JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT T - 3 EXAMINATION-MAY JUNE-2016

B.Tech. IV Semester (BI)

COURSE CODE:15B11BI411

MAX. MARKS: 35

COURSE NAME: Genetic Engineering & Genomics

COURSE CREDITS: 04

MAX. TIME: 2 HRS

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

Q. 1. How would you capture differences in genes expressed in disease/ healthy conditions in a animal system, if whole genome sequence is not available. How would you annotate the differential transcripts for a particular biological function and utilize in developing a suitable drug target?

Q. 2. An eukaryotic genome with 3.2 billion bp size is to be sequenced through a clone-by-clone approach. What different genome resources and technological approaches are required and how those would be generated to complete genome sequence?

(5.0)

Q. 3. Explain whether current high throughput sequencing technologies are generating big biological data? As a computational biologist what technical support can you provide to improvise next generation sequencing technologies?

(5.0)

- Q. 4. Relative quantification of proteins is routinely achieved through gel-based proteomic approaches. However, in current scenario gel-free quantification methodologies have become a $(2.5 \times 2 = 5.0)$ preferred choice.
- a) Name two techniques and their principles which are based on gel-based protein identification methods?
- b) Explain a methodology for gel-free protein quantification and explain its advantages over other primitive methodologies?
- 5. Differentiate the following:
- i) cDNA/gDNA
- ii) RFLP/RAPD
- iii) genetic/physical distance
- iv) 5'RACE/ 3'RACE

- v) DNA marker/ protein marker
- vi) Eukaryote gene/ prokaryote gene
- vii) Illumina NGS platform/ Rosche NGS platform
- viii) Transcriptome/ proteome
- ix) NGS/ shot-gun sequencing
- x) mRNA/tRNA
- xi) Gene prediction/ gene cloning
- xii) Sequence read/ sequence gap
- xiii) BAC/ Cosmid
- xiv) Putative gene/ hypothetical gene
- xv) Plant genome/ Animal genome

(15x1.0 = 15.0)