Shruthi Subramanian

Postdoctoral Scholar Molecular Biology & Hematology

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Research Summary

Postdoctoral scholar in the Maxson Lab at OHSU, studying how somatic mutations alter transcription factor networks and 3D genome organization in myeloid malignancies (CNL, aCML). Expert in combining wet-lab genomics (ChIPmentation, CUT&Tag, Hi-C) with computational pipelines to map enhancerpromoter interactions and gene regulation. Broad interest in chromatin architecture, transcriptomics, and the gene regulatory logic underlying blood disorders.

Research Interests

Epigenetic regulation of hematopoiesis; enhancerpromoter communication; 3D genome organization; transcriptional plasticity in leukemia; integrating multi-omics data to identify novel regulatory drivers and therapeutic vulnerabilities.

Education

2018–2022 **Ph.D. (Medicine)**, *University of New South Wales (UNSW)*, Sydney, Australia
Thesis: *Identifying genome-wide gene regulatory networks in human hematopoietic stem and progenitor cells.*
Supervisors: Prof. John Pimanda, and Dr. Jason Thoms.
Prince of Wales Clinical School and UNSW Tuition Fee Scholarship.

2010–2014 **B.Tech, Bioengineering (First Class with Distinction)**, *SASTRA University*, Thanjavur, India
Semester abroad: Brigham & Women's Hospital, Harvard Medical School (Krichevsky Lab).
DeshVidesh International Research Scholarship.

Research Appointments

2023–Present **Postdoctoral Scholar**, *Maxson Lab, Oregon Health & Science University*, Portland, OR
- Characterizing transcriptional and mutational drivers of CNL/aCML.
- Integrating bulk and single-cell RNA-seq, ATAC-seq, and Hi-C to define 3D gene regulation.
- Collaborating with clinical genomics teams for translational applications.

2018–2022 **Ph.D. Candidate**, *Pimanda Lab, University of New South Wales*, Sydney, Australia
- Generated genome-wide transcription factor binding maps in human HSPCs using ChIPmentation and HiChIP.
- Built enhancerpromoter interaction atlases to link transcription factor occupancy with hematopoietic lineage specification.
- Developed data-processing pipelines integrating RNA-seq, ATAC-seq, and ChIP-seq datasets.

2014–2015 **Research Assistant**, *Krichevsky Lab, Brigham & Womens Hospital, Harvard Medical School*, Boston, MA
- Explored microRNA regulatory pathways in glioblastoma.
- Applied CRISPR-Cas9 editing to interrogate miRNA-10b dependency.
- Contributed to *Molecular Therapy* (2017) publication.

Honors and Awards

2024 Collins Medical Trust Award, project support for CEBPA/3D genome work.

2022 ASH Abstract Achievement Award, American Society of Hematology.

20182022 Prince of Wales Clinical School Scholarship and UNSW Tuition Fee Scholarship.

2014 DeshVidesh International Research Scholarship, SASTRA University.

Selected Publications

[1] El Fatimy R et al. "Genome Editing Reveals Glioblastoma Addiction to MicroRNA-10b". In: *Molecular Therapy* (2017). DOI: 10.1016/j.ymthe.2016.11.004. URL: https://pubmed.ncbi.nlm.nih.gov/28153089/.

[2] Khanna A et al. "Constitutive CHK1 Expression Drives a pSTAT3-CIP2A Circuit that Promotes Glioblastoma Cell Survival and Growth". In: *Molecular Cancer Research* (2020). DOI: 10.1158/1541-7786.MCR-19-0934. URL: https://pubmed.ncbi.nlm.nih.gov/32079743/.

[3] Yeola A et al. "Induction of muscle-regenerative multipotent stem cells from human adipocytes by PDGF-AB and 5-azacytidine". In: *Science Advances* (2021). DOI: 10.1126/sciadv.abd1929. URL: https://pubmed.ncbi.nlm.nih.gov/33523875/.

[4] Thoms JAI et al. "Disruption of a GATA2-TAL1-ERG regulatory circuit promotes erythroid transition in healthy and leukemic stem cells". In: *Blood* (2021). DOI: 10.1182/blood.2020009707. URL: https://pubmed.ncbi.nlm.nih.gov/34075404/.

[5] Subramanian S et al. "Genome-wide transcription factor-binding maps reveal cell-specific changes in the regulatory architecture of human HSPCs". In: *Blood* (2023). DOI: 10.1182/blood.2023021120. URL: https://pubmed.ncbi.nlm.nih.gov/37595278/.

[6] Thoms JAI et al. "BloodChIP Xtra: an expanded database of comparative genome-wide transcription factor binding and gene-expression profiles in healthy human stem/progenitor subsets and leukemic cells". In: *Nucleic Acids Research* (2024). DOI: 10.1093/nar/gkad918. URL: https://pubmed.ncbi.nlm.nih.gov/37870453/.

[7] Pastoors D et al. "MECOM is a master repressor of myeloid differentiation through dose control of CEBPA in acute myeloid leukemia". In: *Blood* (2025). DOI: 10.1182/blood.2025028914. URL: https://pubmed.ncbi.nlm.nih.gov/41060369/.

Technical Skills

Experimental ChIPmentation, HiC, HiChIP, CUT&Tag, CRISPR/Cas9, flow cytometry, tissue culture, primary cell isolation.

Computational R, Python, Linux shell, NGS analysis pipelines, Hi-C/3D genome tools, data visualization.

Other Scientific writing, mentoring undergraduate trainees, presenting at national and international conferences.

Professional Service and Affiliations

Member, Translational Cancer Research Network (TCRN).

Volunteer, Women in Science (Portland Chapter).

Reviewer for hematology and genomics journals.