



# ALPER BÜLBÜL

PHD STUDENT 📍 İSTANBUL, TURKEY 📞 +90 561 516 95 95

## ◦ DETAILS ◦

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## ◦ LINKS ◦

[My Blog](#)  
[Instagram](#)  
[Linkedin](#)  
[Twitter](#)  
[Github](#)

## ◦ SKILLS ◦

Germline Short Variant  
Calling (DeepVariant, etc.)

PLINK

Bcftools, Samtools,  
HTSlib, BWA

Genome Analysis Tool Kit  
(GATK)

Linkage Analysis (MERLIN,  
Allegro, GeneHunter,  
pVAAST)

Knowledge Graph  
Analysis (Exomiser,  
HGPEC)

MD Simulations (AMBER,  
GROMACS, NAMD)

Protein Protein/Ligand  
Docking (Autodock Vina,  
ZDOCK, HADDOCK)

Python (Pandas, Numpy,  
Scipy, etc.)

R (ggplot, DESeq2, EdgeR,  
etc.)

Linux, Bash Scripting

Project Management Tool  
(Git)

## 👤 PROFILE

I am a highly motivated and dedicated individual with a strong passion for advancing the understanding of complex diseases, primary Multiple Sclerosis, through the application of family-based and population-based genetic studies such as Genome-Wide Association Studies (GWAS). Possesses extensive knowledge of genomic data analysis techniques and a keen interest in leveraging this information to predict gene expression, identify patient symptoms, and assess overall disease prognosis and causality. Committed to contributing to the development of innovative solutions for personalized medicine and improving patient outcomes by harnessing the power of genomics and bioinformatics.

## 📁 EMPLOYMENT HISTORY

### Co-founder at Stardust Biotech Inc., İstanbul

February 2020 — November 2022

Biosensor project, which will measure low-concentration breast cancer biomarkers with high accuracy. These biomarkers are measured by aptamers, which are immobilized in gold electrodes, and potentiostats are used for cyclic voltammetry analysis.

TUBITAK, 1512 - Entrepreneurship Support Program

## 🎓 EDUCATION

### B.Sc, Istanbul Technical University, İstanbul

September 2014 — June 2018

Faculty of Science and Letters, Molecular Biology and Genetics Department

### M.Sc, Istanbul Technical University, İstanbul

September 2018 — June 2021

Molecular Biology and Genetics Department Molecular Biology & Genetics and Biotechnology Program

### PhD Student, Acibadem University, İstanbul

January 2022

Graduate School of Health Sciences, Department of Biostatistics and Bioinformatics

## ★ PROJECTS

### Uncovering Genetic Factors in Multiple Sclerosis: Integrating Whole Exome Sequencing, Network Analysis, and Gene Set Enrichment Analysis in a Family-Based Study, Graduate School Of Natural And Applied Sciences, Molecular And Translational Biomedicine Program, Acibadem University, Prof. Dr. Eda TAHIR TURANLI, İstanbul

October 2021

Conducted a research project focused on identifying genetic variants associated with Multiple Sclerosis (MS) in 45 families with affected individuals, using whole exome sequencing data, pVAAST, and Exomiser tools. Performed network analysis to assess gene centrality in families based on the associations identified by Exomiser and pVAAST. Conducted Gene Set Enrichment Analysis (GSEA) with highly central genes in families using the g:Profiler tool, providing further insight into the biological pathways and processes underlying MS.

Machine Learning

Database Management  
(SQLite, MySQL)

Cloud Computing (AWS)

HTML, CSS, JS, Django,  
Flask

Gene Set Enrichment  
Analysis (GSEA)

Network  
Analysis (Cytoscape,  
Networkx, etc.)

**Development of a High-Accuracy Variant Pathogenicity Prediction Tool for Systemic Autoinflammatory Diseases: Integrating 3D Structural Analysis, Protein-Protein Interactions, and Machine Learning, Molecular Biology and Genetics Department, Istanbul Technical University, Prof. Dr. Eda TAHIR TURANLI, Istanbul**

March 2021 — September 2021

Integrated 3D structural analysis of proteins of interest, accounting for the impact of variants on protein stability ( $\Delta\Delta G$ ) and protein-protein interactions using ZDOCK. Prioritized proteins based on their occurrence in disease and their position in the protein-protein interaction network, enhancing the tool's predictive capabilities. Utilized a Random Forest model to predict variant pathogenicity, incorporating features such as protein stability, protein-protein interactions, and disease association. Achieved an Area Under the Curve (AUC) of 95% for the model's performance on a test dataset, demonstrating its high accuracy and potential for advancing SAID research and diagnostics.

**Unraveling the Genetic Basis of Wahap Disease in a Consanguineous Pakistani Family: Parametric Linkage Analysis and Whole Exome Sequencing Approach, Graduate School Of Natural And Applied Sciences, Molecular And Translational Biomedicine Program, Acibadem University, Prof. Dr. Eda TAHIR TURANLI, Istanbul**

April 2022

Conducted parametric linkage analysis on SNP array genotype data from 17 family members to identify regions of the genome potentially harboring disease-causing variants. Analyzed whole exome sequencing data from 3 affected individuals, identifying rare variants potentially associated with the disease.

**Cross-Species Investigation of Replicative Senescence: Reanalysis of RNA Sequencing and Proteomics Datasets from BMRs and Mice, Faculty Of Engineering And Natural Sciences, Molecular Biology And Genetics, Acibadem University, Assoc. Prof. Perinur BOZAYKUT EKER, Istanbul**

March 2022 — August 2022

Conducted a reanalysis of publicly available RNA sequencing and proteomics datasets from Gene Expression Omnibus (GEO) to investigate the effects of replicative senescence across species, including blind mole rats and mice. Utilized a variety of bioinformatics tools and packages, such as Salmon, edgeR, clusterProfiler, GSEA, ggplot2, ComplexHeatmaps, and Cytoscape, for data processing, normalization, annotation, gene set enrichment analysis, and visualization.

**Differential Biomarker Analysis in Multiple Sclerosis Patients with Varying EDSS Scores: A Comparative Study using 2D-DIGE, MS/MS Proteome, Molecular Biology and Genetics Department, Istanbul Technical University, Prof. Dr. Eda TAHIR TURANLI, Istanbul**

June 2020 — September 2021

Utilized proteomics data from (Timucin et al. 2015), which included 2D-DIGE and MS/MS results, as the basis for identifying potential biomarkers associated with disease progression and severity. Applied the Firefly Algorithm, an optimization algorithm with the Support Vector Machine model's accuracy with a group of patients with EDSS scores above or below 5, and significant proteins between the two groups are identified.

**Identification of Small Molecule Ligands Targeting the N-Myc/MAX DNA Binding Complex through Molecular Dynamics Simulations and Virtual Screening, School Of Medicine, Department Of Basic Sciences, Biostatistics And Medical Informatics, Acibadem University, Prof. Dr. EMEL TİMUÇİN, Istanbul**

December 2022 — June 2023

The N-Myc/MAX heterodimer complex, a transcription factor involved in regulating cell growth, differentiation, and apoptosis, has been associated with various cancers. Targeting the DNA binding domain of the N-Myc/MAX complex represents a promising therapeutic approach for the treatment of N-Myc-driven malignancies. In this study, we employed molecular dynamics simulations and virtual screening to identify potential small molecule ligands that target the N-Myc/MAX DNA binding complex.

**Comparative Genomic Analysis and Functional Gene Annotation of Space-Adapted Bacterial Species, School Of Medicine, Department Of Basic Sciences, Biostatistics And Medical Informatics, Acibadem University, Prof. Dr. Uğur SEZERMAN, Istanbul**

December 2022 — Aug 2023

Comparative genomic analysis and functional gene annotation of novel bacterial species isolated from the International Space Station (ISS), I focused on understanding the adaptation of bacteria to space conditions. This involved a detailed comparison of the amino acid compositions of extraterrestrial and terrestrial proteins, particularly noting shifts in proline and glycine. I calculated mutation rates by analyzing amino acid substitutions and utilized tools like g:Profiler and ete3 for functional annotation and phylogenetic analysis.

**Elucidating the Genetic Basis of Ichthyosis in a Family with Multiple Affected Siblings through Homozygosity Mapping, Molecular Biology and Genetics Department, Istanbul Technical University, Prof. Dr. Eda TAHIR TURANLI, İstanbul**

March 2018 — June 2018

Participated in a homozygosity mapping study under the supervision of Prof. Dr. Eda TAHIR TURANLI, investigating the genetic basis of ichthyosis in a family with three affected siblings.

**Identification and Characterization of Novel Biomarkers for Neuro-Behçet's Disease using 2D DIGE and Mass Spectrometry, Molecular Biology and Genetics Department, Istanbul Technical University, Prof. Dr. Eda TAHIR TURANLI, İstanbul**

October 2019 — July 2020

Employed 2D-DIGE (Two-Dimensional Difference Gel Electrophoresis) to separate and compare protein samples from patients with NeuroBehçet's disease and healthy controls and Behçet patients who have no neurological symptoms, enabling the detection of potential biomarker candidates.

**Identification of Potentially Antigenic Peptides of Trypanosoma brucei: Investigating MHC-I and MHC-II Specificity Using Molecular Docking and Multiple Sequence Alignment Profiling, School Of Medicine, Department Of Basic Sciences, Biostatistics And Medical Informatics, Acibadem University, Prof. Dr. Uğur SEZERMAN, İstanbul**

April 2022 — June 2022

Investigated the specificity of MHC class I and class II cell surface receptor proteins for Trypanosoma brucei membrane proteins using a combination of molecular docking with AutoDock and multiple sequence alignment profiling through the Biopython package. Utilized the AutoDock tool to predict antigenic peptide-MHC binding, providing insights into potential immunogenic targets for vaccine development or immunotherapy. Employed the Biopython package to perform multiple sequence alignment profiling, further refining the identification of antigenic peptides.

**Systemic Simulation of Metabolic Pathways in Cancer: Integrating Gene Expression, Metabolite Concentrations, and Enzyme Dynamics to Understand Cancer Complexity and Predict Outcomes, School Of Medicine, Department Of Basic Sciences, Biostatistics And Medical Informatics, Acibadem University, Prof. Dr. Uğur SEZERMAN, İstanbul**

May 2022 — September 2022

Conducted a research project aimed at understanding cancer's complexity and predicting its outcomes by studying the accumulation and significant changes in metabolite concentrations in cancerous cells compared to healthy cells. Utilized gene expression data from breast cancer and healthy tissues to estimate enzyme amounts while retrieving human metabolic pathways and normal protein abundance from KEGG and Pax-Db, respectively. I conducted simulations with the Tellurium package to model cellular responses to changes in enzyme and metabolite levels and performed statistical analysis using the SciPy library.

★ **PUBLICATIONS**

**Investigating the role of common and rare variants in multiplex multiple sclerosis families reveals an increased burden of common risk variation**

October 2022

Elif Everest, Mohammad Ahangari, Ugur Uygunoglu, Melih Tutuncu, Alper Bulbul, Sabahattin Saip, Taskin Duman, Ugur Sezerman, Daniel S. Reich, Brien P. Riley, Aksel Siva & Eda Tahir Turanli

<https://doi.org/10.1038/s41598-022-21484-x>

**Transcriptomics and Proteomics Analyses Reveal JAK Signaling and Inflammatory Phenotypes during Cellular Senescence in Blind Mole Rats: The Reflections of Superior Biology**

August 2022

Nurcan Inci, Erdogan Oguzhan Akyildiz, Abdullah Alper Bulbul, Eda Tahir Turanli, Emel Akgun, Ahmet Tarik Baykal, Faruk Colak and Perinur Bozaykut

<https://doi.org/10.3390/biology11091253>

**Prospective outcome analysis of multiple sclerosis cases reveals candidate prognostic cerebrospinal fluid markers**

Jun 2023

Elif Everest, Ugur Uygunoglu, Melih Tutuncu, Alper Bulbul, Umut Inci Onat, Mehmetcan Unal, Timucin Avsar, Sabahattin Saip, Ugur Bilge, Eda Tahir Turanli, Aksel Siva

<https://doi.org/10.1371/journal.pone.0287463>

**(Congeress Poster), Comprehensive Analysis of Low-Frequency Genetic Variants through Exome Sequencing in Familial Multiple Sclerosis**

Nov 2023

E. Turanli, A. Bulbul, E. Everest, U. Voyvoda, U. Sezerman, K. Bilguvar, C. Boz, C. F. Demir, F. Yetkin, H. Efendi, S. D. Bunul, T. Duman, M. Tecellioglu, M. Terzi, S. Sen, R. Karabudak, M. A. Tuncer, C. Uzunkopru, O. F. Turan, S. Demir, U. Aluclu, H. Gumus, M. Tutuncu, U. Uygunoglu, S. Saip, A. Siva

American Society of Human Genetics Annual Meeting, Washington, DC

**(Oral Presentation), Comparative Analysis of Familial Exome Analysis Tools: Finding Low Frequency Rare Variants in Familial Multiple Sclerosis Cohort**

Oct 2023

E. Tahir Turanlı, A. Bülbül, Berk Gürdamar, Furkan Büyükgöl, U. Voyvoda, U. Sezerman, C. F. Demir, C. Boz, F. Yetkin, H. Efendi, S. D. Bunul, T. Duman, M. Tecelliöğlü, M. Terzi, S. Sen, R. Karabudak, M. A. Tuncer, C. Uzunköprü, O. F. Turan, S. Demir, T. Gündüz, U. Aluclu, H. Gümüs, M. Tütüncü, U. Uygunoğlu, S. Saip and A. Siva

MS Days VIII, Cesme, Izmir

**(Congeress Poster), Identification of a splice variant in PSMB10 gene in a family with undiagnosed autoinflammatory disease**

June 2023

A. Bulbul, D. Sigli, M. Gecgel, U.I. Onat, S. Ugurlu, E. Tahir Turanli

European Human Genetics Conference, Glasgow, Scotland, UK

**(Congeress Poster), Var3DMPred: variant predictor with 3-D and sequence analyses of protein-protein interactions**

July 2022

Abdullah Alper BÜLBÜL, O. Uğur SEZERMAN, Eda TAHİR TURANLI,

8th International Congress of the Molecular Biology Association of Turkey, Acıbadem University Congress Center, Istanbul

**(Congress Poster), Detection of Possible Significant Metabolites by Comparison of Metabolic Simulation Profiles of Healthy and Breast Cancer Tissues**

October 2022

Selin Akkuzu ÖZYEŞER, Abdullah Alper BÜLBÜL, Gül BAŞARAN, O. Uğur SEZERMAN

15th International Symposium on Health Informatics and Bioinformatics METU, Erdemli, Mersin, Turkey

**(Seminer Poster) Identification Of Potentially Antigenic Peptides Of Trypanosoma Brucei, İstanbul**

June 2022

Özdeyiş Hülya İŞGÖRDÜ, Abdullah Alper BÜLBÜL O. Uğur SEZERMAN, Eda TAHİR TURANLI

Graduation Projects Fair, Acibadem University, 25 June 2022

**👤 INTERNSHIPS**

**Research Intern at İstanbul University, Aziz Sancar Institute of Experimental Medicine, Assoc. Prof. Dr. SELÇUK SÖZER TOKDEMİR , İstanbul**

June 2017 — August 2017

Utilized RT-PCR (Reverse Transcription Polymerase Chain Reaction) as the primary molecular technique to investigate the presence and frequency of JAK2 V617F mutation in Polycythemia vera patient samples.

**🌱 EXTRA-CURRICULAR ACTIVITIES**

**Volunteer Tutor at ITU Volunteering Club, İstanbul**

June 2014 — June 2018

In 'Bir Başka Yol' project, volunteered to help high school students from low socioeconomic backgrounds by providing supplementary educational support and tutoring. Offered guidance on study skills, test-taking strategies, and time management techniques to help students excel academically. Provided a positive and supportive learning environment, fostering students' self-confidence and promoting academic success.