

## 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>Director of Computational Genomics</i> , UVA Cancer Center (07/2024–) <i>Associate Professor of Genome Sciences</i> , with Tenure (07/2024–) <i>Associate Professor of Biochemistry and Molecular Genetics</i> (07/2022–) <i>Associate Professor of Biomedical Engineering</i> (07/2022–) <i>Associate Professor of Public Health Sciences</i> (07/2022–06/2024) <i>Resident Faculty Member</i> , Center for Public Health Genomics (11/2016– transition to Department of Genome Sciences 07/2024) <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     **Institute of Physics, Chinese Academy of Sciences**, Beijing, China  
Undergraduate Research Assistant, High-field Physics Group (L05)  
(Thesis Advisor: Jie Zhang, PhD)

## PUBLICATIONS

### Peer-reviewed Journal Articles (reverse chronological order)

Total citations > 18,000; H-index = 42 (Google Scholar)

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

1. Wei Hu, Shengen Shawn Hu, Shaoqi Zhu, Weiqun Peng, Vladimir P. Badovinac, **Chongzhi Zang**, Xudong Zhao<sup>§</sup>, Hai-Hui Xue<sup>§</sup>. "Hdac1 as an early determinant of intermediate-exhausted CD8<sup>+</sup> T cell fate in chronic viral infection." *Proceedings of the National Academy of Sciences USA* in press (2025).
2. Yubao Cheng, Mengwei Hu, Bing Yang, Tyler B. Jensen, Yuan Zhang, Tianqi Yang, Ruihuan Yu, Zhaoxia Ma, Jonathan S. D. Radda, Shengyan Jin, **Chongzhi Zang**, Siyuan Wang. "Perturb-tracing enables high-content screening of multi-scale 3D genome regulators." *Nature Methods* (2025). doi: <https://doi.org/10.1038/s41592-025-02652-z>
3. Shengyuan Wang\*, Zhenjia Wang\*, **Chongzhi Zang**. "Genomic clustering tendency of transcription factors reflects phase-separated transcriptional condensates at super-enhancers." *Nucleic Acids Research* 53, gkaf015 (2025).
4. Shengen Shawn Hu, Hai-Hui Xue, **Chongzhi Zang**. "IGN: Invariable gene set-based normalization for chromatin accessibility profile data analysis." *Computational and Structural Biotechnology Journal* 27, 501–507 (2025).
5. Harish Narasimhan\*, In Su Cheon\*, Wei Qian\*, Shengen Shawn Hu\*, Tanyalak Parimon\*, Chaofan Li, Nick Goplen, Yue Wu, Xiaoqin Wei, Young Min Son, Elizabeth Fink, Gislane de Almeida Santos, Jinyi Tang, Changfu Yao, Lyndsey Muehling, Glenda Canderan, Alexandra Kadl, Abigail Cannon, Samuel Young, Riley Hannan, Grace Bingham, Mohammed Arish, Arka Sen Chaudhari, Jun sub Im, Cameron L. R. Mattingly, Patcharin Pramoonjago, Alberto Marchesvsky, Jeffrey Sturek, Jacob E. Kohlmeier, Yun Michael Shim, Judith Woodfolk, **Chongzhi Zang**<sup>§</sup>, Peter Chen<sup>§</sup>, Jie Sun<sup>§</sup>. "An aberrant immune–epithelial progenitor niche drives viral lung sequelae." *Nature* 634, 961–969 (2024).
6. Yen T.M. Nguyen, Lydia Sibley\*, Piotr Przanowski\*, Xiao-Yu Zhao\*, Michael Kovacs, Shengyuan Wang, Marieke K. Jones, Maureen Cowan, Wenjie Liu, Andrea R. Merchak, Alban Gaultier, Kevin Janes, **Chongzhi Zang**, Tajie Harris, Sarah E. Ewald<sup>§</sup>, Hui Zong<sup>§</sup>. "*Toxoplasma gondii* infection supports the infiltration of T cells into brain tumors." *Journal of Neuroimmunology* 393, 578402 (2024).
7. Nikolai G. Vetr<sup>§</sup>, Nicole R. Gay, MoTrPAC Study Group (including Benjamin G. Ke and **Chongzhi Zang**), Stephen B. Montgomery<sup>§</sup>. The impact of exercise on gene regulation in association with complex trait genetics. *Nature Communications* 15, 3346 (2024).
8. The MoTrPAC Study Group (including Benjamin G. Ke and **Chongzhi Zang**). "Temporal

dynamics of the multi-omic response to endurance exercise training." **Nature** 629, 174–183 (2024).

9. Mengxue Tian, Zhenjia Wang, Zhangli Su, Etsuko Shibata, Yoshiyuki Shibata, Anindya Dutta<sup>§</sup>, **Chongzhi Zang**<sup>§</sup>. "Integrative analysis of DNA replication origins and ORC-/MCM-binding sites in human cells reveals a lack of overlap." **eLife**, doi: <https://doi.org/10.7554/eLife.89548> (2024).
10. Heather M. Raimer Young, Pei-Chi Hou, Anna R. Bartosik, Naomi D. Atkin, Lixin Wang, Zhenjia Wang, Aakrosh Ratan, **Chongzhi Zang**, Yuh-Hwa Wang. "DNA fragility at topologically associated domain boundaries is promoted by alternative DNA secondary structure and topoisomerase II activity." **Nucleic Acids Research**, gkae164 (2024).
11. Xin Zhao, Wei Hu, Sung Rye Park, Shaoqi Zhu, Shengen Shawn Hu, **Chongzhi Zang**, Weiqun Peng, Qiang Shan<sup>§</sup>, Hai-Hui Xue<sup>§</sup>. "The transcriptional cofactor Tle3 reciprocally controls effector and central memory CD8<sup>+</sup> T cell fates." **Nature Immunology** 25, 294–306 (2024).
12. Hyun Jae Cho, Zhenjia Wang, Yidan Cong, Stefan Bekiranov, Aidong Zhang<sup>§</sup>, **Chongzhi Zang**<sup>§</sup>. "DARDN: a deep-learning approach for CTCF binding sequence classification and oncogenic regulatory feature discovery." **Genes** 15(2), 144 (2024).
13. Jose Verdezoto Mosquera, Gaëlle Auguste, Doris Wong, Adam W. Turner, Chani J. Hodonsky, Astrid Catalina Alvarez-Yela, Yipei Song, Qi Cheng, Christian L. Lino Cardenas, Konstantinos Theofilatos, Maxime Bos, Maryam Kavousi, Patricia A. Peyser, Manuel Mayr, Jason C. Kovacic, Johan L. M. Björkegren, Rajeev Malhotra, P. Todd Stukenberg, Alope V. Finn, Sander W. van der Laan, **Chongzhi Zang**, Nathan C. Sheffield, Clint L. Miller. "Integrative single-cell meta-analysis reveals disease-relevant vascular cell states and markers in human atherosclerosis." **Cell Reports** 42, 113380 (2023).
14. Yue Wu, Shengen Shawn Hu, Ruixuan Zhang, Nick P Goplen, Xiaochen Gao, Harish Narasimhan, Ao Shi, Yin Chen, Ying Li, **Chongzhi Zang**, Haidong Dong, Thomas J Braciale, Bibo Zhu<sup>§</sup>, Jie Sun<sup>§</sup>. "Single cell RNA sequencing unravels mechanisms underlying senescence-like phenotypes of Alveolar Macrophages." **iScience** 26, 107197 (2023).
15. Manikarna Dinda, Ryan D. Fine, Shekhar Saha, Zhenjia Wang, **Chongzhi Zang**, Mingguang Li, Jeffrey S. Smith. "Fob1-dependent condensin recruitment and loop extrusion on yeast chromosome III." **PLOS Genetics** 19(4), e1010705 (2023).
16. Hyun Jae Cho, Mia Shu, Stefan Bekiranov, **Chongzhi Zang**, Aidong Zhang. "Interpretable meta-learning of multi-omics data for survival analysis and pathway enrichment." **Bioinformatics**, btad113 (2023).
17. 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).
18. 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).

19. 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).
20. 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).
21. 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).
22. 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).
23. 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).
24. 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).
25. 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).
26. Zhenjia Wang, Yifang Zhang, **Chongzhi Zang**. “BART3D: Inferring transcriptional regulators from differential Hi-C data.” **Bioinformatics** 37, 3075–3078 (2021).
27. Wenjing Ma\*, Zhenjia Wang\*, 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).
28. Zachary V. Thomas, Zhenjia Wang, **Chongzhi Zang**. “BART Cancer: a web resource for transcriptional regulators in cancer genomes.” **NAR Cancer** 3, zcab011 (2021).

29. 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).
30. **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).
31. Celestia Fang\*, Zhenjia Wang\*, 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).
32. Danqi Chen\*, Qiao Yi Chen\*, Zhenjia Wang\*, 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).
33. The ENCODE Project Consortium (including **Chongzhi Zang**), Jill E. Moore\*, Michael J. Purcaro\*, Henry E. Pratt\*, Charles B. Epstein\*, Noam Shores\*, Jessika Adrian\*, Trupti Kawli\*, Carrie A. Davis\*, Alexander Dobin\*, Rajinder Kaul\*, Jessica Halow\*, Eric L. Van Nostrand\*, Peter Freese\*, David U. Gorkin\*, Yin Shen\*, Yupeng He\*, Mark Mackiewicz\*, Florencia Pauli-Behn\*, 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).
34. 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).
35. 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).
36. 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).
  37. 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).
  38. 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).
  39. 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).
  40. 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).
  41. 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).
  42. 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).
  43. 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).
  44. 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).
  45. 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).

46. 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).
47. 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).
48. 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).
49. 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).
50. 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).
51. **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).
52. **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).
53. 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).
54. 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).
55. Hilary K Finucane\*<sup>§</sup>, Brendan Bulik-Sullivan\*<sup>§</sup>, Alexander Gusev, Gosia Trynka, Yakir Reshef, Po-Ru Loh, Verneri 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).
56. 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).
  57. 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).
  58. 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).
  59. 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).
  60. 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).
  61. 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).
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  64. 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).



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66. 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).
67. 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).
68. 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)
69. 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 > 900)
70. 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).
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72. 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+ T cells." **Immunity** 30, 155–167 (2009). (cited > 1000)
73. 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 > 700)
74. Zhibin Wang\*, **Chongzhi Zang\***, Jeffrey A. Rosenfeld\*, Dustin E. Schones, Artem Barski, Suresh Cuddapah, Kairong Cui, Tae-Young Roh, Weiqun Peng, Michael Q. Zhang, Keji Zhao. "Combinatorial patterns of histone acetylations and methylations in the human

genome.” *Nature Genetics* 40, 897–903 (2008). (cited > 2000)

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78. **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 Book Chapter**

79. Qiuling Suo, Hyun Jae Cho, Jingyuan Chou, Stefan Bekiranov, **Chongzhi Zang**, Aidong Zhang. “Knowledge-guided meta learning for disease prediction.” In *Meta-Learning with Medical Imaging and Health Informatics Applications*. 253–273. Academic Press (2023).

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

80. Jing Gao, Kevin Qiu, Kallesh Danappa Jayappa, Qing Yin, Michelle Wang, Allen Hu, Danielle C Llanaeza, Loryn L Blackburn, Jeffrey W Craig, Bijal D Shah, Craig A Portell, Michael E Williams, **Chongzhi Zang**, Jianguo Tao. “Dysregulation of transcription machinery drives the acquisition of BTK inhibitor and Venetoclax treatment resistance in mantle cell lymphoma.” *Blood* 144 (Supplement 1), 6220. *ASH Annual Meeting Abstract* (2024).
81. Nicholas Dunham, Zhenjia Wang, Yaseswini Neelamraju, Yan Guo, Joyce Hardwick, Bernhard Maier, Cem Meydan, Jorge A. Gandara, Tak Lee, Subhash Prajapati, Franck Rapaport, Caroline Sheridan, Paul Zumbo, Michael W. Becker, Lars Bullinger, Martin P Carroll, Richard J. D’Andrea, Richard Dillon, Ross L. Levine, Christopher Mason, Ari M Melnick, Donna S. Neuberg, Stefan Bekiranov, **Chongzhi Zang**, Utpal P. Dave, Francine E. Garrett-Bakelman. “The LMO2-LDB1-TAL1 complex regulates transcription networks in AML relapse.” *Blood* 144 (Supplement 1), 2711. *ASH Annual Meeting Abstract* (2024).
82. Shengen Shawn Hu, Qingying Chen, Megan Grieco, **Chongzhi Zang**. “PATTY: A bias estimation and correction model for bulk and single-cell CUT&Tag data.” *Cancer Research* 84 (6 Supplement), 7435. *AACR Annual Meeting Abstract* 7435 (2024).
83. Shengyuan Wang, Zhenjia Wang, Yuh-Hwa Wang, Hui Li, P. Todd Stukenburg, **Chongzhi Zang**. “Integration analysis of lncRNAs and R-loops in 3D genome organization and gene regulation in the cancer genome.” *Cancer Research* 84 (6 Supplement), 7355. *AACR Annual Meeting Abstract* 7355 (2024).

84. Hongpan Zhang, Jingyi Wang, Zhenjia Wang, **Chongzhi Zang**. "BARTsc: A transcription factor analysis suite for single-cell omics data." **Cancer Research** 84 (6 Supplement), 2342. *AACR Annual Meeting Abstract* 2342 (2024).
85. Zhenjia Wang, Shengyuan Wang, **Chongzhi Zang**. "Genomic clustering tendency of transcription factors reflects phase-separated transcriptional condensates at cancer super-enhancers." **Cancer Research** 84 (6 Supplement), 1695. *AACR Annual Meeting Abstract* 1695 (2024).
86. Yubao Cheng, Tianqi Yang, Mengwei Hu, Bing Yang, Tyler Jensen, Ruihuan Yu, Zhaoxia Ma, Jonathan Radda, Shengyan Jin, **Chongzhi Zang**, Siyuan Wang "Perturb-tracing enables high-content screening of multiscale, global 3D genome regulators." **Biophysical Journal** 123 (3), Supplement 1, 83A (2024).
87. Subhash Prajapati, Cem Meydan, Richard Dillon, Nicholas Dunham, Hao Fan, Jorge A. Gandara, Tak Lee, Yaseswini Neelamraju, Caroline Sheridan, Zhenjia Wang, Paul Zumbo, Michael W. Becker, Lars Bullinger, Martin Carroll, Richard J. D'Andrea, Ross L. Levine, Christopher Mason, Ari M. Melnick, **Chongzhi Zang**, Stefan Bekiranov, Francine E. Garrett-Bakelman. "Loss of CCAAT-Enhancer Binding Protein Delta promotes acute myeloid leukemia cell proliferation and survival by upregulating cyclin D1 expression." **Blood** 142 (Supplement 1), 1380. *ASH Annual Meeting Abstract* (2023).
88. Mengxue Tian, Zhenjia Wang, Zhangli Su, Etsuko Shibata, Yoshiyuki Shibata, Anindya Dutta<sup>§</sup>, **Chongzhi Zang**<sup>§</sup>. "Integrative analysis of genome-wide DNA replication origins in human cells." **Cancer Research** 83 (7 Supplement), 3174. *AACR Annual Meeting Abstract* 3174 (2023).
89. Zhenjia Wang, Yaseswini Neelamraju, Cem Meydan, Nicholas Dunham, Jorge Gandara, Tak Lee, Subhash Prajapati, Franck Rapaport, Caroline Sheridan, Paul Zumbo, Michael Becker, Lars Bullinger, Martin Carroll, Richard D'Andrea, Richard Dillon, Ross Levine, Christopher E. Mason, Ari Melnick, Donna Neuberg, Stefan Bekiranov, **Chongzhi Zang**<sup>§</sup>, Francine E. Garrett-Bakelman<sup>§</sup>. "Gene expression profiles reveal distinct regulatory activities of transcription factors GATA1 and TAL1 upon AML relapse." **Cancer Research** 83 (7 Supplement), 3155. *AACR Annual Meeting Abstract* 3155 (2023).
90. Shengen Shawn Hu, Qingying Chen, Megan Grieco, Lin Liu, **Chongzhi Zang**. "Accurate estimation of open chromatin and intrinsic biases in bulk and single-cell CUT&Tag data." **Cancer Research** 83 (7 Supplement), 871. *AACR Annual Meeting Abstract* 871 (2023).
91. 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).
92. 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).
93. 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).

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95. 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).
96. **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).
97. 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).
98. 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).
99. 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).
100. 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).
101. 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).
102. **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).

## Manuscripts Under Review/Preprints

103. Zhangli Su\*, Mengxue Tian\*, Etsuko Shibata, Yoshiyuki Shibata, Tianyi Yang, Zhenjia Wang, Fulai Jin, **Chongzhi Zang**<sup>§</sup>, Anindya Dutta<sup>§</sup>. "Regulation of epigenetics and chromosome structure by human ORC2." under revision (2025). Preprint at *bioRxiv* doi: <https://doi.org/10.1101/2024.12.18.629220>

## 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/recongnicer>
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

- Dean's Excellence in Faculty Research Award, UVA School of Medicine 2024
- Vivian Pinn Scholar Award, UVA School of Medicine 2024
- University of Virginia Research Award Honor Mention 2021
- University of Virginia Research Excellence Award 2020  
(UVA junior faculty's highest research honor; only recipient from School of Medicine)
- 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 GM133712-06 (MIRA) PI: Zang 09/21/2024–07/31/2029  
Integrative computational models for functional epigenomics and transcriptional regulation  
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: **PI**
3. NIH R21 HG012981 PI: Zang 09/01/2023–08/31/2025  
A multi-level bias correction model for bulk and single-cell CUT&Tag data  
Role: **PI**
4. NIH/NHGRI R25 HG012918 MPI: Brown & Zang 06/01/2024–05/31/2027  
Research Experiences in Genomic Applications of Responsible Data Science (REGARDS)  
Role: **PI**
5. UVA Comprehensive Cancer Center PI: Zang 11/01/2024–10/31/2025  
A novel computational approach for 3D genome dynamics in lung cancer progression  
Role: **PI**

6. UVA Comprehensive Cancer Center      MPI: Wang,Li,Zang,Ratan    05/15/2024–05/14/2025  
Deployment of the Swiss army knife in the human genome - CTCF licensing  
Role: **PI**
  
7. NIH R01 NS116421                              PI: Zhu                              04/15/2021–03/31/2026  
Developmental origin, injury and epigenomic regulation of NF1-associated peripheral nerve  
sheath tumors  
Role: Subcontract PI
  
8. NSF IIS-2106913                              PI: Zhang                              10/01/2021–09/30/2025  
Knowledge-guided meta learning for multi-omics survival analysis  
Role: Co-PI
  
9. NIH R01 CA259573                              PI: Jiang                              01/01/2022–12/31/2026  
Role of UTX condensation in chromatin regulation  
Role: Co-Investigator
  
10. NIH R01 HL168611                              PI: Mohi                              06/15/2023–05/31/2027  
Molecular basis for myelodysplasia induced by U2AF1 mutations  
Role: Co-Investigator
  
11. NIH R21 CA283132                              PI: Li                              09/01/2023–08/31/2025  
Racial disparities and colorectal DNA methylation-driven gene expression  
Role: Co-Investigator
  
12. NIH R01 HL148239                              PI: Miller                              07/01/2024–06/30/2028  
Multimodal genetic regulatory architecture of coronary artery disease  
Role: Co-Investigator
  
13. NIH R01 CA178393                              MPI: Loughran & Ratan      08/15/2024–07/31/2029  
Genomic Architecture of LGL Leukemia  
Role: Co-Investigator
  
14. NIH R01 AG090337                              PI: Sun                              12/01/2024–11/30/2029  
CD38, T cells and post viral lung sequelae during aging  
Role: Co-Investigator
  
15. NIH R01 HL173611                              PI: Mohi                              01/01/2025–11/30/2028  
Molecular basis for progression of myeloproliferative neoplasms induced by JAK2V617F  
Role: Co-Investigator
  
16. Leukemia & Lymphoma Society (LLS)      PI: Tao                              09/01/2023–08/31/2027  
Mantle Cell Lymphoma Research Initiative  
Role: Co-Investigator

***Completed Research Support***

17. NIH R35 GM133712 (MIRA)                      PI: Zang                              09/01/2019–09/20/2024  
Integrative computational models for functional epigenomics and transcriptional regulation  
Role: **PI**

18. NIH 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 due to the funding of NIGMS MIRA (R35) award.
19. Virginia Commonwealth Health Research Board PI: Zang 05/01/2021–07/31/2023  
Aberrant CTCF binding as an epigenetic signature of cancer  
Role: **PI**
20. 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**
21. UVA Comprehensive Cancer Center PI: Zang 11/01/2023–10/31/2024  
BARTsc: a computational method for transcription factor prediction from single-cell data  
Role: **PI**  
Total Award Amount: \$25,000  
Annual Direct Cost: \$25,000  
Effort: N/A
22. UVA Comprehensive Cancer Center PI: Zang 01/01/2023–12/31/2024  
Roles of lncRNAs and R-loops in 3D genome organization and gene regulation in the cancer genome  
Role: **PI**
23. NIH R21 CA274430 PI: Mohi 04/01/2023–03/31/2025  
Targeting of IL-1 signaling in myelofibrosis  
Role: Co-Investigator
24. Chan Zuckerberg Initiative PI: Miller 07/01/2022–12/31/2024  
MetaPlaq: Integrative single-cell meta-analysis for atherosclerosis  
Role: Co-PI
25. NIH R01 ES031402 MPI: Cuddapah & Costa 01/01/2020–10/31/2024  
Persistent transcriptional changes induced by nickel through epigenetic alterations  
Role: Subcontract PI
26. NIH R01 HL148239 PI: Miller 06/01/2019–04/30/2024  
Cis-regulatory architecture of coronary vascular wall loci  
Role: Co-Investigator
27. NIH R01 HL149893 PI: Mohi 01/01/2020–12/31/2023  
The role of PTPN11 in myelofibrosis  
Role: Co-Investigator
28. 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



29. NIH R01 GM132138 PI: Li 09/01/2019–07/31/2023  
Genome-wide investigation of cis-splicing between adjacent genes  
Role: Collaborator
30. 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
31. DOD/CDMRP Impact Award PI: Mohi 09/01/2019–06/30/2022  
Targeted therapies for myeloproliferative neoplasms  
Role: Co-Investigator
32. 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
33. NIH R01 ES024727 PI: Cuddapah 02/01/2017–06/30/2020  
Epigenetic reprogramming by nickel through chromatin domain disruption  
Role: Subcontract PI
34. 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
35. 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
36. 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
37. 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

2023 – now	Computational Biology Summer Institute (CGSI) University of California Los Angeles (UCLA)	Faculty
Spring 2017–	University of Virginia	
	• BIMS 8701/8702: Introduction to Computational Biology I/II	Co-instructor
	• BIMS 8601: Foundations of Computational Genomics	Co-instructor

	<ul style="list-style-type: none"> <li>• BIOC 8014: Chromatin II</li> <li>• BIOC 8145: Bioinformatics &amp; Functional Analysis of Genomes</li> <li>• PHS 5705: Recent Advances in Public Health Genomics</li> <li>• BIMS 6000: Core Course in Integrative Biosciences: Genome Architecture &amp; Dynamics</li> <li>• BME 1501: Introduction to Bioinformatics</li> <li>• BIMS 7100: Research Ethics</li> <li>• BIOL 4910: Undergraduate Research</li> <li>• CHEM 3951: Undergraduate Research</li> </ul>	<p>Co-instructor</p> <p>Co-instructor</p> <p>Co-instructor</p> <p>Co-instructor</p> <p>Guest Lecture</p> <p>Co-instructor</p> <p>Mentor</p> <p>Mentor</p>
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. University Program in Genetics and Genomics Seminar Series, Duke University. Durham, NC. 01/21/2025
2. Keynote talk, Virginia Soft Matter Workshop, James Madison University. Harrisonburg, VA. 10/18/2024
3. Joint Statistical Meetings (JSM). Portland, OR. 08/06/2024
4. Computational Genomics Summer Institute (CGSI), University of California Los Angeles. Los Angeles, CA. 07/17/2024
5. Department Seminar Series, Center for Genetic Medicine, Children's National Hospital. Washington, DC. 06/21/2024
6. Frontiers in Bioinformatics Seminar Series, University of California Los Angeles. Los Angeles, CA. 04/15/2024
7. MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Annual Conference. Atlanta, GA. 03/23/2024
8. Faculty Research Retreat, University of Virginia School of Medicine. Charlottesville, VA. 02/03/2024
9. American Physical Society (APS) March Meeting. Minneapolis, MN. 03/07/2024
10. Center for Statistical Science, Tsinghua University. Beijing, China. 10/30/2023
11. Cold Spring Harbor Asia Meeting: Systems Biology of Gene Regulation and Genome Editing. Suzhou, China. 10/27/2023
12. Seminar Series, The Jackson Laboratory for Genomic Medicine, Farmington, CT. 10/17/2023

13. School of Data Science Research Retreat, University of Virginia. Charlottesville, VA. 09/22/2023
14. Department of Microbiology, Tumor and Cell Biology, Karolinska Institutet. Stockholm, Sweden. 08/02/2023
15. Computational Genomics Summer Institute (CGSI), University of California Los Angeles. Los Angeles, CA. 07/20/2023
16. Distinguished Lectures in Genetics Seminar Series, Cincinnati Children's Hospital Medical Center, Cincinnati, OH. 06/27/2023
17. Gordon Research Conference: Cancer Genetics and Epigenetics. Barga, Italy. 05/25/2023
18. American Association for Cancer Research (AACR) Annual Meeting. Session ED045: Distilling data from single-cell and spatial RNA-seq: a new perspective, a new approach. Orlando, FL. 04/15/2023
19. Carter Immunology Center, University of Virginia. Charlottesville, VA. 02/20/2023
20. Oncological Data Science Seminar Series, Moffitt Cancer Center. Tampa, FL. 09/20/2022 (virtual)
21. International Conference on Intelligent Biology and Medicine (ICIBM 2022). Philadelphia, PA. 08/08/2022
22. Computational Biology Program, Boston Children's Hospital, Harvard Medical School. Boston, MA. 07/29/2022
23. Department of Computational Biomedicine, Cedars-Sinai Medical Center, Los Angeles, CA. 05/31/2022 (virtual)
24. Department of Biology, Johns Hopkins University. Baltimore, MD. 12/03/2021 (virtual)
25. 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
26. Department of Environmental Medicine, New York University. New York, NY. 05/11/2021 (virtual)
27. Child Health Research Center, University of Virginia. Charlottesville, VA. 04/23/2021 (virtual)
28. Foundation of Biomedical Data Science Seminar Series, University of Virginia School of Data Science. Charlottesville, VA. 04/02/2021 (virtual)
29. Computational Biology and Bioinformatics Seminar Series, Duke University. Durham, NC. 03/29/2021 (virtual)
30. Center for Cancer Genomics, Department of Biochemistry and Molecular Genetics, Northwestern University. Chicago, IL. 12/09/2020 (virtual)
31. 14th International Bioinformatics Workshop (IBW 2019), Beijing, China. 08/03/2019
32. State Key Laboratory of Cardiovascular Disease, Peking Union Medical College. Beijing, China. 07/31/2019
33. School of Mathematics, Shandong University. Jinan, China. 07/29/2019
34. Department of Cognitive Science, University of California, San Diego, CA. 12/20/2018
35. Biomedical Pioneering Innovation Center, Peking University. Beijing, China. 08/21/2018
36. Department of Pathology, University of Virginia. Charlottesville, VA. 12/19/2017
37. Department of Biostatistics, Virginia Commonwealth University. Richmond, VA. 11/3/2017
38. Center for Quantitative Biology, Peking University. Beijing, China. 09/29/2017

39. Institute of Biophysics, Chinese Academy of Sciences. Beijing, China. 09/28/2017
40. Beijing Institute for Scientific and Engineering Computing, Beijing University of Technology. Beijing, China. 09/27/2017
41. Center for Statistical Science, Tsinghua University. Beijing, China. 09/25/2017
42. Department of Physics, Fudan University. Shanghai, China. 09/23/2017
43. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Shanghai, China. 09/18/2017
44. School of Life Sciences, Peking University. Beijing, China. 06/08/2016
45. Workshop on Analysis of ChIP-Seq Data, National Cancer Institute, National Institutes of Health. Bethesda, MD. 05/17/2016
46. Laboratory of Genome Integrity, National Cancer Institute, National Institutes of Health. Bethesda, MD. 04/07/2016
47. Department of Immunobiology, Yale University. New Haven, CT. 03/11/2016
48. University of Virginia. Charlottesville, VA. 02/05/2016
49. The Wistar Institute. Philadelphia, PA. 01/29/2016
50. Academy of Mathematics and Systems Science, Chinese Academy of Sciences. Beijing, China. 01/07/2016
51. Peking University Third Hospital. Beijing, China. 01/05/2016
52. Peking University Medical Center. Beijing, China. 01/04/2016
53. University of Illinois College of Medicine, Peoria, IL. 12/17/2015
54. The Stadtman Symposium, National Institutes of Health. Bethesda, MD. 12/10/2015
55. National Heart, Lung, and Blood Institute, National Institutes of Health. Bethesda, MD. 11/20/2015
56. University of Nevada School of Medicine, Reno, NV. 10/06/2015
57. College of Pharmacy, University of Rhode Island. Kingston, RI. 06/24/2015
58. Uniformed Services University of the Health Sciences. Bethesda, MD. 05/29/2015
59. Department of Electrical & Computer Engineering, University of Nebraska, Lincoln, NE. 02/18/2015
60. National Human Genome Research Institute, National Institutes of Health. Bethesda, MD. 02/04/2015
61. National Cancer Institute, National Institutes of Health. Bethesda, MD. 12/19/2014
62. Cancer epigenetics symposium, Harvard Medical School. Boston, MA. 12/14/2014
63. Biophysics Seminar, The George Washington University. Washington, DC. 10/02/2014
64. Workshop on big data analysis in biomedical research, Harvard Medical School. Boston, MA. 06/24/2014
65. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Shanghai, China. 11/28/2013
66. Institute of Systems Biomedicine, Shanghai Jiao Tong University. Shanghai, China. 11/26/2013
67. Computational Biology and Bioinformatics Organization, Broad Institute. Cambridge, MA. 10/16/2013
68. Megakaryocyte and Platelet Biology Joint Meeting, Boston Children's Hospital. Boston, MA.

09/12/2012

69. Department of Animal and Avian Sciences, College of Agriculture and Natural Resources, University of Maryland, College Park, MD. 09/28/2009

## CONTRIBUTED PRESENTATIONS

1. Gordon Research Conference on Single-Cell Genomics. Les Diablerets, Switzerland, 05/2024. (*Poster*)
2. American Association for Cancer Research (AACR) Annual Meeting. San Diego, CA, 04/2024. (*Poster + 4 Posters presented by trainees*)
3. Cold Spring Harbor Meeting Systems Biology: Global Regulation of Gene Expression, 03/2024 (*Poster + 1 Poster by a trainee*)
4. American Physical Society (APS) March Meeting. Minneapolis, MN, 03/2024. (*Talk*)
5. Chan Zuckerberg Science Initiative Single-Cell Biology Annual Meeting. San Diego, CA, 11/2023. (*Talk*)
6. ISMB/ECCB 2023: 31th Conference on Intelligent Systems for Molecular Biology. Lyon, France. 07/2023. (*Poster*)
7. American Association for Cancer Research (AACR) Annual Meeting. Orlando, FL, 04/2023. (*3 Posters presented by trainees*)
8. Keystone Meeting on Epigenetics, Chromatin, Development and Disease. Victoria, BC, Canada, 03/2023. (*Poster*)
9. American Physical Society (APS) March Meeting. Las Vegas, LV, 03/2023. (*Talk*)
10. Chan Zuckerberg Science Initiative Single-Cell Biology Annual Meeting. San Jose, CA, 11/2022. (*Talk*)
11. ISMB 2022: 30th Conference on Intelligent Systems for Molecular Biology. Madison, WI, 07/2022. (*Poster*)
12. Gordon Research Conference on Single-Cell Cancer Biology. Easton, MA, 06/2022. (*3 Posters presented by trainees*)
13. Cold Spring Harbor Meeting on Systems Biology: Global Regulation of Gene Expression, 03/2022. (*3 Posters presented by trainees*)
14. Cold Spring Harbor Meeting on Mechanisms of Eukaryotic Transcription, 09/2021. (*Poster presented by a trainee*)
15. Cold Spring Harbor Meeting on Eukaryotic DNA Replication & Genome Maintenance, 09/2021. (*Poster presented by a trainee*)
16. 2021 NHLBI Systems Biology Symposium (Virtual), 05/2021. (*5 Posters presented by trainees*)
17. American Association for Cancer Research (AACR) Annual Meeting (Virtual), 04/2021. (*Poster*)
18. American Physical Society (APS) March Meeting (Virtual), 03/2021. (*Talk*)
19. American Association for Cancer Research (AACR) Annual Meeting (Virtual), 06/2020. (*Poster*)
20. iPoLS 2020: International Physics of Living Systems Annual Meeting (Virtual), 06/2020. (*Poster*)

21. Cold Spring Harbor Meeting on Systems Biology: Global Regulation of Gene Expression (Virtual), 03/2020. (*Poster presented by a trainee*)
22. Keystone Meeting on Cancer Epigenetics. Keystone, CO, 01/2020. (*Poster*)
23. Physics Meets Biology 2019, Institute of Physics, University of Oxford. Oxford, UK, 09/2019. (*Poster*)
24. RECOMB 2019: 23rd Annual International Conference on Research in Computational Molecular Biology. Washington, DC, 05/2019 (*5 Posters presented by trainees*)
25. Gordon Research Conference on Cancer Genetics and Epigenetics. Lucca, Italy, 04/2019. (*Poster*)
26. American Association for Cancer Research (AACR) Annual Meeting. Atlanta, GA, 04/2019. (*Poster*)
27. American Physical Society (APS) March Meeting. Boston, MA, 03/2019. (*Talk*)
28. ISMB 2018: Conference on Intelligent Systems for Molecular Biology. Chicago, IL, 07/2018. (*Poster*)
29. Biophysics of Epigenetic and Chromatin Dynamics Workshop, Higgs Centre for Theoretical Physics, University of Edinburgh. Edinburgh, UK, 04/2018. (*Poster*)
30. American Physical Society (APS) March Meeting. Los Angeles, CA, 03/2018. (*Talk*)
31. Keystone Meeting on Cancer Epigenetics. Breckenridge, CO, 02/2018. (*Poster*)
32. Cold Spring Harbor Asia Meeting on Precision Cancer Biology. Suzhou, China, 09/2017. (*Poster*)
33. Keystone Meeting on Epigenetics and Human Disease. Seattle, WA, 01/2017. (*Poster*)
34. NCI Symposium on Chromosome Biology. Bethesda, MD, 11/2016. (*Poster*)
35. ENCODE Consortium Meeting. San Diego, CA, 06/2016. (*Poster*)
36. AACR Special Conference on Chromatin and Epigenetics in Cancer. Atlanta, GA, 09/2015. (*Poster*)
37. Keystone Meeting on Cancer Epigenetics. Santa Fe, NM, 02/2014. (*Poster*)
38. NCI Symposium on Chromosome Biology. Bethesda, MD, 04/2013. (*Poster*)
39. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2012. (*Poster*)
40. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2010. (*Poster*)
41. The 7th Asia Pacific Bioinformatics Conference. Beijing, China, 01/2009. (*Best Poster Award Winner*)
42. American Physical Society (APS) March Meeting. New Orleans, LA, 03/2008. (*Talk*)

## MENTEES AND STUDENTS

### ***Postdoctoral Associates Mentored*** (6 completed, 2 ongoing)

1. Zhenjia Wang, PhD (UVA, 01/2017–01/2024)
2. Sheng'en Shawn Hu, PhD (UVA, 11/2017–11/2021, now Res. Asst. Prof. at UVA)
3. Christopher Dampier, MD (UVA, joint with Graham Casey, 07/2019–05/2021)
4. Qingying Chen, PhD (UVA, 01/2021–6/30/2024)

5. William F. Lamberti, PhD (UVA, 01/2021–08/2022, now Asst. Prof. at GMU)
6. Yidan Cong, PhD (UVA, 06/2021–02/2022)
7. Shengyuan Wang, PhD (UVA, 03/2022–)
8. Ziyi Liu, PhD (04/2025–)

**Graduate Students Mentored** (4 masters, 4 PhD rotation; 5 PhD ongoing)

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–)
11. Jingyi Wang (PhD in Biomedical Sciences, UVA, 07/2024–)
12. Sophie O’Keefe (PhD in Biomedical Sciences, UVA, Rotation 1/2025–2/2025)
13. Bhummanat Sittipongpittaya (PhD in Biomedical Sciences, UVA, 1/2025–)

**PhD Thesis Committee Service** (8 completed, 8 ongoing)

*University of Virginia:*

1. Jeffrey Xing (PhD in Biomedical Engineering, 01/2017–10/2020)
2. Yang Yu (PhD in Biology, 12/2020–10/2022)
3. Jacob Wolpe (PhD in Cell Biology, 07/2021–06/2023)
4. Zhijian He (PhD in Biomedical Engineering, UVA, 02/2023–04/2024)
5. Justin Elfman (PhD in Biochemistry and Molecular Genetics, 06/2019–07/2024)
6. Yuanming Liu (PhD in Biology, 01/2021–)
7. Samuel Haddox (PhD in Biochemistry and Molecular Genetics, 02/2021–, Committee Chair)
8. Nicole Kirk (PhD in Microbiology, Immunology, and Cancer Biology, 12/2021–)
9. Jose Verdezoto (PhD in Biochemistry and Molecular Genetics, 05/2022–, Committee Chair)
10. Louisa Quesada (PhD in Biomedical Engineering, 11/2022–)
11. Magda Bujnowska (PhD in Biochemistry and Molecular Genetics, 02/2023–)
12. Yipei Song (PhD in Electrical and Computer Engineering, UVA, 04/2024–)

*External committee service:*

13. Celestia Fang (PhD in Biochemistry and Molecular Genetics, Northwestern University Feinberg School of Medicine, 09/2018–06/2021)
14. Evan Tarbell (PhD in Biochemistry, University at Buffalo, 11/2018–12/2018)
15. Ruoyun Wang (PhD in Molecular & Cell Biology, Dartmouth College, 6/2024)
16. Christy Lee (PhD in Statistics, UCLA, 12/2023–)

**Undergraduate Student Research Supervised** (29 completed, 4 ongoing)

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. Jingyi Wang (UVA, 07/2022–05/2024)
29. Ibrahim Khanani (UVA SRIP program, Duke University, 05/2024–08/2024)
30. Andy Cao (UVA, 08/2022–)
31. Yanbin Xu (UVA, 10/2022–)
32. Grant Atwood (UVA, School of Engineering Summer Research Fellow, 08/2023–)
33. Katherine Zhang (UVA, 08/2024–)

**Visiting Students/Scholars Supervised** (7 completed)

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** (4 completed)

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 DEVELOPMENT AND TRAINING

Leadership in Academic Matters (LAM) Program      Leadership development      Fall 2024  
(University of Virginia Office of the Executive Vice President and Provost)

Research Communications Fellow Program      Communications training      2023–2024  
(University of Virginia Office of the Vice President for Research)

## PROFESSIONAL SERVICE

### *Grant Review/Study Section Service*

*Standing Member*      National Institutes of Health (NIH) Center for Scientific Review  
Maximizing Investigators' Research Award (MRAF) Study Section  
(2023–2026). *Ad hoc Co-Chair* (2023–2024)

*Ad hoc grant reviewer*      UK Research and Innovation (UKRI):  
Medical Research Council (MRC, RCUK) (2017)  
Biotechnology and Biological Sciences Research Council  
(BBSRC, UKRI) (2022)  
Netherlands Organisation for Scientific Research (NWO) (2017)  
US National Institutes of Health (NIH) Center for Scientific Review:

- Member, ZRG1 PSE-B (04): Epidemiology and Statistical Methods Special Emphasis Panel (03/2020)
- Member, ZMH1 ERB-M (06): BRAIN Initiative Cell Census Network (BICCN) Special Emphasis Panel (07/2020)
- Member, ZRG1 CB-K (55): Maximizing Investigators' Research Award (MIRA) for Early Stage Investigators (ESI) Special Emphasis Panel (03/2021)
- Member, ZRG1 GGG-S (55): Maximizing Investigators' Research Award (MIRA) for Early Stage Investigators (ESI) Special Emphasis Panel (03/2022)
- Member, ZRG1 MGG-C (55) Maximizing Investigators' Research Award (MRAA) Special Emphasis Panel (11/2022)
- **Chair**, ZCA1 SRB-P (M1) Cancer Target Discovery and Development Network (CTD2) Special Emphasis Panel (03/2023)

Inova Translational Research Funding Program (2018)  
UVA internal review committee for Virginia CHRB awards (2021)  
UVA Carter Immunology Center internal review committee (2021)  
Wellcome Trust (UK) external grant reviewer (2023)

Canada Research Chairs (2025)

***Journal Editorship Service / Peer Review***

<i>Scientific Editor</i>	<i>PLOS Computational Biology</i> (2024–)
<i>Advisory Board Member</i>	<i>Patterns</i> (Cell Press) (2024–)
<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> (2020–2024)
<i>Ad hoc journal reviewer</i>	<i>Cell</i> <i>Nature Biotechnology</i> <i>Nature Genetics</i> <i>Nature Methods</i> <i>Nature Cancer</i> <i>Nature Communications</i> <i>Science Advances</i> <i>Cell Genomics</i> <i>Cell Systems</i> <i>Genome Research</i> <i>Genome Biology</i> <i>Cancer Research</i> <i>EMBO Journal</i> <i>Nucleic Acids Research</i> <i>Cellular and Molecular Life Sciences</i> <i>Bioinformatics</i> <i>Briefings in Bioinformatics</i> <i>Genomics, Proteomics &amp; Bioinformatics</i> <i>Epigenetics</i> <i>PLOS Computational Biology</i> <i>BMC Bioinformatics</i> <i>BMC Genomics</i> <i>Breast Cancer Research</i> <i>Journal of the American Statistical Association</i> <i>Scientific Reports</i> <i>iScience</i> <i>Cell Discovery</i> <i>Communications Biology</i> <i>Open Biology</i> <i>Patterns</i> <i>PLOS One</i> <i>NAR Cancer</i> <i>Journal of Computational Biology</i> <i>Quantitative Biology</i> <i>IEEE/ACM Transactions on Computational Biology &amp; Bioinformatics</i> <i>Computational Statistics and Data Analysis</i>

*Biomolecules*  
*Frontiers of Medicine*  
*Frontiers in Oncology*

**National/Extramural Community Service**

<i>Co-Chair</i>	American Physical Society (APS) March Meeting Sessions on Genome Organization and Subnuclear Phenomena, 2024–
<i>Faculty Member</i>	Computational Genomics Summer Institute (CGSI), an international summer school hosted by University of California Los Angeles (UCLA), 2023–
<i>Chair</i>	NIH CSR Special Emphasis Panel ZCA1 SRB-P (M1): Cancer Target Discovery and Development Network (CTD2), 2023
<i>Member</i>	Scientific Advisory Board (SAB), Integrated Translational Health Research Institute of Virginia (iTHRIV), 2023–
<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

**University Service/Leadership**

<i>Faculty Advisor</i>	Data Science Shared Resource, UVA Comprehensive Cancer Center, 2/2025–
<i>Committee Member</i>	Faculty Advisory Committee for AI Research, UVA Health, 2/2025–
<i>Director of Computational Genomics</i>	UVA Comprehensive Cancer Center, 7/2024–
<i>Committee Chair</i>	Faculty Search Committee, UVA Precision Medicine/Precision Health Initiative, Department of Genome Sciences and UVA Comprehensive Cancer Center, 2024–2025
<i>Committee Co-Chair</i>	UVA Comprehensive Cancer Center Molecular Epidemiology Faculty Search Committee, 2022
<i>Committee Chair</i>	Emerging Scholars in Genome Sciences Symposium Planning Committee ( <i>Committee Member</i> , 2020–; <i>Committee Chair</i> , 2021–)

Updated: April 14, 2025