JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2024

B.Tech-V Semester (BI)

COURSE CODE (CREDITS): 18B1WBI531 (3)   MAX. MARKS: 25

COURSE NAME: Structural Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar   MAX. TIME: 1 Hour 30 Minutes

Note: (a) All questions are compulsory.

(b) The candidate is allowed to make Suitable numeric assumptions wherever required

for solving problems

Q.No	Question	CO	Marks
Q1	Formulate an energy function which can be utilized to calculate an optimal sequence-structure alignment in fold recognition method?	3	2
Q2	Cite some fundamental differences between the Chou-Fasman and GOR methods.	3	2
Q3	Discuss the three core factors on which successful *ab initio* modeling depends?	3,4	2
Q4	The level of sequence identity between the target protein and the template affect the accuracy of the homology model. Provide examples of what may happen at different thresholds of identity?	3,4	3
Q5	Evaluate the effect of different factors, such as sequence alignment accuracy and template resolution affect the quality of the generated backbone structure. What are the potential consequences of these factors?	4	3
Q6	A researcher has predicted the secondary structure of a protein containing 100 amino acids. The actual secondary structure is as follows: Helix (H): 40 residues, Sheet (E): 30 residues, and Coil (C): 30 residues. The predicted secondary structure contains: Helix (H): 35 residues, Sheet (E): 25 residues, and Coil (C): 40 residues. Calculate the Q3 score for the above protein structure prediction.	4	3
Q7	Calculate the statistical propensities of Alanine and Arginine residues in helix conformation of the given sequence. SS- HHHHHCCCCCCCCCCHHHHHHCCCCCCCC Seq- AVLLTSAPLPTPLESRYRARIYRGNAITV	4,5	6

Q8	Evaluate the first seed window for the given sequence using the given Chou-Fasman parameters.	4,5	4

TABLE 5.2 Chou–Fasman parameters

Residue		P_a
Glu	Hα	1.53
Ala		1.45
Leu		1.34
His	hα	1.24
Met		1.20
Gln		1.17
Trp		1.14
Val		1.14
Phe		1.12
Lys	Iα	1.07
Ile		1.00
Asp	iα	0.98
Thr		0.82
Ser		0.79
Arg		0.79
Cys		0.77
Asn	bα	0.73
Tyr		0.61
Pro	Bα	0.59
Gly		0.53