BIT2014	**Proteomics**	**L**	**T**	**P**	**J**	**C**
		3	0	0	0	3
Pre-requisite	**BIT2006**	**Syllabus version**				
		2.0				

Course Objectives:

1. Enhancing the basic understanding of the emerging technologies related to the analysis of genomes and proteomes
2. Imparting experimental design thinking capability in relation to using appropriate analytical methodologies for the qualitative and quantitative proteomics
3. Extrapolating the design thinking skills to real time scenarios, with special reference to human diseases

Expected Course Outcome:

1. Differentiate genomic and proteomic approaches
2. Design suitable chromatographic and electrophoretic methodologies for the analysis of a given proteome
3. Distinguish the utility of different analytical techniques that can be used to delineate the structural features of proteins
4. Device methodologies for qualitative and qualitative analysis of the proteome with respect to post-translational modification and molecular recognition events involving proteins
5. Apply proteomic approaches to analyse the disease conditions
6. Infer the basic concepts of genomics, transcriptomics and proteomics

Student Learning Outcomes (SLO): **2,5,18**

2. Having a clear understanding of the subject related concepts and of contemporary issues
5. Having design thinking capability
18. Having critical thinking and innovative skills

Module:1	**Introduction and overview of proteomics**	**5 hours**

Overview of protein chemistry, Proteomics and its application, Functional proteomics in post-genomic era, Proteomics experimental workflows, Gene-Protein families link with examples, Human proteome draft

Module:2	**Application of Chromatography in proteomics**	**6 hours**

Application of separation techniques in proteomics - Multidimensional chromatography, use of nanoLC, COFRADIC combined fractional diagonal chromatography, HILIC-hydrophilic interaction liquid chromatography, SAX- strong anion exchange chromatography, SCX- strong cation-exchange chromatography, affinity chromatography, reverse phase and normal phase

Module:3	**Abundance based Proteomics**	**7 hours**

Gel based proteomics. Variations in 2-D gel electrophoresis, Difference Gel Electrophoresis (DIGE), and Mass spectrometry based proteomics- Analysis of data, MALDI, SELDI, Peptide mass fingerprinting, Protein microarray (analytical, functional, reverse phase), protein sequencing

Module:4	**Structural Proteomics**	**6 hours**

Application of X-ray crystallography, Circular Dichroism, Nuclear Magnetic Resonance, Plasmon Resonance, Small Angle X-ray Scattering

Module:5	**Post-translational modification and Tagging of Proteins**	**6 hours**	
Analysis of posttranslational modifications, Phosphorylation, ubiquitination (poly and mono), acetylation, nitration, glycosylation, Sumoylation, disulphide bond formation, signal peptide cleavages. Tagging of proteins with chemical and genetic approaches			
Module:6	**Targetted Proteomics – Macromolecular Interactions**	**7 hours**	
Qualitative and quantitative proteome analysis, Short-gun proteomics for proteome profile (whole proteome and sub-proteome analysis), Expression proteome analysis (isotope-labeling and label-free approaches), Proteomic analysis of protein-protein (including antigen-antibody interactions for epitope mapping), protein-DNA interactions, Identification of ligand receptor pairing and transcriptional regulators.			
Module:7	**Proteomics in Clinical and Drug Discovery Applications**	**6 hours**	
Proteomics in study of diseases, Storage transportation and processing of clinical samples, Proteomic analysis of body fluids, Western Blotting, systems biology approaches and interaction network for drug discovery			
Module:8	**Contemporary issues:**	**2 hours**	
Lecture by Industrial Expert			
	Total Lecture hours:	**45 hours**	
Text Book(s)			
1.	Twyman RM (2013) Principles of Proteomics, Taylor and Francis, Garland Science		
Reference Books			
1. 2. 3. 4.	Westermeier R Naven T (2008) Proteomics in Practice: A Guide to Successful Experimental Design, Wiley-VCH Link AJ, LaBaer J (2009) Proteomics: A Cold Spring Harbor Laboratory Course Manual, Cold Spring Harbor Laboratory Press Hubert R (2006) Protein Biochemistry and Proteomics (The Experimenter Series), Academic Press Proteomics: Methods and Protocols (2017), Methods in Molecular Biology Series, Ed. Lucio Comai · Jonathan E. Katz Parag Mallick, Humana Press. USA.		
Mode of Evaluation: CAT / Assignment / Quiz / FAT / Project / Seminar			
Recommended by Board of Studies	03-08-2017		
Approved by Academic Council	No. 46	Date	24-08-2017