Reg.No. \_\_\_\_\_\_\_\_\_\_\_\_



**UNIVERSITY**

(Karunya Institute of Technology & Sciences)

(Declared as Deemed-to-be University under Sec.3 of the UGC Act, 1956)

**End Semester Examination – April/May– 2017**

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| **Code :** | **16BI3001** | **Duration :** | **3hrs** |
| **Sub. Name :** | **STRUCTURAL BIOINFORMATICS** | **Max. marks :** | **100** |

**ANSWER ALL QUESTIONS (5 x 20 = 100 Marks)**

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| Q. No. | Sub Div. | Questions | Course  Outcome | Marks |
| 1. | a. | Illustate the geometry of peptide chain. | CO1 | 10 |
| b. | Explain the different types of helices in protein secondary structure. | CO1 | 10 |
| (OR) | | | | |
| 2. | a. | Show the process of capping and tailing linkage in eukaryotic mRNA structure. | CO1 | 10 |
|  | b. | Explain the different classes of eukaryotic RNA’s. | CO1 | 10 |
| 3. |  | Give an short stretch of homologous amino acid sequence. How would you predict the secondary structure? Explain the algorithmic procedure. | CO2 | 20 |
| (OR) | | | | |
| 4. | a. | Write a short note on nucleotide structure components. | CO2 | 5 |
|  | b. | Explain the chemical linkage of phospodiester bond in formation of polynucleotide chains. | CO2 | 15 |
| 5. |  | Explain the significance and architecture of macromoleculardata dictionary approach and discuss how it is represented in biological databases. | CO3 | 20 |
| (OR) | | | | |
| 6. |  | Enumerate the inferences from article p3d – python module for structural bioinformatics. | CO3 | 20 |
| 7. |  | Show python procedure and scripting for reading and writing different formats of crystal structure files. Give comments for each line of script. | CO3 | 20 |
| (OR) | | | | |
| 8. |  | Give a schematic explanationon different patterns and interacting domains in macromolecular interactions. | CO3 | 20 |
|  | | **Compulsory:** |  |  |
| 9. |  | Write inferences on cheminformatics python module and explain how small molecular analysis can be done using the module. | CO3 | 20 |

ALL THE BEST