

## EDUCATION

### Orta Doğu Teknik Üniversitesi

September 2021 – Present

#### Bachelor of Science in Biology

Ankara, Türkiye

- *Relevant Coursework:* BIN505: Foundations of Systems Biology, BIN508: NGS and Informatics, BIN506: Protein and DNA-seq Analysis, BIN502: Statistics for Informatics, CENG305: OOP with Java, CENG310: DSA with Python, CENG240: Python for Engineers, Calculus 1&2, Physics 1&2, Biometry, Bioentrepreneurship Biotechnology, Genetics, Evolution.

## RESEARCH EXPERIENCE

### FAR Better Biomedical

November 2025 - Present

#### Genetics + Software Team

Ankara, Türkiye

- Worked on automated T-Cell isolation system using magnetic filters, achieving 96% purity of isolating CD3 T cells,
- Designing of nanobody/antibody using RAbD and SAbPred
- Worked on visualising lab data by building interactive dashboards

### Ankara University

July 2024 – September 2024

#### Research and Development Intern

Ankara, Türkiye

- Design and Deployment of NVIDIA funded project involving building an AI based Analyses device using NVIDIA Jetson Nano 2GB chip running Deep Learning Algorithms and using Computer Vision to detect, classify and count blood cells and types in a given biological sample placed on a modified micro-fluid array
- Responsible for designing the architecture and implementing deep learning models for object classification with a 95 % accuracy level

## PROJECTS

### Preprints

- **Similarity Network Fusion for Multi-Omics Integration and Survival Modeling in TCGA-BRCA (2026)** - Benchmarked Similarity Network Fusion (SNF) against single-omic, early, and late-integration baselines on TCGA-BRCA using RNA-seq, 450k DNA methylation and GISTIC2 copy number data. Implemented spectral clustering, Ridge-regularized Cox survival modeling, covariate-adjusted analyses, and robustness assessments.  
<https://arxiv.org/abs/2603.00212>
- **Multimomics Research of MEF2C Gene (2025)** -Integrated ChIP-seq and RNA-seq to characterize MEF2C transcriptional regulation in human microglia. Identified direct regulatory targets and downstream functional effects associated with MEF2C deficiency using genome-wide binding and differential expression analyses.  
<https://arxiv.org/abs/2510.25780>
- **Somatic Whole-Genome Profiling of the HCC1395 Breast Cancer Cell Line (2025)** - Developed an end-to-end somatic variant analysis pipeline for HCC1395/HCC1395BL (hg38), including BWA alignment, GATK Mutect2 variant calling, VCF filtering, SnpEff annotation, and comprehensive quality control and validation.  
<https://zenodo.org/records/17969212>

### Software/Open-source tools

- **gene-id-resolver (python package)**- Cross-species gene ID conversion tool with automated database updates and deprecated gene handling. Designed for reproducible genomics workflows. 3,000+ downloads.  
<https://pypi.org/project/gene-id-resolver/>
- **EvoMotif (python package)** - Automated discovery of evolutionarily conserved protein motifs using information theory, substitution matrices, and statistical validation frameworks. 2,000+ downloads.  
<https://pypi.org/project/evomotif/>
- **Phredator (python package)** – Rule-based NGS quality control toolkit providing context-aware interpretation of FastQC and MultiQC reports with actionable recommendations. 2,000+ downloads.  
<https://pypi.org/project/phredator/>

## AWARDS & HONORS

- Metuleague winner - METU (2025)
- PFL Bilkent winner - Bilkent (2022)

## ADDITIONAL INFORMATION

*Core Skills:* Python, R, SQL, NGS/WGS, RNA isolation, FastAPI, Flask, PostgreSQL, Docker, CI/CD, Linux, AWS, MATLAB, Java, Git, Machine Learning