Asal Rabiee

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RESEARCH INTERESTS

Drug Discovery, Genomics, Machine Learning, Systems Biology

EDUCATION

B.Sc. in Animal Biology (Concentration: Bioinformatics)　　　　　　　　2021–2026

University of Tehran - GPA: 3.84/4.00 (18.46/20)

- Coursework: Molecular Genetics, Cell and Molecular Biology, Epigenetics and Gene Regulation, Genetic Engineering and Biotechnology, Structural Biochemistry, Metabolic Biochemistry
- Thesis: Benchmarking Protein–Ligand Binding Site Prediction with Pseq2Sites, [GitHub](#)

Minor in Computer Science　　　　　　　　2022–2026

University of Tehran - GPA: 16.39/20 (3.33/4.00)

- Coursework: Introduction to Programming, Database Systems, Bioinformatics

EXPERIENCE

Research Assistant　　　　　　　　2025–2026

School of Biology, College of Science, University of Tehran

- Conducted a feasibility study of **Pseq2Sites**, assessing its applicability for protein–ligand binding site prediction, involving large-scale dataset preprocessing and CNN + attention model training, while identifying key limitations and methodological improvements.
- Performed an independent bioinformatics study on **co-expression networks between ion channels and lncRNAs in gastric cancer**, utilizing RNA-seq (TCGA-STAD), differential expression analysis, WGCNA, and survival modeling, to uncover novel biomarkers and therapeutic targets. (Manuscript in preparation.)

Research Assistant　　　　　　　　2023–2024

University of Tehran (with collaboration of IAU, Uskudar Univ., Semnan Univ., SUT, KMU, TMU)

- Collaborated on a bioinformatics investigation of **Leishmaniasis**, contributing literature review and biomarker-driven drug discovery analyses. Supported integration of QSAR modeling, molecular docking, and molecular dynamics simulations. (Published as preprint)

Research Assistant　　　　　　　　2022–2023

Protein Biotechnology Research Laboratory (PBRL), University of Tehran

- Explored the **therapeutic potential of Cannabidiol (CBD)** via modulation of the Endocannabinoid System (ECS) in Alzheimer's disease, focusing on neuroprotection and synaptic regulation.
- Authored a scholarly review on the **historical and mechanistic exploration of blood sugar homeostasis** through the pioneering work of Nobel laureates Gerty and Carl Cori. (Published in internal scientific journal)

Teaching Assistant　　　　　　　　2023–2025

University of Tehran

- Bioinformatics (Fall 2025, Prof. Kavousi), Neurophysiology and Endocrinology (Winter 2025, Prof. Rezayof), Molecular Genetics (Fall 2024, Prof. Inanloo Rahatloo), Invertebrate Biology (Fall 2024, Prof. Rahimian), Metabolic Biochemistry (Winter 2024, Prof. Habibi Rezaei), Structural Biochemistry (Fall 2023, Prof. Habibi Rezaei), Biostatistics (Fall 2023, Prof. Malek), Calculus II (Winter 2023, Prof. Hosseini)

Laboratory Assistant　　　　　　　　2024–2025

University of Tehran

- Genetics Laboratory (Winter 2025, Prof. Minaei)
- Molecular Genetics Laboratory (Fall 2024, Prof. Minaei)

PUBLICATIONS

- Golnoush Farahzadeh, Arash Rezaeirad, Sorour Hassani, Morva Farajzadeh Tarani, Ayda Peymankar, **Asal Rabiee**, Esmaeil Roohparvar Basmenj. QSAR, Docking and Molecular Dynamic Simulation studies of Leishmanial Inhibitors using bioinformatics approach, *AUTHOREA*, 2024 Aug. DOI: [10.22541/au.172464590.09500449/v1](#)

- **Asal Rabiee**, Mehran Habibi-Rezaei. Deciphering The Mechanisms of Blood Sugar Homeostasis: The Story of Gerty and Carl Cori, *Science Cultivation*, 2023 Jun. URL: https://www.sciencecultivation.ir

SKILLS

Programming:	Python, R, Bash, PostgreSQL, C++, LaTeX
Software Tools:	Open Babel, UCSF Chimera, Oligo7, GenoPro, SnapGene, Cytoscape, IGV, Endnote, Storyline, SPSS
Bioinformatics:	RNA-Seq, Genome Assembly, Multiple Sequence Alignment (MSA), Pairwise/Local Alignments, Reference Mapping, Systems Biology (WGCNA), QSAR, Docking (AutoDock), MD Simulation (GROMACS)
ML and AI:	PyTorch, Scikit-Learn, Transformers
Version Control:	Git, GitHub
Laboratory:	Standard PCR, PCR Primer Design, DNA Electrophoresis, Genomic DNA Extraction (Salting-out), Spectrophotometry, Nanodrop, Centrifugation, ELISA, Blood Smear Preparation, Aseptic Technique, Gram Staining, Streak Plate Method
Personal Skills:	Communication, Team Leadership, Teamwork, Problem-Solving, Critical Thinking, Creativity

PROJECTS

- **Benchmarking Protein–Ligand Binding Site Prediction with Pseq2Sites:** Bachelor thesis project benchmarking deep learning approaches (CNN with attention mechanisms) for sequence-based prediction of protein–ligand binding sites. Focused on large-scale preprocessing of scPDB and PDBbind datasets, implementation of ProtTrans embeddings, and comparative evaluation to highlight strengths, challenges, and opportunities for improving drug discovery pipelines. **GitHub**

- **Exploring Relationships Between Ion Channels and lncRNAs in Gastric Cancer:** Ongoing research project using TCGA-STAD RNA-seq data to investigate gene co-expression networks. Applied differential expression analysis (DESeq2), WGCNA, and survival modeling to identify lncRNA–ion channel modules correlated with clinical traits, aiming to uncover novel biomarkers and therapeutic targets. **GitHub**

- **Genetic Database:** Designed and implemented a normalized relational database (up to BCNF) for efficient genetic data management. Built a complete pipeline including entity–relationship modeling, schema design, and SQL implementation in PostgreSQL. The system supports storing and querying of genes, RNAs, proteins, organisms, and users, with role-based access control and example datasets. **GitHub**

- **Read Mapping and Genome Assembly:** Implemented a full NGS workflow on *E. coli* short-read data, including quality control (FastQC), de novo assembly (SPAdes, Quast), and read mapping (BWA, SAMtools). Validated results by visualizing alignments in IGV and assessing concordance, mapping rates, and read depth, providing hands-on experience with genome assembly and evaluation. **GitHub**

- **Identification of Xylanase Genes:** Designed and implemented a bioinformatics pipeline to identify thermostable xylanase genes from rumen metagenomic datasets. The analysis involved sequence similarity searches (BLAST+), clustering at 97% identity with CD-HIT to generate non-redundant representatives, and conserved region modeling (HMM-based filtering) to refine candidates. Produced a curated set of high-confidence xylanase gene sequences. **GitHub**

- **Hierarchical Data Structure for Genetic Diseases:** Developed a Python-based tree system to organize genetic diseases and associated genes. Implemented search and insertion functions with hash tables for gene attributes (location, exons, type, name) and a menu-driven interface, enabling efficient hierarchical representation of biomedical data. **GitHub**

HONORS

- Ranked 1st in Cumulative GPA among undergraduate students, University of Tehran, 2025.

- Awarded a full scholarship for the Computer Science minor, University of Tehran, 2022.

- Awarded a full scholarship for undergraduate studies, University of Tehran, 2021.

- Top 8.5% in National University Entrance Exam (500,000+ participants), Tehran (2021).