

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
T-3 EXAMINATION, JUNE 2016
B.TECH./BTDD – VI SEMESTER

COURSE NAME: COMPRATIVE AND FUNCTIONAL GENOMICS

COURSE CODE: 10B11BT611

COURSE CREDIT: 04

MAX. MARKS: 35

MAX. TIME: 2 HRS

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

1. The genome of *S. cerevisiae* containsbases and genes 1 marks
2. SNP can be detected throughand 1 marks
3. Draw the structure of phenylalanine? 1 marks
4. In eukaryotic gene the common splicing signal is.....and why it is important to know if you are identifying a gene from genome? 2 marks
5. Why biomarker is needed? Explain with example the application of a biomarker? 2marks
6. Explain pharmacogenomics? Why its study is important? 2marks
7. Describe the equation that is used to determine the charge/mass ratio of an ion in MALDI TOF analysis? 2 marks
8. Give the role of different modifications that occur in proteins that may influence the protein function? 2 marks
9. What is MALDI and give example of matrix that is being commonly used? 2 marks
10. What is profile, Motif and pattern in protein sequence analysis to putatively determine the function of a protein? 2marks
11. Write the strategies to extract protein (soluble/insoluble) from a give protein sample for proteomic analysis? 3 marks
12. Write on protein array? Describe with examples that protein-protein interaction can be performed on glass slides? 5 marks
13. What is illumina solid phase sequencing? Describe the steps involved in it with well labeled diagram? 5 marks
14. If you have been given array of human genome, how do you identify the differentially expressed genes from the given lung cancer and control samples? 5 marks