COURSE TITLE	**FUNDAMENTALS OF GENOMICS AND PROTEOMICS**
COURSE CODE	**01CB1402**
COURSE CREDITS	**4**

Objective:

1 To provide an understanding of the fundamental concepts of genomics and the progression towards proteomics.

2 To enable students to analyze protein–protein interactions for understanding cellular functions and regulatory mechanisms.

Course Outcomes: After completion of this course, student will be able to:

1 Analyze genomic data using annotation and comparative genomics

2 Apply NGS and microarrays for gene expression studies.

3 Utilize the concepts of gene regulation, post-translational modifications to interpret cellular function.

4 Evaluate proteomics and chromatography techniques for protein analysis.

Pre-requisite of course: Knowledge of fundamentals of Biology

Teaching and Examination Scheme

Theory Hours	Tutorial Hours	Practical Hours	ESE	IA	CSE	Viva	Term Work
3	0	2	50	30	20	25	25

Contents : Unit	Topics	Contact Hours
1	**Prokaryotic and Eukaryotic Genome & Proteome** Brief overview of prokaryotic and eukaryotic genome organization & gene structures, Human genome project, The Organization and Structure of Genomes, Mapping and sequencing genomes, Next Generation DNA Sequencing (NGS), Different types of RNA-characteristics & functions, Post-transcriptional modifications, Regulation of gene expression, Protein folding, post-translational modifications & Protein translocation	12
2	**Functional Genomics** Genome annotation, Genetic and physical maps; markers for genetic mapping; Methods and techniques used for gene mapping, physical mapping, Gene Ontology, Overview of Comparative Genomics; Applications of Genome analysis and Genomics, Analysis of RNA expression, Micro array techniques- Types of Microarrays, designing a microarray experiment, Microarray Technology in Treating Disease, Study of Gene Regulation using Chromatin Immunoprecipitation (ChIP), RNA interference (RNAi)	10

DR. SEJAL SAHILKRISHNA SHAH
Digitally signed by (Name of HOD)

DR. RAJENDRASINH BAHADURSINH JADEJA
Digitally signed by (Name of Dean/ Principal)

Contents : Unit	Topics	Contact Hours
3	**Proteomics** Transition from genomics to proteomics, Basics of protein chemistry and proteomics, Technical aspects of different quantitative proteomics methods Chromatography techniques for protein purification/separation, Analysis of protein-protein interactions	10
4	**Mass Spectrometry** Mass spectrometry-based methods for protein identification, De novo sequencing using mass spectrometric data, Correlative mass spectrometric-based identification strategies, 2-D gel electrophoresis coupled with mass spectrometry	10
Total Hours		**42**

Suggested List of Experiments:

Contents : Unit	Topics	Contact Hours
1	**Experiment 1** To explore the human genome using Integrative Genomics Viewer (IGV)	2
2	**Experiment 2** To identify the location of the gene in the human genome with Integrative Genomics Viewer (IGV)	2
3	**Experiment 3** To explore the human genome using the UCSC genome browser	2
4	**Experiment 4** To identify the location of the five genes in the human genome using UCSC genome browser	2
5	**Experiment 5** To identify the SNPs in the five genes in the human genome using UCSC genome browser	2
6	**Experiment 6** To annotate the FASTA file of five proteins using BLASTn	2
7	**Experiment 7** To annotate the FASTA file of five nucleotide sequences using BLASTx	2
8	**Experiment 8** To configure the SRA tool kit in the ubuntu/Linux operating system	2
9	**Experiment 9** To configure the SRA tool kit in Windows operating system	2
10	**Experiment 10** To explore insights into SRA (Sequence Read Archive) data on the NCBI website and tabulate the experimental setup	2
11	**Experiment 11** To extract specific SRA project data using the SRA tool kit from NCBI	2

DR. SEJAL SAHILKRISHNA SHAH
Digitally signed by (Name of HOD)

DR. RAJENDRASINH BAHADURSINH JADEJA
Digitally signed by (Name of Dean/ Principal)

Suggested List of Experiments:

Contents : Unit	Topics	Contact Hours
12	**Experiment 12** To convert the SRA format file into FASTQ file format using the SRA tool kit	2
13	**Experiment 13** To convert FASTQ file format into FASTA format files	2
14	**Experiment 14** To annotate the FASTA file using standalone BLAST	2
Total Hours		**28**

Textbook :

1 Introduction to Proteomics: Principles and Applications, Nawin C. Mishra, Wiley, 2011

2 Principles of Proteomics, Richard M Twyman, Taylor & Francis, 2004

3 Concepts and Techniques in Genomics and Proteomics, N Saraswathy, P Ramalingam, Woodhead Publishing, 2011

References:

1 Discovering Genomics, Proteomics and Bioinformatics, Discovering Genomics, Proteomics and Bioinformatics, Malcolm Campbell, Laurie J. Heyer, Pearson, 2006

2 Principles of Gene Manipulation and Genomics, Principles of Gene Manipulation and Genomics, Sandy B. Primrose, Richard Twyman, Wiley-Blackwell, 2013

3 Introduction to Proteomics: Tools for the New Biology, Introduction to Proteomics: Tools for the New Biology, Daniel C. Liebler, Humana, 2001

Suggested Theory Distribution:

The suggested theory distribution as per Bloom's taxonomy is as follows. This distribution serves as guidelines for teachers and students to achieve effective teaching-learning process

Distribution of Theory for course delivery					
Remember / Knowledge	**Understand**	**Apply**	**Analyze**	**Evaluate**	**Higher order Thinking / Creative**
0.00	0.00	35.00	35.00	30.00	0.00

Instructional Method:

1 The course delivery method will depend upon the requirement of content and need of students. The teacher in addition to conventional teaching method by whiteboard, may also use any of tools such as demonstration, role play, Quiz, brainstorming, MOOCs etc.

2 The internal evaluation will be done on the basis of continuous evaluation of students in the laboratory and class-room.

3 Practical examination will be conducted at the end of semester for evaluation of performance of students in laboratory.

DR. SEJAL SAHILKRISHNA SHAH
Digitally signed by (Name of HOD)

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Digitally signed by (Name of Dean/ Principal)

Supplementary Resources:

1. https://www.youtube.com/watch?v=ZgwNWRul98o
2. https://www.youtube.com/watch?v=JPpKL1uzE0I
3. https://www.youtube.com/watch?v=KkkyD5Q07Q8

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