

# Derrin Bright

Bioinformatics | Biotechnology | AI in Biology

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Portfolio

GitHub

LinkedIn

## Education

**Vellore Institute of Technology (VIT)**

*Bachelor of Technology in Biotechnology*

**CGPA: 8.69** Vellore, India

2022-Present

- **Relevant Courses:** Bioinformatics, Genomics and Proteomics, Molecular Biology, Cell Biology, Genetic Engineering, Biochemistry, Immunology, Biology, Probability and Statistics, Linear Algebra, Calculus

## Technical Skills

<b>Computational Biology Tools</b>	BLAST   AlphaFold   AutoDock Vina   GROMACS   MGLTools   Bioconductor   OpenBabel   Cytoscape   Seurat   GSEA   FIMO
<b>Data Analysis Tools</b>	Neo4J   KNIME   NetworkAnalyst
<b>Programming Tools</b>	R   Python   Bash
<b>Machine Learning Tools</b>	TensorFlow   Keras   NumPy   Pandas   Matplotlib

## Upcoming Research Experience

**Project Intern at Nanyang Technological University, Singapore | Guillaume Thibault Lab** Jan 2026 - June 2026

- Will perform computational analysis of ER stress responses through transcriptomic profiling, differential expression analysis, Weighted Gene Co-expression Network Analysis (WGCNA), and gene regulatory network construction.
- Supervised by Dr. Guillaume Thibault | Guillaume Thibault Lab

## Research Experiences

**Research Intern at Boston University, USA**

Sept 2025 - Present

- Developing an automated bioinformatics pipeline to parse and extract regulatory regions from a large-scale genomic dataset of over 200 viral genomes.
- Conducting a comparative sequence analysis to identify genomic signatures significantly enriched in specific disease-associated subtypes.

**Research Intern at University of Liverpool, UK**

Sept 2025 - Present

- Analyzing bulk RNA-seq data to identify the key molecular drivers and biological pathways involved in the progression of Chronic Lymphocytic Leukemia.
- Developing multiple machine learning models including XGBoost, Logistic Regression, SVM and Random Forest, and applying feature importance analysis to extract transcriptomic features differentiating CLL from RT.

**Research Intern at IIT Bombay, India**

May 2025 - Oct 2025

- Conducted differential expression analysis and WGCNA to identify key gene modules associated with autoimmune disease progression, followed by Gene Set Enrichment Analysis (GSEA) and Protein-Protein Interaction (PPI) network construction to uncover dysregulated pathways and functional gene relationships.
- Implemented predictive models to classify disease vs healthy states based on gene expression, enhancing biological interpretability through integrated network and machine learning approaches.

**Research Intern at Ashoka University, India**

Jan 2025 - Mar 2025

- Analyzed five assembled E. coli genomes for carbapenem and beta-lactam resistance using BLAST and RGI-CARD to identify mutations, and correlated genotype-phenotype relationships through AST report analysis.
- Performed Multiple Sequence Alignment (MSA) of Penicillin-Binding Proteins (PBPs) from the five E. coli genomes against a reference wild-type sequence to detect conserved mutations, and conducted genomic analysis that led to the identification of a 12-base pair insertion in the PBP3 gene, contributing to antibiotic resistance mechanisms.

**Biotech Team Lead at NovaLinks, India**

Feb 2025 - April 2025

- Led a project integrating miRNA analysis and histopathological imaging with machine learning to enhance lung cancer subtype classification and improve diagnostic precision.
- Conducted research on miRNA biomarkers specific to lung cancer and provided biological insights to support the development of an accurate classification model for distinguishing adenocarcinoma from squamous cell carcinoma.

## Technical Projects

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### Transcriptomic Comparison of HPV-Associated Cancers Using Co-Expression Networks

- Extracting and analyzing transcriptomic data from TCGA for HPV-associated cancers to perform both differential expression analysis and WGCNA, identifying key genes and co-expression modules.
- Constructing a PPI network in Cytoscape from a core gene set, and further analyzing these genes with functional enrichment in R to determine their shared biological roles.

### Computational Identification of Antimalarial Leads through Fingerprint Similarity Analysis

[GitHub Link](#)

- Screened a library of antimalarial molecules against a query (chloroquine drug) by generating molecular fingerprints and computing Tanimoto similarity coefficients using KNIME and RDKit nodes.
- Extracted molecular data from the Protein Data Bank (PDB) and visualized pairwise similarity scores as a heatmap to identify high-similarity candidates for antimalarial drug development.

### In Silico Analysis of 3DTC/CEP-6331 Complex using Molecular Docking

[GitHub Link](#)

- Implemented a molecular docking simulation using AutoDock Vina to model the interaction between the 3DTC kinase and the CEP-6331 inhibitor, achieving a predicted binding affinity of -12.23 kcal/mol.
- Analyzed the top binding pose to identify the specific amino acids responsible for the stable interaction, including key hydrophobic (ILE180, LEU274) and polar (LYS228, ASP284) residues.

### Single-Cell Transcriptomic Profiling of the B16 Melanoma's Microenvironment

[GitHub Link](#)

- Processed raw single-cell transcriptomic data from a B16 melanoma model using R (Seurat), applying quality control, normalization, and clustering to map the tumor's cellular heterogeneity.
- Characterized the resulting cell clusters by annotating fourteen distinct cell types within the tumor microenvironment and performed differential expression analysis to identify their unique gene signatures.

### Asthma Risk Prediction using Machine Learning

[GitHub Link](#)

- Optimized asthma risk prediction by developing multiple machine learning models, including Random Forest, SVM, and Gradient Boosting, and finetuning hyperparameters using Grid Search Cross-Validation to maximize accuracy.
- Enhanced model accuracy and reduced data dimensionality by applying Recursive Feature Elimination (RFE) to identify the most predictive features.

### Computational Analysis of Transcriptional Regulation by the MOV10 Protein

[GitHub Link](#)

- Investigated the transcriptomic impact of MOV10's knockdown and overexpression by analyzing a public RNA-seq dataset, identifying hundreds of differentially expressed genes under knockdown and overexpression conditions.
- Uncovered a dual regulatory mechanism for MOV10, where its knockdown and overexpression induce two distinct and often inverse transcriptional responses.

## Honors and Leadership

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**First runner-up in the Biomimicry Innovation Challenge and Showcase, Vellore Institute of Technology, 2024**

**Top 10 Winner of Bio-Inspired Design Fest (BIDFEST) Ideathon, Vellore Institute of Technology, 2024**

**Vice Chairperson at Alpha Bio Cell, VIT University, India**

*January 2024 - December 2024*

- Led several biotechnology and bioinformatics-related events, including hackathons, workshops, and quizzes, enhancing the club's engagement.
- Mentored junior core members and applied leadership, technical, and project management skills to ensure successful event planning and execution.

## Extra-Curricular

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**Volunteer | National Service Scheme, NGO**

*Conducted sessions in government schools on career opportunities and the importance of joining the armed forces.*

**Volunteer | Becoming I Foundation, NGO**

*Taught science, math, and english in government schools, supporting underprivileged communities.*

**Event Coordinator | BioSummit, School of Biosciences and Technology**

*Organized a flagship event connecting academia and food industries, managing food distribution and ensuring smooth execution.*