

Ramin Sakhtemani, Ph.D.

Computational Biologist / Bioinformatician

ramin@sakhtemani.com

linkedin.com/in/ramin-sakhtemani

—

github.com/rayanramin



Work Experience

- **Postdoctoral Research Fellow** **10/2020 – Present**
Massachusetts General Hospital, Boston, MA **Advisor: Michael S. Lawrence, Ph.D.**
 - Comprehensive analysis of NextGen sequencing (WGS, WES, WGBS, ChIP-Seq, Hi-C; bulk and single-cell RNA-seq) from cancer patients and experimental models; Integrating multi-omics data to derive biological insights, including mutational signatures (NMF), differential expression, GSEA, dimensionality reduction (PCA/UMAP/NMF), and biomarker discovery.
 - Collaborated with wet lab scientists and oncologists on interdisciplinary projects.
 - Mined existing datasets and literature to draw scientific conclusions and help wet lab scientists design their next experiment.
 - Translated complex findings into compelling visualizations using tools like ggplot2 and RShiny.
 - Documented the results in scientific reports and manuscripts and presented the results at meetings and conferences.
- **Postdoctoral Scholar** **8/2021 – Present**
Broad Institute of MIT and Harvard
 - Non-paid appointment; collaborated with other computational biologists on studying the clonal evolution of cancer cells in a WES lung cancer cohort.
- **Graduate Research Assistant** **5/2017 – 5/2020**
Wayne State University, Detroit, MI, USA
 - Carried out molecular biology research, DNA extraction, and Illumina DNA library preparation for NextGen sequencing. Genomic Uracil quantification, pull-down and sequencing.
 - Built a pipeline to process, analyze, and map the genomic uracils created by human cytosine deaminase enzymes.
 - Validated the results and contributed to writing scientific manuscripts. Assisted with drafting grant proposals and their submission.

Computational Biology & Biochemistry Skills

- Programming languages (R, MATLAB, Linux shell, Bash, and some Python)
- Bioinformatics tools (BWA, STAR, Samtools, bedtools, Seurat, DESeq2, GSEA, NAMD, etc.)
- Statistics, Analysis, and Visualization (R, RStudio, MATLAB, ggplot2, RShiny, IGV, VMD)
- Machine Learning (familiar with the caret package, KNN, random forest, etc.)
- HPC and Cloud Computing (AWS, Google Cloud); Version Control (Git/GitHub); Nextflow
- PyMOL, SnapGene, VS Code; FlowJo, ChemDraw, Fusion360, EndNote, Art & Graphics, etc.
- Next-Generation Sequencing: Experienced in Illumina DNA library Prep and Sequencing
- UPD-Seq: co-developed and optimized a novel DNA sequencing method to map genomic uracils
- CRISPR-Cas9: gRNA design and base editing; detection of off-target sites using UPD-Seq
- Gene cloning: Gibson Assembly or Restriction Enzymes cloning of genes in inducible plasmids
- Molecular Biology: routine wet lab skills, including PCR, DNA/RNA extraction, qRT-PCR, FACS analysis, gel electrophoresis, western blots, and uracil quantification assay.

Education

- **Ph.D. in Biochemistry** **08/2014 – 08/2020**
Wayne State University, Detroit, MI, USA **Advisor: Ashok S. Bhagwat, Ph.D.**
Studied the biochemistry of human AID/APOBEC cytosine deaminases. Co-developed a novel sequencing method (UPD-Seq) and created the bioinformatics pipeline to map the genomic uracils created by cytosine deaminases.
 - **B.Sc. in Applied Chemistry** **09/2010 – 07/2014**
University of Tehran, Tehran, Iran
-

Notable Publications

- Isozaki, H., Sakhtemani, R., et al. (2023). Therapy-induced APOBEC3A drives evolution of persistent cancer cells. *Nature*, 620, 393–401
 - Sakhtemani, R., Butt, Y., et al. (2024). Distinguishing preferences of human APOBEC3A and APOBEC3B for cytosines in hairpin loops, and reflection of these preferences in APOBEC-signature cancer genome mutations. *Nature Communications*, 15(1), 2369.
 - Sakhtemani, R., Langenbucher, A., Bowen, D., et al. (2021). An extended APOBEC3A mutation signature in cancer. *Nature Communications*, 12(1), 1602.
 - Sakhtemani, R., Senevirathne, Stewart, J., et al. (2019). Genome-wide mapping of regions preferentially targeted by the human DNA-cytosine deaminase APOBEC3A using uracil-DNA pulldown and sequencing. *Journal of Biological Chemistry* 294, 15037-15051.
-

Notable Talks, Seminars and Poster Presentations

- Tufts University **2022 & 2023**
Guest lecturer for BioInquiry through Sequencing; Pre-College course
 - Deaminet 2022, 3rd International Conference on Base Editing Enzymes and Applications **1/2022**
 - Deaminet 2020 (1st International Conference on Base Editing Enzymes and Applications) **1/2020**
Talk Title: “Using UPD-Seq to map targets and off-targets of CRISPR-Cas9”
 - 21st Annual Chemistry Graduate Research Symposium **10/2019**
 - American Society for Virology Conference **7/2019**
 - Mutagenesis Gordon Research Seminar **6/2018**
 - 20th Annual Midwest DNA Repair Symposium **5/2018**
-

Honors and Awards

- Best Biological Chemistry Graduate Student Award, WSU **6/2019**
 - Thomas C. Rumble Graduate Fellowship **9/2018–5/2019**
 - Joseph Jasper Scholarship **5/2018–9/2018**
 - Thomas C. Rumble Graduate Fellowship **9/2017–5/2018**
-

Additional skills

- Electronics, CAD modeling & 3D-Printing
- Persian as a native language