

CUET PG 2026 Bioinformatics Question Paper

Time Allowed :1 Hour 30 Minutes	Maximum Marks :300	Total Questions :75
---------------------------------	--------------------	---------------------

General Instructions

Read the following instructions very carefully and strictly follow them:

- The Question Paper consists of 75 Multiple Choice Questions (MCQs).
- Total marks for the exam is 300.
- The total duration is 90 minutes; a timer on the screen will display the remaining time, and the exam will automatically submit when the time reaches zero.
- For every correct answer, 4 marks (+4) will be awarded to the candidate, and a 1 mark (-1) will be deducted for every incorrect answer.
- Question papers are available in both English and Hindi.

1. Which algorithm is used for performing Global Sequence Alignment?

- (A) Smith–Waterman Algorithm
- (B) Needleman–Wunsch Algorithm
- (C) BLAST Algorithm
- (D) FASTA Algorithm

2. What is the primary difference between PAM and BLOSUM scoring matrices?

- (A) PAM matrices are based on global alignments, while BLOSUM matrices are based on local alignments
- (B) PAM matrices are used only for DNA sequences, while BLOSUM matrices are used for proteins
- (C) PAM matrices are derived from highly divergent sequences, while BLOSUM matrices use closely related sequences
- (D) PAM matrices are heuristic methods, while BLOSUM matrices use dynamic programming

3. Which biological database is considered a curated, secondary database for protein sequences?

- (A) GenBank
- (B) UniProtKB/Swiss-Prot
- (C) EMBL
- (D) DDBJ

4. In the Michaelis-Menten equation, what does the constant K_m represent?

- (A) Maximum reaction velocity
 - (B) Substrate concentration at half of V_{max}
 - (C) Enzyme concentration
 - (D) Rate of enzyme degradation
-

5. Which amino acid is responsible for forming disulfide bridges in a protein structure?

- (A) Glycine
 - (B) Cysteine
 - (C) Lysine
 - (D) Alanine
-

6. What is the specific function of the BLASTn program?

- (A) Compare protein sequences
 - (B) Compare nucleotide sequences
 - (C) Predict protein structure
 - (D) Align protein structures
-

7. Which tool is most commonly used for Multiple Sequence Alignment (MSA)?

- (A) BLAST
 - (B) ClustalW
 - (C) FASTA
 - (D) Needleman–Wunsch
-

8. The p53 protein is primarily known for which cellular role?

- (A) DNA replication
 - (B) Tumor suppression
 - (C) Protein synthesis
 - (D) Cell membrane transport
-

9. Which molecular technique is used to detect specific mRNA molecules in a sample?

- (A) Southern Blot
 - (B) Northern Blot
 - (C) Western Blot
 - (D) PCR
-

10. In computer science, what does the Markov Property assume about future states?

- (A) Future states depend on all previous states
 - (B) Future states depend only on the current state
 - (C) Future states depend only on the initial state
 - (D) Future states are completely random
-

11. Which database serves as the main archive for 3D macromolecular structures?

- (A) GenBank
 - (B) Protein Data Bank (PDB)
 - (C) UniProt
 - (D) EMBL
-

12. What is the purpose of Emulsion PCR (ePCR) in Next-Generation Sequencing?

- (A) To sequence DNA directly without amplification
 - (B) To amplify individual DNA fragments in isolated microreactors
 - (C) To detect proteins in sequencing samples
 - (D) To separate RNA molecules from DNA
-

13. Which component is strictly part of a Microprocessor System Unit, excluding peripherals?

- (A) Keyboard
 - (B) Monitor
 - (C) CPU
 - (D) Printer
-

14. How does a 2D array differ from a 1D array in a programming language like C++?

- (A) A 2D array stores characters only
 - (B) A 2D array has rows and columns
 - (C) A 2D array stores only integers
 - (D) A 2D array cannot store multiple values
-

15. Which type of bond characterizes the primary structure of DNA?

- (A) Hydrogen bond
 - (B) Ionic bond
 - (C) Phosphodiester bond
 - (D) Disulfide bond
-