Sizhao Lu M.D. Ph.D.

RESEARCH ASSISTANT PROFESSOR
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Summary

My expertise spans from developing preclinical models of complex diseases to investigating molecular signaling pathways. I have extensive experience in bioinformatics analysis of omics data and its applications in research. I am particularly passionate about uncovering the genetic foundations of diseases and advancing personalized treatment approaches.

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 Skills: in vivo and in vitro experimental models; biochemical assays; molecular cloning; immunoprecipitation; immunofluorescent staining; flow cytometry*

Instructor **January 2021 - September 2023**

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

- *Key Skills: RNA-seq; metabolomics and data analysis; genetic lineage tracing model*

Research Assistant Professor **October 2023 - present**

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

- *Key Skills: scRNA-seq; CyTOF; small animal hemodynamic analysis; biomechanical analysis*

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

Strand, K. A., **Lu, S.**, Mutryn, M. F., Linfeng, L., Qiong, Z., T., E., J., J. A., Dubner Allison M., Moulton Karen S., Nemenoff Raphael A., Koch Keith A., LaBarbera Daniel V., & Weiser-Evans Mary C.M. (2020). High Throughput Screen Identifies the DNMT1 (DNA Methyltransferase-1) Inhibitor, 5-Azacytidine, as a Potent Inducer of PTEN (Phosphatase and Tensin Homolog). Arteriosclerosis, Thrombosis, and Vascular Biology, 40(8), 1854–1869. https://doi.org/10.1161/ATVBAHA.120.314458

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

Link to "My Bibliography": https://www.ncbi.nlm.nih.gov/myncbi/sizhao.lu.1/bibliography/public/

Bioinformatics skills

Programming:

Python: anaconda; Jupyter; Pandas; anndata; Scanpy; scvi-tools; squidpy; CellRank; PyDESeq2; Pytometry; LIANA; UCSC Cell Browser

R: tidyr; ggplot2 limma; Seurat

Linux/Unix: Bash scripting; slurm batch system; RNA-seq aligner (STAR, HISAT2), MultiQC