PART 2

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EDITION 1

INSTITUTE AND UNIVERSITY EXAMS | NEET / NEXT EXAMS

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BIOCHEMISTRY
COMPENDIUM

As per the Competency-Based Medical Education Curriculum (NMC)

BRIEF NOTES FOR COMPETENCIES

VIVA QUESTIONS WITH ANSWERS

SHORT QUESTIONS & ANSWERS

LONG QUESTIONS & ANSWERS

MCQS WITH EXPLANATIONS

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A Comprehensive Guide for Biochemistry

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sage.edu.in@gmail.com
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This first edition of the *Comprehensive Guide for Biochemistry* has been carefully crafted to provide a thorough and up-to-date resource for students and educators in the field of Biochemistry. The contents have been reviewed by experts to ensure accuracy and relevancy, reflecting current knowledge and practices in Biochemistry education.

Dedication

This book is dedicated to all students and educators who strive for excellence in the field of Biochemistry . May this guide serve as a reliable companion on your journey of discovery and learning.

Revision

Updates and revisions for subsequent editions will be made available as necessary to ensure that the material remains current and continues to meet the evolving needs of Biochemistry education.

For suggestions and feedback, please contact Sage Helix 360 at sage.edu.in@gmail.com

Disclaimer

While every effort has been made to ensure the accuracy of the information contained herein, the publisher and the author assume no responsibility for errors, omissions, or changes to the data. This guide is intended for educational purposes and should not be used as a substitute for professional medical advice.

Preface

Welcome to **Biochemistry Compendium** by Sage Helix 360, your comprehensive companion for conquering NEET UG and PG examinations.

Why Choose This Book?

We, at Sage Helix 360, have meticulously crafted this book to provide you with a learning experience that is both **comprehensive and strategic**. We understand the demands of competitive exams like NEET UG and PG. Here's what sets this book apart:

Exam-Oriented Content: Every chapter is meticulously structured to align perfectly with NEET UG and PG exam patterns. You'll find a strategic blend of question formats including **Viva Questions with Answers, Short Questions and Answers, Long Questions and Answers, Multiple Choice Questions (MCQs).** This diverse range of questions reflects the actual exam format, allowing you to practice and familiarize yourself with the types of questions you'll encounter.

- **Effective Learning Tools:** We believe in empowering your learning through clear and concise explanations. The book incorporates **crisp explanations, well-labelled diagrams, and strategically placed tables** to enhance your understanding and retention of key concepts. Visual aids are a powerful tool for grasping complex information, and we've utilized them extensively to make your learning journey more engaging.
- **Self-Assessment and Reinforcement:** We understand the importance of testing your knowledge. Each chapter concludes with a comprehensive question bank encompassing MCQs. The answer keys, complete with explanations, offer valuable insights into your strengths and weaknesses. By actively engaging with these questions, you'll solidify your understanding and identify areas that require further practice.

We wish you the very best in your academic journey and a fulfilling career in the medical field.

The Sage Helix 360 Team

Acknowledgements

Creating a comprehensive educational resource such as *Biochemistry Compendium* is a monumental task that requires the dedication, expertise, and collaboration of many individuals. We would like to extend our sincere gratitude to everyone who contributed to the making of this book.

Sage Helix 360

We are also profoundly grateful to **Sage Helix 360** team for their pivotal role in the publication and design of this guide.

- **Publishing Team:** We thank our publishing team for their steadfast support throughout this project. Their coordination, project management, and adherence to deadlines have been vital in bringing this book to life. Their understanding of the academic market and their ability to navigate the complexities of publishing have been invaluable.
- **Editorial Team:** Our editorial team deserves special recognition for their tireless efforts in refining the content of this guide. Their thorough reviews, insightful suggestions, and keen eye for detail have enhanced the accuracy and readability of the material. Their commitment to maintaining the highest editorial standards has ensured that this book is both authoritative and student-friendly.
- **Design Team:** The design team at Sage Helix 360 has played a crucial role in creating a visually appealing and user-friendly layout for this book. Their creativity, technical skills, and attention to visual detail have resulted in a design that complements and enhances the educational value of the content. Their innovative approach to incorporating diagrams, charts, and illustrations has made this guide an engaging and effective learning tool.

Contributors and Reviewers

We would like to acknowledge the contributions of numerous **subject matter experts** and **peer reviewers** who have provided their valuable feedback during the development of this guide. Their expertise has been instrumental in validating the accuracy and relevance of the content. Their constructive feedback has ensured that this guide meets the educational needs of its intended audience and reflects the latest advancements in the field of Biochemistry

Students and Educators

Finally, we extend our heartfelt thanks to the **students and educators** who have provided insights, suggestions, and feedback throughout the creation of this guide. Your experiences

and perspectives have been crucial in shaping a book that is not only comprehensive but also practical and relevant to your needs. We hope that this guide will serve as a valuable resource in your studies and teaching, and that it will inspire a deeper understanding and appreciation of Biochemistry .

Conclusion

In closing, the *Biochemistry Compendium* is the result of a collaborative effort, and we are immensely proud of what we have achieved together. We hope that this guide will serve as a cornerstone for Biochemistry education, helping students to navigate and excel in this complex field.

With profound gratitude,

The Team at Sage Helix 360

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BI 5

Chemistry and Metabolism of Proteins

BI 5.1

Describe and discuss the structural organization of proteins.

5.1.1

Detail Overview

Proteins perform most of the functions in the cell therefore considered as the central cell components. Their functions are hard to understand without knowing their structures. This note provides an overview of the four main organizational levels of proteins:

1. Primary Structure:

- The foundation of a protein, it refers to the linear sequence of amino acids making up the polypeptide chain.
- There are 20 different amino acids, each with a unique side chain (R group) influencing its chemical properties and folding potential.
- The order of amino acids is determined by DNA and is crucial for function. Changing even one amino acid can drastically alter the protein's shape and activity.

2. Secondary Structure:

- Refers to the local folding patterns of the polypeptide chain, stabilized by hydrogen bonds formed between backbone N-H and C=O groups.
- **Two major types:**

α-helix: A tightly packed right-handed coil, where every fourth amino acid forms a hydrogen bond. Common in structural proteins like keratin.

β-sheet: Two or more polypeptide chains arranged side-by-side or oppositely facing, connected by hydrogen bonds. Forms sheets or pleated structures found in enzymes and antibodies.

3. Tertiary Structure:

- The overall three-dimensional shape of the entire polypeptide chain, resulting from interactions between R groups and backbone atoms.
- **Stabilized by a combination of forces:**

Hydrogen bonds: Between polar side chains and main chain atoms.

Ionic bonds: Between oppositely charged side chains.

Disulfide bonds: Covalent bonds formed between cysteine residues.

Hydrophobic interactions: Nonpolar side chains cluster inside the protein to minimize contact with water.

- The tertiary structure defines a protein's functional surface, pockets, and grooves, crucial for ligand binding and enzyme activity.

4. Quaternary Structure:

- Applies to proteins composed of multiple polypeptide chains assembled in a specific arrangement.
- Stabilized by the same forces as tertiary structure, plus additional interactions between subunits.
- **Examples:** Hemoglobin (four subunits) and antibodies (two heavy and two light chains).

5.1.2

Viva Questions with Answers

1. What are the building blocks of proteins?

Answer: Amino acids, are made up of amino, carboxyl, R-side chain and central carbon (alpha).

2. How are amino acids linked together?

Answer: With peptide linkages, which are formed between a carboxyl group of one amino acid and the amino group of another.

3. What is the primary structure of a protein?

Answer: The primary structure is a linear sequence of amino acids in one of the polypeptide chains. Determines the positioning of variable side chains that play a role in protein structure and function.

4. What are the types of secondary structures in proteins?

Answer: They are alpha helix (right-handed or left-handed helix) and beta-sheet (beta-pleated) secured by internal hydrogen bonds between amino acids.

5. How do secondary structures form tertiary structures?

Answer: The interactions of the R-side chains (hydrophobic, ionic, hydrogen bonds, and disulfide linkages) twist the polypeptides into complex three-dimensional shapes.

6. What is the functional unit of a protein?

Answer: The Domain, is a folded stable unit of the protein tertiary structure that confers specific functional capabilities of the protein.

7. What determines the stability of a protein structure?

Answer: It is the combination of several forces such as hydrogen bonds, hydrophobic interactions, ionic bonds and sulphur bonds.

8. How does protein structure relate to function?

Answer: The protein's distinctive 3D shape causes the formation of certain areas and surfaces that are vital in attaching ligands, substrates, and other proteins for its task.

9. What are the different levels of protein organization?

Answer: Primary (polypeptide chain), secondary (alpha helices/beta sheets), tertiary (the folding into maximum 3D structure) and quaternary (more than one polypeptide chain in this case in a complex).

10. How can changes in protein structure affect function?

Answer: Genetic mutations, protein misfolding, or post-translational modifications are all examples of factors that can change the structure of a protein with deleterious consequences that include loss of function, aggregation and even diseases.

5.1.3

Short Questions and Answers

1. Explain the concept of peptide bonds and their significance in determining the primary structure of a protein.

Answer: Peptide bonds are covalent bonds that arise out of the reaction between the α-amino and the α-carboxyl groups from two different amino acids in a condensation reaction thus producing a polypeptide chain. The sequence of amino acids that are joined together by peptide bonds is referred to as the primary structure of a protein. Like informing the unique structure of the protein, the linear sequence of amino acids keeps memory wires that specify their order. Revolutionary alteration in the properties and function of any protein can occur by just changing one of the amino acids in its sequence.

2. Compare and contrast the two major types of secondary structure: α-helices and β-sheets. How do the properties of different amino acid side chains influence these structures?

Answer: Both α-helices and β-sheets arise from regular, repeating patterns of hydrogen bonds between the backbone atoms of the polypeptide chain. α-helices are spiral structures held together by H-bonds between backbone NH and CO groups spaced four residues apart. They favour amino acids with small, non-polar side chains that minimize steric hindrance and promote tight packing. β-sheets are formed by pleated strands of polypeptide chains linked by H-bonds between backbone NH and CO groups of adjacent strands. They can be parallel or antiparallel and accommodate amino acids with various side chains, though bulky residues may disrupt the sheet structure.

3. Describe the forces and interactions that contribute to the formation of the tertiary structure of a protein. Illustrate with an example.

Answer: The 3D folding of a single polypeptide chain into a unique, functional shape is referred to as the tertiary structure.

This complex architecture arises from a combination of non-covalent interactions, including:

- **Hydrogen bonds:** Formed between backbone and side chain atoms, stabilizing specific conformations.
- **Ionic bonds:** Electrostatic attractions between charged side chains (e.g., lysine and glutamate) can hold folded domains together.
- **Hydrophobic interactions:** Non-polar side chains cluster to minimize exposure to water, driving protein folding inward.
- **Disulfide bridges:** Covalent linkages formed between cysteine side chains further stabilize tertiary structure.

For example, the tertiary structure of myoglobin relies on a combination of these forces: α-helices fold and pack together via hydrophobic interactions and H-bonds, while a strategically placed disulfide bridge between two helices adds rigidity and maintains the protein's oxygen-binding pocket.

4. Discuss the concept of protein domains and their functional significance in protein architecture.

Answer: Protein domains are independently folding and often evolutionarily conserved units within a polypeptide chain. They typically have specific structural and functional roles, allowing for modularity and versatility in protein design. Multiple domains can combine to form complex proteins with diverse functions. For example, an antibody molecule contains several domains: one for antigen binding, another for Fc receptor interaction, and others for hinge-like flexibility. Domain organization is crucial for interpreting protein function and exploring targeted therapies.

5. How does the quaternary structure of a protein, involving multiple polypeptide chains, influence its function? Provide an example.

Answer: Quaternary structure describes the arrangement and interactions between multiple polypeptide chains in a protein complex. This assembly adds another layer of complexity and functional specialization. For instance, haemoglobins' quaternary structure consists of four polypeptide chains, each with an α-helix and heme group. Their specific assembly allows for cooperative oxygen binding and efficient release in response to changing oxygen levels, a process crucial for oxygen transport.

6. Explain the concept of intrinsically disordered proteins (IDPs) and their unique structural and functional properties.

Answer: Unlike most proteins with defined folded structures, some IDPs lack a stable 3D conformation under physiological conditions. These proteins often contain long stretches of hydrophilic and charged amino acids, making them dynamic and adaptable. IDPs often function as molecular switches or scaffolds, interacting with other proteins or biomolecules in a context-dependent manner. Their flexibility allows them to participate in diverse and complex cellular processes.

7. Describe the role of post-translational modifications (PTMs) in modulating protein structure and function.

Answer: PTMs are chemical alterations of proteins after translation, adding a layer of diversity and regulation beyond the encoded sequence. Examples include phosphorylation, acetylation, methylation, and glycosylation. These modifications can alter protein structure, folding stability, interactions with other molecules, and enzymatic activity. For instance, phosphorylation of a protein kinase might activate it, while glycosylation on an immune receptor might modulate its binding affinity.

5.1.4

Multiple Choice Questions

1. Which amino acid side chain has the highest pKa and is most commonly involved in hydrogen bonds?

(A) Alanine
(B) Glycine
(C) Glutamic Acid
(D) Cysteine

Answer: (C) Glutamic Acid.

Explanation: *Depending on the ionization level of the glutamic side chain which carries a carboxylic acid, Glutamic is the one with the highest pKa value of 4.25.*

2. The alpha helix is a secondary structure element stabilized by:

(A) Ionic Bonds
(B) Disulfide Bridges
(C) Hydrogen Bonds
(D) Van Der Waals Forces

Answer: (C) Hydrogen bonds.

Explanation: *The α helix is a spiral formed due to hydrogen bonds between the NH group of an amino acid and the CO group of another amino acid that is located four amino acids away in the sequence.*

3. Which protein structure level defines the overall 3D arrangement of polypeptide chains?

(A) Primary Structure
(B) Secondary Structure
(C) Tertiary Structure
(D) Quaternary Structure

Answer: (C) Tertiary structure.

Explanation: *The three-dimensional structure where one polypeptide protein folds into one unique 3D structure owing to various interactions such as hydrogen bonding, hydrophobic interactions and ionic interactions is known as tertiary structure.*

4. Haemoglobin is an example of a protein with:

(A) Alpha Helices Only
(B) Beta Sheets Only
(C) Both Alpha Helices And Beta Sheets
(D) Neither Alpha Helices Nor Beta-Sheets

Answer: (C) Both alpha helices and beta sheets.

Explanation: *Haemoglobin possesses alpha-helical and beta-sheet structures, which form an elaborate tertiary structure that enhances oxygen binding.*

5. Which amino acid residue destabilizes alpha helix formation due to its bulky side chain?

(A) Glycine
(B) Proline
(C) Serine
(D) Alanine

Answer: (B) Proline.

Explanation: *The presence of proline within the helix creates a stiff region that does not allow the accommodation of the hydrogen bonding that is characteristic of alpha-helical conformations.*

6. Disulfide bridges are covalent bonds formed between the sulfur atoms of:

(A) Histidine Residues
(B) Cysteine Residues
(C) Tyrosine Residues
(D) Methionine Residues

Answer: (B) Cysteine residues.

Explanation: *The covalent link formed, and referred to as a disulphide bond is between two cysteine residues oxidised, which functions to stabilise and retain the structural integrity of proteins.*

7. The fibrous protein keratin found in hair is primarily composed of:

(A) Alpha Helices
(B) Beta Sheets
(C) Random Coils
(D) Disulfide Bridges

Answer: (B) Beta sheets.

Explanation: *The rich composition of keratin with beta-sheet portions enhances the strength and rigidity of the molecule.*

8. Chaperones are proteins that assist in:

(A) Protein Folding
(B) Protein Degradation
(C) Signal Transduction
(D) Enzyme Catalysis

Answer: (A) Protein folding.

Explanation: *Nucleated chaperones assist in the folding of newly synthesized or misfolded proteins into their biologically active states.*

9. Myoglobin, a protein with similar function to haemoglobin, differs in its:

(A) Amino Acid Sequence
(B) Quaternary Structure
(C) Heme Group Binding Affinity
(D) Overall Size And Shape

Answer: (D) Overall size and shape.

Explanation: *Polypeptides consisting of a single chain are myoglobin's, whilst tetramers having four polypeptide subunits are haemoglobins. Structural differences are responsible for the higher oxygen trapping of myoglobin.*

10. Denaturation of a protein refers to the loss of its:

(A) Primary Structure
(B) Secondary Structure
(C) Tertiary Structure
(D) All Of The Above

Answer: (C) Tertiary structure.

Explanation: *Denaturation leads to alteration in the overall three-dimensional form of a protein and loss of its biological activity for which it was intended, though the primary structure of the protein is preserved.*

11. A chain of amino acids linked by peptide bonds is termed:

A) Primary Structure
B) Secondary Structure
C) Tertiary Structure
D) Quaternary Structure

Answer: A) Primary structure

Explanation: *Hemen Sol the basic description of the existing mesyl positioned at the primary factor, understanding of which is simplistic.*

12. Which type of secondary structure element is stabilized by intramolecular hydrogen bonds between the main chain N-H and C=O groups?

A) A-Helix
B) B-Sheet
C) Random Coil
D) Pleated Sheet

Answer: A) α-helix

Explanation: *In an α-helix, hydrogen bonds are formed between the amino acid N-H and C=O which are four residues down the chain coupled with the side chains leading to the coiling of the structure.*

13. Which amino acid side chain contributes significantly to β-sheet formation due to its ability to form multiple hydrogen bonds?

A) Alanine
B) Cysteine
C) Proline
D) Serine

Answer: C) Proline

Explanation: *Owing to proline which violates the basic structural rules of all amino acids itself software, because of the rigid molecular ring*

environment of proline, it is mostly only made to the hirsute ends of β- sheets extending structures.

14. Disulfide bonds arise from the oxidation of which amino acid side chain functional group?

A) Amine
B) Carboxyl
C) Hydroxyl
D) Thiol

Answer: D) Thiol

Explanation: *Cystines can make covalent disulfide linkages to cysteine residues and participate in the folding and stabilization of structures of proteins at the tertiary and quaternary protein levels.*

15. Haemoglobin, a globular protein, exhibits which level of protein structure?

A) Primary Only
B) Primary And Secondary
C) Primary, Secondary, And Tertiary
D) Primary, Secondary, Tertiary, And Quaternary

Answer: D) Primary, secondary, tertiary, and quaternary

Explanation: *Haemoglobin molecules including four chains of polypeptides (quaternary structure) are twisted and turned into different shapes (tertiary structure), alpha baying and beta barreling are secondary forms based on the primary structure consisting of amino acids.*

16. Which disease state arises from the misfolding of a specific protein in the brain?

A) Sickle Cell Anemia
B) Alzheimer's Disease
C) Cystic Fibrosis
D) Muscular Dystrophy

Answer: B) Alzheimer's disease

Explanation: *Amyloid plaques which are comprised of aggregated and misfolded β-amyloid proteins are hallmarks of either the mild or advanced Alzheimer's disease, pointing out the importance of the geometry of the protein in the disease states.*

17. Enzymes exhibit high specificity for their substrates due to:

A) Their Tertiary Structure Provides A Unique Binding Pocket
B) Their Primary Sequence Determining Specific Amino Acid Interactions
C) The Presence Of Disulfide Bonds Contributing To Stability
D) All Of The Above

Answer: D) All of the above

Explanation: *Specificity on enzyme involves several aspects; both the shape of the active site (tertiary structure) and specific residues of an enzyme (substrate binding) involved in disulphide bonds as well for example touch or dis(with) help); these were crucial towards achieving catalytic efficiency.*

18. Which mutation type is least likely to significantly affect protein folding and function?

A) Single Amino Acid Substitution
B) Insertion Of A Few Amino Acids
C) Deletion Of Several Amino Acids
D) Change In A Disulfide Bond Location

Answer: A) Single amino acid substitution

Explanation: *A single substitution may do very little about overall folding and function depending on the amino acid but more especially the part of the protein that is substituted. However, large insertions, deletions or shifts in the positions of disulfide bonds are known to lead to changes in secondary and tertiary structures with a corresponding change in the function of the protein.*

19. Design of new drugs often involves the manipulation of which level of protein structure?

A) Primary
B) Secondary
C) Tertiary
D) Quaternary

Answer: C) Tertiary

Explanation: *One of the common drug design strategies is to create inhibitors or activators for specific interactions within the folded protein (tertiary structure) would goal is to regulate its function. Targeting primary or secondary structures is usually not possible or productive.*

20. Which technology allows visualization of the three-dimensional structure of proteins at the atomic level?

A) Electrophoresis
B) Chromatography
C) X-Ray Crystallography
D) Western Blotting

Answer: C) X-Ray crystallography

Explanation: X-*ray crystallography is a powerful technique since it allows for the precise identification of the spatial arrangement of atoms within proteins and thus enhances the understanding of protein structure and function.*