

COURSE CODE (CREDITS): 20MS1BT214 (2)

MAX. MARKS: 35

COURSE NAME: GENOMICS AND PROTEOMICS

COURSE INSTRUCTORS: DR JATA SHANKAR

MAX. TIME: 2 Hours

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*Note: All questions are compulsory. Marks are indicated against each question in square brackets.*

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- Q1. What is Human Genome sequencing project, how it is useful to study the functional genomics? (3 marks)
- Q2. If mouse is model organism, name human gene and their orthologs in this species is useful studies which human diseases? (3 marks)
- Q3. What are the characteristics of DNA Microarray that enabled the technology to be widely accepted for whole genome expression analysis? (3 marks)
- Q4. What is the Protein array/chip that enabled the technology to be widely accepted for functional proteomics studies? (3 marks)
- Q5. Post translational modification is important for eukaryotic protein to perform biological functions, what are these modification in the proteins? What is significance these modification for the cells? (3 marks)
- Q6. Yeast two hybrid system is a successful technique to study protein-protein interaction, describe the technique with example how two proteins interact in the yeast model system? (5 marks)
- Q7. If you have provided with genomic facilities and mice oligo chip, how to proceed to identify the differential expressed gene from the lung tissue from cancerous and normal mice model? (5 marks)
- Q8. Describe the method 'MALDI TOF' for the identification of the proteins? What are the protein databases for the protein identification? (5 marks)
- Q9. Describe the methodology of Sanger's and Pyrosequencing? Highlight the significances and its uses? (5 marks)