

BIOINFORMATICS PROJECT TOPIC LIST

- 1. Sequence alignment analysis of Mpox Virus
- 2. Personalized drug in type II diabetes using Pharmacovigilance approach
- 3. Developing a Computational Model for Predicting the Emergence of New Mpox or SARS-CoV-2 Escape Variants with Enhanced Immune Evasion
- 4. Understanding efficacy of personalized medicine in Alzheimer's disease treatment: A Molecular docking approach
- 5. Studying the cervical cancer and it's drugs target using multiple omics data analysis
- 6. Identification of potential drug targets of miR-4454 in CARS disease using bioinformatics databases and network pharmacology
- 7. Investigating the role of cervical cancer and its drug targets using proteomics data analysis
- 8. Identification of Disease-Causing Mutations: A Bioinformatics Database Approach (breast cancer)
- 9. Exploring genomics variants on cervical cancer a bioinformatics approach
- 10. Decoding genetic blueprint of type II diabetes through bioinformatics
- 11. Computational Drug Discovery Targeting Mpox: Virtual Screening and Molecular Docking Analysis of Potential Antiviral Compounds
- 12. Sequence alignment and homology modeling
- 13. Bioinformatics approaches to investigate antimicrobial resistance in humans

- 14. Predicting Drug Resistance in Cancer Using Multi-Omics Data Integration
- 15. Metagenomic Analysis of Gut Microbiota and Its Impact on Immune Response in Autoimmune Diseases
- 16. Designing Novel Therapeutic Strategies for Rare Genetic Diseases Using CRISPR-Based Functional Genomics
- 17. Exploring Epigenetic Modifications in Cardiovascular Diseases Through Computational Epigenomics
- 18. Integrative Analysis of Single-Cell RNA Sequencing Data to Uncover Cellular Heterogeneity in Tumor Microenvironment
- 19. Predictive Modeling of Drug-Drug Interactions in Personalized Medicine Using Network Pharmacology
- 20. Bioinformatics Approaches to Identify Biomarkers for Early Detection of Chronic Kidney Disease
- 21. Characterizing the Impact of Epitranscriptomics on Cancer Progression Using RNA Sequencing Data
- 22. Modeling Protein-Protein Interactions in Neurodegenerative Disease Using Structural Bioinformatics
- 23. Exploring Genetic and Epigenetic Factors Contributing to Drug Response Variability in Cancer Therapy
- 24. Investigating the Role of Circular RNAs in Cancer Metastasis Using Computational Approaches
- 25. Utilizing Bioinformatics and CADD pipelines to Identify Novel Therapeutic Targets of Mpox
- 26. Analyzing the Impact of Post-Translational Modifications on Protein Function in Disease States
- 27. Ligand-Based Virtual Screening for Discovery of Novel Dengue Virus or Mpox Virus Entry Inhibitors
- 28. Design and Optimization of Novel Inhibitors for Dengue Virus NS3 or Mpox Virus Protease Using Structure-Based Drug Design
- 29. Identifying Potential Inhibitors of Mpox with Enhanced Pharmacological Profiles:
 An In-Silico Drug Discovery to Development Approach

- 30. Structure-Based Multi-Target Screening, Molecular Docking, and DFT Analysis for Anti-Cancer Drug Discovery
- 31. Exploration of Hub Genes and therapeutics drug candidates in cancer through an Integrated Bioinformatics Framework
- 32. Single-Nucleotide Polymorphism (SNP) Analysis for Personalized Nutrition Based on Gut Microbiome
- 33. Pan-genome Analysis of Antibiotic-Resistant Klebsiella pneumoniae Strains
- 34. CRISPR Guide RNA Design for Improving Stress Tolerance in Rice
- 35. Mining Plant Metabolome Databases to Predict Bioactive Compounds for Herbal Drug Discovery
- 36. Role of Skin Microbiome in Psoriasis and Eczema: Comparative Metagenomic Study
- 37. Constructing a Systems Biology Model to Simulate Inflammatory Pathways in Rheumatoid Arthritis
- 38. Automated QSAR Modeling and Prediction of Anti-TB Compounds
- 39. Development of a Bioinformatics Workflow for scRNA-seq Quality Control and Cell Type Annotation
- 40. In Silico Identification of Neoantigens for Personalized Immunotherapy in Glioblastoma
- 41. Gene-Disease Network Analysis in Rare Mitochondrial Disorders
- 42. Identification of Neoantigens for Personalized Cancer Vaccines Use AI to predict cancer-specific neoantigens from tumor sequencing data to guide vaccine development.
- 43. Gene Regulatory Network Analysis for Cancer Use graph neural networks to infer and analyze gene regulatory networks in different cancer types