Name: **Enrolment No:**	

UPES

End Semester Examination, May 2025

Course: Bioinformatics and Computational Biology — **Semester : VI**

Program: B.Tech Biotechnology — **Duration : 3 Hours**

Course Code: HSBT3008 — **Max. Marks: 100**

Instructions:

S. No.	Section A Short answer questions/ MCQ/T&F (20Qx1.5M= 30 Marks)	Marks	COs
Q 1	Computational biology only deals with protein folding simulations. **(True/False)**	**1.5**	**CO1**
Q 2	Which of the following is a key aim of bioinformatics? a) Replace lab work b) Store biological data c) Engineer proteins d) Perform surgery	**1.5**	**CO1**
Q 3	GenBank is a protein sequence database. **(True/False)**	**1.5**	**CO1**
Q 4	Which of the following was the first widely used global alignment algorithm? a) FASTA b) BLAST c) Smith-Waterman d) Needleman-Wunsch	**1.5**	**CO1**
Q 5	NCBI provides tools like BLAST, Primer-BLAST, and ClinVar. **(True/False)**	**1.5**	**CO1**
Q 6	Which database stores gene expression data? a) PDB b) SRA c) GEO d) ChEMBL	**1.5**	**CO2**
Q 7	RNA-seq data can be found in the Sequence Read Archive (SRA). **(True/False)**	**1.5**	**CO2**
Q 8	Which of the following is NOT typically found in a GenBank entry?	**1.5**	**CO2**

	a) Annotations b) 3D structure c) Nucleotide sequence d) References		
Q 9	Which organization developed AlphaFold? a) Google Brain b) IBM Watson c) DeepMind d) OpenAI	**1.5**	**CO2**
Q 10	Which of the following databases focuses on biological pathways? a) UniProt b) Reactome c) PDB d) SRA	**1.5**	**CO2**
Q 11	PAM matrices are used to find conserved regulatory sequences. **(True/False)**	**1.5**	**CO2**
Q 12	Which type of alignment does the Smith-Waterman algorithm perform? a) Global b) Local c) Semi-global d) None	**1.5**	**CO2**
Q 13	Sequence alignment is a prerequisite for phylogenetic tree construction. **(True/False)**	**1.5**	**CO3**
Q 14	Which of the following best represents an unrooted tree? a) Circular plot b) Ladder c) Tree without a common ancestor d) Bar graph	**1.5**	**CO3**
Q 15	Clustal Omega is a tool for multiple sequence alignment. **(True/False)**	**1.5**	**CO3**
Q 16	Which of the following helps visualize protein-drug interaction in 3D? a) PyMOL b) BLASTN c) RAxML d) Reactome	**1.5**	**CO3**
Q 17	Cryo-EM does not require crystallization of the molecule. **(True/False)**	**1.5**	**CO3**

Q 18	Which of the following is used for visualizing molecular structures? a) Excel b) Word c) PyMOL d) Tableau	**1.5**	**CO3**
Q 19	BLOSUM matrices are derived from alignments of highly divergent sequences. **(True/False)**	**1.5**	**CO3**
Q 20	The one key outcome of AlphaFold2's development as highlighted in the 2024 Nobel Prize announcement is: a) Eradication of protein misfolding diseases b) Prediction of structures of nearly all known proteins c) Automated synthesis of proteins in bacteria d) Discovery of quantum protein folding algorithms	**1.5**	**CO3**
Section B (4Qx5M=20 Marks)			
Q 1	Define Ramachandran plot. How does it help in validating a protein model?	**5**	**CO1**
Q 2	Describe how the GEO database is used in gene expression analysis. Provide an example of its application.	**5**	**CO2**
Q 3	Describe the function of scoring matrices in sequence alignment. Why are PAM and BLOSUM commonly used?	**5**	**CO2**
Q 4	Explain the difference between global and local sequence alignment with suitable examples.	**5**	**CO3**
Section C (2Qx15M=30 Marks)			
Q 1	**You are given a task to study the structure and function of the tumor suppressor protein p53, which plays a key role in preventing cancer. Your objective is to analyze its secondary structure, predict its 3D model, and visualize it.** a) As a starting point, you are asked to review the **secondary structure elements** present in p53. Define **alpha helices** and **beta sheets**, and briefly explain the **forces** that stabilize them. **(5 Marks)** b) Next, you use the **SWISS-MODEL tool** to predict the 3D structure of p53. Explain how SWISS-MODEL uses **homology modeling** to assist in structure prediction. **(5 Marks)**	**15**	**CO2**

	c) Finally, you are instructed to visualize the modeled p53 structure using **PyMOL**.List and explain **three key features** of PyMOL that make it useful in **molecular visualization** and protein analysis. **(5 Marks)**		
Q 2	**You are part of a bioinformatics research team working on predicting and validating the 3D structure of a newly discovered protein.** a) Your team is discussing different techniques used to determine biomolecular structures. Choose **any two techniques** your team might consider and explain: How the technique works (principle), What level of detail (resolution) it provides, one key advantage and one limitation of each and how each technique is useful in bioinformatics research **(10 Marks)** b) After building a 3D model of the protein, your teammate suggests checking the **Ramachandran plot**. Explain what the Ramachandran plot shows and **how it helps validate** the accuracy of a protein model. **(5 Marks)**	**15**	**CO3**
Section D (2Qx10M=20 Marks)			
Q 1	Explain how tools like AlphaFold and PyMOL have transformed protein structure prediction and visualization. **(5 Marks)** Discuss one example where structure prediction helped in understanding a disease or designing a drug. **(5 Marks)**	**10**	**CO3**
Q 2	Define phylogenetic tree? Explain the types of phylogenetic trees. **(5 marks)** Discuss how sequence alignment data is used to understand evolutionary relationships. **(5 Marks)**	**10**	**CO2**