21. When we extract carotenoids from its source we see that is:
A. Violet in color B. Yellow green in color
C. Blue green in color D. Yellow to orange red in color

22. Glycolysis takes place in the _____ of cell:
A. Golgi complex D. Cytoplasm C. Nucleus D. Mitochondria

23. How many molecules of ATP would be utilized for phosphorylation of one glucose molecule during glycolysis?
A. One B. Two C. Four D. Three

24. Which of the following photosystem is involved in cyclic photophosphorylation?
A. PS I and PS II B. PS III C. PS II D. PS I

25. The photosynthetic pigments of plants are arranged as clusters in thylakoid membranes. The reaction centers of these clusters consist of _____ molecules:
A. ATP B. Glucose C. Chlorophyll D. Carotenoids

26. The following flowchart depicts the steps of the Calvin Cycle. Which option according to you fits in as the correct answer of the missing step?
A. Hydrogenase B. Ribulose bisphosphate C. Oxaloacetate D. Pyruvate

27. In chemiosmosis the proton (H^+) pumps moves from:
A. Stroma to Lumen B. Lumen to Stroma C. Stroma to Cytoplasm D. Cytoplasm to Stroma

28. In chemiosmosis the proton (H^+) pumps moves from:
A. Stroma to Lumen B. Lumen to Stroma C. Stroma to Cytoplasm D. Cytoplasm to Stroma

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31. How many molecules of ATP would be utilized for phosphorylation of one glucose molecule during glycolysis?
A. One B. Two C. Four D. Three

32. Which of the following photosystem is involved in cyclic photophosphorylation?
A. PS I and PS II B. PS III C. PS II D. PS I

ANSWERS KEY

1. A	2. B	3. B	4. D	5. B	6. C	7. B	8. C	9. A	10. A	11. A	12. B
13. D	14. B	15. A	16. C	17. B	18. C	19. A	20. B	21. D	22. D	23. B	24. D
25. C	26. B	27. B	28. B	29. C	30. B	31. B	32. D				

Chapter 07 STRUCTURAL AND COMPUTATIONAL BIOLOGY

Student Learning Outcomes (SLOs)

After studying this chapter, the students will be able to:
- Define structural biology.
- Explain that structure determination of biomolecules are important.
- Describe how X-ray crystallography works.
- Outline the online databases where biomolecule structures are available.
- Describe computational biology.
- Define sequence homology.
- Define structural homology.

- **Structural Biology:** Which deals with the study of **three dimensional (3D)** structures of **macromolecules** (including proteins and nucleic acids) at atomic levels.
- **Use Structural Biology:** Provides the detailed information about the structure of **biomolecule**, its **functions**, dynamics and interaction with ligands and other macromolecules.

APPLICATIONS OF STRUCTURAL BIOLOGY

Q. **Describe the applications of structural biology.** (Exercise L.O.1)

- Structural biology has a wide range of applications especially in the field of medical research.
- Some of these are discussed here:

(1) Determining the Active sites and Domains:

- Structural biologists can determine the **three-dimensional (3D)** structures of macromolecules such as proteins and nucleic acids.
- The 3D structures reveal the exact **location, shape,** and **environment of the active sites** and different domains distinct structural units with independent functions of macromolecules.
- **Example:** Structural studies of the **enzyme HIV-1 reverse transcriptase** have identified its polymerase domain:
  (i) Polymerase Domain: Domains which synthesizes DNA.
  (ii) RNase H domain: Which breaks down the **RNA** strand of RNA-DNA hybrids.

Check Understanding!
1. Which of the following best explains the function of the active site in an enzyme?
A. It stores genetic information
B. It binds to the substrate to catalyze a reaction
C. It breaks down the enzyme itself
D. It transports proteins across membranes

➢ **Importance of Knowing Domains:**
- **Help to Design Antiviral Drug:** Knowing the location and structure of these **domains** has helped in the design of **antiviral drugs** that specifically target them.
- Similarly, the structure of serine **proteases** reveals its well-defined active site, which is responsible for breaking down **peptide bonds.**

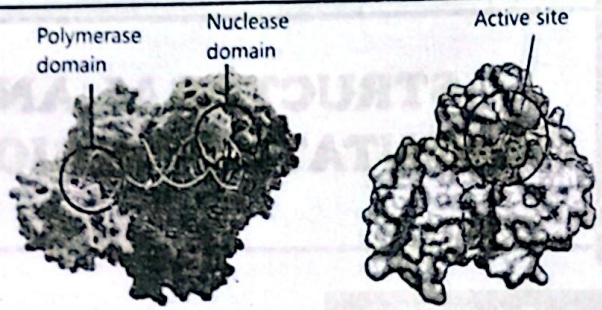


Figure : (a) 3D structure of HIV-1 reverse transcriptase (b) 3D structure of serine protease

(2) Identifying Drug Targets:

- **Drug Target:** The place made up of proteins on a **disease causing molecule**, where a drug can work is called **"drug target"**.
- **Structural biology** helps the scientists to find the right place on a **disease-causing molecule** where a drug can work. These places are usually proteins and are called **drug targets**. By studying the **3D shape** of these proteins, scientists can find specific **spots** where a drug can attach and stop the protein from working.

Check Understanding!
2. Why is understanding protein domains useful in biotechnology and medicine?

- **Example (Use of Structural Biology in COVID-19):** In COVID-19, scientists used **structural biology** to study the **spike protein** of the coronavirus (SARS-CoV-2). This protein helps the virus to **enter human cells**. By knowing its 3D structure, scientists identified it as a **drug target**.
- **Importance/Use:** Thus, they designed **vaccines** and **medicines** that block the spike protein, preventing the virus from infecting more cells.

(3) Identifying Host-Pathogen Interactions

- **To Study Host-Pathogen Interaction:** Structural biology also helps in understanding **how pathogens** (like viruses or bacteria) interact with the host's body cells. This is called **host-pathogen interaction.**
- By studying the **3D structures** of both the **pathogen and the host cell** proteins, scientists can see how the pathogen attaches to and enters the host cell, and which molecules are involved in the process.
- **Example:** Structural biologists studied the **spike protein of coronavirus**, which sticks out from the surface of the virus.
- They also looked at a protein on human cells that acts as **receptor of virus spike** protein. So, the scientists discovered exactly how the virus **enters human cells**. This information was vital in developing the drugs that can bind with receptor proteins.
- **Importance/Use:** Such drug inhibits the interaction of the virus with the receptor and consequently blocks the entry of virus into the host cells.

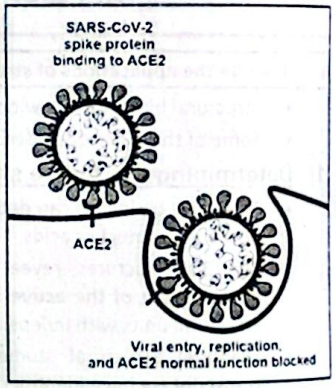


Figure : Mechanism of corona virus binding with receptorof human cell.

(4) Identifying Protein Misfolding:

- The functionality of proteins depends on the correct folding into **three dimensional shapes**.
- **Effect of Incorrect Folding:** Several diseases (including **cyctic fibrosis, Parkinsons, Alziemer's**) originate due to incorrect folding of proteins.
- **Importance/Use:** Structural biology provides **understanding** of intricate folding pathways and how misfolding leads to the diseases.

X-RAY CRYSTALLOGRAPHY

Q. Write a note on principle and working of x-ray crystallography. (Exercise L.O.2)

- **Technique Developed By:** X-ray crystallography was **developed in 1912** by **William Henry Bragg** and **William Lawrence Bragg.**
- In 1915 they were awarded Nobel Prize in Physics for their work.
- Since then it has been used to analyze the **diverse substances** including minerals, **salts, metals, proteins, carbohydrates,** nucleic acids and vitamins.

Mechanism of X-Ray Crystallography:

- In this technique, **x-rays beam strikes** crystals and atoms and molecules in the crystals diffract the x-rays beam in specific directions.
- From the **angles** and intensities of diffracted beams, a 3D picture of electron density within the crystals are produced. The **electron density** is used to create 3D structure of the molecule.
- In order to **understand** the working of X-ray crystallography, let us take the example of protein structure determination.

Check Understanding!
3. How did structural biology contribute to the development of COVID-19 vaccines or treatments?
A. By predicting weather changes
B. By sequencing plant DNA
C. By revealing the 3D structure of the spike protein
D. By observing white blood cells

Steps Involve in X-Ray Crystallography: (The method can be divided into following steps)

(i) Protein Crystallization:

- Protein crystallization means **turning** a purified protein into a **solid crystal form**. Crystals are needed because they arrange protein molecules in a **regular, repeating pattern**, which is important for getting a clear image during the X-ray process.
- To make **crystals**, scientists slowly mix the protein with special solutions that cause the protein molecules to stick together in an orderly way. This process can take **hours, days,** or **even weeks**.
- It often requires careful control of temperature, pH, and salt concentration. Once a clear and stable protein **crystal** is formed, it can be used in the next steps.

(ii) Production of a Diffraction Pattern:

- Once a good quality crystal is formed, it is mounted on the **x-ray machine**. The x-rays beam is bombarded at the crystal at various angles.
- The atoms in the crystal diffract the x-rays beam and a diffraction pattern (which is a series of spots) is created on the **detectors**.

(iii) Creating Density Map:

- The angles and intensities of these spots contain information about the arrangement of atoms in the crystal.
- Diffraction pattern is used to make a **density map.**

(iv) Determination of Protein Structure:

- Then the data is analyzed **mathematically** by using computational programs.
- These calculations transform data into the **3D structure of protein**, thus we can understand the structure of that protein.

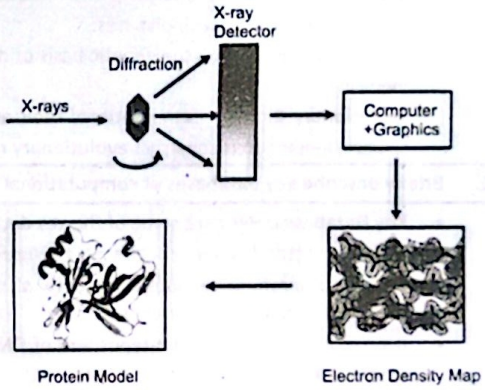


Figure: Schematic representation of X-ray crystallography

COMPUTATIONAL BIOLOGY

- **Computational Biology:** An interdisciplinary field that uses computational techniques and tools to solve biological problems is called **computational biology.**
- It integrates knowledge from **biology, computer science, mathematics,** and **statistics** to analyze and **interpret biological data.**
- **Importance:** The importance of computational biology lies in its ability to handle large datasets, uncover **hidden patterns,** and **generate** predictive models that can lead to new biological insights and applications.

➢ Major Areas of Computational Biology:

Check Understanding!
4. How did structural biology contribute to understanding SARS-CoV-2 (COVID-19 virus)?

(I) **Genomics:** The study of **genomes,** which are the complete set of DNA within a single cell of an organism. Genomics involves sequencing, assembling, and analyzing the function and structure of genomes.
Use: It helps in understanding genetic variations, gene function, and evolutionary relationships.

(II) **Proteomics:** The large-scale study of proteins, including their structures and functions. Proteins are essential molecules that perform many functions within organisms.
Use: Proteomics aims to map the entire set of proteins (the proteome) produced by an organism and understand their interactions and roles in cellular processes.

(III) **Bioinformatics:** The application of **computer technology** to manage and analyze biological data.
Use: Bioinformatics tools and techniques are used to store, retrieve, and analyze DNA, RNA, and protein sequences.

➲ Applications of Computational Biology:

Though computation **biology has vast application,** some of these are discussed here.

(I) **Discovery of Drug:** Computational biology helps in **identifying potential** drug targets and simulating the effects of drugs on biological systems.
It accelerates the drug discovery process by predicting how drugs interact with proteins and other molecules.

(ii) **Genetic Research:** By analyzing DNA sequences, computational biology helps to identify genetic variations associated with diseases.
It aids in understanding the genetic basis of diseases and can lead to the development of personalized medicine.

(iii) **Evolutionary Biology:** Computational tools are used to compare genetic information across different species, helping to reconstruct **evolutionary relationships** and understand the process of evolution.

Q. Briefly describe key databases of computational biology. (Exercise LO.)

- **Key Databases:** Here are some of the key databases used to analyze nucleic acid and proteins.
- **GenBank:** https://www.ncbi.nlm nih.gov/nuccore/
- It is a comprehensive public database of nucleotide sequences and supporting bibliographic and biological annotations (comment).
- It provides access to a vast repository of DNA sequences from various organisms, facilitating genetic research and comparative genomics.

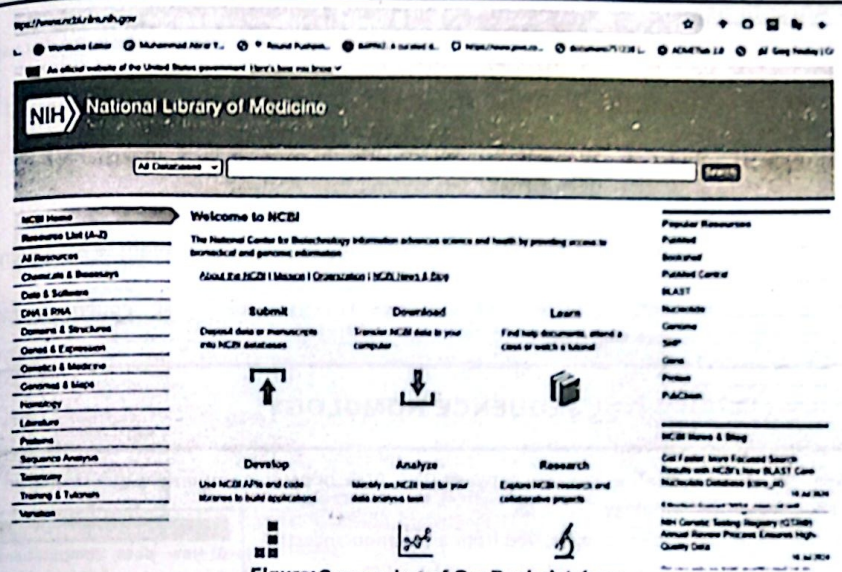


Figure: Screenshot of GenBank database

➢ Protein Data Bank (PDB):

Check Understanding!
5. Which of the following fields in computational biology focuses on studying complete sets of genes?
A. Bioinformatics B. Proteomics
C. Genomics D. Cytogenetics

- This database provides **3D structural** data of large biological molecules, such as proteins and nucleic acids.
- It is important for studying the structures of macromolecules, understanding their functions, and designing drugs that target specific protein structures.

Figure: Screenshot of protein databank

➢ Ensembl:

- It is a genome browser providing information on genome sequences, gene models, and comparative genomics for various species.
- Ensembl helps to access and visualize genomic data, supporting studies in genomics and evolutionary biology.

Key Algorithms:

In addition to above mentioned databases, some algorithms being used in data analysis are discussed below

(i) BLAST (Basic Local Alignment Search Tool):

- It is used for comparing primary biological sequence information, such as the amino-acid sequences of proteins or the nucleotides of DNA sequences.
- It helps identify homologous sequences, predict functions of unknown genes, and study evolutionary relationships.

(ii) FASTA:

- It is a sequence alignment tool that compares a query sequence to a database of sequences to find regions of similarity.
- It is used for searching protein and nucleotide databases, identifying sequence homology, and analyzing sequence alignments.

SEQUENCE HOMOLOGY

- **Sequence Homology:** The similarity between DNA, RNA, or protein sequences due to shared ancestry is called **sequence homology.**
- Homologous sequences have evolved from a common ancestral sequence and can be categorized into two main types:

Check Understanding!
6. How does computational biology support evolutionary biology?

i. **Orthologs:** Sequences in different species that originated from a common ancestral gene during speciation.
   - Orthologs often retain the same function across species.

ii. **Paralogs:** Sequences within the same species that originated from gene duplication.
   - Paralogs can evolve new functions even if they originally arise from the same ancestral gene.

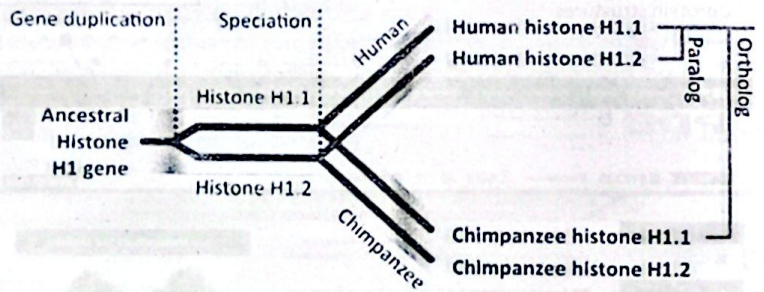


Figure: Types of Homologous Sequences

Importance:

- Sequence homology provides an insight into the evolutionary relationships between organisms. By comparing homologous sequences, scientists can conclude the evolutionary history and divergence of species.
- Furthermore sequence homology provides a clue about the function of an unknown gene or protein. If an unknown gene/protein is homologous to a gene/protein with a known function, it is likely to have a similar function.
- Additionally, Identifying homologous genes involved in diseases across different species helps in understanding disease mechanisms and developing treatments.

- **Help to Study Diseases:** Homologous genes in model organisms can be studied to gain insights into human diseases.

Structural Homology:

- **Definition:** The similarity in the **three-dimensional** structures of proteins or other macromolecules due to shared ancestry is called structural homology.
- Proteins with similar structures often perform similar functions, even if their sequences are not highly similar. The **three-dimensional** structure of a protein provides critical information about its function.
- **Prediction of Functions of New Proteins:** Understanding structural homology helps in predicting the function of newly discovered proteins.
- **Helps to Design Drugs:** Furthermore, structural homology is crucial in drug design, as drugs are often designed to interact with specific protein structures.
- **Designing of More Effective Drugs:** Understanding the structural relationships between proteins can help in designing more effective drugs.
- Also studying the **structural homology** of proteins helps in understanding the evolutionary processes that shape protein functions and interactions.

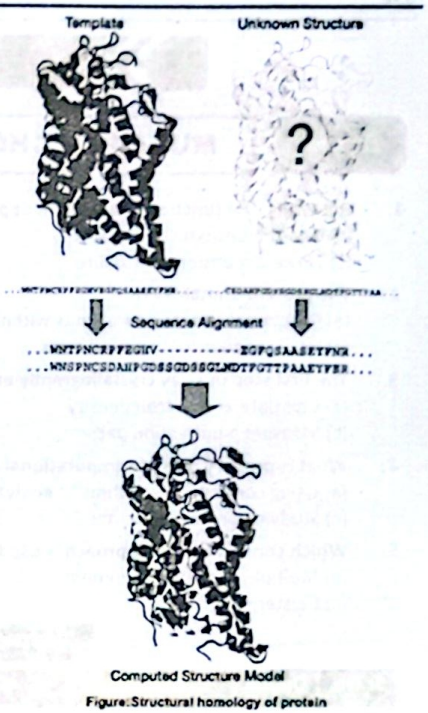


Figure: Structural homology of protein

Check Understanding (Solutions)

Sr. #	Option	Explanation
1.	B	• The active site is the specific region of an enzyme where the substrate binds. It has a unique shape that fits the substrate, allowing the enzyme to catalyze the chemical reaction efficiently.
2.	S.Q	• Protein domains are distinct structural units within a protein that often have specific functions. • Knowing domains allows scientists to predict the function of unknown proteins. • It is crucial in drug design, such as creating antivirals that block viral protein domains. • Domains also help in engineering fusion proteins for research or therapeutic use.
3.	C	• Structural biology allowed researchers to map the spike protein of SARS-CoV-2, enabling the design of vaccines and antibodies that could effectively bind and neutralize the virus.
4.	S.Q	• Structural biology revealed the 3D structure of the virus's spike protein. • This knowledge enabled scientists to design vaccines and antibodies that could bind and neutralize the virus. • It also guided antiviral drug development, such as remdesivir targeting viral enzymes. • This demonstrates how structure leads to precise therapeutic strategies.
5.	C	• Genomics is the study of the structure, function, and mapping of entire genomes and genetic sequences.
6.	S.Q	• It uses sequence alignment and phylogenetic tools to trace species evolution. • Genomic data help build evolutionary trees and find conserved genes. • It reveals genetic divergence and adaptation patterns. • This enhances understanding of biological complexity across species.

Exercise

Exercise — MULTIPLE CHOICE QUESTIONS (MCQs) — Section 01

1. **Generally, the function of a protein depends on its:**
   (a) One-dimensional structure (b) Two-dimensional structure
   (c) Three-dimensional structure (d) Four-dimensional structure
2. **The protein domains are:**
   (a) Functional and structural units within protein (b) Secondary structural elements
   (c) Linear sequences of amino acids (d) Specific regions for post-translational modification
3. **The first step in x-ray crystallography experiment is:**
   (a) Compute an electron density (b) Build a model of your molecule
   (c) Measure a diffraction pattern (d) Grow a crystal
4. **What is primary role of computational biology?**
   (a) Using computer algorithms to analyze data (b) Identifying genetic mutations
   (c) Studying protein functions (d) Analyzing the expression patterns
5. **Which computational approach is used to predict protein structure based on amino acid sequence?**
   (a) Multiple sequence alignment (b) Homology modelling
   (c) Clustering analysis (d) BLAST searches

Answer Key with Explanations

Sr.No.	Option	Answer	Explanations
1.	(c)	Three-dimensional structure	• Protein function depends on its 3D shape, which determines its biological interactions.
2.	(a)	Functional and structural units within protein	• Protein domains are specific parts that fold independently and perform distinct functions.
3.	(d)	Grow a crystal	• X-ray crystallography begins by growing a crystal to analyze its diffraction pattern.
4.	(a)	Using computer algorithms to analyze data	• Computational biology uses algorithms to study and interpret complex biological data.
5.	(b)	Homology modelling	• Homology modelling predicts a protein's structure using similarity to known structures.

Exercise — SHORT ANSWER QUESTIONS — Section 02

Q.1 Define domains of the protein.

Ans. Protein Domains:

- Protein domains are distinct **structural and functional** regions within a protein.
- Each domain folds independently into a stable **three-dimensional structure.**
- Domains often carry out specific functions like binding or catalysis.
- They allow a single protein to perform multiple functions.

Q.2 How corona virus enters the host cells?

Ans. Entry of Coronavirus into Host Cells:

- Coronavirus **uses its spike (S) protein** to bind to the receptor site on the host cell surface.

- This binding triggers fusion of the viral envelope with the host cell membrane.
- The viral RNA genome is then released into the cytoplasm.
- This initiates the process of viral replication and infection.

Q.3 Define genomics.

Ans. Genomics:

- Genomics is the study of the **complete DNA** content (genome) of an organism.
- It includes sequencing, mapping, and analysis of genes.
- It helps in understanding gene functions, mutations, and regulation.
- Genomics is essential in medicine, agriculture, and evolutionary biology.

Q.4 Differentiate between genomics and proteomics.

Ans. Difference between Genomics and Proteomics:

Genomics	Proteomics
• The study of **genomes**, which are the complete set of DNA within a single cell of an organism. Genomics involves sequencing, assembling, and analyzing the function and structure of genomes. • **Use:** It helps in understanding genetic variations, gene function, and evolutionary relationships.	• The large-scale study of proteins, including their structures and functions. Proteins are essential molecules that perform many functions within organisms. • **Use:** Proteomics aims to map the entire set of proteins (the proteome) produced by an organism and understand their interactions and roles in cellular processes.

Q.5 What is GenBank? Describe it briefly.

Ans. GenBank:

- GenBank is a public database of nucleotide sequences maintained by NCBI.
- It contains DNA sequences submitted by scientists worldwide.
- It helps researchers compare and analyze genetic information.
- GenBank supports research in genetics, medicine, and evolutionary studies.
- It is a comprehensive public database of nucleotide sequences and supporting bibliographic and biological annotations (comment).
- It provides access to a vast repository of DNA sequences from various organisms, facilitating genetic research and comparative genomics.

Q.6 Write a short note on protein data bank.

Ans. Short Note on Protein Data Bank (PDB):

- Protein Data Bank (PDB) is a global archive of 3D structural data of biological macromolecules.
- It stores experimentally determined structures of proteins, DNA, RNA, and complex assemblies.
- Data is submitted by scientists using techniques like X-ray crystallography and NMR.
- PDB helps researchers understand molecular functions, drug design, and protein interactions.

Exercise — LONG ANSWER QUESTIONS — Section 03

Q.1 Describe the applications of structural biology.

Ans. See Page No. (217)

Q.2 Write a note on principle and working of x-ray crystallography.

Ans. See Page No. (219)

Q.3 Briefly describe key databases of computational biology.

Ans. See Page No. (220)

Exercise

INQUISITIVE ANSWER QUESTIONS

Q.1 Consider there is a pandemic of a new unknown disease, and the causative agent is a virus. You also know that virus belongs to X family. How structural biology can be helpful in preventing the disease?

Ans. Role of Structural Biology can be Helpful in Preventing the Disease:

- **Understanding Virus Structure:** Structural biology reveals the 3D shape of the virus, especially surface proteins, which are critical for vaccine and drug development.
- **Identifying Drug Targets:** It helps locate specific viral sites that can be targeted by antiviral drugs to stop the virus from replicating.
- **Vaccine Development:** By identifying stable and immune-triggering parts of the virus, it guides the design of effective vaccines.
- **Tracking Mutations:** Structural studies help monitor how mutations affect the virus, allowing for timely updates in vaccines and treatments.
- **Studying Host Interaction:** It shows how the virus binds to human cells, enabling the creation of entry-blocking therapies.

Q.2 Suppose you find an unknown protein and determine amino acid sequence by Edman degradation/mass spectrometry. How you can exploit the computational biology to predict the structure and function of the protein.

Ans. Use of Computational Biology to Predict the Structure and Function of the Protein:

- **Sequence Comparison:** Use BLAST to find similar protein sequences and infer possible function.
- **Domain Identification:** Check conserved regions using tools like Pfam to guess the role of the protein.
- **Structure Modeling:** Predict 3D structure using Alpha Fold or SWISS-MODEL based on known templates.
- **Function Prediction:** Link structure and domains to possible activity or role in the cell.
- **Drug Target Use:** If relevant, model can help screen drugs that bind to the protein.

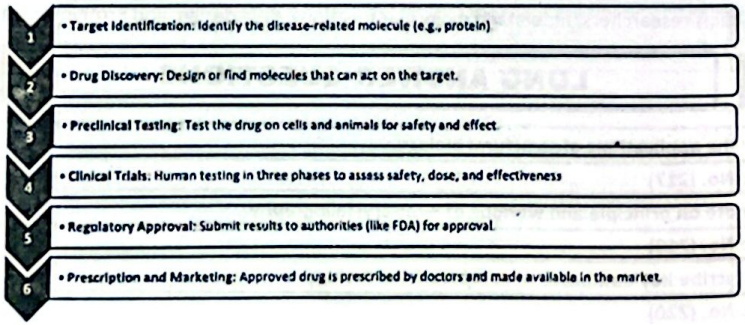
Q.3 Homology models of macromolecules differ from experimentally determined structures of the macromolecules. Please comment.

Ans. Homology Models of Macromolecules Differ from Experimentally Determined Structures of Macromolecules:

- **Source of Structure:** Homology models are predicted using known structures of similar proteins, while experimental structures (e.g., X-ray, cryo-EM) are based on actual physical data of the target molecule.
- **Accuracy:** Homology models are less accurate, especially in regions with low sequence similarity. Experimental structures provide high-resolution, real atomic details.
- **Assumptions vs. Reality:** Homology models rely on the assumption that similar sequences have similar structures. Experimental methods reveal the actual structure without assumptions.
- **Use and Reliability:** Homology models are useful for predictions and hypotheses, while experimental structures are trusted for precise biological and drug research.

Q.4 Draw a flow chart to describe the steps involved in drug development till its prescription.

Ans.



ADDITIONAL MCQs

Q.1 Why is identifying functional domains in a protein important in medical research?
A. Domains determine the protein's color
B. Domains help to design antiviral or therapeutic drugs
C. Domains are only present in DNA
D. Domains are irrelevant in drug targeting

Q.2 What is meant by a "drug target" in medical science?
A. A compound that treats diseases
B. A biological molecule that drugs interact with to produce effects
C. A machine used in laboratories
D. A symptom of a disease

Q.3 Why is identifying host-pathogen interactions important in drug development?
A. It allows production of stronger antibiotics
B. It identifies how host cells can be protected or pathogens blocked
C. It removes all pathogens instantly
D. It's unrelated to drug development

Q.4 What is one major consequence of protein misfolding in cells?
A. Enhanced enzyme activity
B. Increased metabolic rate
C. Diseases such as Alzheimer's or cystic fibrosis
D. Better immune responses

Q.5 Who are credited with developing X-ray crystallography for studying molecular structures?
A. Watson and Crick
B. Rosalind Franklin and Maurice Wilkins
C. William Henry Bragg and William Lawrence Bragg
D. Linus Pauling and Frederick Sanger

Q.6 What is the first essential step in the process of X-ray crystallography?
A. Building a density map
B. Crystallizing the protein
C. Firing X-rays into a solution
D. Analyzing DNA sequences

Q.7 What is produced when X-rays are directed at a protein crystal in X-ray crystallography?
A. Protein sequence
B. DNA helix
C. Diffraction pattern
D. Amino acid list

Q.8 Why is the electron density map important in crystallography?
A. It shows the protein's hydrophobic regions only
B. It visualizes the crystal growth
C. It helps model the 3D structure of the protein
D. It detects the protein's charge

Q.9 What is the final goal of the X-ray crystallography process?
A. To photograph the crystal
B. To identify the primary sequence
C. To determine the three-dimensional structure of a protein
D. To increase protein synthesis

Q.10 What best describes the role of computational biology?
A. Using AI to synthesize proteins directly
B. Applying computer science to analyze and model biological data
C. Designing vaccines manually in wet labs
D. Isolating genetic materials for study

Q.11 How does bioinformatics support genomics?
A. By sequencing amino acids directly
B. By visualizing organelles through electron microscopy
C. By developing algorithms to store, retrieve, and analyze genetic data
D. By converting proteins into DNA

Q.12 What distinguishes proteomics as a branch of computational biology?
A. It measures plant pigment levels
B. It evaluates the lipid content of membranes
C. It investigates protein expression, structure, and interactions
D. It isolates DNA for sequencing

Q.13 How does computational biology contribute to drug discovery?
A. It helps in vaccine transportation
B. It predicts molecular interactions to identify drug targets
C. It manufactures drugs directly
D. It identifies allergies in patients

Q.14 Which tool is commonly used to store and visualize 3D structures of proteins?
A. KEGG B. Ensembl C. Protein Data Bank (PDB) D. Gene Ontology

Q.15 What is the role of Ensembl in computational biology?
A. Synthesizing proteins from scratch
B. Managing large-scale protein sequencing labs
C. Providing genome data and annotations of various species
D. Measuring temperature effects on enzymes

Q.16 Which of the following best describes the role of computational biology in evolutionary studies?
A. Editing of ancient DNA
B. Comparison of gene sequences to establish phylogenetic relationships
C. Field collection of fossils
D. Scanning of tissue samples

Q.17 What type of data is commonly retrieved from the Protein Data Bank (PDB)?
A. Gene expression charts B. Protein 3D structures
C. Metabolic pathways D. RNA interference patterns

ANSWER KEY

1. B	2. B	3. B	4. C	5. C	6. B	7. C	8. C	9. C	10. B	11. C	12. C
13. B	14. C	15. C	16. B	17. B							

ADDITIONAL SHORT ANSWER QUESTIONS

1. What is the significance of the active site in enzymes?

Ans. Significance of the Active site in Enzymes:
- The active site is the part of an enzyme where substrate molecules bind.
- It has a specific 3D shape that fits only particular substrates (lock and key model).
- It facilitates the chemical reaction by lowering the activation energy.
- The shape and charge of the active site determine enzyme specificity.

2. Define a drug target and explain its significance in medicine.

Ans. Drug Target and its Significance:
- A drug target is a specific molecule in the body, usually a protein, that a drug interacts with to cause a biological effect.
- It helps in designing drugs that are highly specific, minimizing side effects.
- Examples include enzymes, receptors, and viral proteins.
- Identifying the correct target is key to effective and safe therapy.

3. Why is studying host-pathogen interaction important in infectious diseases?

Ans. Importance studying host-pathogen interaction:
- These interactions reveal how pathogens infect host cells and how the immune system responds.
- They help identify targets for drugs or vaccines, like blocking viral entry proteins.
- In COVID-19, understanding ACE2 and spike protein interaction was critical.
- It supports better treatment and prevention strategies.

4. What is protein misfolding and why is it significant in biology and medicine?

Ans. Protein Misfolding and its Significant:
- Protein misfolding refers to proteins failing to attain their correct 3D structure.
- Misfolded proteins often lose function or form toxic aggregates.
- Diseases like Alzheimer's, Huntington's, and cystic fibrosis are linked to misfolding.
- Understanding this helps develop chaperone therapies or inhibitors of aggregation.

5. Who developed X-ray crystallography and why was it significant?

Ans. X-ray crystallography:
- X-ray crystallography was developed by William Henry Bragg and William Lawrence Bragg in the early 20th century.
- They discovered that X-rays diffracted by crystals could be used to reveal atomic structures.
- This technique became essential for studying proteins, DNA, and complex molecules.
- Their work laid the foundation for structural biology.

6. Why is protein crystallization important in X-ray crystallography?

Ans. Importance of Protein Crystallization:
- Crystallization arranges protein molecules into a repeating, ordered pattern.
- Only a well-formed crystal can produce a clear diffraction pattern.
- It's the first and most challenging step in the process.
- Without crystals, X-ray data cannot be collected effectively.

7. What is a diffraction pattern, and how is it generated?

Ans. Diffraction Pattern:
- When X-rays are directed at a protein crystal, the rays scatter and interfere to produce a diffraction pattern.
- This pattern contains information about electron density.
- It looks like a series of spots on a photographic plate or detector.
- It's the second step and key to building the protein's structure.

8. How is an electron density map used in protein structure determination?

Ans. Use of Electron Density Map:
- After obtaining a diffraction pattern, mathematical algorithms convert it into a 3D electron density map.
- This map shows where electrons are most dense in the crystal.
- Scientists fit a protein model into this map to determine its structure.
- It's a crucial step before finalizing the atomic structure.

9. What is the final outcome of the X-ray crystallography process?

Ans. Final Outcome of the X-ray Crystallography:
- The goal is to determine the complete 3D structure of the protein at atomic resolution.
- This reveals how the protein functions, interacts, and can be targeted by drugs.
- It's widely used in drug design, enzyme studies, and vaccine development.
- For example, the COVID-19 spike protein structure was solved this way.

10. What is computational biology and how does it differ from traditional biology?

Ans. Computational Biology differ from Traditional Biology:

- Computational biology uses mathematical modeling, simulations, and data analytics to study biological systems.
- Unlike traditional lab-based biology, it focuses on in silico (computer-based) approaches.
- It allows the analysis of large-scale biological data.
- It's essential in genomics, proteomics, drug discovery, and systems biology.

11. How does genomics contribute to personalized medicine?

Ans. Contribution of genomics to Personalized Medicine:

- Genomics helps identify genetic variations among individuals.
- These insights can predict disease risks and drug responses.
- It enables the design of tailored treatments based on one's genetic profile.
- Genomics is a key part of precision medicine.

12. What is the scope of proteomics in disease diagnosis and treatment?

Ans. Scope of Proteomics:

- Proteomics analyzes the expression, structure, and function of proteins.
- Abnormal protein levels or modifications often signal disease.
- It helps identify biomarkers for diagnosis and potential therapeutic targets.
- It plays a role in cancer research and neurodegenerative diseases.

13. How is bioinformatics essential for managing biological data?

Ans. Use of Bioinformatics in Biological Data:

- Bioinformatics provides tools for storage, annotation, and interpretation of biological datasets.
- It is crucial for managing the massive data from sequencing technologies.
- It aids in gene prediction, protein modeling, and pathway analysis.
- Bioinformatics accelerates research in genomics and systems biology.

14. How is computational biology used in modern drug discovery?

Ans. Use of Computational Biology used in Modern Drug Discovery:

- Computational biology helps identify molecular targets and simulate drug-receptor interactions.
- It uses virtual screening and molecular docking techniques to predict the best drug candidates.
- This reduces time and cost compared to experimental drug testing.
- It is essential in designing specific and effective therapies.

15. What is the role of the Ensembl database in genomics research?

Ans. Role of Ensembl Database in Genomics Research:

- Ensembl provides annotated genome sequences for humans and other species.
- It supports gene prediction, comparative genomics, and variant analysis.
- Researchers use it to study gene functions and evolutionary relationships.
- It is updated regularly and freely accessible online.

16. Why is the Protein Data Bank (PDB) important in biology and medicine?

Ans. Importance of PDB:

- PDB stores three-dimensional structures of proteins and other macromolecules.
- These structures are key to understanding protein function and designing drugs.
- It supports research in molecular biology, biochemistry, and pharmacology.
- Structures are derived from techniques like X-ray crystallography and NMR.

17. What is the significance of protein structure modelling in computational biology?

Ans. Significance of Protein Modelling in Computational Biology:

- Protein modelling helps predict the 3D shape of proteins from sequences.
- This reveals active sites, binding pockets, and folding patterns.
- It's crucial in drug design and understanding disease mechanisms.
- Methods like homology modelling and ab initio predictions are commonly used.

SELF-ASSESSMENT Chapter # 07

Total Mark: 30

Q.1 Encircle the correct option. (1 x 6 = 06)

i. **Why is identifying host-pathogen interactions important in drug development?**
(a) It allows production of stronger antibiotics
(b) It identifies how host cells can be protected or pathogens blocked
(c) It removes all pathogens instantly (d) It's unrelated to drug development

ii. **What is the first essential step in the process of X-ray crystallography?**
(a) Building a density map (b) Crystallizing the protein
(c) Firing X-rays into a solution (d) Analyzing DNA sequences

iii. **How does computational biology contribute to drug discovery?**
(a) It helps in vaccine transportation
(b) It predicts molecular interactions to identify drug targets
(c) It manufactures drugs directly (d) It identifies allergies in patients

iv. **Which of the following best describes the role of computational biology in evolutionary studies?**
(a) Editing of ancient DNA
(b) Comparison of gene sequences to establish phylogenetic relationships
(c) Field collection of fossils (d) Scanning of tissue samples

v. **The protein domains are:**
(a) Functional and structural units within protein (b) Secondary structural elements
(c) Linear sequences of amino acids (d) Specific regions for post-translational modification

vi. **What is primary role of computational biology?**
(a) Using computer algorithms to analyze data (b) Identifying genetic mutations
(c) Studying protein functions (d) Analyzing the expression patterns

Q.2 Write short answers of the following questions. (2 x 8 = 16)

i. What is the principle behind X-ray crystallography, and how is it used to determine biomolecular structure?
ii. What are some online databases that provide access to biomolecular structures, and how are they used in research?
iii. How does computational biology contribute to our understanding of biological systems and processes, and what are its applications?
iv. How does sequence homology analysis provide insights into biomolecular structure and function, and what are its limitations?
v. Define genomics.
vi. What is GenBank? Describe it briefly.
vii. How does genomics contribute to personalized medicine?
viii. What is the role of the Ensembl database in genomics research?

Q.3 Extensive Questions. (4 x 2 = 8)

(a) Describe the applications of structural biology.
(b) Briefly describe key databases of computational biology.