YANXIAO ZHANG, Ph.D.

Ludwig Institute for Cancer Research
9500 Gilman Drive, MC 0653
La Jolla, CA 92093, USA

Phone: 734-355-8039
Email: shz254@health.ucsd.edu
https://shawnzhangyx.github.io/

Research Interests

I have extensive experiences in developing state-of-art Bioinformatics algorithms/methods and performing large-scale integrative analysis to uncover new mechanisms of gene regulation in mammalian development and disease. I will continue to develop new computational tools and combine computational and experimental approaches to study transcriptional regulation and molecular basis of cancer and other age-related diseases.

Education

2016 **Ph.D in Bioinformatics**, University of Michigan, Ann Arbor, Michigan, USA
2016 **M.A. in Statistics**, University of Michigan, Ann Arbor, Michigan, USA
2010 **B.S. in Biotechnology**, Peking University, Beijing, China

Research Experience

Ludwig Institute for Cancer Research, San Diego, California, USA
Aug 2016 – present ***Postdoctoral Fellow in Dr. Bing Ren's lab***

- Discovered retrotransposon HERV-H in demarcating chromatin domains in human pluripotent stem cells.
- Characterized the chromatin landscape (1,128 ChIP-seq and 132 ATAC-seq datasets) of mouse organogenesis.
- Characterized chromatin architecture changes during cardiomyocyte differentiation and identified genes involved in congenital heart diseases.
- Analyzed single-nucleus ATAC-seq data to investigate changes in chromatin accessibility during mouse aging.

University of Michigan, Ann Arbor, Michigan, USA
Jan 2011 – Apr 2016 ***Ph.D candidate (Thesis advisor: Dr. Maureen Sartor)***

- Developed a peak-calling software program for replicated ChIP-seq data.
- Characterized subtypes of human papillomavirus associated head and neck cancers.
- Investigated the regulatory mechanisms of oncogenic fusion protein PAX8/PPARγ in thyroid cancer.

Funding

NIH K99/R00 Pathway to Independence Award 09/01/2020 - 08/31/2025
(NCI)

Dissecting the cis-regulatory roles of transposable elements in human cancers. This project aims to uncover the potential enhancer and insulator roles of transposable elements and investigate the mechanism of their over expression and contribution to cancer development.

Honors & Awards

2018 Keystone Symposia Future of Science Fund scholarship
2015 Endowment for the Basic Sciences Award, University of Michigan
2012, 2015 Rackham Conference Travel Award, University of Michigan
2012 New Investigator Award, 1st head and neck cancer stem cell symposium
2011 Rackham International Student Fellowship, University of Michigan
2010 MAAS/Dean's fellowship, University of Michigan

2009 Suzhou Industrial Park Scholarship, Peking University
2008 Yang Fuqing & Wang Yangyuan Academician Scholarship, Peking University
2005 Chinese National Physics & Biology Olympiads, First Places

Publications

First/co-first author papers (*equal contribution)

6) Gorkin D*, Barozzi I*, Zhao Y*, **Zhang Y***, Huang H*,..., (35 authors), ...,Visel A, Pennacchio LA, Ren B. "An atlas of dynamic chromatin landscapes in the developing mouse fetus", *Nature*, 2020

5) **Zhang Y***, Li T*, Preissl S*, Amaral ML, Grinstein, JD, Farah, EN, Destici E, Qiu Y, Hu R, Lee AY, Chee S, Ma K, Ye Z, Zhu Q, Huang H, Fang R, Yu L, Izpisua Belmonte JC, Evans SM, Chi NC, Ren B. "Transcriptionally active HERV-H retrotransposons demarcate topologically associating domains in human pluripotent stem cells" *Nature Genetics*, 2019 [**highlighted story in that issue; commentary by Michael I. Robson & Stefan Mundlos ; recommended by F1000.**]

4) **Zhang Y**, Yu J, Grachtchouk V, Lumeng C, Sartor M, Koenig R. "Genomic binding of PAX8-PPARG fusion protein regulates cancer-related pathways and alters the immune landscape of thyroid cancer.", *Oncotarget*, 2016

3) **Zhang Y**, Koneva LA, Virani S, Arthur AE, Virani A, Hall PB, Warden CD, Carey TE, Chepeha DB, McHugh JB, Wolf GT, Rozek LS, Sartor MA. "Subtypes of HPV-positive head and neck cancers are associated with HPV characteristics, copy number alterations, PIK3CA mutation, and pathway signatures.", *Clinical Cancer Research*, 2016

2) **Zhang Y***, Yu J*, Lee C*, Xu B, Sartor MA, Koenig RJ. "Genomic binding and regulation of gene expression by the thyroid carcinoma-associated PAX8-PPARG fusion protein." *Oncotarget*, 2015

1) **Zhang Y***, Lin YH*, Johnson TD, Rozek LS, Sartor MA. "PePr: a peak-calling prioritization pipeline to identify consistent or differential peaks from replicated ChIP-Seq data." *Bioinformatics*, 2014

Co-author papers

17) Yu M*, Abnousi A*, **Zhang Y**, Li G, Lee L, Chen Z, Fang R, Wen J, Sun Q, Li Y, Ren B, Hu M. "SnapHiC: a computational pipeline to map chromatin contacts from single cell Hi-C data" Nature Methods(in press), 2021;

16) Huang H, Zhu Q, Jussila A, Han Y, Bintu B, Kern C, Conte M, **Zhang Y**, Bianco S, Chiariello A, Yu M, Hu R, Tastemel M, Juric I, Hu M, Nicodemi M, Zhuang X, Ren B. "CTCF mediates dosage and sequence-context-dependent transcriptional insulation through formation of local chromatin domains" *Nature Genetics*, 2021 May 17;

15) Hocker JD, Poirion OB, Zhu F, Buchanan J, Zhang K, Chiou J, Wang T, Hou X, Li YE, **Zhang Y**, Farah E, Wang A, McCulloch AD, Gaulton KJ, Ren B, Chi NC, Preissl S. "Cardiac Cell Type-Specific Gene Regulatory Programs and Disease Risk Association" *Science Advances*, 2021 May 1;

14) Fang R, Preissl S, Li Y, Hou X, Lucero J, Wang X, Motamedi A, Shiau AK, Zhou X, Xie F, Mukamel EA, Zhang K, **Zhang Y**, Behrens MM, Ecker J, Ren B. "Comprehensive analysis of single cell ATAC-seq data with SnapATAC",*Nature Communications*, 2021

13) Zhu C, **Zhang Y**, Li YE, Lucero J, Behrens MM, Ren B. "Joint profiling of histone modifications and transcriptome in single cells from mouse brain", *Nature Methods*, 2021

12) The ENCODE Project Consortium, Moore J, [...], Weng Z. "Expanded encyclopaedias of DNA elements in the human and mouse genomes", *Nature*, 2020

11) Qin T*, Koneva L*, Liu Y*, **Zhang Y**, Virani A, Virani S, Arthur AE, Zarins KR, Carey TE, Chepeha D, Wolf GT, Rozek LS, Sartor MA. "Significant association between host transcriptome-derived HPV oncogene E6* influence score and carcinogenic pathways, tumor size, and survival in head and neck cancer", *Head & Neck*, 2020

10) Zhang Z, Zhou C, Li X, Barnes SD, Deng S, Hoover E, Chen CC, Lee YS, **Zhang Y**, Wang C, Metang LA, Wu C, Tirado CR, Johnson NA, Wongvipat J, Navrazhina K, Cao Z, Choi D, Huang CH, Linton E, Chen X, Liang Y, Mason CE, de Stanchina E, Abida W, Lujambio A, Li S, Lowe SW, Mendell JT, Malladi VS, Sawyers CL, Mu P. "Loss of CHD1 Promotes Heterogeneous Mechanisms of Resistance to AR-Targeted Therapy via Chromatin Dysregulation", *Cancer Cell*, 2020

9) Arvanitis M, Tampakakis E, **Zhang Y**, Wang W,Auton A, 23andMe Research Team, Dutta D, Glavaris S, Chatterjee N, Keramati A, Chi N, Ren B, Post WS, Battle A. "Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure", *Nature Communication*, 2020

8) Li G*, Liu Y*, **Zhang Y**, Kubo N, Yu M, Fang R, Kellis M, Ren B. "Joint profiling of DNA methylation and chromatin architecture in single cells", *Nature Methods*, 2019

7) Hao Y, Waller T, Nye D, Li J, **Zhang Y**, Hume R, Rolls M, Collins C. "Degeneration of injured axons and dendrites requires restraint of a protective JNK signaling pathway by the transmembrane protein Raw" *Journal of Neuroscience*, 2019

6) Juric I*, Yu M*, Abnousi A, Raviram R, Fang R, Zhao Y, **Zhang Y**, Qiu Y, Yang Y, Li Y, Ren B, Hu M. "MAPS: model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments" *PLoS computational biology*, 2019

5) Qin T, **Zhang Y**, Zarins KR, Jones TR, Virani S, Peterson LA, McHugh JB, Chepeha D, Wolf GT, Rozek LS, Sartor MA. "Expressed HNSCC variants by HPV-status in a well-characterized Michigan cohort." *Scientific Reports*, 2018

4) Preissl S, Fang R, Huang H, Zhao Y, Raviram R, Gorkin D, **Zhang Y**, Sos B, Afzal V, Dickel D, Kuan S, Visel A, Pennacchio L, Zhang K, Ren B. "Single nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell type-specific transcriptional regulation" *Nature Neuroscience*, 2018

3) Koneva L, **Zhang Y**, Virani S, Hall P, McHugh J, Chepeha D, Wolf G, Carey T, Rozek L, Sartor M. "HPV integration in head and neck cancer correlates with survival and suggests candidate drivers.", *Molecular Cancer Research*, 2017

2) Xiong X, **Zhang Y**, Yan J, Jain S, Chee S, Ren B, Zhao H. "A Scalable Epitope Tagging Approach for High Throughput ChIP-Seq Analysis.", *ACS synthetic biology*, 2017

1) Xu B, O'Donnell M, O'Donnell J, Yu J, **Zhang Y**, Sartor MA, Koenig RJ. "Adipogenic Differentiation of Thyroid Cancer Cells Through the Pax8-PPARG Fusion Protein Is Regulated by Thyroid Transcription Factor 1 (TTF-1)", *Journal of Biologcal Chemistry*, 2016

Preprints & manuscripts under review

1) Rajderkar S, Barozzi I, Zhu Y, Hu R, **Zhang Y**,... Dickel D, Visel A, Pennacchio L. "Topologically Associating Domain Boundaries are Commonly Required for Normal Genome Function", bioRxiv, 2021

Software & Web application

Peak-calling Prioritization pipeline for ChIP-seq data (PePr)
OmicsPedia website: online community for sharing knowledge of genomics data analysis

Teaching experience

Spring 2019 — Guest lecturer
• BIOM272/274 "Seminars in Genetics and Molecular Cell Biology"

Winter 2012 — Graduate Student Teaching Assistant
• BIOSTAT646/BIOINF545: "High-throughput Molecular Genomic and Epigenomic Data Analysis"

Mentoring Experience

2020 — Qing Liu (Undergraduate student)
2019 - 2021 — Luisa Amaral (Bioinformatics PhD student; contributed substantially to the HERV-H and aging project)
2018 — James Deng (MD-PhD Rotation student)
Yawei Wu (Undergraduate student; currently PhD student at WUSTL)
2017 — Krystyna Kolodziej (Bioinformatics rotation student)

Invited Talk

Nov 2020 — The Center for Public Health Genomics (CPHG) at the University of Virginia. "Multiomics analysis of chromatin structure and function"

Conference Oral Presentations

2019 Keystone symposium 3D Genome: Gene Regulation and Disease."Primate-Specific Retrotransposon HERV-H Demarcates Chromatin Domains in Lineage Specification and Evolution"

2018 Cold Spring Harbor Asia meeting for Systems Biology and Gene Regulation , "Endogenous Retrovirus HERV-H Delineates Chromatin Domains in Human Pluripotent Stem Cells"

2017 CvDC Bench to Bassinet Face-to-face meeting, "Chromatin organization dynamics in human cardiomyocyte differentiation"

2015 UM Head and Neck Cancer S.P.O.R.E. Meeting, "Subtypes of HPV-positive head and neck cancers are associated with HPV characteristics, copy number variations, PIK3CA mutation, and pathway signatures"

2013 NCIBI Tools and Technology Seminar Series, "PePr: a Peak-calling and Prioritization pipeline to test group differences in ChIP-Seq data"

2012 The 10th Annual Rocky Mountain Bioinformatics Conference, "PePr: a peak-calling and prioritization pipeline to test group differences in ChIP-seq data"

Academic Community Involvement

Reviewer (*Ad hoc*) for: Genome Biology, PLOS Computational Biology, Nucleic Acids Research, Scientific Reports, BMC Bioinformatics, PLOSone

$\sim\sim\sim$ Last updated: August 25, 2021$\sim\sim\sim$