidine.

R. 3-Phosphoglycerate is an intermediate in glycolysis and contributes to the synthesis of serine.

S. Phosphoenolpyruvate is a precursor for the synthesis of aspartate

71. **Topic:** Carboxypeptidase

Answer (A)

Explanation: Carboxypeptidase A requires zinc for its enzyme activity, aiding in protein breakdown. Chlorophyll a uses magnesium, myoglobin uses iron, and vitamin B12 uses cobalt. Zinc is essential only for carboxypeptidase A's function.

72. **Topic:** Structure and function of biomolecules

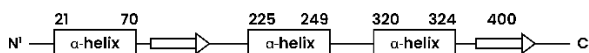
Answer (A, D)

Explanation: Chondroitin-4-sulfate (A) is a heteropolysaccharide, made of alternating units of glucuronic acid and N-acetylgalactosamine, often found in cartilage.

Heparin (D) is also a heteropolysaccharide, composed of repeating disaccharide units with sulfate groups, involved in blood clot prevention. On the other hand, Chitin (B) and Cellulose (C) are homopolysaccharides, made of a single type of sugar (N-acetylglucosamine for chitin and glucose for cellulose).

NAT

1. **Explanation:**



The number of amino acid residues forming each α -helix is:

From 21 to 70 = 50 residues

From 225 to 249 = 25 residues

From 320 to 324 = 5 residues

Total number of residues forming α -helix = 50 + 25 + 5 = 80 residues

The percentage of residues forming α -helix with total 400 amino acids = $\left(\frac{80}{400}\right) \times 100 = 20\%$

2. **Explanation:**

Dielectric constant of water = 80

$$\text{Energy} \propto \frac{1}{\text{Dielectric constant}}$$

$$\frac{\text{Energy}_{\text{water}}}{\text{Energy}_{\text{vacuum}}} = \frac{\text{Dielectric constant}_{\text{vacuum}}}{\text{Dielectric constant}_{\text{water}}}$$

$$\frac{-6}{\text{Energy}_{\text{vacuum}}} = \frac{1}{80}$$

$$\text{Energy}_{\text{vacuum}} = 80 \times (-6) = -480 \text{ kJ/mol}$$

3. **Explanation:**

For glutamic acid:

$$\text{pI} = \frac{\text{pK}_1 + \text{pK}_R}{2} = \frac{2.2 + 4.2}{2} = \frac{6.4}{2} = 3.2$$

For Lysine:

$$\text{pI} = \frac{\text{pK}_2 + \text{pK}_R}{2} = \frac{9.2 + 10.2}{2} = \frac{19.4}{2} = 9.7$$

The difference in pI of lysine and glutamic acid = 9.7 - 3.2 = 6.50

4. **Explanation:**

$\text{pK}_1 = 1.8$, $\text{pK}_2 = 9.2$ and $\text{pK}_R = 6.0$

Histidine is a basic amino acid, therefore:

$$\text{pI} = \frac{\text{pK}_2 + \text{pK}_R}{2} = \frac{9.2 + 6.0}{2} = \frac{15.2}{2} = 7.6$$

5. **Explanation:**

Apply Henderson-Hasselbalch equation:

$$\text{pH} = \text{pKa} + \log\left(\frac{\text{Na}_2\text{HPO}_4}{\text{NaH}_2\text{PO}_4}\right)$$

$$7 = 6.8 + \log\left(\frac{\text{Na}_2\text{HPO}_4}{\text{NaH}_2\text{PO}_4}\right)$$

$$0.2 = \log\left(\frac{\text{Na}_2\text{HPO}_4}{\text{NaH}_2\text{PO}_4}\right)$$

$$\text{antilog}(0.2) = \left(\frac{\text{Na}_2\text{HPO}_4}{\text{NaH}_2\text{PO}_4}\right)$$

$$1.58 = \left(\frac{\text{Na}_2\text{HPO}_4}{\text{NaH}_2\text{PO}_4}\right)$$

6. **Explanation:** The correct answer for the maximum number of disulfide bonds that can be formed by 7 cysteine residues is 48.

To calculate this, we can use the formula: $2^n - 1$

Where n is the number of cysteine residues. In this case, n = 7, so we get: $2^7 - 1 = 128 - 1 = 127$

However, we need to divide this number by 2, because each disulfide bond involves two cysteine residues, so we get: $127 / 2 = 63.5$

Since we can't have a half disulfide bond, we round down to get: 63 disulfide bonds.

However, we need to subtract the number of non-disulfide bonds (i.e. the number of possible ways to choose 7 cysteine residues without forming a disulfide bond), which is:

7 choose 1 + 7 choose 2 + 7 choose 3 + 7 choose 4 + 7

choose 5 + 7 choose 6 = 64

So the final answer is: 63 - 64 = 48

Therefore, the maximum number of disulfide bonds of different combinations that can possibly be formed by these seven cysteine residues is 48.

7. **Explanation: 100 μ M**

200 μ L has 20 nanomoles of an oligonucleotide
 Means 1000 μ L (1 ml) will have 100 nanomoles
 1000 mL will have 100 X 1000 nanomoles
 = 100 micromoles/1000 mL
 = 100 μ M

8. **Explanation:** In this case, we can assume that the solution of pH 10 is the weaker acid (due to its lower concentration of hydrogen ions) and the solution of pH 4 is the stronger base (due to its higher concentration of hydrogen ions).

Since the two solutions are mixed in equal volumes, we can assume that the resulting solution has a total volume of 200 mL and a total concentration of hydrogen ions of:

$$[H^+] = (1 \times 10^{-4} \text{ mol/L} \times 100 \text{ mL} / 200 \text{ mL}) + (1 \times 10^{-4} \text{ mol/L} \times 100 \text{ mL} / 200 \text{ mL}) = 5.05 \times 10^{-5} \text{ mol/L}$$

Using the formula $\text{pH} = -\log [H^+]$, we get: $\text{pH} = -\log(5.05 \times 10^{-5})$ $\text{pH} = 4.29$ (rounded off to two decimal places)

Therefore, the pH of the resulting solution is approximately 4.29 to 4.31

9. **Explanation:** In an α -helix, each amino acid contributes to the formation of hydrogen bonds with the amino acid located four residues ahead in the sequence. Therefore, the number of main chain hydrogen bonds in a helix is calculated as (number of amino acid residues - 4). For a helix spanning 60 amino acid residues: Number of H-bonds = 60 - 4 = 56. So, the answer is 56.10. **Explanation:** Let's reevaluate the pKa using the Henderson-Hasselbalch equation:

$$\text{pH} = \text{pKa} + \log([A^-]/[HA])$$

Given that $\text{pH} = 4.8$, $[A^-] = 0.087 \text{ M}$, and $[HA] = 0.01 \text{ M}$, we can rearrange the equation to solve for pKa:

$$\text{pKa} = \text{pH} - \log([A^-]/[HA])$$

$$\text{pKa} = 4.8 - \log(0.087/0.01)$$

$$\text{pKa} \approx 4.8 - \log(8.7)$$

$$\text{pKa} \approx 4.8 - 0.9395$$

$$\text{pKa} \approx 3.8605$$

Rounded off to one decimal place, the calculated pKa of lactic acid is approximately 3.93

11. **Explanation:** The molar extinction coefficient (ϵ) can be calculated using the Beer-Lambert Law: $A = \epsilon \cdot c \cdot l$
 Where:

A is the absorbance (0.90 for 90% absorption, as it ranges from 0 to 1). c is the concentration of the biomolecule in molarity (10^{-2} M).

l is the path length of the cuvette in centimeters (10 mm, which is equivalent to 1.0 cm). Rearranging the equation to solve for ϵ :

$$\epsilon = A / c \cdot l$$

l

Plug in the values:

$$\epsilon = 1/10^{-2} \cdot 1$$

$$\epsilon = 10^2$$

$$\epsilon = 100 \text{ M}^{-1} \text{ cm}^{-1}$$

So, the molar extinction coefficient of the biomolecule at 280 nm is $100 \text{ M}^{-1} \text{ cm}^{-1}$.

12. **Explanation:** The linking number (Lk) in a closed, circular DNA molecule can be calculated using the formula: $Lk = Tw - Wr$

where:

Tw is the twist, the number of turns of the DNA helix. Wr is the writhe, the number of supercoils.

The twist (Tw) can be calculated as = Number of base pairs / Base pairs per turn $Tw = \text{Base pairs per turn} / \text{Number of base pairs}$

Given that the plasmid is 5250 base pairs long and has 10.5 base pairs per turn for B DNA: $Tw = 500$

Now, substitute Tw and Wr into the linking number formula: $Lk = 500 - 10$ $Lk = 490$

Therefore, the linking number of the plasmid is 490.