Dr. Tatashanken

## JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT **T2 EXAMINATIONS, OCTOBER-2019**

Biotechnology (PhD)

Course Code: 13M11BT114

MAX. MARKS: 25 Course Name: High Throughput Technologies MAX. TIME: 1.5 Hours

Course Credits: 03

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Marks are indicated in square brackets against each question.

- Q. 1 For genome wide expression analysis, DNA microarray has been extensively used. What are the characteristics of DNA microarray that allowed this technology to a one of choice to study large number of samples? (3) COII
- Q2. What are the different types of DNA microarray available to that can be used to study expression analyses, what are the features of these types of arrays? (3) COII
- Q3. a. What is SNP? (1) COI
  - b. How SNP are introduced into a genome and what are the factors? (1)
  - c. Name two common methods to screen SNPs in a gene? (1)
- O4. In genomic laboratory set up, if you have been provided with DNA chip of human genome, how would you be able to identify the differentially expressed genes in cancerous lung tissue in comparison to the control tissue? (5) COII & COIII
- Q5. Data from DNA microarray often needs normalization; what are the factors contribute to the technical or systemic bias? Represent the equation that can be applied to normalize the gene expression data? (3) COII
- Q.6 Answer the following: [2x4] [COIII]
  - a) Omics Technology
  - b) Secretomes
  - c) Genotoxicity
  - d) High throughput technology for biomarker discovery