JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- Oct 2017

B.Tech Vth Semester

COURSE CODE: 15B11BI511   MAX. MARKS:15

COURSE NAME: Structural Bioinformatics

COURSE CREDITS: 4   MAX. TIME: One Hr

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means.

Q1. Differentiate between primary, secondary, tertiary, and quaternary protein structures.   **2 Marks**

Q2. Imagine as a crystallographer you have to convey the list of residues, the refinement program used, and stereochemistry of your protein. Which REMARK sections will you use?   **3 Marks**

Q3. Explain the statement "Difficulties in obtaining data leads us to propose general principles from observed cases", from the point of view of protein fold evolution.   **2 Marks**

Q4. List the two proteins that are called as "living fossils".   **2 Marks**

Q5. Sometimes SCOP and CATH have disagreements to what is a domain. Why do you think there are disagreements in the domain definition?   **2 Marks**

Q6. Name some of the existing structural alignment software/tools. While a complete match between two structures are ideal, why do different algorithms give different structural alignments?   **2 Marks**

Q7. What are the benefits of internal coordinates compared to external coordinates?   **2 Marks**

BI-3 , BT