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| Department of Biotechnology | LP: BT22603<br>Rev. No: 00<br>Date: 18-01-2025 |
| B.Tech: Biotechnology Regulation: 2022<br>PG Specialisation: N/A<br>Sub. Code / Sub. Name: BT22603 – Genomics and Proteomics<br>Unit: I | |

**Unit Syllabus:** GENOMICS SEQUENCING TECHNOLOGIES 12 Hrs

Next Generation Sequencing (NGS), Sequencing File formats, Basic pipeline for data analysis - quality check, adaptor trimming, Genome assembly, Genome annotation, Concepts of sequencing coverage and sequencing depth, phred score. Chip-Seq, DNAse-Seq, ATAC-seq, MNase-seq, FAIRE-seq.

Practical Sessions: Introduction to Bioinformatics Tools: Utilizing online resources - NCBI, UniProt, and Ensembl for sequence data retrieval and analysis, Genome browsers: UCSC and Ensembl, Finding genes from Genome browsers, Finding Transcripts from Genome browsers.

**Objective:** Familiarize students with Next-Generation Sequencing (NGS) technologies and bioinformatics tools for sequence analysis.

| Session No * | Topics to be covered | Ref | Teaching Aids |
|---|---|---|---|
| 1. | Maxam and Gilber, Sanger Sequencing and Next Generation Sequencing (NGS) | TB1; Pg. (93-104) | GCR/LCD |
| 2. | Sequencing File formats, Basic pipeline for data analysis - quality check, adaptor trimming, | Weblink - 1 | GCR/LCD |
| 3. | Genome Mapping and assembly<br>Genome annotation | TB1; Pg. (81-90)<br>TB1; Pg. (98-100)<br>TB1; Pg. (104-109) | GCR/LCD |
| 4. | Concepts of sequencing coverage and sequencing depth, phred score | Weblink - 2 | BB/Video Lecture |
| 5. | Chip-Seq, DNAse-Seq | Journal Article-3 | BB/LCD |
| 6. | ATAC-seq, MNase-seq, FAIRE-seq | Journal Article-3 | BB/LCD |
| 7. | Sequence Data Retrieval from NCBI | Laboratory Manual | NCBI |
| 8. | Protein Sequence Analysis Using UniProt | Laboratory Manual | UniProt |
| 9. | Genome Browsing with UCSC Genome Browser | Laboratory Manual | UCSC Genome Browser |
| 10. | Identifying Genes Using Ensembl Genome Browser | Laboratory Manual | Ensembl |
| 11. | Transcript Analysis in Ensembl | Laboratory Manual | Ensembl |
| 12. | Comparative Genome Analysis Using UCSC | Laboratory Manual | UCSC Browser |
| **Content beyond syllabus covered (if any): Nil** | | | |

* Session duration: 50 minutes

Sub. Code / Sub. Name: BT22603 – Genomics and Proteomics

Unit : II

**Unit Syllabus:** GENOMICS APPLICATIONS 12 Hrs

Transcriptomics: RNA sequencing, Microarray, Epigenomics: Techniques for Studying DNA Methylation, Histone Modifications, Comparative Genomics, Single Cell Genomics.

Practical Sessions: NGS Data Analysis: NGS data preprocessing, quality control, and read alignment using FASTQC, Trimmomatic, and Bowtie2.Transcriptomics Data Analysis: Differential gene expression analysis using GEO2R.

**Objective:** Enable understanding of genomics applications such as transcriptomics, epigenomics, and metagenomics.

| Session No * | Topics to be covered | Ref | Teaching Aids |
|---|---|---|---|
| 13. | Transcriptomics: RNA Sequencing | TB1; Pg. (292) | GCR/LCD |
| 14. | Microarray | TB1; Pg. (266-292) | GCR/LCD/Video Lecture |
| 15. | Epigenomics: Techniques for Studying DNA Methylation | Journal Article-4 | GCR/LCD |
| 16. | Histone Modifications - ChIP-on-chip, ChIP–SAGE, ChIP–Seq | Weblink - 3 | BB/LCD |
| 17. | Comparative Genomics | TB1; Pg. (115-154) | BB/LCD |
| 18. | Single Cell Genomics | Journal Article-5 | BB/LCD |
| 19. | NGS Data Preprocessing with Trimmomatic | Laboratory Manual | Trimmomatic |
| 20. | Quality Control of NGS Data Using FASTQC | Laboratory Manual | FASTQC |
| 21. | Read Alignment Using Bowtie2 | Laboratory Manual | Bowtie2 |
| 22. | Differential Gene Expression Analysis Using GEO2R | Laboratory Manual | GEO2R |
| 23. | Visualization of NGS Read Quality Metrics | Laboratory Manual | FASTQC |
| 24. | Post-alignment Analysis Using Bowtie2 Output | Laboratory Manual | Bowtie2 |

**Content beyond syllabus covered (if any): Nil**

* Session duration: 50 mins

Sub. Code / Sub. Name: BT22603 – Genomics and Proteomics

Unit : III

**Unit Syllabus:** PROTEOMICS - PROTEIN IDENTIFICATION AND INTERACTION 12 Hrs

Two-dimensional Gel Electrophoresis (2D-PAGE), Protein Fractionation Techniques: Affinity chromatography, ion-exchange chromatography, size-exclusion chromatography, ultracentrifugation, Protein Sequencing: Edman degradation, Protein-Protein Interaction Analysis: yeast two-hybrid (Y2H) assays, co-immunoprecipitation (Co-IP), and tandem affinity purification (TAP)

Practical Sessions: Protein gel Image analysis using ImageJ and protein simulation studies.

**Objective:** Provide knowledge of protein identification techniques and protein-protein interaction analysis.

| Session No * | Topics to be covered | Ref | Teaching Aids |
|---|---|---|---|
| 25. | Two-dimensional Gel Electrophoresis (2D-PAGE), Protein Fractionation Techniques: Affinity chromatography | TB2; Pg. (25-36) | GCR/LCD |
| 26. | ion-exchange chromatography, size-exclusion chromatography, ultracentrifugation | TB2; Pg. (36-38) | GCR/LCD |
| 27. | Protein Sequencing: Edman degradation | TB2; Pg. (48-51) | GCR/LCD |
| 28. | Protein-Protein Interaction Analysis: yeast two-hybrid (Y2H) assays | TB2; Pg. (145-149) | BB/LCD |
| 29. | Co-immunoprecipitation (Co-IP) | TB2; Pg. (139-140) | BB/LCD |
| 30. | Tandem affinity purification (TAP) | TB2; Pg. (153-155) | BB/LCD |
| 31. | Protein Gel Image Analysis Using ImageJ | Laboratory Manual | ImageJ |
| 32. | Quantification of Protein Bands and DNA Using ImageJ | Laboratory Manual | ImageJ |
| 33. | Simulation of Protein Folding Using PyMOL | Laboratory Manual | PyMOL |
| 34. | Energy Minimization of Protein Models | Laboratory Manual | GROMACS |
| 35. | Molecular Dynamics Simulation Using GROMACS | Laboratory Manual | GROMACS |
| 36. | Visualization of Protein Structure and Dynamics | Laboratory Manual | VMD |

**Content beyond syllabus covered (if any): Nil**

* Session duration: 50 mins

Sub. Code / Sub. Name: BT22603 – Genomics and Proteomics

Unit : IV

**Unit Syllabus:** QUANTITATIVE PROTEOMICS 12 Hrs

Basics of Mass-spectrometry (MS), Types of MS, Peptide mass fingerprinting, stable isotope labeling (e.g., SILAC, TMT, iTRAQ), label-free quantification, and selected reaction monitoring (SRM), Data independent acquisition (DIA).

Practical Sessions: Protein-protein interaction network analysis using databases STRING or BioGRID

**Objective:** Familiarize with mass spectrometry-based proteomics and quantitative analysis methods.

| Session No * | Topics to be covered | Ref | Teaching Aids |
|---|---|---|---|
| 37. | Basics of Mass-Spectrometry (MS) | TB2; Pg. (52-53) | GCR/LCD |
| 38. | Types of Mass-Spectrometry | TB2; Pg. (54-57) | GCR/LCD |
| 39. | Peptide mass fingerprinting, | TB2; Pg. (58-61) | GCR/LCD |
| 40. | Stable isotope labeling (e.g., SILAC, TMT, iTRAQ) | TB2; Pg. (77-84) | BB/LCD |
| 41. | label-free quantification | TB2; Pg. (77) | BB/LCD |
| 42. | selected reaction monitoring (SRM) and Data independent acquisition (DIA) | Journal Article-1 | BB/LCD |
| 43. | Retrieving Protein-Protein Interaction Data Using STRING | Laboratory Manual | STRING |
| 44. | Visualizing Protein Interaction Networks in STRING | Laboratory Manual | STRING |
| 45. | Exploring Functional Enrichment Analysis in STRING | Laboratory Manual | STRING |
| 46. | Downloading Interaction Data from BioGRID | Laboratory Manual | BioGRID |
| 47. | Comparative Analysis of Interactions from STRING and BioGRID | Laboratory Manual | STRING, BioGRID |
| 48. | Building Custom Protein-Protein Interaction Networks | Laboratory Manual | Cytoscape for STRING/BioGRID data |

**Content beyond syllabus covered (if any): Nil**

* Session duration: 50 mins

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Unit : V

**Unit Syllabus:** STRUCTURAL PROTEOMICS 12 Hrs

Nuclear magnetic resonance (NMR) spectroscopy: Fundamentals of the NMR phenomenon, relationship between NMR spectra and molecular structure. Recording of routine spectra (1H and 13C), essentials of data processing (e.g., weightingfunctions). 1D NMR, 2D NMR techniques, X-ray crystallography, Cryo-electron microscopy (cryo-EM).

Practical Sessions: Introduction to molecular visualization tools: PyMOL or Jmol for protein structure visualization, Ramachandran plot. Mass Spectrometry tools: Basic data processing using softwares – Proteome Discoverer, MaxQuant, OpenMS, CompOMICS, Unipept, Tabloid Proteome, Ionbot.

**Objective:** Equip with advanced structural biology techniques such as NMR spectroscopy and X-ray crystallography.

| Session No * | Topics to be covered | Ref | Teaching Aids |
|---|---|---|---|
| 49. | Nuclear magnetic resonance (NMR) spectroscopy - Magnetic Properties of Nuclei, Chemical Shift, Excitation and Relaxation | RB1; Pg. (1-10) | GCR/LCD |
| 50. | NMR – Pulsed Experiments, Coupling Constant, Quantitation and Complex Splitting, Commonly studied nuclides | RB1; Pg. (11-22) | GCR/LCD |
| 51. | NMR Spectrometer Sample Preparation, Acquistion Parameters, Processing Parameters<br>Chemical Shift | RB1; Pg. (31-51)<br>RB1; Pg. (62-88) | GCR/LCD |
| 52. | 2D NMR techniques | RB1; Pg. (172-208) | BB/LCD |
| 53. | X-ray crystallography | RB2; Pg. (1-31) | BB/LCD |
| 54. | Cryo-electron microscopy (cryo-EM). | Journal Article-2 | BB/LCD |
| 55. | Protein Structure Visualization Using PyMOL | Laboratory Manual | PyMOL |
| 56. | Protein Structure Visualization Using Jmol | Laboratory Manual | Jmol |
| 57. | Analysis of Protein Dihedral Angles with Ramachandran Plot | Laboratory Manual | MolProbity |
| 58. | Basic Mass Spectrometry Data Processing Using OpenMS | Laboratory Manual | OpenMS |
| 59. | Peptide Analysis Using UniPept | Laboratory Manual | UniPept |
| 60. | Protein Identification with CompOmics Tools | Laboratory Manual | CompOmics (Peptide Shaker) |

**Content beyond syllabus covered (if any): Nil**

* Session duration: 50 mins

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## REFERENCES:

### Text Books

1. Lesk, Arthur M. Introduction to Genomics. United Kingdom, Oxford University Press, 2017.
2. Twyman, Richard, et al. Principles of Proteomics. United Kingdom, CRC Press, 2013.

### Reference Books

1. Lambert, Joseph B, Mazzola, Eugene P. Nuclear Magnetic Resonance Spectroscopy: An Introduction to Principles, Applications, and Experimental Methods. United Kingdom: Pearson Education, 2004.
2. Clegg, William. X-ray Crystallography. United Kingdom: Oxford University Press, 2015.

### Journal Article

1. Van Bentum, M., & Selbach, M. (2021). An Introduction to Advanced Targeted Acquisition Methods. Molecular & cellular proteomics: MCP, 20, 100165. https://doi.org/10.1016/j.mcpro.2021.100165
2. Milne, J. L., Borgnia, M. J., Bartesaghi, A., Tran, E. E., Earl, L. A., Schauder, D. M., Lengyel, J., Pierson, J., Patwardhan, A., & Subramaniam, S. (2013). Cryo-electron microscopy--a primer for the non-microscopist. The FEBS journal, 280(1), 28–45. https://doi.org/10.1111/febs.12078
3. Klein, D. C., & Hainer, S. J. (2020). Genomic methods in profiling DNA accessibility and factor localization. Chromosome research: an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology, 28(1), 69–85. https://doi.org/10.1007/s10577-019-09619-9
4. Marzese, D. M., & Hoon, D. S. (2015). Emerging technologies for studying DNA methylation for the molecular diagnosis of cancer. Expert review of molecular diagnostics, 15(5), 647–664. https://doi.org/10.1586/14737159.2015.1027194
5. Kalisky, T., & Quake, S. R. (2011). Single-cell genomics. Nature methods, 8(4), 311–314. https://doi.org/10.1038/nmeth0411-311

### Weblink

1. https://genomics-fungi.sschmeier.com/ngs-qc/index.html
2. https://www.cd-genomics.com/resource-sequencing-depth-and-coverage.html#:~:text=Coverage%3A%20Refers%20to%20the%20percentage,represented%20by%20a%20Phred%20score.
3. https://www.cusabio.com/c-20827.html?srsltid=AfmBOopqYtCPy8Mq-h0HFTqZALtHGbwQOjigYDv5PBjAeqsrZmm3IgpQ

| | Prepared by | Approved by |
|---|---|---|
| Signature | | 20/1/25 |
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| Designation | Assistant Professor | HOD-Biotechnology |
| Date | 18-01-2025 | 18-01-2025 |
| Remarks *: the same lesson plan will be followed in the subsequent semester/year | | |
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* If the same lesson plan is followed in the subsequent semester/year it should be mentioned and signed by the Faculty and the HOD