

**Yuannyu Zhang (Yuannv Zhang), PhD**  
Assistant Professor  
Children's Research Institute, Department of Pediatrics,  
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**Education:**

**Harbin Medical University** **2008.8- 2012.7**  
Ph.D. in Bioinformatics

**Harbin Medical University** **2004.9- 2008.7**  
B.M (Bachelor of Medicine)

**Work Experience:**

**Children's Medical Center Research Institute, Department of Pediatrics, University of Texas Southwestern Medical Center**

Visiting scholar	2015.5-2015.11
Visiting scholar	2016.6-2016.12
Postdoctoral Researcher in Bioinformatics	2017.3-2019.8
Assistant Instructor	2019.8-2020.3
Assistant Professor	From 2020.4

**CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences** **2014.10-2017.10**  
Assistant professor

**Shanghai Jiao Tong University School of Medicine** **2012.9-2014.9**  
Postdoctoral Researcher in Bioinformatics

**Research synopsis:**

**1. Non-coding Variants in Leukemia:** By analyzing WGS data from dozens of human leukemia patients, I identified SNVs, Indels and structural variants located in non-coding regulatory regions<sup>1</sup>. Then by combining enhancer perturbation and motif analysis, we characterized and validated pathogenic genomic variants in human leukemia.

**2. In Site Capture of Regulatory Elements:** We developed a new approach to isolate endogenous cis-element-regulating protein complexes and long-range DNA interactions by repurposing the CRISPR/Cas9 system<sup>2,3</sup>. The new system, named CAPTURE, offers several advantages compared to traditional ChIP or protein-based affinity assays, including high sensitivity, high specificity and adaptability for multiplexing approaches.

**3. Epigenetic and Metabolic Control of Hematopoiesis:** We compared the proteomic and transcriptomic changes in human primary HSPCs and erythroid cells, and found that observed defects in hematopoiesis most likely originated from metabolite imbalances that

impinge on critical enzymes involved in epigenetic modifications, subsequently leading to altered transcript abundance<sup>4</sup>.

**4. Characterization of Cancer Genes:** I identified candidate driver mutations and pathways from thousands of mutations detected from 207 hepatocellular carcinoma (HCC) patients; a novel pipeline which can be easily applied to other cancer types<sup>5,6</sup>.

Note: the superscript corresponds to the index of papers in 'PUBLICATIONS' section.

**Computer/Bioinformatics skills:**

1. Operating Systems: Linux.
2. Programming Languages: R, Matlab, Bash, Python.
3. **NGS pipelines: WES, WGS, ChIP-Seq, ATAC-Seq, RNA-Seq, Capture-3C and Hi-C.**
4. Others: **Metabolomics, Proteomics**, Bioconductor, Cytoscape, Inkscape/Illustrator, GraphPad Prism.

**Selected Publications (Selected from >30 Publications):**

1. Kailong Li\*, **Yuannu Zhang\***, Xin Liu\*, Yuxuan Liu\*, Zhimin Gu, Hui Cao, Kathryn E. Dickerson, Mingyi Chen, Weina Chen, Zhen Shao, Min Ni, Jian Xu, Non-Coding Variants Connect Enhancer Dysregulation with Nuclear Receptor Signaling in Hematopoietic Malignancies. *Cancer Discovery* 2020, 10(5):724-745. \***co-first author** PMID: 32188707
2. Xin Liu\*, Yong Chen\*, Yuannu Zhang\*, Yuxuan Liu, Nan Liu, Giovanni A. Botten, Hui Cao, Stuart H. Orkin, Michael Q. Zhang, Jian Xu, Multiplexed capture of spatial configuration and temporal dynamics of locus-specific 3D chromatin by biotinylated dCas9, *Genome Biology* 2020, 21(1):59 \***co-first author** PMID: 32138752
3. Xin Liu\*, **Yuannu Zhang\***, Yong Chen\*, Mushan Li\*, Feng Zhou\*, Kailong Li, Hui Cao, Min Ni, Yuxuan Liu, Zhimin Gu, Kathryn E Dickerson, Shiqi Xie, Gary C Hon, Zhenyu Xuan, Michael Q Zhang, Zhen Shao, Jian Xu, In Situ Capture of Chromatin Interactions by Biotinylated dCas9. *Cell* 2017, 170: 1028-1043 \***co-first author** PMID: 28841410
4. Xin Liu\*, **Yuannu Zhang\***, Min Ni\*, Hui Cao, Robert AJ Signer, Dan Li, Mushan Li, Zhimin Gu, Zeping Hu, Kathryn E Dickerson, Samuel E Weinberg, Navdeep S, Chandel, Ralph J DeBerardinis, Feng Zhou, Zhen Shao, Jian Xu, Quantitative Proteomic and Transcriptomic Analysis Reveals Post-Transcriptional Regulation of Mitochondrial Biogenesis during Erythropoiesis. *Nature Cell Biology* 2017. 19:626-638. \***co-first author** PMID: 28504707
5. **Yuannu Zhang**, Zhaoping Qiu, Lin Wei, Ruqi Tang, Baofeng Lian, Yingjun Zhao, Xianghuo He, Lu Xie, Integrated analysis of mutation data from various sources identifies key genes and signaling pathways in hepatocellular carcinoma. *PLoS One*, 2014. 9(7): p. e100854. PMID: 24988079
6. **Yuannu Zhang**, Jiguang Xia, Yujing Zhang, Yao Qin, Da Yang, Lishuang Qi, Wenyuan Zhao, Chenguang Wang, Zheng Guo, Pitfalls in experimental designs for characterizing the transcriptional, methylational and copy number changes of oncogenes and tumor suppressor genes. *PLoS One*, 2013. 8(3): p. e58163. PMID: 23472150

**Complete List of Published Work in MyBibliography:**

<https://www.ncbi.nlm.nih.gov/myncbi/yuannu.zhang.1/bibliography/public/>