Name of the Programme: M.Sc. Biotechnology

Course Code: GBT 624

Title of the Course: GENOMICS AND PROTEOMICS

Number of Credits: 2

Effective from AY: 2022-23

Pre-requisites for the Course:	Basic knowledge in Molecular Biology /Biochemistry.	
Course Objectives:	1) To develop required knowledge and skills in the students so that they are able to acquire the following competency in genomics and proteomics which aims to look into the genome and protein properties from a global perspective. 2) To provide basic knowledge about sample preparation, mass spectrometry workflow, different chromatography technologies and quantitative proteomics.	
Content:	**MODULE I** ● Brief overview of prokaryotic and eukaryotic genome organization; extra-chromosomal DNA: bacterial plasmids, mitochondria and chloroplast. ● Genetic and physical maps; markers for genetic mapping; methods and techniques used for gene mapping, physical mapping, linkage analysis, cytogenetic techniques, FISH technique in gene mapping, somatic cell hybridization, radiation hybrid maps, in situ hybridization, comparative gene mapping. ● Human Genome Project, genome sequencing projects for microbes, plants and animals, accessing and retrieving genome project information from the web. ● Identification and classification of organisms using molecular markers- 16S rRNA typing/sequencing, SNPs; ● Use of genomes to understand the evolution of eukaryotes ● Track emerging diseases and design new drugs; determining gene location in genome sequence.	**No. of hours** 15

	MODULE II ● Introduction to Proteomics ● Proteomics technologies- Sample preparation, Protein extraction and quantification, Gel-based proteomics: 2D-PAGE, isoelectric focusing. ● Mass spectrometry-based proteomics: mass spectrometry, MALDI-TOF, sample preparations, liquid chromatography, and quantitative proteomics techniques such as iTRAQ, SILAC and TMT using mass spectrometry. ● Protein-protein interaction, protein-DNA interactions, yeast 2-hybrid system, protein chips and functional proteomics. ● Proteome databases. ● Clinical and biomedical applications of proteomics; Challenges in proteomics. ● Introduction to metabolomics, lipidomics, metagenomics, translational research and systems biology.	15
Pedagogy:	Lectures, tutorials, assignments, demonstration.	
References/ Readings:	1. A. Batiza, Bioinformatics, genomics, and proteomics: getting the big picture. Infobase Publishing, 2005. 2. B. Cummings, Bioinformatics, 2nd Edition, 2007. 3. B. R. Glick & J.J. Pasternak, Molecular Biotechnology, 3rd Edition, ASM Press, 1998. 4. B. Kobe , M. Gussand, T. Huber, A.M. Campbell & L. J. Heyer, Structural Proteomics: High-Throughput Methods (Methods in Molecular Biology) Discovering Genomics and Proteomics, Humana Press, 2008. 5. D.C. Liebler, Introduction of Proteomics: Tools for the new Biology. Totowa, NJ: Humana Press, 2002. 6. S.C. Suhai, Genomics and proteomics: functional and computational aspects Springer, 2000.	
Course Outcomes:	Students will be able to 1. acquire knowledge and gain understanding of the fundamentals of genomics and proteomics, transcriptomics and metabolomics. 2. analyse various analytical problems based on techniques of	

	proteomics like 2D and MALDI and methods of protein separation, detection and quantitation. 3. evaluate various applications of genomics and proteomics in agriculture, human health and industry. 4. have the necessary learning to radically advance their understanding of life and transform medicine.

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