

CURRICULUM VITAE

Chongzhi Zang, PhD

Assistant Professor
University of Virginia
P.O. Box 800717, Charlottesville, VA 22908, USA
+1-434-243-5397 | zang@virginia.edu | <https://zanglab.github.io/>

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 –	University of Virginia , Charlottesville, VA <i>Assistant Professor of Public Health Sciences (primary) (11/2016–)</i> <i>Resident Faculty Member, Center for Public Health Genomics (11/2016–)</i> <i>Assistant Professor of Biochemistry and Molecular Genetics (12/2016–)</i> <i>Assistant Professor of Biomedical Engineering (09/2017–)</i> <i>Faculty Member, UVA Cancer Center (03/2017–)</i> <i>Faculty Member, Data Science Institute (03/2017–)</i>
07/2010 – 10/2016	Harvard University/Dana-Farber Cancer Institute , Boston, MA <i>Research Fellow, Department of Data Science, Dana-Farber Cancer Institute (07/2010–10/2016)</i> <i>Postdoctoral Fellow, Department of Biostatistics, Harvard T.H. Chan School of Public Health (10/2010–10/2016)</i> (Mentor: Xiaole Shirley Liu, PhD)
05/2007 – 06/2010	National Institutes of Health , Bethesda, MD <i>Predoctoral Research Assistant, Laboratory of Epigenome Biology, National Heart, Lung, and Blood Institute</i> (PhD Co-advisor: Keji Zhao, PhD)
09/2005 – 06/2010	The George Washington University , Washington, DC <i>Graduate Research Assistant, Department of Physics (09/2006–06/2010)</i> <i>Graduate Teaching Assistant, Department of Physics (09/2005–05/2008)</i> (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

Total citations > 10,000; H-index = 25 (Google Scholar)

*: equal-contributing authors; §: co-corresponding authors.

1. 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§, Chongzhi Zang§. “Cancer-specific CTCF binding facilitates oncogenic transcriptional dysregulation.” *Genome Biology* 21, 247 (2020).
2. 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§, Chunyuan Jin§, Max Costa§. “Polyadenylation of histone H3.1 mRNA promotes cell transformation by displacing H3.3 from gene regulatory elements.” *iScience* 23, 101518 (2020).
3. Chongzhi Zang§, Yiren Wang, Weiqun Peng§. “RECOGNICER: a coarse-graining approach for identifying broad domains from ChIP-seq data.” *Quantitative Biology* in press (2020).
4. The ENCODE Project Consortium, 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 Victorson, Kevin P. White, Axel Visel, Gene W. Yeo, Christopher B. Burge, Eric Lécuycer, 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§, Richard M. Myers§, Bing Ren§, Brenton R. Graveley§, Mark B. Gerstein§, Len A. Pennacchio§, Michael P. Snyder§, Bradley E. Bernstein§, Barbara Wold§, Ross C. Hardison§, Thomas R. Gingeras§, John A. Stamatoyannopoulos§, Zhiping Weng§. “Expanded encyclopaedias of DNA elements in the human and mouse genomes.” *Nature* 583, 699–710 (2020).
5. The ENCODE Project Consortium, Michael P. Snyder§, 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).

6. 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[§], X. Shirley Liu[§], Kevin White[§], Mark Gerstein[§]. “An integrative ENCODE resource for cancer genomics.” *Nature Communications* 11, 3696 (2020).
7. Qiang Shan*, Sheng'en Hu*, Xia Chen, Derek B. Danahy, Vladimir P. Badovinac, Chongzhi Zang[§], Hai-Hui Xue[§]. “Ectopic Tcf1 expression instills a stem-like program in exhausted CD8+ T cells to enhance viral and tumor immunity.” *Cellular & Molecular Immunology*, doi:10.1038/s41423-020-0436-5 (2020).
8. 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).
9. Cynthia C Jose*, Zhenjia Wang*, Vinay Singh Tanwar, Xiaoru Zhang, Chongzhi Zang[§], Suresh Cuddapah[§]. “Nickel induced transcriptional changes persist post exposure through epigenetic reprogramming.” *Epigenetics and Chromatin* 12, 75 (2019).
10. Teng Fei*, Wei Li*, Jingyu Peng*, Tengfei Xiao, Chen-Hao Chen, Alexander Wu, Jialiang Huang, Chongzhi Zang, X. Shirley Liu[§], Myles Brown[§]. “Deciphering essential cistromes using genome-wide CRISPR screens.” *Proceedings of the National Academy of Sciences USA* 116, 25186–25195 (2019).
11. Qingsu Cheng, Mina Khoshdeli, Bradley S. Ferguson, Kosar Jabbari, Chongzhi Zang[§], Bahram Parvin[§]. “YY1 is a cis-regulator in the organoid models of high mammographic density.” *Bioinformatics*, btz812 (2019).
12. 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).
13. 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).
14. 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[§], Myles Brown[§]. “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).
15. 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).
 16. 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).
 17. 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[§], X. Shirley Liu[§]. “Cistrome Cancer: a web resource for integrative gene regulation modeling in cancer.” *Cancer Research* 77, e19–e22 (2017).
 18. Eric Severson*, Kelly L. Arnett*, Hongfang Wang*, Chongzhi Zang*, Len Taing, Hudan Liu, Warren S. Pear, X. Shirley Liu, Stephen C. Blacklow[§], Jon C. Aster[§]. “Genome-wide identification and characterization of Notch transcription complex-binding sequence-paired sites in leukemia cells.” *Science Signaling* 10, 477, eaag1598 (2017).
 19. Shenglin Mei, Qian Qin, Qiu Wu, Hanfei Sun, Rongbin Zheng, Chongzhi Zang, Muyuan Zhu, Jiaxin Wu, Xiaohui Shi, Len Taing, Tao Liu, Myles Brown, Clifford A. Meyer[§], X. Shirley Liu[§]. “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).
 20. 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[§], X. Shirley Liu[§]. “ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline.” *BMC Bioinformatics* 17, 404 (2016).
 21. 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[§], X. Shirley Liu[§]. “Modeling cis-regulation with a compendium of genome-wide histone H3K27ac profiles.” *Genome Research* 26, 1417–1429 (2016).
 22. 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).
 23. 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 bias correction and data integration

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

24. 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[§], X. Shirley Liu[§]. “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).
25. 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).
26. Hilary K Finucane*[§], Brendan Bulik-Sullivan*[§], 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[§], Alkes L Price[§]. “Partitioning heritability by functional annotation using genome-wide association summary statistics.” *Nature Genetics* 47, 1228–1235 (2015).
27. 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).
28. Alexander Gusev[§], 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. Köhler, 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[§]. “Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases.” *The American Journal of Human Genetics* 95, 535–552 (2014).
29. 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[§], Warren S. Pear[§]. “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).
30. Annouck Luyten*, Chongzhi Zang*, X. Shirley Liu[§], Ramesh A. Shivdasani[§]. “Active enhancers are delineated *de novo* during hematopoiesis with limited lineage fidelity among specified primary blood cells.” *Genes and Development* 28, 1827–1839 (2014).
31. Alexander Stoeck, Serguei Lejnine, Andrew Truong, Li Pan, Hongfang Wang, Chongzhi Zang, Jing Yuan, Chris Ware, John MacLean, Philip W Garrett-Engele, 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).

32. 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).
33. Hongfang Wang*, Chongzhi Zang*, Len Taing, Kelly Arnett, Yinling Joey Wong, Warren S. Pear, Stephen C. Blacklow, X. Shirley Liu[§], Jon C. Aster[§]. “NOTCH1-RBPJ complexes drive target gene expression through dynamic interactions with superenhancers.” *Proceedings of the National Academy of Sciences USA* 111, 715–710 (2014).
34. 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[§], X. Shirley Liu[§], Myles Brown[§]. “Refined DNase-seq protocol and data analysis reveals intrinsic bias in transcription factor footprint identification.” *Nature Methods* 11, 73–78 (2014).
35. Su Wang, Hanfei Sun, Jian Ma, Chongzhi Zang, Chenfei Wang, Juan Wang, Qianzi Tang, Clifford A. Meyer, Yong Zhang[§], X. Shirley Liu[§]. “Targets analysis by integration of transcriptome and ChIP-seq data with BETA.” *Nature Protocols* 8, 2502–2515 (2013).
36. 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).
37. 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).
38. 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).
39. 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)
40. Chunyuan Jin*, Chongzhi Zang*, Gang Wei, Kairong Cui, Weiqun Peng, Keji Zhao[§], Gary Felsenfeld[§]. “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 > 700)

41. 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[§], Nan-ping Weng[§]. “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).
42. 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 > 800)
43. 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[§], Keji Zhao[§]. “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)
44. 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 > 500)
45. 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)
46. HAO Zuoqiang, ZHANG Jie, YU Jin, ZHANG Zhe, ZHONG Jiayong, ZANG Chongzhi, JIN Zhan, WANG Zhaohua, WEI Zhiyi. “Fluorescence measurement and acoustic diagnostics of plasma channels in air.” *Acta Physica Sinica* 55, 299–303 (2006). (In Chinese)
47. ZANG Chongzhi, ZHANG Jietian[§], 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)
48. ZANG Chongzhi, ZHANG Jietian[§], PENG Peizhi. “Discussion of data processing method for measuring NMR relaxation time.” *Physics Experimentation* (ISSN 1005-4642) 25(5), 45–47 (2005). (In Chinese)
49. ZANG Chongzhi, PENG Peizhi, ZHANG Jietian[§], LU Sihua. “Teaching experimentation of MRI.” *Physics Experimentation* (ISSN 1005-4642) 24(8), 3–7 (2004). (In Chinese)

Peer-reviewed Conference Abstracts

50. 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).

51. 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).
52. 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).
53. 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).
54. 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).
55. 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).
56. 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).
57. 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).
58. 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).
59. 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. 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/>
3. 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/>
4. 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/>
5. 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>
6. BARTweb: Interactive web server for performing BART analysis. <http://bartweb.org>
7. SICER2: An updated bioinformatics tool for SICER: Identification of broad enriched regions from ChIP-seq data. <https://zanglab.github.io/SICER2/>
8. BARTcancer: A database resource for computationally predicted transcriptional regulator activities in 15 human cancers from The Cancer Genome Atlas (TCGA). <https://zanglab.github.io/bartcancer/>

HONORS AND AWARDS

- | | |
|-----------|--|
| 2019–2024 | NIH/NIGMS Maximizing Investigators' Research Award (R35) |
| 2018 | 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 |
| 2017–2020 | NIH/NCI Transition Career Development Award (K22) |
| 2014 | Travel Award, Harvard Program in Quantitative Genomics |

2012–2015 Leukemia and Lymphoma Society Fellow Award
2010 Dimitris N. Chorafas Foundation Prize
2009 Parke Prize in Theoretical Physics, The George Washington University
2009 The Best Poster Award, the 7th Asia-Pacific Bioinformatics Conference
2008 Chinese Government Award for Outstanding Self-financed Student Abroad
2008 Student Travel Grant Award, American Physical Society (APS)
2004 2nd Award for Undergraduate Research, School of Physics, Peking University
2001 Freshman Fellowship, Peking University
2000 1st Prize, Beijing Region; 3rd Prize, National Final, Chinese Physics Olympiad

RESEARCH SUPPORT

Current Research Support

1. NIH/NIGMS R35 GM133712 PI: Zang 09/01/2019–07/31/2024
Integrative computational models for functional epigenomics and transcriptional regulation
Role: PI
2. NIH/NIAID 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. NIH/NHLBI R01 HL148239 PI: Miller 06/01/2019–04/30/2024
Cis-regulatory architecture of coronary vascular wall loci
Role: Co-investigator
4. NIH/NINDS R01 NS115531 PI: Zhu 07/01/2019–06/30/2023
Investigating and targeting pathways of malignant peripheral nerve sheath tumor (MPNST)
Role: Co-investigator
5. DOD/CDMRP Impact Award PI: Mohi 09/01/2019–06/30/2022
Targeted therapies for myeloproliferative neoplasms
Role: Co-investigator
6. NIH/NIEHS R01 ES031402 MPI: Cuddapah, Costa 01/01/2020–10/31/2024
Persistent transcriptional changes induced by nickel through epigenetic alterations
Role: Co-investigator
7. NIH/NHLBI R01 HL149893 PI: Mohi 01/01/2020–12/31/2023
The role of PTPN11 in myelofibrosis
Role: Co-investigator

8. NIH/NIA U01 AG070960 PI: Yan 09/30/2020–05/31/2023
Machine learning-based multi-omics modeling and CRISPR/Cas9-mediated gene editing in elucidating molecular transducer of physical activity
Role: Co-investigator

Completed Research Support

9. NIH/NCI K22 CA204439 PI: Zang 09/01/2017–08/31/2020*
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 the funding of NIGMS MIRA (R35) award.
10. 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
11. NIH/NIEHS R01 ES024727 PI: Cuddapah 02/01/2017–06/30/2020
Epigenetic reprogramming by nickel through chromatin domain disruption
Role: Co-investigator
12. 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: Co-investigator
13. Jayne Koskinas Ted Giovanis Foundation for Health and Policy See 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
14. 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
15. 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	
	PHS5705: Public Health Genomics	Lecture
	BIOC8145: Functional Analysis of Genomes	Lectures

	BIMS7100: Research Ethics BIOL4910: Undergraduate Research CHEM3951: Undergraduate Research	Discussion Leader Mentor Mentor
05/2016	NIH/NCI Bioinformatics Workshop	Guest Instructor
11/2014	NIH/NCI Bioinformatics Workshop	Guest Instructor
11/2013	Tongji University: Computational Genomics	Guest Lecture
09/2005–05/2008	The George Washington University Physics 001, Physics 002 Astronomy 001, Astronomy 002	Teaching Assistant Lab & Recitation Lab Instructor

INVITED TALKS

- 14th International Bioinformatics Workshop (IBW 2019), Beijing, China. 08/03/2019
- State Key Laboratory of Cardiovascular Disease, Peking Union Medical College. Beijing, China. 07/31/2019
- School of Mathematics, Shandong University. Jinan, China. 07/29/2019
- Department of Cognitive Science, University of California, San Diego, CA. 12/20/2018
- Biomedical Pioneering Innovation Center, Peking University. Beijing, China. 8/21/2018
- Department of Pathology, University of Virginia. Charlottesville, VA. 12/19/2017
- Department of Biostatistics, Virginia Commonwealth University. Richmond, VA. 11/3/2017
- Center for Quantitative Biology, Peking University. Beijing, China. 09/29/2017
- Institute of Biophysics, Chinese Academy of Sciences. Beijing, China. 09/28/2017
- Beijing Institute for Scientific and Engineering Computing, Beijing University of Technology. Beijing, China. 09/27/2017
- Center for Statistical Science, Tsinghua University. Beijing, China. 09/25/2017
- Department of Physics, Fudan University. Shanghai, China. 09/23/2017
- CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Shanghai, China. 09/18/2017
- Department of Biochemistry and Molecular Genetics, University of Virginia. Charlottesville, VA. 12/15/2016
- School of Life Sciences, Peking University. Beijing, China. 06/08/2016
- Workshop on Analysis of ChIP-Seq Data, National Cancer Institute, National Institutes of Health. Bethesda, MD. 05/17/2016
- Laboratory of Genome Integrity, National Cancer Institute, National Institutes of Health. Bethesda, MD. 04/07/2016
- Department of Immunobiology, Yale University. New Haven, CT. 03/11/2016

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

CONTRIBUTED PRESENTATIONS

1. American Association for Cancer Research (AACR) Annual Meeting (Virtual), 06/2020. (*Poster*)
2. iPoLS 2020: International Physics of Living Systems Annual Meeting (Virtual), 06/2020. (*Poster*)

3. Keystone Meeting on Cancer Epigenetics. Keystone, CO, 01/2020. (*Poster*)
4. Physics Meets Biology 2019, Institute of Physics, University of Oxford. Oxford, UK, 09/2019. (*Poster*)
5. RECOMB 2019: 23rd Annual International Conference on Research in Computational Molecular Biology. Washington, DC, 05/2019 (*5 Posters by lab members*)
6. Gordon Research Conference on Cancer Genetics and Epigenetics. Lucca, Italy, 04/2019. (*Poster*)
7. American Association for Cancer Research (AACR) Annual Meeting. Atlanta, GA, 04/2019. (*Poster*)
8. American Physical Society (APS) March Meeting. Boston, MA, 03/2019. (*Talk*)
9. ISMB 2018: Conference on Intelligent Systems for Molecular Biology. Chicago, IL, 07/2018. (*Poster*)
10. Biophysics of Epigenetic and Chromatin Dynamics Workshop, Higgs Centre for Theoretical Physics, University of Edinburgh. Edinburgh, UK, 04/2018. (*Poster*)
11. American Physical Society (APS) March Meeting. Los Angeles, CA, 03/2018. (*Talk*)
12. Keystone Meeting on Cancer Epigenetics. Breckenridge, CO, 02/2018. (*Poster*)
13. Cold Spring Harbor Asia Meeting on Precision Cancer Biology. Suzhou, China, 09/2017. (*Poster*)
14. Keystone Meeting on Epigenetics and Human Disease. Seattle, WA, 01/2017. (*Poster*)
15. NCI Symposium on Chromosome Biology. Bethesda, MD, 11/2016. (*Poster*)
16. ENCODE Consortium Meeting. San Diego, CA, 06/2016. (*Poster*)
17. AACR Special Conference on Chromatin and Epigenetics in Cancer. Atlanta, GA, 09/2015. (*Poster*)
18. Keystone Meeting on Cancer Epigenetics. Santa Fe, NM, 02/2014. (*Poster*)
19. NCI Symposium on Chromosome Biology. Bethesda, MD, 04/2013. (*Poster*)
20. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2012. (*Poster*)
21. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2010. (*Poster*)
22. The 7th Asia Pacific Bioinformatics Conference. Beijing, China, 01/2009. (*Best Poster Award Winner*)
23. American Physical Society (APS) March Meeting. New Orleans, LA, 03/2008. (*Talk*)

MENTEES AND STUDENTS

Postdoctoral Associates

Zhenjia Wang, PhD (UVA, 01/2017–)

Sheng'en Shawn Hu, PhD (UVA, 11/2017–)

Christopher Dampier, MD (UVA, joint with Graham Casey, 07/2019–)

Graduate Students

Wuwei Tan (MS in Statistics, UVA, 03/2017–05/2018)
Yushan Brandon Feng (MS in Statistics, UVA, 05/2018–05/2019)
Seung Hyun Lee (MS in Statistics, UVA, 09/2018–05/2019)
Yifan Zhang (PhD in Biomedical Engineering, UVA, 08/2018–12/2019)
Audrey Putelo (PhD in Biomedical Sciences, UVA. Rotation 07/2020–08/2020)
Mengxue Tian (PhD in Biomedical Sciences, UVA, 07/2020–)
Hongpan Zhang (PhD in Biomedical Sciences, UVA, 07/2020–)
Jose Verdezoto (PhD in Biomedical Sciences, UVA, 10/2020–)

Undergraduate Students

Celina Shih (Johns Hopkins University, 05/2017–07/2017)
Yiren Wang (Peking University, 07/2017–06/2018)
Yayi Feng (UVA, 09/2017–05/2020)
Stephany Perez-Rojas (UVA, 01/2018–05/2020)
John Zhang (UVA, 02/2018–05/2020)
Yuantao Chen (UVA, 02/2018–)
Jeffrey Yoo (UVA, 02/2018–05/2020)
Naifei Pan (UVA, 04/2018–02/2019)
Alexander An (UVA, 05/2018–08/2018)
Zhou Lu (UVA, 08/2018–05/2020)
Allison Ryu (UVA, 09/2018–12/2018)
Aaron Ho (UVA, 10/2018–05/2020)
Benjamin Ke (UVA, 01/2019–)
Sophia Park (UVA, 01/2019–08/2019)
Tianhe Li (UVA, 01/2019–05/2020)
Maggie Bujor (UVA, 02/2019–)
Leyao Li (UVA, 03/2019–05/2020)
Megan Grieco (UVA, 04/2019–)
Xinyue Qiu (UVA, 04/2019–)
Zack Thomas (UVA, 04/2019–)
Sekou Rowe (NSF REU student, Howard University, 05/2019–08/2019)
Minaal Khan (UVA, 09/2019–)
Kendall Davis (UVA, 10/2019–)
Anvitha Chimata (UVA, 10/2019–)
Andrew Vanichkachorn (UVA, 10/2019–)
Joe Barrett (UVA, 01/2020–)
Alex Li (UVA, 01/2020–)
Jingwen Wang (UVA, 01/2020–)
Shahbaz Nizam (UVA, 02/2020–)
Emilie Neulen (UVA, 02/2020–)
Raymond Wen (UVA, 02/2020–)
Jasmine Dogu (UVA, 05/2020–)
Soumil Madhiwala (UVA, 05/2020–)
Sifan Tao (06/2020–)

Aaron Mun (UVA, 07/2020–)
Kuki Davey (UVA, 07/2020–)
Alex Hickman (UVA, 07/2020–)

Visiting Students/Scholars

Qi Li (PhD Candidate in Statistics, Tsinghua University, 01/2018–02/2018, 03/2019)
Wen Shen (Undergraduate Student, Nanjing University, 02/2018–05/2018)
Rongquan He, MD (PhD Candidate, Guangxi Medical University, 03/2018–02/2019)
Wenjing Ma (Beijing University of Posts and Telecommunications, 08/2018–06/2019)
Gang Chen, MD, PhD (Professor of Pathology, Guangxi Medical University, 09/2018–08/2019)
Ruoyao Shi (Undergraduate Student, Jilin University, 10/2019–05/2020)

PhD Committee

Jeffrey Xing (PhD in Biomedical Engineering, UVA, 01/2017–)
Celestia Fang (PhD in Biochemistry and Molecular Genetics, Northwestern University Feinberg School of Medicine, 09/2018–)
Evan Tarbell (PhD in Biochemistry, University at Buffalo, 11/2018–12/2018)
Justin Elfman (PhD in Biochemistry and Molecular Genetics, UVA, 06/2019–)

PROFESSIONAL SERVICES

Ad hoc grant reviewer Research Councils UK (RCUK) (2017)
 Netherlands Organisation for Scientific Research (NWO) (2017)
 Inova Translational Research Funding Program (2018)
 NIH Center for Scientific Review (CSR) (2020–)

Ad hoc journal reviewer Nature Biotechnology
 Nature Genetics
 Nature Methods
 Nature Communications
 Genome Research
 Genome Biology
 EMBO Journal
 Nucleic Acids Research
 Cancer Research
 Bioinformatics
 Epigenetics
 PLoS Computational Biology
 BMC Bioinformatics
 BMC Genomics
 Journal of the American Statistical Association
 Scientific Reports
 Cell Discovery
 PLoS One

IEEE/ACM Transactions on Computational Biology &
Bioinformatics
Computational Statistics and Data Analysis
Biomolecules

Guest Editor

PLoS Computational Biology

Mentor, Biomedical Data Science Innovation Club, 2020–2021

Co-Chair, AACR Annual Meeting Minisymposium: Transcriptional Gene Regulation in Cancer, 2020

Organizing Committee, Emerging Scholars in Genome Sciences Symposium, UVA, 2020–

Updated: September 2020