


Name:			
Enrolment No:			
<p style="text-align: center;">UPES End Semester Examination, May 2025</p>			
Course: Computational Biology and Bioinformatics		Semester : VI	
Program: INT BMSC MICROBIOLOGY		Duration : 3 Hours	
Course Code: HSMB3019		Max. Marks: 100	
Instructions: Attempt all the sections.			
S. No.	Section A Short answer questions/ MCQ/T&F (20Qx1.5M= 30 Marks)	Marks	Cos
Q1.	Global alignment is defined as _____.	1.5	CO1
Q2.	Origin of Species was authored by _____.	1.5	CO1
Q3.	Define the term nucleoside.	1.5	CO1
Q4.	Write the full form for HTVS.	1.5	CO1
Q5.	The three types of biological databases are _____.	1.5	CO1
Q6.	Define the term genome.	1.5	CO1
Q7.	Write the names of structure classification databases.	1.5	CO1
Q8.	Define pairwise alignment.	1.5	CO1
Q9.	Give four examples of software used for pharmacophore mapping.	1.5	CO1
Q10.	The double helix model of DNA was proposed by _____.	1.5	CO1
Q11.	Write the full form for HBD.	1.5	CO2
Q12.	Define the term molecular docking.	1.5	CO2
Q13.	A hit compound is _____.	1.5	CO2
Q14.	Give three examples of protein-protein interaction databases.	1.5	CO2
Q15.	Write the full form for SAR.	1.5	CO2
Q16.	Draw structure of two amino acids.	1.5	CO2
Q17.	Define the term pharmacodynamics.	1.5	CO2
Q18.	Homology modelling involves _____.	1.5	CO2
Q19.	Define the term phylogram.	1.5	CO2
Q20.	Rooted trees are _____.	1.5	CO2
<p style="text-align: center;">Section B (4Qx5M=20 Marks)</p>			
Q1.	Explain the term phylogenetic tree. Draw the diagram of a typical phylogenetic tree.	2.5+2.5	CO3

Q2.	Define a lead compound in relation to drug discovery.	5	CO3
Q3.	Classify biological databases.	5	CO4
Q4.	Discuss the advantages of human genome project.	5	CO3
<p style="text-align: center;">Section C (2Qx15M=30 Marks)</p>			
Q1.	Define molecular docking. Discuss in detail about the steps involved in docking.	3+12	CO5
Q2.	Give examples of databases consisting of protein structures. Write a detailed note on uniprot.	3+12	CO5
<p style="text-align: center;">Section D (2Qx10M=20 Marks)</p>			
Q1.	Define sequence alignment. Discuss in detail about the various types of alignment methods.	2+8	CO4
Q2.	Define the term GWAS. Discuss the use of microGWAS pipeline.	2+8	CO4