



**Programme – B.Tech. Biotechnology**

L	T	P/S	SW/F W	TOTAL CREDIT UNITS
3	0	2	0	4

**Course Title: Essentials of Genomics and Proteomics**

**Course Code: GCMB401**

**Credit Units: 03+1**

**Course Objectives:** The course recognizes the developing fundamental and prominent high throughput techniques across the fields of genomics, transcriptomics and proteomics. The students would be able to value their applications in elucidating complex biological queries in the scientific world.

**Pre-requisites:** Molecular biology, Cell Biology, Genetics, Recombinant DNA technology, Bioinformatics and Computational Biology courses

**Student Learning Outcomes:** Upon the completion of the course the student will be able to

- The student will be able to illustrate the key concepts of high throughput techniques used in genomics, transcriptomics and proteomics. -  
Relate to the complexity of Genome annotation efforts and infer the significance of genomic variations in disease, forensics and evolution - Students will be able to establish the modalities of proteomic studies that are applied in latest research in life sciences.
- Apply concepts of dynamic protein biology and create processes of application to translate across biological systems

**Course Contents/Syllabus:**

	Weightage (%)
Module I	10

<p><b>Descriptors/Topics – Genomics Overview</b>  Genome definition, Genomics and its diversifications – Structural Genomics, Functional Genomics,  Pharmacogenomics, Personal Genomics  Genome organization – Differences in prokaryotes, eukaryotes and viruses, Repeat content of the genome, C value paradox; Model Genomes (E.coli, Arabidopsis, C.elegans)</p>	
<p><b>Module II – Whole Genome Sequencing techniques and annotation</b></p>	<b>30</b>
<p><b>Massively parallel Genome Sequencing Techniques</b> – Common features of Second Generation Sequencing Techniques, Pyrosequencing, Virtual Terminator Sequencing, SOLiD  <b>De novo Whole Genome Sequencing strategies</b> – De novo sequencing and assembly strategies - Whole Genome</p>	
<p>Shotgun and Hierarchical Shotgun, Genome finishing – Gaps and their resolution, Human Genome Project - findings and impact, Reference based assembly and alignment algorithms for short reads  <b>Genome Annotation</b> – concepts of Open Reading Frame, <i>in silico</i> annotation approaches – de novo, homology based annotation – common gene finding algorithms and wet lab confirmation methods – mRNA, ESTs</p>	
<p><b>Module III Molecular markers and applications</b></p>	<b>10</b>
<p><b>Variations in genomes and Molecular markers</b> –  Concepts, assays and Applications – Dominant and codominant markers, RFLP, AFLP, CAPS, SSRs, RAPDs, SNPs, Copy number variations (CNVs), Variations and diseases</p>	
<p><b>Module IV</b></p>	<b>30</b>
<p><b>Descriptors/Topics - Elucidation of Transcriptomes and Proteomes</b>  <b>Transcriptome analysis</b> - ESTs, SAGE, RNAseq; ENCODE project; Microarray Chips and applications- ChIPSeq, ChIP-chip, Subtractive Hybridization – Concepts and applications  Proteomes and Sub- proteomes (structure, function and expression correlations); Expression and Analytical Proteome analysis; Quantitative Proteomics  <b>Proteomic technologies</b> -Gel based proteome investigations (1D/ 2D- GE, IEF,DIGE); Sequence based technologies - Mass spectrometry (ESI, MALDI and hybrid); LC/MS-MS; Differential Display proteomics; Protein sequence determination – Edman versus Peptide sequencing and mass fingerprinting; Identification of post-translational modifications; DEEP SEQ MS; Protein de novo sequencing and top down proteomics; Applications of X-Ray and NMR for structure determination; Computational tools for structure</p>	

<p><b>Descriptors/Topics: Interaction proteomics and applications of proteomics</b>  Proteomic analysis of protein-protein, protein-DNA interactions - experimental and computational methods (Co-IP, Y2H approaches, Phage display); Proteome interaction maps  <b>Structure function relationship</b> - Protein function from structure; Structural proteomics; Proteomics experimental workflows; Protein Engineering Techniques; Basics of Metabolic networks, Protein databases and bioinformatics processing; Experimental design in proteomics  <b>Proteomics applications</b> - Pharmacogenomics; Metabolomics, Metaproteomics, Proteogenomics and introduction to systems biology</p>	<b>20</b>
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**Pedagogy for Course Delivery:**

Lectures – 43 Class  
test – 2  
Total – 45 hours

**Lab/ Practical details, if applicable:**

Practical: 13  
Practical Test: 2  
Total: 15

**List of Experiments:**

- **Introductions to Genome browser (NCBI, UCSC) and protein databases (SWISS-PROT, TrEMBL, PDB)**
- **Homology Search using BLAST – BLASTn, BLASTp**
- **Homology search using BLAST – Psi BLAST**
- **Multiple Sequence Alignment using CLUSTALW and CLUSTALX, identification of conserved domains**
- **Multiple sequence alignment and phylogeny**
- **Primer3, Restriction digestion, VecScreen, Mapviewer**
- **Gene Structural Annotation Tools - ORF finder, GeneScan, GeneFinder / GENEMARK, Repeat Masker**
- **DNA sequencing methods, gene finding tools and Genome annotation**
- **Genomic browsers and databases, Orthology prediction**
- **Translate, SMSuite, MIAME, Melanie, Analysis of 2D- IEF data**
- **Protein Database, SOPMA, GOR 4, Rasmol, THMM, Pepdide Cutter, Peptide Mass**
- **Melanie, Flicker, PROFOUND, MASCOT, Alibaba**
- **Metabolic pathways resources: KEGG, Biocarta**

**Assessment/ Examination Scheme:**

<b>Theory L/T (%)</b>	<b>Lab/Practical/Studio (%)</b>	<b>End Term Examination</b>
<b>75</b>	<b>25</b>	<b>100</b>

**Theory Assessment (L&T):**

<b>Continuous Assessment/Internal Assessment</b>					<b>End Term Examination</b>
<b>Components (Drop down)</b>	<b>Class Test</b>	<b>Home Assignment</b>	<b>Presentation/ Seminar/ Viva</b>	<b>Attendance</b>	
<b>Weightage (%)</b>	15	5	5	5	70

**Lab/ Practical/ Studio Assessment:**

	<b>Continuous Assessment/Internal Assessment</b>				<b>End Term Examination</b>			
<b>Components (Drop down)</b>	<b>Performance</b>	<b>Lab record</b>	<b>Viva</b>	<b>Attendance</b>	<b>Lab record</b>	<b>Performance</b>	<b>Viva</b>	<b>Total</b>
<b>Weightage (%)</b>	10	10	5	5	10	40	20	70

**Text & References:**

- **Discovering Genomics, Proteomics and Bioinformatics, 2nd Edition. Campbell AM & Heyer LJ, Benjamin Cummings 2007; CSH Press, NY.**

**ISBN-10: 8131715590**

- **Principles of Proteomics. R.M Twyman (2004). (BIOS Scientific publishers). ISBN-10: 1859962734**
- **Principles of Gene Manipulation and Genomics- Primrose S & Twyman R, 7th Edition, Blackwell, 2006. ISBN-10: 1405135441**
- **Principles of Genome Analysis and Genomics. Primrose SB & Twyman RM. 2007. Blackwell. ISBN-10: 1405101202**
- **Introduction to Genomics. A.M Lesk, Oxford University press, 2007. ISBN-10: 0199557489**
- **A Primer of Genome Science. Greg Gibson and Spencer V. Muse. 2nd ed. 2004. SINAUER Associates Inc. ISBN-10: 0878932364**

- **Genome III – T.A. Brown Garland Science Publ. June 08, 2006. ISBN-10: 0815341385**
- **Introduction to Proteomics: Tools for the New Biology. Daniel C. Liebler, Humana Press Inc., 2002. ISBN-10: 0896039919**
- **Bioinformatics – Sequence and Genome Analysis – David W. Mount –Cold Spring Harbor Laboratory Press, U.S.; 2nd Revised edition, 2004. ISBN-10: 9746520709**
- **Essential Bioinformatics – Xing Xiong – Cambridge University Press, New York, 2006. ISBN-10: 0521706106**
- **Bioinformatics and Functional Genomics – Jonathan Pevsner - 2nd edition, Wiley-Blackwell, 2009. ISBN-10: 0471210048**

**Any other Study Material:**

- **Proteomic to study genes and genomes (2000). Nature 405: 837-846.**
- **Application of DNA microarrays in Biology (2005) Ann. review of Biochemistry 74: 53-82.**
- **Functional Proteomics (2005) Clin Chim Acta 357: 140-150.**
- **Mass spectrometry for proteomics (2008), Curr Opin Chem Biol. Oct;12(5):483-90.**
- **ChIPSeq and beyond – Nature reviews Genetics Volume 13, 2012, 840-852**
- **Sequencing Technologies – The next Generation – Nature reviews Genetics Volume 11, 2010, 31-46**
- **Proteomics: Challenges, Techniques and Possibilities to Overcome Biological Sample Complexity – Human Genomics and Proteomics, 2009. • NCBI online tutorials and Videos**
- **Genome TV – You tube videos form NIH**