**Karunya University**
**(Karunya Institute of Technology and Sciences)**
(Declared as Deemed to be University under Sec.3 of the UGC Act, 1965)

**End Semester Examinations - 2015-16 Even Semester - May 2016**

**15BI3001 Structural Bioinformatics**

**Set A**

**Time : 3 hrs**
**Total Marks: 100**

1. A) Illustrate and explain the geometry of peptide chain and peptide bond formation. (10)

   B) Explain the components of tertiary structure of a protein and its role in protein modification. (10)

**OR**

2. A) Exhibit the cloverleaf structure of transfer RNA. Also discuss the functions and its features. (10)

   B) Explain the contribution, types and role of ribosomal RNA in eukaryotes and prokaryotes. (10)

3. A) Write a short note on structure and properties of purine and pyrimidine bases. (5)

   B) llustrate the components of nucleotide structure. Explain the chemical linkage between monomer units in nucleic acids. (15)

**OR**

4. A) What are supercoils in double stranded circular DNA? Briefly explain its functions in DNA molecule. (10)

   B) Explain the steps involved in X-Ray crystallography technique to determine the protein structure.(10)

5. A) Define liquid crystals. Illustrate and explain crystallization energy diagram. Discuss the types of crystals and various factors that affect crystallization. (15)

   B) Show how surprising patterns produced by bragg's diffraction. (5)

**OR**

6. Discuss in detail how crystallographic data represented in PDB database. Explain about PDB file entry and semantic elements of mmCIF data dictionary file formats.(20)

7. Discuss in detail your inference from research paper – Novel technique for protein structure determination using semi-automated map fitting procedure.(20)

**OR**

8. Write your observations and explain from research paper entitled - Automated main-chain model building by template matching and iterative fragment extension.(20)

9. A) Why protein-protein interactions are so important? Explain how protein interaction information represented in different PPI's databases. (10)

   B) Explain about any two algorithms used to determine protein secondary structure prediction. (10)

**Wishing you All the Best**