

BACHELOR WITH BIOTECHNOLOGY AS MAJOR

6th SEMESTER

BTG 622J3: OMICS: Genomics, Transcriptomics and Proteomics

CREDITS: THEORY – 4, PRACTICAL – 2

- **Course Learning Objective:** aim of this course is to acquaint students with Omics – genomics, transcriptomics and proteomics.
- **Course outcome:** A student will be able to;
 - distinguish genomes on basis of complexity.
 - do genome analysis – sequencing, assembly and annotation.
 - select and use different techniques used for transcriptome analysis.
 - identify the different techniques in-use for proteome study.

UNIT- 1 (15 HOURS)

Genomics – Introduction, types: size, structural, epigenomics, mutational and metagenomics. Genome analysis: genome complexity (cot curve), repetitive and unique sequences, C-value paradox, genome mapping (FISH, restriction mapping), molecular markers (RAPD, AFLP, STS, EST).

UNIT - 2 (15 HOURS)

Genome sequencing, Introduction to DNA sequencing, methods of DNA sequencing (Maxam & Gilbert, Sanger and NGS- Illumina). Metagenomics: 16S rRNA typing/sequencing. Whole genome sequence: genome assembly and annotation. Human Genome Project.

UNIT - 3 (15 HOURS)

Global gene expression analysis: cDNA-Microarrays and oligonucleotide arrays: Technique of cDNA Micro array, Micro array design, Data representation and applications. Expression sequence tags (ESTs) and their significance. MiRNAs and siRNAs: biogenesis and function. Serial analysis of gene expression (SAGE), SAGE data analysis, role of SAGE in gene discovery.

UNIT - 4 (15 HOURS)

Proteomics: Introduction, strategies in analysis of proteome: Pulldown of interacting partners of a protein, Tandem-Affinity purification (TAP) and Immunoprecipitation. Identification of proteins by mass spectrometry, 2D-Gel electrophoresis, trypsin digestion, liquid

chromatography (LC) for separation of peptides and mass spectrometry (MALDI-MS and ESI-MS). Analysis: Peptide mass finger printing.

PRACTICALS (2 CREDITS)

1. Analysis of genome by commercially available kits.
2. Study of DNA denaturation and renaturation (http://www.scfbio-iitd.res.in/chemgenome/Tm_predictor.jsp)
3. Demonstration of real time PCR and SDM.
4. Visit to mass spectrometry facility/any advanced science instrumentation facility.

BOOKS RECOMMENDED

1. Robert B Northrop, Anne N Connor: Introduction to Molecular Biology, Genomics and Proteomics for Biomedical Engineers, CRC Press.
2. Brown TA, Genomes, 3rd Edition, Garland Science.
3. Campbell AM & Heyer LJ, Discovering Genomics, Proteomics and Bioinformatics, 2nd Edition, Benjamin Cummings.
4. Carl, Branden and Tooze, John. Introduction to Protein Structure, Garland Publishing (Taylor and Francis Group). New York
5. Kamp RM, Methods in proteome and protein analysis, Springer.