Sizhao Lu M.D., Ph.D.

RESEARCH ASSISTANT PROFESSOR

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Summary

- Extensive training in molecular biology, biochemistry, bioinformatics and genomics.
- Led multiple research projects investigating the pathogenesis of complex diseases leveraging my expertise in *in vivo* disease models and bioinformatics.
- Passionate about uncovering the genetic foundations of diseases and advancing personalized treatment approaches.

Career Objective

Molecular biologist and bioinformatician seeking to leverage advanced academic expertise in developing innovative genomic technologies and personalized therapeutic solutions. Committed to translating scientific knowledge into practical applications that advance healthcare outcomes.

Education

Medical College of Qingdao University, Qingdao, China   **August 2005 - June 2010**
M.D. in Medicine

University of Nebraska Medical Center, Omaha, NE   **August 2010 - July 2015**
Ph.D. in Biochemistry and Molecular Biology

University of Colorado Anschutz Medical Campus, Aurora, US   **August 2024 - June 2025**
Certificate in Personalized and Genomic Medicine

Experience

Postdoctoral Fellow   **October 2015 - December 2020**

Dr. Weiser-Evans Laboratory University of Colorado Anschutz Medical Campus.

Key technical achievement: Quantitative imaging analysis of fibrosis

Instructor   **January 2021 - September 2023**

Division of Renal Diseases and Hypertension, University of Colorado Anschutz Medical Campus

Key technical achievement: Assembly of unbiased immunofluorescent image analysis workflow using Cellpose, FIJI, and Python.

Research Assistant Professor   **October 2023 - present**

Division of Renal Diseases and Hypertension, University of Colorado Anschutz Medical Campus

Key technical achievement: Bioinformatics analysis of scRNA-seq and spatial transcriptomics data focusing on differential expression, enrichment, trajectory and cell-cell communication analysis and visualization using scverse packages.

Core Skills

Molecular Biology:
- RNA and DNA extraction
- PCR & qPCR
- Western blotting
- Molecular cloning
- Reporter assay
- Immunoprecipitation
- Immunofluorescent staining
- Flow cytometry

Omics Methods:
- RNA-seq
- ATAC-seq
- scRNA-seq (10x Chromium)
- Spatial Transcriptomics
- Metabolomics

Python:
- Anaconda
- Jupyter
- Pandas
- Anndata
- Scanpy
- scvi-tools
- Scvelo
- Squidpy
- CellRank
- LIANA
- PyDESeq2
- Pytometry
- GPU acceleration (Cuda)
- cellpose

R:
- Tidyr
- ggplot2
- limma
- Seurat

Linux/Unix:
- Bash scripting
- Slurm batch system
- RNA-seq aligner (STAR, HISAT2)
- Cell/Space Ranger
- Git/GitHub
- Gene Expression Omnibus (GEO) database submission and access

Honors/Awards and Funding

Graduate Studies Fellowship Scholarship — **2012 - 2015**
University of Nebraska Medical Center

Postdoctoral Fellowship Award — **2018 - 2020**
American Heart Association

ATVB Travel Award for Young Investigators — **2019**
American Heart Association

Travel Award — **2020**
UCD Postdoctoral Association

Career Development Award (under review) — **2025 - 2028**
American Heart Association

Select Publications

Lu, S., Mott, J. L., & Harrison-Findik, D. D. (2015). Saturated Fatty Acids Induce Post-transcriptional Regulation of HAMP mRNA via AU-rich Element-binding Protein, Human Antigen R (HuR). Journal of Biological Chemistry, 290(40), 24178–24189. https://doi.org/10.1074/jbc.M115.648212

Lu, S., Jolly, A. J., Strand, K. A., Dubner, A. M., Mutryn, M. F., Moulton, K. S., Nemenoff, R. A., Majesky, M. W., & Weiser-Evans, M. C. M. (2020). Smooth muscle–derived progenitor cell myofibroblast differentiation through KLF4 downregulation promotes arterial remodeling and fibrosis. JCI Insight, 5(23). https://doi.org/10.1172/jci.insight.139445

Lu, S., Jolly, A. J., Dubner, A. M., Strand, K. A., Mutryn, M. F., Hinthorn, T., Noble, T., Nemenoff, R. A., Moulton, K. S., Majesky, M. W., & Weiser-Evans, M. C. (2024). KLF4 in smooth muscle cell-derived progenitor cells is essential for angiotensin II-induced cardiac inflammation and fibrosis (p. 2024.06.04.597485). bioRxiv. https://doi.org/10.1101/2024.06.04.597485

d'Escamard, V., Kadian-Dodov, D., Ma, L., **Lu, S.**, King, A., Xu, Y., Peng, S., V'Gangula, B., Zhou, Y., Thomas, A., Michelis, K. C., Bander, E., Bouchareb, R., Georges, A., Nomura-Kitabayashi, A., Wiener, R. J., Costa, K. D., Chepurko, E., Chepurko, V., … Kovacic, J. C. (2024). Integrative gene regulatory network analysis discloses key driver genes of fibromuscular dysplasia. Nature Cardiovascular Research, 3(9), 1098–1122. https://doi.org/10.1038/s44161-024-00533-w