JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST – 1 EXAMINATION, SEPTEMBER 2016

B.TECH V SEMESTER

COURSE CODE: 15B11BI511   MAX. MARKS: 15

COURSE NAME: Structural Bioinformatics   MAX. TIME: 1 HR

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

1. Explain briefly as to why Ribosome and Ubiquitin are called as "living fossils"? **2 Marks**

2. Among the various hierarchical levels between SCOP and CATH, list the levels that share similar/identical definition in SCOP and CATH. **2 Marks**

3. Explain the limitation of PDB format and describe the solution prescribed. **2 Marks**

4. You have been told to design an algorithm that compares two protein structures, where the application of the algorithm is to identify similar active site residues. List the considerations of designing the algorithm and draw a flowchart of implementing the algorithm. **3 Marks**

5. Why are proteins belonging to a structural "family" likely to be related with respect to their evolution?

        2 Marks

OR

5. List the analogy based methods for automated functional annotation of proteins. **2 Marks**

6. In an α-helix, the R-groups on the amino acid residues are found on the outside of the helix spiral (True or False) **1 Mark**

7. For the given molecule, write the adjacency and incidence matrices, edge and vertex lists. Identify the molecule. **3 Marks**