GIDEON SHAKED

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EDUCATION

University of Michigan — Ann Arbor, MI
M.S. in Bioinformatics — August 2025 – Present (expected December 2026)

- Relevant courses: Machine Learning for Drug Discovery, Developmental Genetics, Computational Systems Biology, Probability & Statistics for Bioinformatics

University of Michigan — Ann Arbor, MI
B.S. in Computer Science — August 2022 – April 2026

- Relevant courses: Foundations of Large Language Models, Introduction to Machine Learning, Data Mining, Practical Data Science, Organic Chemistry

INDUSTRY EXPERIENCE

Octant Bio — San Francisco Bay Area, CA
AI Drug Discovery Consultant — September 2026 – Present
Computational Drug Discovery Intern — June 2026 – August 2026

- Created Octomind (blog post), an agentic lab-in-the-loop drug discovery system on Databricks and AWS where AI agents design, make, test, and analyze compounds (the full DMTA cycle) computationally and in the lab
- Built Octomind's memory as an LLM-maintained knowledge base, distilling drug program meetings, documents, and results into cited records, and designed agentic search and retrieval evals on top of it
- Cloned lentiviral constructs with Kozak sequences that modulate p53 and luciferase reporter translation, then transduced them into HPV-positive cervical cancer cells to optimize an HPV assay

AfterQuery — Remote
AI Evaluation and Post-Training Researcher, Life Sciences — December 2025 – Present

- Built OmicsBench (paper), a benchmark for evaluating AI agents on long-horizon, multi-turn bioinformatics tasks on the scale of entire research studies, with task data acquired by multiple frontier AI labs for post-training
- Post-trained LLMs with reinforcement learning and distillation on agentic life sciences workflows in RL environments of my own design, with rewards from deterministic verifiers and rubric-guided LLM judges

RESEARCH EXPERIENCE

University of Michigan — Ann Arbor, MI
Research Assistant I — September 2023 – Present
Undergraduate Research Assistant (UROP) — September 2022 – September 2023
Advisors: Alex (Lam) Tsoi and Matthew Patrick

- Developed a cell-type-aware model for imputing unmeasured genes in spatial transcriptomics (10x Xenium) from a single-cell RNA-seq reference, and an accompanying ML model to predict gene-level imputation accuracy
- Created Loopsim (paper), an open-source tool that tests Hi-C chromatin loops for enrichment at disease-associated loci, and used it to link psoriasis risk variants to chromatin loops in dendritic cells

Broad Institute of MIT and Harvard — Cambridge, MA
Visiting Researcher — June 2025 – August 2025
Advisor: Evan Macosko

- Designed network propagation algorithms to predict how missense mutations alter downstream gene expression, seeding AlphaMissense scores into gene regulatory networks built from single-cell RNA-seq
- Measured how predicted mutation effects decayed with distance in gene regulatory networks to characterize the limits of network propagation for perturbation prediction

University of California, Los Angeles — Los Angeles, CA
Research Intern — June 2024 – July 2024
Advisor: Jason Ernst

- Built a hidden Markov model of chromatin states from 10x Multiome single-cell ATAC-seq data to track how enhancers and promoters gain and lose chromatin accessibility as fibroblasts are reprogrammed into iPSCs
- Integrated reference epigenome maps and transcription factor binding datasets to identify the regulatory programs that switch on pluripotency and shut down fibroblast identity (paper)

Tel Aviv University Tel Aviv, Israel
Research Intern June 2023 – July 2023
Advisors: Ron Shamir and Ran Elkon

- Used protein-protein interaction networks and active module identification algorithms to find disease-associated gene modules, then evaluated existing drugs that target those modules as repurposing candidates (paper)
- Rebuilt legacy gene expression analysis suite as a web app (Expander) and added new bioinformatics algorithms

SKILLS

ML & AI	PyTorch, scikit-learn, Unsloth, Harbor, Daytona, Weights & Biases
Comp. Bio & Comp. Chem	Scanpy, AnnData, Seurat, Biopython, RDKit, PyMOL, Rosetta
Languages & Compute Platforms	Python, R, C++, Bash, AWS, GCP, Databricks, Slurm

AWARDS AND HONORS

Nucleate DojoHouse Biotech Co-Living Program 2025
Selected for biotech co-living program funded by 1517 Fund, Emergent Ventures, and Amaranth Foundation

Bruins In Genomics Research Excellence Award, UCLA 2024
Awarded for outstanding research in functional genomics

NSF Research Experience for Undergraduates (REU), UCLA Bruins in Genomics 2024
Selected for competitive NSF-funded summer research program in genomics and computational biology

Undergraduate Research Opportunity Program (UROP), University of Michigan 2022
Selected for program pairing first and second-year students with faculty research mentors

SELECTED PROJECTS

Predicting Loss-of-Function Mechanisms in Melanocortin-4 Receptor Variants

- Trained a random forest on a compact set of structure- and sequence-derived features to predict experimental activity from Octant Bio's deep mutational scanning data across ∼4,600 MC4R variants
- Identified each mutation's dominant loss-of-function mechanism (misfolding, disrupted drug binding, or impaired downstream signaling) with SHAP feature attribution

Agentic Peer Review | GitHub

- Built a multi-agent workflow in which AI coding agents iteratively review codebases and fix the issues they find, with configurable issue categories such as security and performance