GRADUATE SCHOOL ADMISSIONS (GS)

TIFR BIOLOGY

Topic Wise Sorted PYQs with Detailed Explanation

15 Years' 2010 - 2024

Useful for
IIT JAM, GAT-B, CUET (PG), GATE, Autonomous, Deemed,
Private, State & Central Universities Entrance Exams

Kailash Choudhary
Digambar Jagtap

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PREFACE

It gives me immense pleasure to present this compilation of TIFR (Tata Institute of Fundamental Research) Biology Previous Year Question Papers along with detailed explanations. This book is designed to serve as a comprehensive and valuable resource for all aspiring candidates preparing for the TIFR Biology entrance examination.

This book contains topic-wise & Year wise sorted TIFR Biology (Graduate School Admissions) Previous year questions answers and explanations. The questions are categorized according to the TIFR Biology syllabus and are divided into four sections: 1. Biology, 2. Chemistry, 3. Physics, 4. General. Each section comprises chapters that start with previous year’s exam questions. This organized structure will greatly benefit those preparing for the TIFR Biology exam systematically.

Previous year question papers play a crucial role in any competitive examination preparation. They provide valuable insights into the exam pattern, marking scheme, and the types of questions asked. By solving these papers, candidates get familiar with the level of difficulty and the areas that require more attention. Moreover, analysing and understanding the solutions to these questions helps build a strong foundation and enhances the ability to approach new problems effectively.

This book presents authentic question papers directly sourced from previous years' TIFR Biology entrance examinations. The questions have been carefully curated to represent the diversity of topics covered in the syllabus. By practicing these questions, candidates gain valuable insights into the evolving trends in the examination, allowing them to align their preparation strategy accordingly.

Each question in this book is accompanied by a detailed explanation that goes beyond mere solutions. The explanations aim to provide a step-by-step approach to solving the problems, highlighting the underlying principles and concepts. Complex topics are broken down into simpler parts to ensure that candidates grasp the essence of each question effectively. The inclusion of previous year question papers allows candidates to assess their progress over time. Regular practice and self-assessment help identify strengths and weaknesses, enabling focused preparation on areas that need improvement.

The focus of this book is not just on providing correct answers but on developing conceptual clarity. By understanding the underlying principles, candidates can apply their knowledge to solve novel and challenging problems. This approach fosters a deeper appreciation for biology as a science and helps aspirants excel in their future research pursuits.

The more familiar candidates are with the examination format, the more confident they feel during the actual exam. Practicing with previous year papers reduces exam anxiety and helps candidates perform to the best of their abilities. It is hoped that this book will inspire and empower all aspiring biologists to pursue their dreams of contributing to the advancement of knowledge and making significant discoveries in the field of biology.

Kailash Choudhary
Digambar Jagtap

ACKNOWLEDGEMENT

As we present this comprehensive collection of solutions to the previous year's questions from TIFR Biology entrance exams, we extend our heartfelt gratitude to all those who have played a pivotal role in its realization.

First and foremost, we express our deepest thanks to Mr. Radheshyam Choudhary, the Founding CEO of IFAS Edutech Pvt. Ltd., for his continuous support, continual motivation, and critical insights that have helped us transform our dream into a reality. Your determination to empower students has been instrumental in shaping this book into a valuable resource for TIFR aspirants.

We express our deepest thanks to the esteemed faculty and subject matter experts whose wisdom and knowledge have been the cornerstone of this endeavor. Their expertise, guidance, and relentless pursuit of excellence have shaped this book into a valuable resource for TIFR aspirants. Mr. Dadasaheb Sondge, Mr. Pranshu Dwivedi, Mr. Vishal Bhujbal, Mr. Lalji Kanojiya, Ms. Mamta Marar, Mr. Dipak Kumar, and Mr. Yogesh Bishnoi deserve our warmest gratitude. Your passion for teaching has been contagious, igniting in us a love for learning and a desire to develop deeper into the subjects we cherish

We also want to thank Mr. Siddharth Gangwar, Mr. Omkar Girkar, Ms. Prajakta Choughule, Mr. Rohit Walke, Ms. Jeel Patel, Ms. Priyanka Jena, Ms. Vaishnavi Bhilare and Ms. Pradnya Nikam for their thorough review and aid in structuring the book. You have always been willing to go the extra mile, clarifying concepts, and providing personalized attention to ensure our understanding. Your profound knowledge, expertise, and commitment to education have been the guiding force behind the accuracy and rigor of the solutions presented herein.

Our appreciation also goes out to the editorial and support team at IFAS who have worked tirelessly to ensure the highest standards of quality and clarity in this book. Your meticulous efforts in reviewing, editing, and organizing the content have been invaluable in making this book accessible and user-friendly.

We are immensely grateful to the students whose enthusiasm and thirst for knowledge have been a constant source of inspiration. Your inquisitive minds and dedication to learning have motivated us to deliver the best possible solutions to the challenging questions that TIFR examinations pose. Your trust in our expertise drives us to continually strive for excellence in education. It is our sincere hope that this book becomes a trusted companion in your pursuit of knowledge and success.

With heartfelt gratitude,

Kailash Choudhary
Digambar Jagtap

TIFR – BIOLOGY

(Graduate School Admissions)

The Tata Institute of Fundamental Research is India's premier institution for advanced research in fundamental sciences. The Institute runs a graduate programme leading to the award of Ph.D., Integrated M.Sc.-Ph.D. as well as M.Sc. degree in certain subjects. With its distinguished faculty, world class facilities and stimulating research environment, it is an ideal place for aspiring scientists to initiate their career.

The Graduate Programme at TIFR is classified into the following Subjects -

Biology, Chemistry, Computer & Systems Science (including Communications and Machine Learning), Mathematics, Physics, Science Education.

Fellowship

For Ph.D. and I-Ph.D. programmes, the academic year starts from August 1, every year.

The academic year for M.Sc. programme begins from July 1, every year.

Ph.D.

Students receive a monthly fellowship of Rs. 31,000/- (+ hostel accommodation OR HRA as applicable) enhanced to Rs. 35,000/- after registration.

I-Ph.D.

Students receive a monthly fellowship of Rs. 21,000/- (+ hostel accommodation OR HRA as applicable) for the first year. At the end of the first year, upon satisfactory performance, the fellowship is enhanced to Rs. 31,000/- per month (further raised to Rs. 35,000/- after registration for Ph.D.).

M.Sc. (Biology)

Students receive a monthly fellowship of Rs 16,000/- (+HRA as applicable).

M.Sc. (Wildlife Biology & Conservation)

EXAM PATTERN

The exam consists of 4 sections, split into 2 sub-sections, General A and B, Physics A and B, Chemistry A and B, and Biology A and B.

All questions are multiple choice and have ONLY ONE correct answer.

Answer them by clicking the radio button next to the relevant option.

All sections have a total of 15 questions, with 10 in sub-section A and 5 in sub-section B.

All questions have a negative marking (of 0.5). Correct answers in the A sub-section are worth 1 mark, and in the B sub-section, 2 marks.

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TIFR BIOLOGY
Graduate School Admissions (GS 2024)

SECTION I - BIOLOGY

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MOLECULAR BIOLOGY

CELL SIGNALING

IMMUNOLOGY

DEVELOPMENTAL BIOLOGY

PLANT PHYSIOLOGY

ANIMAL PHYSIOLOGY

TAXONOMY

GENETICS

ECOLOGY

EVOLUTION

MICROBIOLOGY

TECHNIQUES

SECTION II - CHEMISTRY

SECTION III - PHYSICS

SECTION IV - MATHEMATICS

SECTION – I

BIOLOGY

BIOCHEMISTRY : NUMBER OF QUESTIONS ASKED IN TIFR

Chapter Name		2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
1	**Acid, pH, Buffer & Solutions**	-	-	1	-	-	-	-	-	-	-	-	2	-	-	-
2	**Thermodynamics**	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
3	**Amino acids**	-	-	-	-	-	1	-	-	-	-	-	2	1	4	1
4	**Proteins**	-	-	-	-	-	-	1	-	1	-	-	1	2	-	-
5	**Nucleotides & Nucleic acids**	-	-	-	-	-	-	-	-	-	-	-	3	1	1	-
6	**Carbohydrates & Glycobiology**	-	-	-	-	-	-	-	-	-	-	-		-	1	-
7	**Enzymes**	1	-	1	1	-	1	-	-	-	-	-	1	3	1	1
8	**Metabolism**	1	-	-	1	-	-	-	1	1	1	-	-	-	-	-

ACID, pH, BUFFER & SOLUTIONS

TIFR - PREVIOUS YEAR EXAM QUESTIONS

(TIFR - 2012)

1. A student conducted an experiment where CO_2 and N_2were bubbled through water in beakers A and B respectively. He recorded the pH in each of the solutions every 5 min. What is the most valid conclusion the student could draw from these results:

	pH reading	
Time (min)	A	B
5	7.5	7.5
10	7.2	7.3
15	7.0	7.5
20	6.8	7.4

(1) The change in pH was too small to be significant
(2) Bubbling CO_2 through water makes it more acidic
(3) Bubbling N_2 through water makes it more acidic
(4) Both CO_2 and N_2 make water more acidic

(TIFR - 2021)

2. 700 ml of colourless solution is present in each of two bottles, A and B. The label on A reads, 1 M $NaCl$, while that on B reads 1 mole NaCl. Which of the following statements is correct?

(1) The amount of $NaCl$ in in each bottle is the same
(2) The concentration of $NaCl$ in each bottle is the same
(3) Bottle A has less amount of $NaCl$ than Bottle B
(4) The concentration of $NaCl$ is more in Bottle A than in Bottle B

(TIFR - 2021)

3. The pKa of a monobasic organic acid is 4.2. The pH at which 95% of the acid will be in ionized form is:

(1) 5.02
(2) 5.38
(3) 2.92
(4) 3.71

Answer Key		
1	**2**	**3**
2	3	2

EXPLANATIONS

1. **Correct Answer is (2)**
   Explanation: When CO2 (carbon dioxide) is bubbled through water, it dissolves and forms carbonic acid, as shown in the following reaction:
   CO2 + H2O -> H2CO3. The student conducted the experiment by bubbling CO2 through water in beaker A and N2 through water in beaker B. He recorded the pH in each of the solutions every 5 minutes. After a period of time, he found that the pH of the solution in beaker A decreased, while the pH of the solution in beaker B did not change. This indicates that bubbling CO2 through water makes it more acidic, while bubbling N2 through water does not change the pH of the water.

2. **Correct Answer is (3)**
   Explanation: A 1 M NaCl solution means that there is 1 mole of NaCl dissolved in 1 liter of solution. So, in a 700 ml solution, there will be 0.7 moles of NaCl.
   A 1 mole NaCl solution means that there is 1 mole of NaCl in the solution, regardless of the volume of the solution. So, in a 700 ml solution, there will be 1 mole of NaCl.
   Therefore, Bottle A has less amount of NaCl than Bottle B.

3. **Correct Answer is (3)**
   Explanation: To determine the pH at which 95% of the acid will be in ionized form, we can use the Henderson-Hasselbalch equation:
   pH = pKa + log([A-]/[HA])
   Where: pH = the pH of the solution pKa = the negative logarithm of the acid dissociation constant (4.2 in this case) [A-] = concentration of the ionized form of the acid [HA] = concentration of the non-ionized form of the acid
   Since we want to find the pH at which 95% of the acid is in the ionized form, we can set [A-] to 0.95 and [HA] to 0.05 (since 95% in the ionized form means 5% in the non-ionized form).
   Let's plug these values into the Henderson-Hasselbalch equation:
   pH = 4.2 + log(0.95/0.05)
   pH = 4.2 + log(19)
   Now, let's calculate the logarithm:
   log(19) ≈ 1.278
   Now, add this value back to the pKa:
   pH ≈ 4.2 + 1.278 ≈ 5.478
   Now, we need to round the pH value to one decimal place since the pKa was given to one decimal place. The answer will be approximately:
   pH ≈ 5.5
   Among the given options, the closest pH value is (2) 5.38.

THERMODYNAMICS

TIFR - PREVIOUS YEAR EXAM QUESTIONS

(TIFR - 2021)

1. According to the third law of thermodynamics, entropy of a perfect crystal at absolute zero temperature is

   (1) Always negative (2) Always positive

   (3) Equal to zero (4) Equal to one

Answer Key
1
3

EXPLANATIONS

1. **Correct Answer is (3)**

   Explanation: The third law of thermodynamics states that the entropy of a perfect crystal at absolute zero temperature is exactly zero. At absolute zero (0 Kelvin or -273.15 degrees Celsius), a perfect crystal is in its lowest possible energy state, and there is only one way to arrange the particles with minimum disorder. As a result, the entropy is zero, as there is no randomness or disorder present at this temperature.

CHAPTER-3
BIOCHEMISTRY

AMINO ACIDS

TIFR - PREVIOUS YEAR EXAM QUESTIONS

(TIFR - 2015)

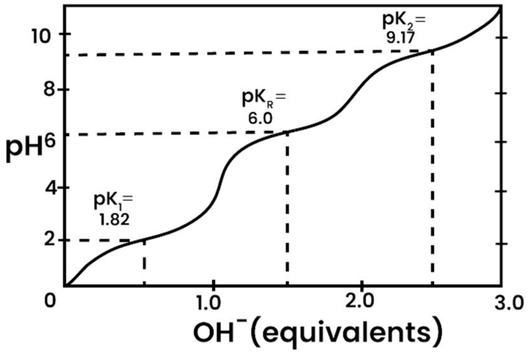
1. Animal cells are labelled with radioactive amino acids. In which of the following molecules would you detect radioactivity:

I. Proteins
II. RNA
III. Ribosomes
IV. Glycolipids

(1) I (2) I & III
(3) II (4) I & IV

(TIFR - 2021)

2. Which amino acid may produce following titration curve profile?



(1) Phe (2) His
(3) Val (4) Leu

(TIFR - 2021)

3. Which of the following amino acids do you expect to find in higher proportion within histones compared to a cytoskeletal protein?

(1) K and R (2) L and A
(3) D and E (4) F and W

(TIFR - 2022)

4 Which one of the following statements is wrong?

(1) Cellulose is a polysaccharide
(2) Uracil is a pyrimidine
(3) Serine is a sulphur containing amino acid
(4) Sucrose is a disaccharide

(TIFR - 2023)

5. Amino acids have different chemical properties that determine whether they are found on the surface of globular proteins. Which of the following series of amino acids is ordered according to how likely it will be found on the surface of a protein:

(1) Arginine > Leucine > Aspartic acid> Phenylalanine
(2) Threonine > Arginine > Phenylalanine > Asparagine
(3) Arginine > Phenylalanine > Threonine > Glycine
(4) Aspartic acid > Threonine > Leucine > Phenylalanine

(TIFR - 2023)

6. You synthesise a short peptide [AMxVFxGNxM], where x is any amino acid with a charged side chain. How many possible peptides can be synthesised?

(1) 15 (2) 243
(3) 125 (4) 27

(TIFR - 2023)

7. If you have a polypeptide of size 11 kilo Daltons, what would be the mass of the open reading frame that codes for the polypeptide? The average mass of an amino acid and a nucleotide is considered to be 110 Daltons and 330 Daltons, respectively.

(1) 99990 (2) 99000
(3) 90900 (4) 99900

(TIFR - 2023)

8. A newly discovered extra-terrestrial organism was found to contain proteins that are made up of 75 different amino acids. Assuming that one codon codes for a unique amino acid, which of the following is possibly correct about its DNA and codons?

(1) The DNA could be composed of 4 bases and the organism has a triplet codon.
(2) The DNA could be composed of 3 bases and the organism has a triplet codon.
(3) The DNA could be composed of 3 bases and the organism has a quartet codon.
(4) The DNA could be composed of 2 bases and the organism has a quartet codon.

(TIFR - 2024)

9. A peptide has the following sequence ATHMARAMEN. At pH 3.7, the net charge of the peptide is likely to be

(1) +2 (2) +1
(3) -1 (4) -2

Answer Key

1	2	3	4	5	6	7	8	9
2	2	1	2	4	3	1	3	2

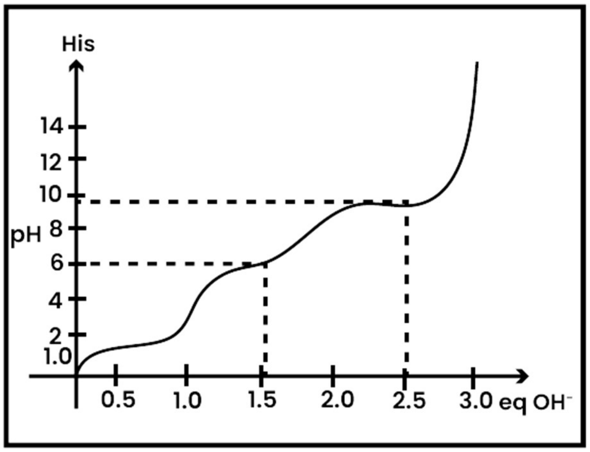
EXPLANATIONS

1. **Correct Answer is (2)**

Explanation:- Proteins and ribosomes can be detected for radioactivity because amino acids are radiolabeled. Proteins are made up of amino acids, so if you label animal cells with radioactive amino acids, you will be able to detect radioactivity in the proteins. Ribosomes are the organelles responsible for protein synthesis. They are made up of RNA and proteins. If you label animal cells with radioactive amino acids, you will be able to detect radioactivity in the ribosomes.

2. **Correct Answer is (2)**

Explanation: In the titration curve of histidine, the pka1 value is around 1.8, pI value is around 6, and pk2 value is around 9.8.



3. **Correct Answer is (1)**

Explanation: DNA is negatively charged and histones are composed of mostly positively charged amino acids, they are abundant in lysine and arginine. Due to this positive charge on histone, they remain closely associated with the negatively charged DNA through electrostatic force of attraction.

4. **Correct Answer is (2)**

Explanation: Uracil is a common and naturally occurring **pyrimidine nucleobase** in which the pyrimidine ring is substituted with two oxo groups at positions 2 and 4. Found in RNA, it base pairs with adenine and replaces thymine during DNA transcription.

5. **Correct Answer is (4)**

Explanation: In globular proteins, the hydrophobic amino acids are buried in the interior of the protein, while the hydrophilic amino acids are exposed to the solvent. Aspartic acid and leucine are both hydrophobic amino acids, so they are more likely to be found in the interior of the protein. Threonine is a polar amino acid, so it is more likely to be found on the surface of the protein. Phenylalanine is also a polar amino acid, but it is more hydrophobic than threonine, so it is less likely to be found on the surface of the protein.

6. **Correct Answer is (3)**

Explanation: The number of amino acids with a charged side chain is typically 5: Aspartic acid (Asp), Glutamic acid (Glu), Lysine (Lys), Arginine (Arg), and Histidine (His).

Thus, For each "x" position = 5 choices of charged amino acids.

There are 3 "x" positions in the peptide sequence,

Then Number of possible peptides = 5 (choices for the first "x") × 5 (choices for the second "x")× 5 (choices for the third "x")

$=5^3= 125$.

7. **Correct Answer is (1)**

Explanation: given, molecular weight of protein = 11 KD

= 11,000 Dalton

Average molecular weight is = $\frac{11,000}{110}$ = 100

That means ORF is made up of 100 amino acid.

Now for 1 amino acid code there are 3 nucleotides required,

There for, for 100 amino acid = 100 × 3 = 300 nucleotides.

Here also considered stop codon and that is made up of 3 nucleotides, thus 300 + 3 = 303,

Now total molecular weight is = 303 × 330(average mol. wt. of nucleotides) = 99,990

8. **Correct Answer is (3)**

Explanation: The DNA could be composed of 3 bases and the organism has a quartet codon. If the DNA is composed of 3 bases and the organism has a quartet codon, then there are 3^4 = 81 possible codons. This is enough codons to code for 75 different amino acids.

9. **Correct Answer is (2):-**

N-terminus (A, Alanine): Typically, the N-terminal amine group has a pKa around 8-9. At pH 3.7, it is protonated and positively charged.

(+1)R (Arginine): Arginine has a pKa around 12.5, so at pH 3.7, it's protonated and positively charged. **(+1) H (Histidine):** Histidine has a pKa around 6.0. At pH 3.7, it's close to its pKa is close to the pH, it may be partially protonated, contributing less to the overall positive charge.

(0) E (Glutamic acid): Glutamic acid has a pKa around 4.1 for its side chain carboxyl group. At pH 3.7, it's slightly below its pKa, so it is likely protonated and neutral.

(0) C-terminus (N, Asparagine): The C-terminal carboxyl group typically has a pKa around 2-3. At pH 3.7, it is deprotonated and negatively charged.

(-1) Adding these up: [+1 (N-terminal A)] + [+1 (R)] + [-1 (C-terminal N)] = +1.

The exact charge can depend on the specific environment and interactions within the peptide, which might affect the ionization states of these groups.

CHAPTER-4
BIOCHEMISTRY

PROTEINS

TIFR - PREVIOUS YEAR EXAM QUESTIONS

(TIFR - 2016)

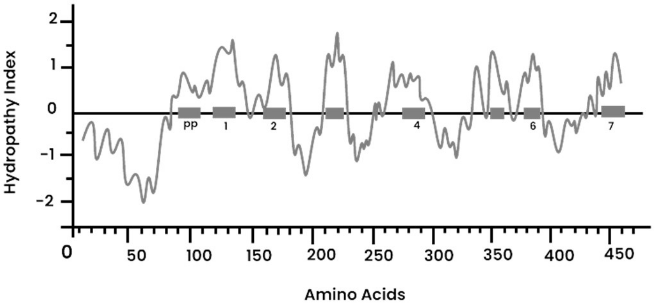
1. The α-helix in proteins is formed due to
   (1) Intramolecular hydrogen bonds
   (2) Intermolecular hydrogen bonds
   (3) van der Waals interactions between amino acids
   (4) Ionic interactions

(TIFR - 2018)

2. Which of these events contributes the most in proper folding of a polypeptide to its native state in an aqueous solvent?
   (1) Loss of hydrogen bonding between the polar amino acids and water
   (2) Hydrophobic effect which sequesters the non-polar residues away from water
   (3) Formation of new intermolecular hydrogen bonding between polar amino acids
   (4) Formation of di-sulphide linkages between free cysteine residues located at a distance along the primary sequence

(TIFR - 2021)

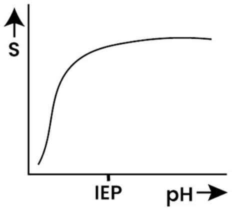
3. In the below hydropathy plot of a protein, positive values are regions of the protein that are considered hydrophobic based on primary amino acid sequence. What type of protein is this?



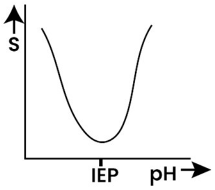
   (1) Lipid-anchored membrane protein
   (2) Multiple-pass integral membrane protein
   (3) Cytosolic protein
   (4) Cannot say. I need more information.

(TIFR - 2022)

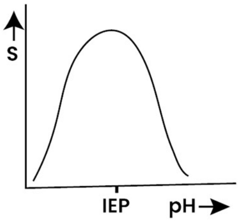
4. Which of the following show the appropriate solubility (S) curve of globular protein in polar solvent when plotted as a function of pH. IEP is the isoelectric point of the protein.



1.



2.



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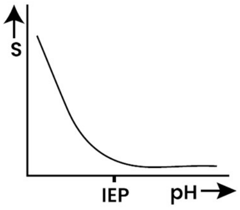

4.

(TIFR - 2022)

5. Identify the statement about haemoglobin that is not correct:
   (1) Oxygen binds the porphyrin ligands of the haem groups
   (2) Oxygen binding is sensitive to pH
   (3) Carbon Monoxide is toxic as it binds haemoglobin with a higher affinity than oxygen
   (4) Oxygen binding to Haemoglobin is reversible.

Answer Key				
1	**2**	**3**	**4**	**5**
1	2	2	2	1

EXPLANATIONS

1. **Correct Answer is (1)**
   Explanation: The alpha helix is a secondary structure of proteins that is formed by hydrogen bonds between the backbone carbonyl oxygens and amide hydrogens of amino acids that are four residues apart. These hydrogen bonds are called intramolecular hydrogen bonds because they occur within the same molecule.

2. **Correct Answer is (2)**
   Explanation: The proper folding of a polypeptide into its native state in an aqueous solvent is primarily driven by the hydrophobic effect. The hydrophobic effect is a significant driving force in protein folding and is a result of the interaction between non-polar (hydrophobic) residues in the polypeptide and water molecules.

3. **Correct Answer is (2)**
   Explanation: Hydropathy plots are used to predict the transmembrane regions in a protein based on the hydrophobicity of its amino acid sequence. In a multiple-pass integral membrane protein, the regions with positive values in the hydropathy plot correspond to the hydrophobic transmembrane domains that span the lipid bilayer of the cell membrane. These hydrophobic regions anchor the protein into the membrane, allowing it to pass through the lipid bilayer multiple times.

4. **Correct Answer is (2)**
   Explanation: The protein solubility increased when the pH increased. Maximum protein solubility was observed at pH=8.0, because in this condition, the protein's positive and negative net charged molecules interact more with water. Protein solubility is lower in acidic pH than in alkaline pH.

5. **Correct Answer is (1)**
   Explanation: The correct statement is that oxygen binds to the iron atom at the center of the heme groups in hemoglobin, not the porphyrin ligands. Hemoglobin is an iron-containing protein, and each subunit of hemoglobin contains a heme group with an iron atom at its center. Oxygen binds reversibly to the iron in the heme group, allowing hemoglobin to transport oxygen in the blood.