

Unit 7: Structural and Computational Biology

Multiple Choice Questions

MULTIPLE CHOICE QUESTIONS (EXERCISE)

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

SLO BASED MULTIPLE CHOICE QUESTIONS

Applications of Structural Biology

6. What is the primary focus of structural biology?
 - (a) Studying metabolic pathways
 - (b) Determining 3D atomic level structures of macromolecules
 - (c) Gene sequencing
 - (d) Gene expression
7. Which technique is used to determine the 3D-structure of proteins?
 - (a) Electron microscopy
 - (b) Mass spectrometry
 - (c) Spectrometry
 - (d) X-ray crystallography
8. The active site of enzyme is important in designing a drug, because:
 - (a) It determines enzyme physiology
 - (b) It is where a substrate binds
 - (c) It provides information about drug
 - (d) It is made up of lipids
9. How did structural biology contribute to COVID-19 research?
 - (a) By measuring blood sugar level
 - (b) By sequencing the human genome
 - (c) By determining 3D structure of spike protein
 - (d) By analyzing bacterial cell wall
10. The structural studies of enzyme HIV-L reverse transcriptase have identified its:
 - (a) Polymerase domain
 - (b) RNase H Domain
 - (c) Nuclease domain
 - (d) All of above
11. The place on a disease-causing molecule where a drug can work are called:
 - (a) Drug targets
 - (b) Off targets
 - (c) Counter target
 - (d) Active
12. Protein misfolding is associated with which of the following diseases?
 - (a) Influenza
 - (b) Hypertension
 - (c) Alzheimer's
 - (d) Gout

X-ray Crystallography

13. The first step in x-ray crystallography is:
 - (a) Protein crystallization
 - (b) Production of a diffraction pattern
 - (c) Creating density map
 - (d) Determination of protein structure
14. In x-ray diffraction technique, the diffraction pattern is used to:
 - (a) Make good quality crystal
 - (b) Create a density map
 - (c) Make density gradient
 - (d) Diagnose disease

Computational Biology

15. The field that uses computational tools to analyze biological data is:
 - (a) Quantum physics
 - (b) Geography
 - (c) Geophysics
 - (d) Computational biology
16. Which of the following is not the area in computational biology?
 - (a) Genomics
 - (b) Proteomics
 - (c) Ergonomics
 - (d) Bioinformatics
17. Sequencing, assembling and analyzing the function and structure of genomes is studied in:
 - (a) Bioinformatics
 - (b) Proteomics
 - (c) Structural biology
 - (d) Genomics
18. Mapping the entire set of proteins produced by an organism and to understand their interactions and roles in cellular process, is achieved in:
 - (a) Proteomics
 - (b) Bioinformatics
 - (c) Genomics
 - (d) Biodynamics
19. Which field of biology helps in identifying genetic variations associated with diseases?
 - (a) Structural biology
 - (b) Social biology
 - (c) Computational biology
 - (d) biomathematics

20. "<https://www.ncbi.nlm.nih.gov/nuccore/>" is a link for:

- (a) GenBank (b) EmBL
(c) PDP (d) DDBJ

21. Which database stores 3D structures of macromolecules?

- (a) Ensembl (b) PDB
(c) GenBank (d) BLAST

22. The database of nucleotide sequences and supporting bibliographic annotations is:

- (a) GenBank (b) FASTA
(c) BLAST (d) PDB

23. A genome browser providing information on genome sequences, gene models and comparative genomics for various species is:

- (a) FASTA (b) GenBank
(c) BLAST (d) Ensembl

24. Which one of the following is a sequence alignment tool that compares a query sequence to a database of sequences?

- (a) BLAST (b) FASTA
(c) EMBL (d) PDB

25. A researcher wants to search protein and nucleotide databases to identify sequence homology, which one is most appropriate to study?

- (a) FASTA (b) GenBank
(c) Swiss port (d) UniPort KB

Sequence Homology

26. What is sequence homology?

- (a) Similarity in sequences due to shared ancestry.
(b) 3D-structure of proteins due to shared ancestry
(c) Large-scale study of proteins
(d) None of above

27. Orthologs are:

- (a) Genes in same species
(b) Human histone H1.1 and H1.2
(c) Sequences in different species
(d) Arise from same ancestral gene

28. Human histone H1.1 and Human histone H1.2 are:

- (a) Paralog (b) Ortholog
(c) Metalog (d) both (a) and (b)

29. Human histone H1.1 and Chimpanzee histone H1.1 are:

- (a) Paralog (b) Metalog
(c) Ortholog (d) Algorithm

30. How does structural homology helps in drug designing?

- (a) By identifying similar protein structures for targeted drug binding
(b) By identifying homologous genes
(c) By providing an insight into evolutionary relationships of genes
(d) By gene sequencing

31. If two proteins have structural homology what can be inferred:

- (a) They likely share functional similarities
(b) They have identical DNA sequences
(c) They share orthologs
(d) Does not give clue about unknown gene

32. The tool used for sequence alignment in bioinformatics:

- (a) PDB (b) FASTA
(c) GenBank (d) Ensembl

33. Which bioinformatics tools acts like a 'Google Search' for DNA sequences?

- (a) Photoshop (b) Excel
(c) BLAST (d) PDB

34. The biologists compare protein structures to unknown genes?

- (a) To assign possible functions
(b) To study novel proteins
(c) To discover drugs
(d) To make an act

35. Identify the missing step in X-ray crystallography:

1. Crystallize protein → 2. X-ray diffraction 3 → ? → 4. 3D model

- (a) Calculate electron density maps
- (b) Calculate charge of electrons
- (c) Homogenization
- (d) Protein fractionation

36. A researcher is studying a newly discovered protein, linked to a rare disease. The protein's sequence shows no match in BLAST, the next possible step is:

- (a) Modify protein sequence
- (b) Check for structural homology using PDB
- (c) Reanalyze the protein structure
- (d) Go for x-ray crystallography

37. Orthology differ from paralogs in:

- (a) Orthologs arise from speciation paralogs from gene duplication
- (b) Orthologs arise from gene duplication and paralogs from speciation
- (c) Orthologs have identical genetic sequences
- (d) Both (a) and (c)

38. The limitation of homology modeling is:

- (a) Depends on protein function
- (b) Only specific for carbohydrates
- (c) Requires a template structure with maximum similarities
- (d) None of above

ANSWER KEY

1.	c	2.	a	3.	d	4.	a	5.	b	6.	b	7.	d
8.	b	9.	c	10.	d	11.	a	12.	c	13.	a	14.	b
15.	d	16.	c	17.	d	18.	a	19.	c	20.	a	21.	b
22.	a	23.	d	24.	b	25.	a	26.	a	27.	c	28.	a
29.	c	30.	a	31.	a	32.	b	33.	c	34.	a	35.	a
36.	b	37.	a	38.	c								