

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. Resulting work has been disseminated in multiple research articles and manuscripts.
- Passionate about uncovering the genetic foundations of diseases and advancing personalized treatment approaches.

Career Objective

Aiming to transition my academic expertise in molecular biology and bioinformatics to industry, seeking a position where I can join teams in developing novel genomic technologies and advancing personalized therapeutic solutions.

Education

Medical College of Qingdao University, Qingdao, China <i>M.D. in Medicine</i>	August 2005 - June 2010
University of Nebraska Medical Center, Omaha, NE <i>Ph.D. in Biochemistry and Molecular Biology</i>	August 2010 - July 2015
University of Colorado Anschutz Medical Campus, Aurora, US <i>Certificate in Personalized and Genomic Medicine</i>	August 2024 - June 2025

Experience

Postdoctoral Fellow <i>Dr. Weiser-Evans Laboratory University of Colorado Anschutz Medical Campus.</i> <u>Key technical achievement:</u> Imaging analysis of fibrosis	October 2015 - December 2020
Instructor <i>Division of Renal Diseases and Hypertension, University of Colorado Anschutz Medical Campus</i> <u>Key technical achievement:</u> Assembly of unbiased immunofluorescent image analysis workflow using Cellpose, FIJI, and Python.	January 2021 - September 2023
Research Assistant Professor <i>Division of Renal Diseases and Hypertension, University of Colorado Anschutz Medical Campus</i> <u>Key technical achievement:</u> 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.	October 2023 - present

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)

R:

- TidyR
 - ggplot2
 - limma
 - Seurat
- ### Linux/Unix:
- Bash scripting
 - Slurm batch system
 - RNA-seq aligner (STAR, HISAT2)
 - MultiQC
 - Cell/Space Ranger
 - Git/GitHub
 - Gene Expression Omnibus (GEO) database submission and access

Honors/Awards and Funding

Graduate Studies Fellowship Scholarship <i>University of Nebraska Medical Center</i>	2012 - 2015
Postdoctoral Fellowship Award <i>American Heart Association</i>	2018 - 2020
ATVB Travel Award for Young Investigators <i>American Heart Association</i>	2019
Travel Award <i>UCD Postdoctoral Association</i>	2020
Career Development Award (under review) <i>American Heart Association</i>	2025 - 2028

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>