

## CURRICULUM VITAE

### Chongzhi Zang, PhD

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#### EDUCATION AND TRAINING

Peking University	B.S., Physics	07/2005
The George Washington University	Ph.D., Physics	09/2010
Harvard University/Dana-Farber Cancer Institute	Postdoctoral training, Computational Biology	10/2016

#### APPOINTMENTS

11/2016 –	<b>University of Virginia</b> , Charlottesville, VA <i>Associate Professor of Public Health Sciences</i> (primary) (07/2022–) <i>Associate Professor of Biochemistry and Molecular Genetics</i> (07/2022–) <i>Associate Professor of Biomedical Engineering</i> (07/2022–) <i>Resident Faculty Member</i> , Center for Public Health Genomics (11/2016–) <i>Full Member</i> , UVA Comprehensive Cancer Center (01/2017–) <i>Assistant Professor of Public Health Sciences, Biochemistry and Molecular Genetics, Biomedical Engineering</i> (11/2016–06/2022)
07/2010 – 10/2016	<b>Harvard University/Dana-Farber Cancer Institute</b> , Boston, MA <i>Postdoctoral Research Fellow</i> , Department of Data Science, Dana-Farber Cancer Institute (07/2010–10/2016) <i>Postdoctoral Fellow</i> , Department of Biostatistics, Harvard T.H. Chan School of Public Health (10/2010–10/2016) (Postdoctoral Mentor: Xiaole Shirley Liu, PhD)
05/2007 – 06/2010	<b>National Institutes of Health</b> , Bethesda, MD <i>Predocctoral Research Assistant</i> , Laboratory of Epigenome Biology, National Heart, Lung, and Blood Institute (PhD Co-advisor: Keji Zhao, PhD)
09/2005 – 06/2010	<b>The George Washington University</b> , Washington, DC <i>Graduate Research Assistant</i> , Department of Physics (09/2006–06/2010) <i>Graduate Teaching Assistant</i> , Department of Physics (09/2005–05/2008) (PhD Advisor: Weiqun Peng, PhD)
02/2004 – 07/2005	<b>Institute of Physics, Chinese Academy of Sciences</b> , Beijing, China <i>Undergraduate Research Assistant</i> , High-field Physics Group (L05) (Thesis Advisor: Jie Zhang, PhD)

## PUBLICATIONS

### Peer-reviewed Journal Articles

Total citations > 13,000; H-index = 34 (Google Scholar)

\*: equal-contributing authors; §: co-corresponding authors. Underscored: Dr. Zang's trainees.

1. Shengen Shawn Hu, Lin Liu, Qi Li, Wenjing Ma, Michael J. Guertin, Clifford A. Meyer, Ke Deng, Tingting Zhang, **Chongzhi Zang**. "Intrinsic bias estimation for improved analysis of bulk and single-cell chromatin accessibility profiles using SELMA." **Nature Communications** 13, 5533 (2022).
2. Yuchao Jiang<sup>§</sup>, Yuriko Harigaya, Zhaojun Zhang, Hongpan Zhang, **Chongzhi Zang**, Nancy R. Zhang<sup>§</sup>. "Nonparametric single-cell multiomic characterization of trio relationships between transcription factors, target genes, and cis-regulatory regions." **Cell Systems** 13, 737–751 (2022).
3. William F. Lamberti, **Chongzhi Zang**. "Extracting physical characteristics of higher-order chromatin structures from 3D image data." **Computational and Structural Biotechnology Journal** 20, 3387–3398 (2022).
4. Ryan J. Smith\*, Hongpan Zhang\*, Shengen Shawn Hu\*, Theodora Yung, Roshane Francis, Lilian Lee, Mark W. Onaitis, Peter B. Dirks, **Chongzhi Zang**<sup>§</sup>, Tae-Hee Kim<sup>§</sup>. "Single-cell chromatin profiling of the primitive gut tube reveals regulatory dynamics underlying lineage fate decisions." **Nature Communications** 13, 2965 (2022).
5. Adam W. Turner\*, Shengen Shawn Hu\*, Jose Verdezoto Mosquera, Wei Feng Ma, Chani J. Hodonsky, Doris Wong, Gaëlle Auguste, Yipei Song, Katia Sol-Church, Emily Farber, Soumya Kundu, Anshul Kundaje, Nicolas G. Lopez, Lijiang Ma, Saikat Kumar B, Ghosh, Suna Onengut-Gumuscu, Euan A. Ashley, Thomas Quertermous, Alope V. Finn, Nicholas J. Leeper, Jason C. Kovacic, Johan L. M. Björkegren, **Chongzhi Zang**<sup>§</sup>, Clint L. Miller<sup>§</sup>. "Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk." **Nature Genetics** 54, 804–816 (2022).  
  
Summarized in Research Briefing: **Nature Genetics** 54, 750–751 (2022).
6. Qiang Shan\*, Shengen Shawn Hu\*, Shaoqi Zhu, Xia Chen, Vladimir P. Badovinac, Weiqun Peng, **Chongzhi Zang**<sup>§</sup>, Hai-Hui Xue<sup>§</sup>. "Tcf1 preprograms the mobilization of glycolysis in central memory CD8<sup>+</sup> T cells during recall responses." **Nature Immunology** 23, 386–398 (2022).
7. Avik Dutta, Dipmoy Nath, Yue Yang, Bao T. Le, Mohammad Ferdous-Ur Rahman, Patrick Faughnan, Zhenjia Wang, Matthew Stuver, Rongquan He, Wuwei Tan, Robert E. Hutchison, Jason M. Foulks, Steven L. Warner, **Chongzhi Zang**, Golam Mohi. "Genetic ablation of Pim1 or pharmacologic inhibition with TP-3654 ameliorates myelofibrosis in murine models." **Leukemia** 36, 746–759 (2022).
8. Bi Shi\*, Wei Li\*, Yansu Song\*, Zhenjia Wang\*, Rui Ju, Aleksandra Ulman, Jing Hu, Francesco Palomba, Yanfang Zhao, John Philip Le, William Jarrard, David Dimoff, Michelle A. Digman, Enrico Gratton, **Chongzhi Zang**, Hao Jiang. "UTX condensation underlies its

tumor suppressive activity." **Nature** 597, 726–731 (2021).

9. Naomi D. Atkin, Heather M. Raimer, Zhenjia Wang, **Chongzhi Zang**, Yuh-Hwa Wang. "Assessing acute myeloid leukemia susceptibility in rearrangement-driven patients by DNA breakage at topoisomerase II and CCCTC-binding factor/cohesin binding sites." **Genes, Chromosomes and Cancer** 60, 808–821 (2021).
10. Zhenjia Wang, Yifang Zhang, **Chongzhi Zang**. "BART3D: Inferring transcriptional regulators from differential Hi-C data." **Bioinformatics** 37, 3075–3078 (2021).
11. Wenjing Ma<sup>\*</sup>, Zhenjia Wang<sup>\*</sup>, Yifan Zhang, Neal E. Magee, Yayi Feng, Ruoyao Shi, Yang Chen, **Chongzhi Zang**. "BARTweb: a web server for transcriptional regulator association analysis." **NAR Genomics and Bioinformatics** 3(2), lqab022 (2021).
12. Zachary V. Thomas, Zhenjia Wang, **Chongzhi Zang**. "BART Cancer: a web resource for transcriptional regulators in cancer genomes." **NAR Cancer** 3, zcab011 (2021).
13. Avik Dutta, Yue Yang, Bao T. Le, Yifan Zhang, Omar Abdel-Wahab, **Chongzhi Zang**, Golam Mohi. "U2af1 is critical for survival and function of hematopoietic stem/progenitor cells." **Leukemia** 35, 2382–2398 (2021).
14. **Chongzhi Zang**<sup>§</sup>, Yiren Wang, Weiqun Peng<sup>§</sup>. "RECOGNICER: a coarse-graining approach for identifying broad domains from ChIP-seq data." **Quantitative Biology** 8, 359–368 (2020).
15. Celestia Fang<sup>\*</sup>, Zhenjia Wang<sup>\*</sup>, Cuijuan Han, Stephanie L Safgren, Kathryn A Helmin, Emmalee R Adelman, Kyle P Eagen, Alexandre Gaspar-Maia, Maria E Figueroa, Benjamin D Singer, Aakrosh Ratan, Panagiotis Ntziachristos<sup>§</sup>, **Chongzhi Zang**<sup>§</sup>. "Cancer-specific CTCF binding facilitates oncogenic transcriptional dysregulation." **Genome Biology** 21, 247 (2020).
16. Danqi Chen<sup>\*</sup>, Qiao Yi Chen<sup>\*</sup>, Zhenjia Wang<sup>\*</sup>, Yusha Zhu, Thomas Kluz, Wuwei Tan, Jinquan Li, Feng Wu, Lei Fang, Xiaoru Zhang, Rongquan He, Steven Shen, Hong Sun, **Chongzhi Zang**<sup>§</sup>, Chunyuan Jin<sup>§</sup>, Max Costa<sup>§</sup>. "Polyadenylation of histone H3.1 mRNA promotes cell transformation by displacing H3.3 from gene regulatory elements." **iScience** 23, 101518 (2020).
17. The ENCODE Project Consortium (including **Chongzhi Zang**), Jill E. Moore<sup>\*</sup>, Michael J. Purcaro<sup>\*</sup>, Henry E. Pratt<sup>\*</sup>, Charles B. Epstein<sup>\*</sup>, Noam Shores<sup>\*</sup>, Jessika Adrian<sup>\*</sup>, Trupti Kawli<sup>\*</sup>, Carrie A. Davis<sup>\*</sup>, Alexander Dobin<sup>\*</sup>, Rajinder Kaul<sup>\*</sup>, Jessica Halow<sup>\*</sup>, Eric L. Van Nostrand<sup>\*</sup>, Peter Freese<sup>\*</sup>, David U. Gorkin<sup>\*</sup>, Yin Shen<sup>\*</sup>, Yupeng He<sup>\*</sup>, Mark Mackiewicz<sup>\*</sup>, Florencia Pauli-Behn<sup>\*</sup>, Brian A. Williams, Ali Mortazavi, Cheryl A. Keller, Xiao-Ou Zhang, Shaimae I. Elhajjajy, Jack Huey, Diane E. Dickel, Valentina Snetkova, Xintao Wei, Xiaofeng Wang, Juan Carlos Rivera-Mulia, Joel Rozowsky, Jing Zhang, Surya B. Chhetri, Jialing Zhang, Alec Victorsen, Kevin P. White, Axel Visel, Gene W. Yeo, Christopher B. Burge, Eric Lécuyer, David M. Gilbert, Job Dekker, John Rinn, Eric M. Mendenhall, Joseph R. Ecker, Manolis Kellis, Robert J. Klein, William S. Noble, Anshul Kundaje, Roderic Guigó, Peggy J. Farnham, J. Michael Cherry<sup>§</sup>, Richard M. Myers<sup>§</sup>, Bing Ren<sup>§</sup>, Brenton R. Graveley<sup>§</sup>, Mark B. Gerstein<sup>§</sup>, Len A. Pennacchio<sup>§</sup>, Michael P. Snyder<sup>§</sup>, Bradley E. Bernstein<sup>§</sup>, Barbara Wold<sup>§</sup>, Ross C. Hardison<sup>§</sup>, Thomas R. Gingeras<sup>§</sup>, John A. Stamatoyannopoulos<sup>§</sup>, Zhiping Weng<sup>§</sup>. "Expanded encyclopaedias of DNA elements in the human and mouse genomes." **Nature**

583, 699–710 (2020).

18. The ENCODE Project Consortium (including **Chongzhi Zang**), Michael P. Snyder<sup>§</sup>, Thomas R. Gingeras, Jill E. Moore, Zhiping Weng, Mark B. Gerstein, Bing Ren, Ross C. Hardison, John A. Stamatoyannopoulos, Brenton R. Graveley, Elise A. Feingold, Michael J. Pazin, Michael Pagan, Daniel A. Gilchrist, Benjamin C. Hitz, J. Michael Cherry, Bradley E. Bernstein, Eric M. Mendenhall, Daniel R. Zerbino, Adam Frankish, Paul Flicek, Richard M. Myers. “Perspectives on ENCODE.” **Nature** 583, 693–698 (2020).
19. Jing Zhang\*, Donghoon Lee\*, Vineet Dhiman\*, Peng Jiang\*, Jie Xu\*, Patrick McGillivray\*, Hongbo Yang\*, Jason Liu, William Meyerson, Declan Clarke, Mengting Gu, Shantao Li, Shaoke Lou, Jinrui Xu, Lucas Lochovsky, Matthew Ung, Lijia Ma, Shan Yu, Qin Cao, Arif Harmanci, Koon-Kiu Yan, Anurag Sethi, Gamze Gürsoy, Michael Rutenberg Schoenberg, Joel Rozowsky, Jonathan Warrell, Prashant Emani, Yucheng T. Yang, Timur Galeev, Xiangmeng Kong, Shuang Liu, Xiaotong Li, Jayanth Krishnan, Yanlin Feng, Juan Carlos Rivera-Mulia, Jessica Adrian, James R Broach, Michael Bolt, Jennifer Moran, Dominic Fitzgerald, Vishnu Dileep, Tingting Liu, Shenglin Mei, Takayo Sasaki, Claudia Trevilla-Garcia, Su Wang, Yanli Wang, **Chongzhi Zang**, Daifeng Wang, Robert J. Klein, Michael Snyder, David M. Gilbert, Kevin Yip, Chao Cheng, Feng Yue<sup>§</sup>, X. Shirley Liu<sup>§</sup>, Kevin White<sup>§</sup>, Mark Gerstein<sup>§</sup>. “An integrative ENCODE resource for cancer genomics.” **Nature Communications** 11, 3696 (2020).
20. Qiang Shan\*, Sheng'en Hu\*, Xia Chen, Derek B. Danahy, Vladimir P. Badovinac, **Chongzhi Zang**<sup>§</sup>, Hai-Hui Xue<sup>§</sup>. “Ectopic Tcf1 expression instills a stem-like program in exhausted CD8+ T cells to enhance viral and tumor immunity.” **Cellular & Molecular Immunology** 18, 1262–1277 (2021). doi:10.1038/s41423-020-0436-5 (2020).
21. Luke T. Oostdyk, Zhenjia Wang, **Chongzhi Zang**, Hui Li, Michael J. McConnell, Bryce M. Paschal. “An epilepsy-associated mutation in the nuclear import receptor KPNA7 reduces nuclear localization signal binding.” **Scientific Reports** 10, 4844 (2020).
22. Qingsu Cheng, Mina Khoshdeli, Bradley S. Ferguson, Kosar Jabbari, **Chongzhi Zang**<sup>§</sup>, Bahram Parvin<sup>§</sup>. “YY1 is a cis-regulator in the organoid models of high mammographic density.” **Bioinformatics** 36, 1663–1667 (2020).
23. Cynthia C Jose\*, Zhenjia Wang\*, Vinay Singh Tanwar, Xiaoru Zhang, **Chongzhi Zang**<sup>§</sup>, Suresh Cuddapah<sup>§</sup>. “Nickel induced transcriptional changes persist post exposure through epigenetic reprogramming.” **Epigenetics and Chromatin** 12, 75 (2019).
24. Teng Fei\*, Wei Li\*, Jingyu Peng\*, Tengfei Xiao, Chen-Hao Chen, Alexander Wu, Jialiang Huang, **Chongzhi Zang**, X. Shirley Liu<sup>§</sup>, Myles Brown<sup>§</sup>. “Deciphering essential cistromes using genome-wide CRISPR screens.” **Proceedings of the National Academy of Sciences USA** 116, 25186–25195 (2019).
25. Kushani K. Shah, Robert H. Whitaker, Theodore Busby, Jing Hu, Bi Shi, Zhenjia Wang, **Chongzhi Zang**, William J. Placzek, Hao Jiang. “Specific inhibition of DPY30 activity by ASH2L-derived peptides suppresses blood cancer cell growth.” **Experimental Cell Research** 382(2), 111485 (2019).
26. Zhenjia Wang, Mete Civelek, Clint L. Miller, Nathan C. Sheffield, Michael J. Guertin, **Chongzhi Zang**. “BART: a transcription factor prediction tool with query gene sets or

- epigenomic profiles." *Bioinformatics* 34, 2867–2869 (2018).
27. Tengfei Xiao\*, Wei Li\*, Xiaoqing Wang, Han Xu, Jixin Yang, Qiu Wu, Ying Huang, Joseph Geradts, Peng Jiang, Teng Fei, David Chi, **Chongzhi Zang**, Qi Liao, Jonathan Rennhack, Eran Andrechek, Nanlin Li, Simone Detre, Mitchell Dowsett, Rinath M. Jeselsohn, X. Shirley Liu<sup>§</sup>, Myles Brown<sup>§</sup>. "Estrogen-regulated feedback loop limits the efficacy of estrogen receptor–targeted breast cancer therapy." *Proceedings of the National Academy of Sciences USA* 115, 7869–7878 (2018).
  28. Cynthia C Jose, Lakshmanan Jagannathan, Vinay Singh Tanwar, Xiaoru Zhang, **Chongzhi Zang**, Suresh Cuddapah. "Nickel exposure induces persistent mesenchymal phenotype in human lung epithelial cells through epigenetic activation of ZEB1." *Molecular Carcinogenesis* 57, 794–806 (2018).
  29. André L. Martins, Ninad M. Walavalkar, Warren D. Anderson, **Chongzhi Zang**, Michael J. Guertin. "Universal correction of enzymatic sequence bias reveals molecular signatures of protein/DNA interactions." *Nucleic Acids Research* 46 (2), e9 (2017).
  30. Shenglin Mei, Clifford A. Meyer, Rongbin Zheng, Qian Qin, Qiu Wu, Peng Jiang, Bo Li, Xiaohui Shi, Binbin Wang, Jingyu Fan, Celina Shih, Myles Brown, **Chongzhi Zang**<sup>§</sup>, X. Shirley Liu<sup>§</sup>. "Cistrome Cancer: a web resource for integrative gene regulation modeling in cancer." *Cancer Research* 77, e19–e22 (2017).
  31. Eric Severson\*, Kelly L. Arnett\*, Hongfang Wang\*, **Chongzhi Zang**\*, Len Taing, Hudan Liu, Warren S. Pear, X. Shirley Liu, Stephen C. Blacklow<sup>§</sup>, Jon C. Aster<sup>§</sup>. "Genome-wide identification and characterization of Notch transcription complex-binding sequence-paired sites in leukemia cells." *Science Signaling* 10, 477, eaag1598 (2017).
  32. Shenglin Mei, Qian Qin, Qiu Wu, Hanfei Sun, Rongbin Zheng, **Chongzhi Zang**, Muyuan Zhu, Jiabin Wu, Xiaohui Shi, Len Taing, Tao Liu, Myles Brown, Clifford A. Meyer<sup>§</sup>, X. Shirley Liu<sup>§</sup>. "Cistrome Data Browser: an integrated data portal for ChIP-Seq and chromatin accessibility data in human and mouse." *Nucleic Acids Research* 45 (D1), D658–D662 (2016).
  33. Qian Qin, Shenglin Mei, Qiu Wu, Hanfei Sun, Lewyn Li, Len Taing, Sujun Chen, Fugen Li, Tao Liu, **Chongzhi Zang**, Han Xu, Yiwen Chen, Clifford A. Meyer, Yong Zhang, Myles Brown, Henry W. Long<sup>§</sup>, X. Shirley Liu<sup>§</sup>. "ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline." *BMC Bioinformatics* 17, 404 (2016).
  34. Su Wang\*, **Chongzhi Zang**\*, Tengfei Xiao, Jingyu Fan, Shenglin Mei, Qian Qin, Qiu Wu, Xujuan Li, Kexin Xu, Housheng Hansen He, Myles Brown, Clifford A. Meyer<sup>§</sup>, X. Shirley Liu<sup>§</sup>. "Modeling cis-regulation with a compendium of genome-wide histone H3K27ac profiles." *Genome Research* 26, 1417–1429 (2016).
  35. **Chongzhi Zang**\*, Annouck Luyten\*, Christina Chen, X. Shirley Liu, Ramesh A. Shivdasani. "NF-E2, FLI1 and RUNX1 collaborate at areas of dynamic chromatin to activate transcription in mature mouse megakaryocytes." *Scientific Reports* 6, 30255 (2016).
  36. **Chongzhi Zang**\*, Tao Wang\*, Ke Deng, Bo Li, Sheng'en Hu, Qian Qin, Tengfei Xiao, Shihua Zhang, Clifford A. Meyer, Housheng Hansen He, Myles Brown, Jun S. Liu, Yang Xie<sup>§</sup>, X. Shirley Liu<sup>§</sup>. "High-dimensional genomic data bias correction and data integration

using MANCIE.” *Nature Communications* 7, 11305 (2016).

37. Han Xu\*, Kexin Xu\*, Housheng H. He, **Chongzhi Zang**, Chen-Hao Chen, Yiwen Chen, Qian Qin, Su Wang, Chenfei Wang, Sheng'en Hu, Fugen Li, Henry Long, Myles Brown<sup>§</sup>, X. Shirley Liu<sup>§</sup>. “Integrative analysis reveals the transcriptional collaboration between EZH2 and E2F1 in the regulation of cancer-related gene expression.” *Molecular Cancer Research* 14, 163–172 (2015).
38. Peng Jiang, Hongfang Wang, Wei Li, **Chongzhi Zang**, Bo Li, Yinling Joey Wong, Clifford A. Meyer, Jun S. Liu, Jon C. Aster, X. Shirley Liu, “Network analysis of gene essentiality in functional genomics experiments.” *Genome Biology* 16, 239 (2015).
39. Hilary K Finucane\*<sup>§</sup>, Brendan Bulik-Sullivan\*<sup>§</sup>, Alexander Gusev, Gosia Trynka, Yakir Reshef, Po-Ru Loh, Verner Anttila, Han Xu, **Chongzhi Zang**, Kyle Farh, Stephan Ripke, Felix R Day, ReproGen Consortium, Schizophrenia Working Group of the Psychiatric Genomics Consortium, The RACI Consortium, Shaun Purcell, Eli Stahl, Sara Lindstrom, John RB Perry, Yukinori Okada, Soumya Raychaudhuri, Mark Daly, Nick Patterson, Benjamin M Neale<sup>§</sup>, Alkes L Price<sup>§</sup>. “Partitioning heritability by functional annotation using genome-wide association summary statistics.” *Nature Genetics* 47, 1228–1235 (2015).
40. Hongfang Wang, **Chongzhi Zang**, X. Shirley Liu, Jon C. Aster. “The role of Notch receptors in transcriptional regulation.” *Journal of Cellular Physiology* 230(5), 982–988 (2015).
41. Alexander Gusev<sup>§</sup>, S. Hong Lee, Gosia Trynka, Hilary Finucane, Bjarni J Vilhjálmsson, Han Xu, **Chongzhi Zang**, Stephan Ripke, Brendan Bulik-Sullivan, Eli Stahl, Schizophrenia Working Group of the Psychiatric Genomics Consortium, SWE-SCZ Consortium, Anna K. Kähler, Christina M. Hultman, Shaun M. Purcell, Steven A. McCarroll, Mark Daly, Bogdan Pasaniuc, Patrick F. Sullivan, Benjamin M. Neale, Naomi R. Wray, Soumya Raychaudhuri, Alkes L. Price<sup>§</sup>. “Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases.” *The American Journal of Human Genetics* 95, 535–552 (2014).
42. Yumi Yashiro-Ohtani\*, Hongfang Wang\*, **Chongzhi Zang**, Kelly L. Arnett, Will Bailis, Yugong Ho, Birgit Knoechel, Claudia Lanauze, Lumena Louis, Katherine S. Forsyth, Sujun Chen, Yoonjie Chung, Jonathan Schug, Gerd A. Blobel, Stephen A. Liebhaber, Bradley E. Bernstein, Stephen C. Blacklow, X. Shirley Liu, Jon C. Aster<sup>§</sup>, Warren S. Pear<sup>§</sup>. “Long-range enhancer activity determines Myc sensitivity to Notch inhibitors in T cell leukemia.” *Proceedings of the National Academy of Sciences USA* 111(46), E4946–E4953 (2014).
43. Annouck Luyten\*, **Chongzhi Zang**\*, X. Shirley Liu<sup>§</sup>, Ramesh A. Shivdasani<sup>§</sup>. “Active enhancers are delineated *de novo* during hematopoiesis with limited lineage fidelity among specified primary blood cells.” *Genes and Development* 28, 1827–1839 (2014).
44. Alexander Stoeck, Serguei Lejnine, Andrew Truong, Li Pan, Hongfang Wang, **Chongzhi Zang**, Jing Yuan, Chris Ware, John MacLean, Philip W Garrett-Engle, Michael Kluk, Jason Laskey, Brian B. Haines, Christopher Moskaluk, Leigh Zawel, Stephen Fawell, D. Gary Gilliland, Theresa Zhang, Brandon Kremer, Birgit Knoechel, Bradley E Bernstein, Warren S. Pear, X. Shirley Liu, Jon C Aster, Sriram Sathyanarayanan. “Discovery of biomarkers predictive of GSI response in triple negative breast cancer and adenoid cystic carcinoma.” *Cancer Discovery* 4(10), 1154–1167 (2014).
45. Xiaoqi Zheng, Qian Zhao, Huajun Wu, Wei Li, Haiyun Wang, Clifford A. Meyer, Qian Alvin

- Qin, Han Xu, **Chongzhi Zang**, Peng Jiang, Fuqiang Li, Yong Hou, Jianxing He, Jun Wang, Jun Wang, Peng Zhang, Yong Zhang, X. Shirley Liu. "MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes." *Genome Biology* 15, 419 (2014).
46. Hongfang Wang\*, **Chongzhi Zang**\*, Len Taing, Kelly Arnett, Yinling Joey Wong, Warren S. Pear, Stephen C. Blacklow, X. Shirley Liu<sup>§</sup>, Jon C. Aster<sup>§</sup>. "NOTCH1-RBPJ complexes drive target gene expression through dynamic interactions with superenhancers." *Proceedings of the National Academy of Sciences USA* 111, 715–710 (2014).
  47. Housheng Hansen He\*, Clifford A. Meyer\*, Sheng'en Shawn Hu\*, Mei-Wei Chen, **Chongzhi Zang**, Yin Liu, Prakash K. Rao, Teng Fei, Han Xu, Henry Long<sup>§</sup>, X. Shirley Liu<sup>§</sup>, Myles Brown<sup>§</sup>. "Refined DNase-seq protocol and data analysis reveals intrinsic bias in transcription factor footprint identification." *Nature Methods* 11, 73–78 (2014).
  48. Su Wang, Hanfei Sun, Jian Ma, **Chongzhi Zang**, Chenfei Wang, Juan Wang, Qianzi Tang, Clifford A. Meyer, Yong Zhang<sup>§</sup>, X. Shirley Liu<sup>§</sup>. "Targets analysis by integration of transcriptome and ChIP-seq data with BETA." *Nature Protocols* 8, 2502–2515 (2013).
  49. Hong Hao, Douglas S. Kim, Bernward Klocke, Kory R. Johnson, Kairong Cui, Norimoto Gotoh, **Chongzhi Zang**, Janina Gregorski, Linn Gieser, Weiqun Peng, Yang Fann, Martin Seifert, Keji Zhao, Anand Swaroop. "Transcriptional regulation of rod photoreceptor homeostasis revealed by *in vivo* NRL targetome analysis." *PLoS Genetics* 8(4), e1002649 (2012).
  50. Jeremy A. Daniel, Margarida A. Santos\*, Zhibin Wang\*, **Chongzhi Zang**\*, Mila Jankovic, Anna Gazumyan, Kristopher R. Schwab, Arito Yamane, Darius Filsuf, Young-Wook Cho, Kai Ge, Weiqun Peng, Michel C. Nussenzweig, Rafael Casellas, Gregory R. Dressler, Keji Zhao, André Nussenzweig. "PTIP promotes chromatin changes critical for immunoglobulin switch recombination." *Science* 329, 917–923 (2010).
  51. Lai Wei\*, Golnaz Vahedi\*, Hong-Wei Sun, Wendy T. Watford, Hiroaki Takatori, Haydee L. Ramos, Hayato Takahashi, Jonathan Liang, Gustavo Gutierrez-Cruz, **Chongzhi Zang**, Weiqun Peng, John J. O'Shea, Yuka Kanno. "Discrete roles of STAT4 and STAT6 transcription factors in tuning epigenetic modifications and transcription during T helper cell differentiation." *Immunity* 32, 840–851 (2010).
  52. Zhibin Wang\*, **Chongzhi Zang**\*, Kairong Cui\*, Dustin E. Schones, Artem Barski, Weiqun Peng, Keji Zhao. "Genome-wide mapping of HATs and HDACs reveals distinct functions in active and inactive genes." *Cell* 138, 1019–1031 (2009). (cited > 1000)
  53. Chunyuan Jin\*, **Chongzhi Zang**\*, Gang Wei, Kairong Cui, Weiqun Peng, Keji Zhao<sup>§</sup>, Gary Felsenfeld<sup>§</sup>. "H3.3/H2A.Z double variant-containing nucleosomes mark 'nucleosome-free regions' of active promoters and other regulatory regions." *Nature Genetics* 41, 941–945 (2009). (cited > 800)
  54. Yasuto Araki\*, Zhibin Wang\*, **Chongzhi Zang**, William H. Wood, Dustin E. Schones, Kairong Cui, Tae-Young Roh, Brad Lhotsky, Robert P. Wersto, Weiqun Peng, Kevin G. Becker, Keji Zhao<sup>§</sup>, Nan-ping Weng<sup>§</sup>. "Genome-wide analysis of histone methylations reveals chromatin state-based regulation of gene transcription and function of memory CD8+ T cells." *Immunity* 30, 912–925 (2009).

55. **Chongzhi Zang**, Dustin E. Schones, Chen Zeng, Kairong Cui, Keji Zhao, Weiqun Peng. "A clustering approach for identification of enriched domains from histone modification ChIP-Seq data." *Bioinformatics* 25, 1952–1958 (2009). (cited > 900)
56. Gang Wei\*, Lai Wei\*, Jinfang Zhu, **Chongzhi Zang**, Jane Hu-Li, Zhengju Yao, Kairong Cui, Yuka Kanno, Tae-Young Roh, Wendy Watford, Dustin E. Schones, Weiqun Peng, Hong-wei Sun, William E. Paul, John J. O'Shea<sup>§</sup>, Keji Zhao<sup>§</sup>. "Global mapping of H3K4me3 and H3K27me3 reveals specificity and plasticity in lineage fate determination of differentiating CD4<sup>+</sup> T cells." *Immunity* 30, 155–167 (2009). (cited > 1000)
57. Kairong Cui\*, **Chongzhi Zang\***, Tae-Young Roh, Dustin E. Schones, Richard W. Childs, Weiqun Peng, Keji Zhao. "Chromatin signatures in multipotent hematopoietic stem cells indicate the fate of bivalent genes during differentiation." *Cell Stem Cell* 4, 80–93 (2009). (cited > 600)
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60. **ZANG Chongzhi**, ZHANG Jietian<sup>§</sup>, PENG Peizhi. "Experimental study of the relationship between NMR relaxation time and the concentration of solutions." *Physics Bulletin* (ISSN 0509-4038) 2005 (10), 30–32 (2005). (In Chinese)
61. **ZANG Chongzhi**, ZHANG Jietian<sup>§</sup>, PENG Peizhi. "Discussion of data processing method for measuring NMR relaxation time." *Physics Experimentation* (ISSN 1005-4642) 25(5), 45–47 (2005). (In Chinese)
62. **ZANG Chongzhi**, PENG Peizhi, ZHANG Jietian<sup>§</sup>, LU Sihua. "Teaching experimentation of MRI." *Physics Experimentation* (ISSN 1005-4642) 24(8), 3–7 (2004). (In Chinese)

#### **Peer-reviewed Conference Papers/Abstracts**

63. William F. Lamberti, **Chongzhi Zang**. "Quantifying differences between machine learning classification models applied to cancer microscopy data." *Microscopy and Microanalysis* 28 (S1), 3006–3008 (2022).
64. Jingyuan Chou, Stefan Bekiranov, **Chongzhi Zang**, Mengdi Huai, Aidong Zhang. "Analysis of meta-learning approaches for TCGA pan-cancer datasets." *IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM)* December 16. (2020).
65. Zhenjia Wang, Wenjing Ma, Yifan Zhang, Neal E Magee, Yang Chen, **Chongzhi Zang**. "BART: An integrative bioinformatics toolkit and web server for functional transcription factor prediction." *Cancer Research* 80 (16 Supplement), 3214. *AACR Annual Meeting Abstract* 3214 (2020).



66. Celestia Fang, Zhenjia Wang, Carlos A. Martinez, Panagiotis Ntziachristos, **Chongzhi Zang**. "Global alteration of CTCF binding in the cancer genome." **Cancer Research** 79 (13 Supplement), 5181. *AACR Annual Meeting Abstract 5181* (2019).
67. Tengfei Xiao, Wei Li, Xiaoqing Wang, Han Xu, Qiu Wu, Peng Jiang, Jixin Yang, Teng Fei, **Chongzhi Zang**, Qi Liao, Jonathan Rennhack, Eran Andrechek, Nanlin Li, Rinath Jeselsohn, X. Shirley Liu, Myles Brown. "CRISPR screens identified drivers of endocrine resistance and synthetic lethal vulnerabilities in breast cancer." **Molecular Cancer Therapeutics** 16(10 Supplement), PR06. In: *Proceedings of the AACR Precision Medicine Series: Opportunities and Challenges of Exploiting Synthetic Lethality in Cancer* (2017).
68. **Chongzhi Zang\***, Tao Wang\*, Ke Deng, Bo Li, Sheng'en Hu, Qian Qin, Tengfei Xiao, Shihua Zhang, Clifford A. Meyer, Housheng Hansen He, Myles Brown, Jun S. Liu, Yang Xie, X. Shirley Liu. "High-dimensional genomic data integration and bias correction using MANCIE." **Cancer Research** 76, B24. *AACR Special Conference: Chromatin and Epigenetics in Cancer* (2015).
69. Hongfang Wang, Yumi Yashiro-Ohtani, **Chongzhi Zang**, Yinling Joey Wong, Will Bailis, Birgit Knoechel, Bradley Bernstein, Steve Blacklow, X Shirley Liu, Warren S Pear, Jon C Aster. "Alternative Super-Enhancer States Determine MYC Sensitivity to Notch and Brd4 Inhibitors in T Lymphoblastic Leukemia/Lymphoma." **Blood** 124 (21), *ASH Annual Meeting Abstracts* 863 (2014).
70. Hongfang Wang\*, **Chongzhi Zang\***, Len Taing, Hoifung Wong, Yumi Yashiro-Ohtani, Stephen Blacklow, Warren S. Pear, X. Shirley Liu, Jon C. Aster. "Genome-wide analysis of NOTCH1, ETS family factors, and RUNX1 binding in human T lymphoblastic leukemia cells reveals distinct regulatory elements." **Blood** 120 (21), *ASH Annual Meeting Abstracts* 1277 (2012).
71. Hong Hao, Douglas S. Kim, Kory Johnson, **Chongzhi Zang**, Kairong Cui, Janina Gregorski, Fann Yang, Keji Zhao, Anand Swaroop. "Chip-seq aided elucidation of Nrl-centered transcription regulatory network and implications for retina degeneration." **Investigative Ophthalmology and Visual Science** 52 (6), 38 (2011).
72. Kalpana Subedi, Yasuto Araki, Supriyo De, William Wood, Alexei Sharov, **Chongzhi Zang**, Dustin Schones, Brad Lhotsky, Dawood Dudekula, Kevin Becker, Minoru Ko, Weiqun Peng, Keji Zhao, Nan-ping Weng. "Dynamic changes of gene expression in concordance with histone modifications in CD8 T cells after activation." **The Journal of Immunology** 186, 159.2 (2011).
73. Hong Hao, Douglas S. Kim, Kory Johnson, **Chongzhi Zang**, Kairong Cui, Janina Gregorski, Fann Yang, Keji Zhao, Anand Swaroop. "Global target analysis of Nrl, the key transcriptional regulator of photoreceptor differentiation and homeostasis." **Investigative Ophthalmology and Visual Science** 51 (5), 5952 (2010).
74. **Chongzhi Zang**, Dustin E. Schones, Chen Zeng, Kairong Cui, Keji Zhao, Weiqun Peng. "Genome-wide identification of ChIP-Seq enriched regions based on a statistical model." In: **Proceedings of the 7th Asia-Pacific Bioinformatics Conference**, edited by Michael Q. Zhang, Michael S. Waterman, Xuegong Zhang. Beijing: Tsinghua University Press, 835 (2009).

## SOFTWARE AND RESOURCES

1. SICER: Spatial-clustering approach for the Identification of ChIP-Enriched Regions, a ChIP-Seq data analysis method and software package. <http://home.gwu.edu/~wpeng/Software.htm>
2. RECOGNICER: Recursive Coarse-Graining approach for the Identification of ChIP-Enriched Regions, a ChIP-Seq ultra-broad peak calling method. <https://github.com/zanglab/reconicer>
3. MANCIE: Matrix Analysis and Normalization by Concordant Information Enhancement, a computational method for high-dimensional genomic data integration. <https://cran.r-project.org/web/packages/MANCIE/>
4. MARGE: Model-based Analysis of Regulation of Gene Expression, a comprehensive computational method for inference of cis-regulation of gene expression leveraging public H3K27ac genomic profiles in human or mouse. <http://cistrome.org/MARGE/>
5. BART: Binding Analysis for Regulation of Transcription, a bioinformatics tool for predicting functional transcription factors that bind at genomic cis-regulatory regions to regulate gene expression in the human or mouse genomes, given a query gene set or a ChIP-seq dataset as input. <https://zanglab.github.io/bart/>
6. BART3D: Binding Analysis for Regulation of Transcription for Three-Dimensional (3D) genomics data, a bioinformatics tool for identifying transcription regulators associated with genomic regions with differential chromatin interactions, given a pair of Hi-C datasets as input. <https://github.com/zanglab/bart3d>
7. BARTweb: Interactive web server for performing BART analysis. <http://bartweb.org>
8. SICER2: An updated bioinformatics tool for SICER: Identification of broad enriched regions from ChIP-seq data. <https://zanglab.github.io/SICER2/>
9. BART Cancer: A database resource for computationally predicted transcriptional regulator activities in 15 human cancers from The Cancer Genome Atlas (TCGA). <https://zanglab.github.io/bartcancer/>
10. SELMA: Simplex Encoded Linear Model for Accessible chromatin, a computational model to accurately estimate and correct intrinsic enzymatic cleavage biases in chromatin accessibility profiling data. <https://github.com/zang-lab/SELMA>
11. IGN: Invariable Gene Normalization, a gene set based normalization method for chromatin accessibility profile data analysis. <https://github.com/zang-lab/IGN>

## HONORS AND AWARDS

- |                                                                                                                         |      |
|-------------------------------------------------------------------------------------------------------------------------|------|
| • University of Virginia Research Award                                                                                 | 2021 |
| • University of Virginia Research Excellence Award<br>(highest research award for junior faculty across the university) | 2020 |
| • MilliPub Club, University of Virginia School of Medicine                                                              | 2018 |

- Seed Award, Jayne Koskinas Ted Giovanis Foundation for Health and Policy 2018
- Phi Beta Psi Sorority National Project Research Grant 2018
- Travel Award, Harvard Program in Quantitative Genomics 2014
- Leukemia and Lymphoma Society Fellow Award 2012–2015
- Dimitris N. Chorafas Foundation Prize 2010
- Parke Prize in Theoretical Physics, The George Washington University 2009
- The Best Poster Award, the 7th Asia-Pacific Bioinformatics Conference 2009
- Chinese Government Award for Outstanding Self-financed Student Abroad 2008
- Student Travel Grant Award for March Meeting, American Physical Society 2008
- 2nd Award for Undergraduate Research, School of Physics, Peking University 2004
- Peking University Freshman Fellowship 2001
- 1st Prize, Beijing Region; 3rd Prize, National Final, Chinese Physics Olympiad 2000

## RESEARCH SUPPORT

Total award amount includes both direct and indirect costs funded to Dr. Zang's institution.  
Annual direct cost refers to the amount funded to Dr. Zang's lab per year.

### *Current Research Support*

1. NIH R35 GM133712 PI: Zang 09/01/2019–07/31/2024  
Integrative computational models for functional epigenomics and transcriptional regulation  
(Maximizing Investigators' Research Award, MIRA)  
Role: PI
2. NIH R01 AI112579 MPI: Xue & Zang 05/01/2020–04/30/2025  
Tcf1 programs recall and reverses exhaustion in CD8 T cell response  
Role: MPI
3. Virginia Commonwealth Health Research Board PI: Zang 05/01/2021–04/30/2023  
Aberrant CTCF binding as an epigenetic signature of cancer  
Role: PI
4. NSF IIS-2106913 PI: Zhang 10/01/2021–09/30/2024  
Knowledge-guided meta learning for multi-omics survival analysis  
Role: co-PI
5. NIH R01 NS115531 PI: Zhu 07/01/2019–06/30/2023  
Investigating and targeting pathways of malignant peripheral nerve sheath tumor (MPNST)  
Role: Subcontract PI
6. NIH R01 ES031402 MPI: Cuddapah, Costa 01/01/2020–10/31/2024  
Persistent transcriptional changes induced by nickel through epigenetic alterations  
Role: Subcontract PI
7. NIH R01 NS116421 PI: Zhu 04/01/2021–03/31/2026  
Developmental origin, injury and epigenomic regulation of NF1-associated peripheral nerve sheath tumors  
Role: Subcontract PI

8. NIH R01 HL148239 PI: Miller 06/01/2019–04/30/2024  
Cis-regulatory architecture of coronary vascular wall loci  
Role: Co-Investigator
9. NIH R01 HL149893 PI: Mohi 01/01/2020–12/31/2023  
The role of PTPN11 in myelofibrosis  
Role: Co-Investigator
10. DOD/W81XWH-21-1-0008 PI: Mohi 01/01/2021–12/31/2023  
Novel targeted therapy for metastatic triple-negative breast cancer  
Role: Co-Investigator
11. NIH R01 GM132138 PI: Li 09/01/2019–07/31/2023  
Genome-wide investigation of cis-splicing between adjacent genes  
Role: Collaborator
12. NIH/NCI R01 CA259573 PI: Jiang 01/01/2022–12/31/2026  
Role of UTX condensation in chromatin regulation  
Role: Co-Investigator
13. Chan Zuckerberg Initiative PI: Miller 07/01/2022–12/31/2023  
MetaPlaQ: Integrative single-cell meta-analysis for atherosclerosis  
Role: Co-PI

***Completed Research Support***

14. NIH/NCI K22 CA204439 PI: Zang 09/01/2017–08/31/2019\*  
Quantitative modeling for chromatin regulation of gene expression in cancer  
Role: PI  
\* Funded for 3 years but Year 03 fund was relinquished on 08/31/2019 due to Dr. Zang's funding of NIGMS MIRA (R35) award.
15. Phi Beta Psi Charity Trust Research Grant PI: Zang 08/15/2018–08/14/2020  
Integrative modeling of multi-source genomic data for functional gene regulation in colorectal cancer  
Role: PI
16. DOD/CDMRP Impact Award PI: Mohi 09/01/2019–06/30/2022  
Targeted therapies for myeloproliferative neoplasms  
Role: Co-Investigator
17. NIH U01 AG070960 PI: Yan 09/30/2020–05/31/2022  
Machine learning-based multi-omics modeling and CRISPR/Cas9-mediated gene editing in elucidating molecular transducer of physical activity  
Role: Co-Investigator
18. NIH/NIEHS R01 ES024727 PI: Cuddapah 02/01/2017–06/30/2020  
Epigenetic reprogramming by nickel through chromatin domain disruption  
Role: Subcontract PI

19. NFRI MPNST Pre-Clinical Research PI: Zhu 07/01/2018–01/31/2020  
Involvement of PRC2 in malignant transformation and metastatic spread of NF1-associated MPNSTs  
Role: Subcontract PI
20. Jayne Koskinas Ted Giovanis Foundation for Health and Policy Seed Award 8/1/18–6/30/19  
Inferring lineage program regulating transcription factors for neuronal cell type identity from multi-modal single cell transcriptome and epigenome data  
Role: Co-PI
21. American Cancer Society IRG 81-001-26 PI: Zang 12/18/2017–12/17/2018  
Integrative modeling of functional gene regulation in colorectal cancer  
Role: Project PI
22. Leukemia & Lymphoma Society Fellowship PI: Zang 07/01/2012–06/30/2015  
Computational studies on transcriptional regulation of Notch1 in T-ALL  
Role: PI

## TEACHING

Spring 2017–	University of Virginia	
	• BIMS 8601: Foundations of Computational Genomics	Co-instructor
	• BIOC 8014: Chromatin II	Co-instructor
	• BIOC 8145: Bioinformatics & Functional Analysis of Genomes	Co-instructor
	• PHS 5705: Recent Advances in Public Health Genomics	Co-instructor
	• BIMS 6000: Core Course in Integrative Biosciences: Genome Architecture & Dynamics	Co-instructor
	• BME 1501: Introduction to Bioinformatics	Guest Lecture
	• BIMS 7100: Research Ethics	Co-instructor
	• BIOL 4910: Undergraduate Research	Mentor
	• CHEM 3951: Undergraduate Research	Mentor
04/2021	New York University EHSC-GA-2050: Epigenetics and Environmental Diseases	Guest Lecture
05/2016	NIH/NCI Bioinformatics Workshop	Guest Instructor
11/2014	NIH/NCI Bioinformatics Workshop	Guest Instructor
09/2005–05/2008	The George Washington University Physics 001, Physics 002 Astronomy 001, Astronomy 002	Teaching Assistant Lab & Recitation Lab Instructor

## INVITED TALKS

1. Distinguished Lectures in Genetics Seminar Series, Cincinnati Children's Hospital Medical Center, Cincinnati, OH. (invited for 06/27/2023)
2. Oncological Data Science seminar series, Moffitt Cancer Center. Tampa, FL. 09/20/2022
3. International Conference on Intelligent Biology and Medicine (ICIBM 2022). Philadelphia, PA. 08/08/2022
4. Computational Biology Program, Boston Children's Hospital, Harvard Medical School. Boston, MA. 07/29/2022
5. Department of Computational Biomedicine, Cedars-Sinai Medical Center, Los Angeles, CA. 05/31/2022
6. Department of Biology, Johns Hopkins University. Baltimore, MD. 12/03/2021
7. Division of Biostatistics and Bioinformatics, Department of Epidemiology and Public Health and Department of Neurosurgery, University of Maryland School of Medicine. Baltimore, MD. 06/03/2021
8. Department of Environmental Medicine, New York University. New York, NY. 05/11/2021
9. Child Health Research Center, University of Virginia. Charlottesville, VA. 04/23/2021
10. Foundation of Biomedical Data Science Seminar Series, University of Virginia School of Data Science. Charlottesville, VA. 04/02/2021
11. Computational Biology and Bioinformatics Seminar Series, Duke University. Durham, NC. 03/29/2021
12. Center for Cancer Genomics, Department of Biochemistry and Molecular Genetics, Northwestern University. Chicago, IL. 12/09/2020
13. 14th International Bioinformatics Workshop (IBW 2019), Beijing, China. 08/03/2019
14. State Key Laboratory of Cardiovascular Disease, Peking Union Medical College. Beijing, China. 07/31/2019
15. School of Mathematics, Shandong University. Jinan, China. 07/29/2019
16. Department of Cognitive Science, University of California, San Diego, CA. 12/20/2018
17. Biomedical Pioneering Innovation Center, Peking University. Beijing, China. 08/21/2018
18. Department of Pathology, University of Virginia. Charlottesville, VA. 12/19/2017
19. Department of Biostatistics, Virginia Commonwealth University. Richmond, VA. 11/3/2017
20. Center for Quantitative Biology, Peking University. Beijing, China. 09/29/2017
21. Institute of Biophysics, Chinese Academy of Sciences. Beijing, China. 09/28/2017
22. Beijing Institute for Scientific and Engineering Computing, Beijing University of Technology. Beijing, China. 09/27/2017
23. Center for Statistical Science, Tsinghua University. Beijing, China. 09/25/2017
24. Department of Physics, Fudan University. Shanghai, China. 09/23/2017
25. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Shanghai, China. 09/18/2017
26. School of Life Sciences, Peking University. Beijing, China. 06/08/2016
27. Workshop on Analysis of ChIP-Seq Data, National Cancer Institute, National Institutes of Health. Bethesda, MD. 05/17/2016
28. Laboratory of Genome Integrity, National Cancer Institute, National Institutes of Health. Bethesda, MD. 04/07/2016

29. Department of Immunobiology, Yale University. New Haven, CT. 03/11/2016
30. University of Virginia. Charlottesville, VA. 02/05/2016
31. The Wistar Institute. Philadelphia, PA. 01/29/2016
32. Academy of Mathematics and Systems Science, Chinese Academy of Sciences. Beijing, China. 01/07/2016
33. Peking University Third Hospital. Beijing, China. 01/05/2016
34. Peking University Medical Center. Beijing, China. 01/04/2016
35. University of Illinois College of Medicine, Peoria, IL. 12/17/2015
36. The Stadtman Symposium, National Institutes of Health. Bethesda, MD. 12/10/2015
37. National Heart, Lung, and Blood Institute, National Institutes of Health. Bethesda, MD. 11/20/2015
38. University of Nevada School of Medicine, Reno, NV. 10/06/2015
39. College of Pharmacy, University of Rhode Island. Kingston, RI. 06/24/2015
40. Uniformed Services University of the Health Sciences. Bethesda, MD. 05/29/2015
41. Department of Electrical & Computer Engineering, University of Nebraska, Lincoln, NE. 02/18/2015
42. National Human Genome Research Institute, National Institutes of Health. Bethesda, MD. 02/04/2015
43. National Cancer Institute, National Institutes of Health. Bethesda, MD. 12/19/2014
44. Cancer epigenetics symposium, Harvard Medical School. Boston, MA. 12/14/2014
45. Biophysics Seminar, The George Washington University. Washington, DC. 10/02/2014
46. Workshop on big data analysis in biomedical research, Harvard Medical School. Boston, MA. 06/24/2014
47. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Shanghai, China. 11/28/2013
48. Institute of Systems Biomedicine, Shanghai Jiao Tong University. Shanghai, China. 11/26/2013
49. Computational Biology and Bioinformatics Organization, Broad Institute. Cambridge, MA. 10/16/2013
50. Megakaryocyte and Platelet Biology Joint Meeting, Boston Children's Hospital. Boston, MA. 09/12/2012
51. Department of Animal and Avian Sciences, College of Agriculture and Natural Resources, University of Maryland, College Park, MD. 09/28/2009

## CONTRIBUTED PRESENTATIONS

1. ISMB 2022: 30th Conference on Intelligent Systems for Molecular Biology. Madison WI, 07/2022. (*Poster*)
2. Gordon Research Conference on Single-Cell Cancer Biology. Easton, MA, 06/2022. (3 *Posters presented by lab members*)
3. Cold Spring Harbor Meeting on Systems Biology: Global Regulation of Gene Expression, 03/2022. (3 *Posters presented by lab members*)

4. Cold Spring Harbor Meeting on Mechanisms of Eukaryotic Transcription, 09/2021. (*Poster presented by a lab member*)
5. Cold Spring Harbor Meeting on Eukaryotic DNA Replication & Genome Maintenance, 09/2021. (*Poster presented by a lab member*)
6. 2021 NHLBI Systems Biology Symposium (Virtual), 05/2021. (*5 Posters presented by lab members*)
7. American Association for Cancer Research (AACR) Annual Meeting (Virtual), 04/2021. (*Poster*)
8. American Physical Society (APS) March Meeting (Virtual), 03/2021. (*Talk*)
9. American Association for Cancer Research (AACR) Annual Meeting (Virtual), 06/2020. (*Poster*)
10. iPoLS 2020: International Physics of Living Systems Annual Meeting (Virtual), 06/2020. (*Poster*)
11. Cold Spring Harbor Meeting on Systems Biology: Global Regulation of Gene Expression (Virtual), 03/2020. (*Poster presented by a lab member*)
12. Keystone Meeting on Cancer Epigenetics. Keystone, CO, 01/2020. (*Poster*)
13. Physics Meets Biology 2019, Institute of Physics, University of Oxford. Oxford, UK, 09/2019. (*Poster*)
14. RECOMB 2019: 23rd Annual International Conference on Research in Computational Molecular Biology. Washington, DC, 05/2019 (*5 Posters presented by lab members*)
15. Gordon Research Conference on Cancer Genetics and Epigenetics. Lucca, Italy, 04/2019. (*Poster*)
16. American Association for Cancer Research (AACR) Annual Meeting. Atlanta, GA, 04/2019. (*Poster*)
17. American Physical Society (APS) March Meeting. Boston, MA, 03/2019. (*Talk*)
18. ISMB 2018: Conference on Intelligent Systems for Molecular Biology. Chicago, IL, 07/2018. (*Poster*)
19. Biophysics of Epigenetic and Chromatin Dynamics Workshop, Higgs Centre for Theoretical Physics, University of Edinburgh. Edinburgh, UK, 04/2018. (*Poster*)
20. American Physical Society (APS) March Meeting. Los Angeles, CA, 03/2018. (*Talk*)
21. Keystone Meeting on Cancer Epigenetics. Breckenridge, CO, 02/2018. (*Poster*)
22. Cold Spring Harbor Asia Meeting on Precision Cancer Biology. Suzhou, China, 09/2017. (*Poster*)
23. Keystone Meeting on Epigenetics and Human Disease. Seattle, WA, 01/2017. (*Poster*)
24. NCI Symposium on Chromosome Biology. Bethesda, MD, 11/2016. (*Poster*)
25. ENCODE Consortium Meeting. San Diego, CA, 06/2016. (*Poster*)
26. AACR Special Conference on Chromatin and Epigenetics in Cancer. Atlanta, GA, 09/2015. (*Poster*)
27. Keystone Meeting on Cancer Epigenetics. Santa Fe, NM, 02/2014. (*Poster*)
28. NCI Symposium on Chromosome Biology. Bethesda, MD, 04/2013. (*Poster*)
29. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2012. (*Poster*)



30. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2010. (*Poster*)
31. The 7th Asia Pacific Bioinformatics Conference. Beijing, China, 01/2009. (*Best Poster Award Winner*)
32. American Physical Society (APS) March Meeting. New Orleans, LA, 03/2008. (*Talk*)

## **MENTEES AND STUDENTS**

### ***Postdoctoral Associates Mentored***

1. Zhenjia Wang, PhD (UVA, 01/2017–)
2. Sheng'en Shawn Hu, PhD (UVA, 11/2017–)
3. Christopher Dampier, MD (UVA, joint with Graham Casey, 07/2019–05/2021)
4. Qingying Chen, PhD (UVA, 01/2021–)
5. William F. Lamberti, PhD (UVA, 01/2021–08/2022)
6. Yidan Cong, PhD (UVA, 06/2021–02/2022)
7. Shengyuan Wang, PhD (UVA, 03/2022–)

### ***Graduate Students Mentored***

1. Wuwei Tan (MS in Statistics, UVA, 03/2017–05/2018)
2. Yushan Brandon Feng (MS in Statistics, UVA, 05/2018–05/2019)
3. Seung Hyun Lee (MS in Statistics, UVA, 09/2018–05/2019)
4. Yifan Zhang (Biomedical Engineering, UVA, 08/2018–12/2019)
5. Audrey Putelo (PhD in Biomedical Sciences, UVA. Rotation 07/2020–08/2020)
6. Jose Verdezoto (PhD in Biomedical Sciences, UVA, Rotation 10/2020–11/2020)
7. Jamel Simpson (PhD in Biomedical Sciences, UVA, Rotation 1/2021–2/2021)
8. Mengxue Tian (PhD in Biomedical Sciences, UVA, 07/2021–)
9. Hongpan Zhang (PhD in Biomedical Sciences, UVA, 07/2021–)
10. Zhaoxia Ma (PhD in Biomedical Sciences, UVA, 09/2021–)

### ***PhD Thesis Committee Service***

1. Jeffrey Xing (PhD in Biomedical Engineering, UVA, 01/2017–10/2020)
2. Celestia Fang (PhD in Biochemistry and Molecular Genetics, Northwestern University Feinberg School of Medicine, 09/2018–06/2021)
3. Evan Tarbell (PhD in Biochemistry, University at Buffalo, 11/2018–12/2018)
4. Justin Elfman (PhD in Biochemistry and Molecular Genetics, UVA, 06/2019–)
5. Yang Yu (PhD in Biology, UVA, 12/2020–)
6. Yuanming Liu (PhD in Biology, UVA, 1/2021–)
7. Samuel Haddox (PhD in Biochemistry and Molecular Genetics, UVA, 02/2021–, Committee Chair)
8. Jacob Wolpe (PhD in Cell Biology, UVA, 07/2021–)
9. Nicole Kirk (PhD in Microbiology, Immunology, and Cancer Biology, UVA, 12/2021–)
10. Jose Verdezoto (PhD in Biochemistry and Molecular Genetics, UVA, 05/2022–, Committee Chair)

### ***Undergraduate Student Research Supervised***

1. Celina Shih (Johns Hopkins University, 05/2017–07/2017)
2. Yayi Feng (UVA, 09/2017–05/2020)
3. Stephany Perez-Rojas (UVA, 01/2018–05/2020)
4. John Zhang (UVA, 02/2018–05/2020)
5. Yuantao Chen (UVA, 02/2018–05/2021)
6. Jeffrey Yoo (UVA, 02/2018–05/2020)
7. Naifei Pan (UVA, 04/2018–02/2019)
8. Alexander An (UVA, 05/2018–08/2018)
9. Zhou Lu (UVA, 08/2018–05/2020)
10. Allison Ryu (UVA, 09/2018–12/2018)
11. Aaron Ho (UVA, 10/2018–05/2020)
12. Benjamin Ke (UVA, 01/2019–07/2022)
13. Sophia Park (UVA, 01/2019–08/2019)
14. Tianhe Li (UVA, 01/2019–05/2020)
15. Leyao Li (UVA, 03/2019–05/2020)
16. Megan Grieco (UVA, 04/2019–07/2022)
17. Xinyue Qiu (UVA, 04/2019–05/2021)
18. Zack Thomas (UVA, 04/2019–05/2021)
19. Sekou Rowe (NSF REU student, Howard University, 05/2019–08/2019)
20. Minaal Khan (UVA, 09/2019–08/2021)
21. Kendall Davis (UVA, 10/2019–08/2021)
22. Anvitha Chimata (UVA, 10/2019–08/2021)
23. Andrew Vanichkachorn (UVA, 10/2019–07/2022)
24. Jingwen Wang (UVA, 01/2020–05/2021)
25. Emilie Neulen (UVA, 02/2020–08/2022)
26. Kuki Davey (UVA, 07/2020–05/2022)
27. Alex Hickman (UVA, 07/2020–05/2021)
28. Ivory Tang (UVA, 08/2021–)
29. Jingyi Wang (UVA, 07/2022–)
30. Andy Cao (UVA, 08/2022–)

### ***Visiting Students/Scholars Supervised***

1. Yiren Wang (Graduate from Peking University, 07/2017–06/2018)
2. Qi Li (PhD Candidate in Statistics, Tsinghua University, 01/2018–02/2018, 03/2019)
3. Wen Shen (Undergraduate Student, Nanjing University, 02/2018–05/2018)
4. Rongquan He, MD (PhD Candidate, Guangxi Medical University, 03/2018–02/2019)
5. Wenjing Ma (Graduate from Beijing University of Posts and Telecommunications, 08/2018–06/2019)
6. Gang Chen, MD, PhD (Professor of Pathology, Guangxi Medical University, 09/2018–08/2019)
7. Ruoyao Shi (Undergraduate Student, Jilin University, 10/2019–05/2020)

### ***High School Students Supervised***

1. Katherine Zhang (Thomas Jefferson High School for Science and Technology, Class of 2024, 06/2022–08/2022)
2. Elizabeth McClung (Rockbridge County High School, Class of 2023, UVA Advance Summer Program, 07/2022–08/2022)
3. Riya Shah (McLean High School, Class of 2023, UVA Advance Summer Program, 07/2022–08/2022)

4. Chris Stewart (Monticello High School, Class of 2023, UVA Advance Summer Program, 07/2022–08/2022)

## PROFESSIONAL SERVICE

<i>Ad hoc grant reviewer</i>	<p>UK Research and Innovation (UKRI): Medical Research Council (MRC, RCUK) (2017) Biotechnology and Biological Sciences Research Council (BBSRC, UKRI) (2022)</p> <p>Netherlands Organisation for Scientific Research (NWO) (2017)</p> <p>US National Institutes of Health (NIH) Center for Scientific Review:</p> <ul style="list-style-type: none"><li>• ZRG1 PSE-B (04): Epidemiology and Statistical Methods Special Emphasis Panel (03/2020)</li><li>• ZMH1 ERB-M (06): BRAIN Initiative Cell Census Network (BICCN) Special Emphasis Panel (07/2020)</li><li>• ZRG1 CB-K (55): Maximizing Investigators' Research Award (MIRA) for Early Stage Investigators (ESI) Special Emphasis Panel (03/2021)</li><li>• ZRG1 GGG-S (55): Maximizing Investigators' Research Award (MIRA) for Early Stage Investigators (ESI) Special Emphasis Panel (03/2022)</li><li>• ZRG1 MGG-C (55) Maximizing Investigators' Research Award (MRAA) Special Emphasis Panel (11/2022)</li></ul> <p>Inova Translational Research Funding Program (2018)</p> <p>UVA internal review committee for Virginia CHRB awards (2021)</p> <p>UVA Carter Immunology Center internal review committee (2021)</p>
<i>Ad hoc journal reviewer</i>	<p><i>Nature Biotechnology</i></p> <p><i>Nature Genetics</i></p> <p><i>Nature Methods</i></p> <p><i>Nature Communications</i></p> <p><i>Genome Research</i></p> <p><i>Genome Biology</i></p> <p><i>EMBO Journal</i></p> <p><i>Nucleic Acids Research</i></p> <p><i>Cancer Research</i></p> <p><i>Cellular and Molecular Life Sciences</i></p> <p><i>Bioinformatics</i></p> <p><i>Briefings in Bioinformatics</i></p> <p><i>Epigenetics</i></p> <p><i>PLOS Computational Biology</i></p> <p><i>BMC Bioinformatics</i></p> <p><i>BMC Genomics</i></p> <p><i>Breast Cancer Research</i></p> <p><i>Journal of the American Statistical Association</i></p> <p><i>Scientific Reports</i></p> <p><i>iScience</i></p> <p><i>Cell Discovery</i></p>

*Communications Biology*  
*Open Biology*  
*PLOS One*  
*NAR Cancer*  
*Journal of Computational Biology*  
*Quantitative Biology*  
*IEEE/ACM Transactions on Computational Biology & Bioinformatics*  
*Computational Statistics and Data Analysis*  
*Biomolecules*  
*Frontiers of Medicine*  
*Frontiers in Oncology*

<i>Editorial Board Member</i>	<i>Immunoinformatics</i> (2022–)
<i>Topical Advisory Board</i>	<i>Epigenomes</i> (2021–)
<i>Guest Editor</i>	<i>PLOS Computational Biology</i> (2020–)
<i>Committee Co-Chair</i>	UVA Comprehensive Cancer Center Molecular Epidemiology Faculty Search Committee, 2022
<i>Faculty Mentor</i>	Biomedical Data Science Innovation Lab: Challenges in Brain Analytics and Integration, 2020–2021
<i>Co-Chair</i>	American Association for Cancer Research (AACR) Annual Meeting Minisymposium: Transcriptional Gene Regulation in Cancer, 2020
<i>Planning Committee</i>	Emerging Scholars in Genome Sciences Symposium, UVA, 2020– <i>Committee Chair</i> , 2021–

Updated: September 30, 2022