Y M Rajotham

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- Oct 2017

B.Tech BI (V Semester)

COURSE CODE: 15B11BI511 MAX. MARKS:25

COURSE NAME: Structural Bioinformatics

COURSE CREDITS: 4 MAX. TIME: One Hour Thirty Minutes

Note: *All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Each question is of 5 marks.*

---

1. Describe the various hydrogen bond models to determine the secondary structural features in a protein. Compare and contrast DSSP and STRIDE.

2. A new organism has been identified for its unique biodegradation properties. The genome has been sequenced and 90% of the genes has been annotated. How do you think the 10% of the unannotated genes can be identified using structural genomic method?

3. 2D structure prediction of alpha helices is easier or has higher accuracy than beta strands. Why?

4. There are two proteins A and B having sequence identity to two other proteins C and D (whose structures are known), at 30% and 70, respectively. What do you think are the limitations to predict the 3D structure of proteins A and B. Explain in detail.

5. Compare and contrast the three different De novo structure prediction methods. Why is there a debate on Rosetta with regards to classified as a De novo prediction method?