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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

Aug 2016 – present **Ludwig Institute for Cancer Research**, San Diego, California, USA
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.

Jan 2011 – Apr 2016 **University of Michigan**, Ann Arbor, Michigan, USA
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/PPAR γ in thyroid cancer.

Funding

NIH K99/R00 Pathway to Independence Award
(NCI)

09/01/2020 - 08/31/2025

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, Izipisua 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

- 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*, Abnoui 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 Biological Chemistry*, 2016

Preprints & manuscripts under review

- 3) 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, Bing Ren, Neil C Chi, Sebastian Preissl. "Cardiac Cell Type-Specific Gene Regulatory Programs and Disease Risk Association" [bioRxiv](#), 2020 Sept 11;
- 2) Huang H, Zhu Q, Jussila A, Han Y, Bintu B, Kern C, Conte M, **Zhang Y**, Bianco S, Chiariello A, Yu M, Hu R, 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" [bioRxiv](#), 2020 July 08;
- 1) Fang R, Preissl S, Hou X, Lucero J, Wang X, Motamedi A, Shiau AK, Mukamel EA, **Zhang Y**, Behrens MM, Ecker J, Ren B. "Fast and Accurate Clustering of Single Cell Epigenomes Reveals Cis-Regulatory Elements in Rare Cell Types" [bioRxiv](#), 2019 April 22;

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 - 2020	Luisa Amaral (Bioinformatics rotation and current 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"
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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

Reviewers (*Ad hoc*) for:

Genome Biology
PLOS Computational Biology
Nucleic Acids Research
Scientific Reports
BMC Bioinformatics
PLOSone

~~~ Last updated: November 18, 2020~~~