JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST -1 EXAMINATION- FEB-2024

B. Tech-VIII Semester [All Except Bio]	
COURSE CODE(CREDITS): 21B1WBT833 (3)	MAX. MARKS: 15
COURSE NAME: Computational Biology for Engineers	MAX TIME: 1 Horn
COURSE INSTRUCTOR: Dr. Raj Kumar, Dr. Tiratha Raj Singh, Dr. Sh	ikha Mittal
Note: All questions are compulsory Marks and it is	adia iviittai.
Note: All questions are compulsory. Marks are indicated against each que brackets.	estion in square
Orackers.	
Q.1. Discuss the significance of central dogma of molecular biology. Exp	
how it is crucial for the development of Computational biology domain?	plain in your own terms
	(CO-1,2) [1.5]
Q.2. How many distinct sub-strings will be generated from the sequence 'C	JACAGT'9
A = A + A + A + A + A + A + A + A + A +	and the second s
Q.3. Realize the mathematical parameters of distances and similarities. A ('AGTACTG' and 'AGAG') using the consists and similarities.	11
deling the scoring system as follows: Match	= +2. Mismatch = 0
GOP2, GEP = -1.	(CO-2) [2.5]
O4 Dim	(00 2) [2.5]
Q4. Differentiate between -	(CO-1)[2]
a) Nucleoside and Nucleotide	(00 1)[2]
b) Transition and Transversion	
05. Define hiological databases Buntain	
Q5. Define biological databases. Explain nucleic acid, protein and structura examples	l databases with
	(CO-1,2)[3]
Q6. Write down the single letter codes for the given amino acids:	(00 1) 501
a) Alanine, c) Leucine.	(CO-1) [2]
b) Cysteine, d) Aspartic acid, f) Phenylalanine	
Water the property of the control of	
Q7. Write the general structure of an amino acid. Write down the general equescribe the polypertide formation	uation for used to

(CO-1,2)[3]

describe the polypeptide formation.