

## 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>Assistant Professor of Public Health Sciences</i> (primary) (11/2016–) <i>Resident Faculty Member</i> , Center for Public Health Genomics (11/2016–) <i>Assistant Professor of Biochemistry and Molecular Genetics</i> (12/2016–) <i>Assistant Professor of Biomedical Engineering</i> (09/2017–) <i>Faculty Member</i> , UVA Cancer Center (03/2017–) <i>Faculty Member</i> , Data Science Institute (03/2017–)
07/2010 – 10/2016	<b>Harvard University/Dana-Farber Cancer Institute</b> , Boston, MA <i>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) (Mentor: Xiaole Shirley Liu, PhD)
05/2007 – 06/2010	<b>National Institutes of Health</b> , Bethesda, MD <i>Predoctoral 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*

Total citations > 10,000; H-index = 26 (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. Chongzhi Zang§, Yiren Wang, Weiqun Peng§. “RECOGNICER: a coarse-graining approach for identifying broad domains from ChIP-seq data.” *Quantitative Biology*, doi: 10.1007/s40484-020-0225-2 (2020).
3. 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).
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 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§, 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<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).
7. 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*, 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<sup>§</sup>, Suresh Cuddapah<sup>§</sup>. “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<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).
11. 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*, 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<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).
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<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).
18. 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).
19. 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).
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<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).
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<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).
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<sup>§</sup>, X. Shirley Liu<sup>§</sup>. “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<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).
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\*<sup>§</sup>, Brendan Bulik-Sullivan\*<sup>§</sup>, Alexander Gusev, Gosia Trynka, Yakir Reshef, Po-Ru Loh, Verner Anttila, Han Xu, Chongzhi Zang, Kyle Farh, Stephan Ripke, Felix R Day, ReproGen Consortium, Schizophrenia Working Group of the Psychiatric Genomics Consortium, The RACI Consortium, Shaun Purcell, Eli Stahl, Sara Lindstrom, John RB Perry, Yukinori Okada, Soumya Raychaudhuri, Mark Daly, Nick Patterson, Benjamin M Neale<sup>§</sup>, Alkes L Price<sup>§</sup>. “Partitioning heritability by functional annotation using genome-wide association summary statistics.” *Nature Genetics* 47, 1228–1235 (2015).
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<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).
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<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).
30. 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).
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<sup>§</sup>, Jon C. Aster<sup>§</sup>. “NOTCH1-RBPJ complexes drive target gene expression through dynamic interactions with superenhancers.” *Proceedings of the National Academy of Sciences USA* 111, 715–710 (2014).
  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<sup>§</sup>, X. Shirley Liu<sup>§</sup>, Myles Brown<sup>§</sup>. “Refined DNase-seq protocol and data analysis reveals intrinsic bias in transcription factor footprint identification.” *Nature Methods* 11, 73–78 (2014).
  35. 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).
  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<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 > 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<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<sup>+</sup> 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<sup>§</sup>, Keji Zhao<sup>§</sup>. “Global mapping of H3K4me3 and H3K27me3 reveals specificity and plasticity in lineage fate determination of differentiating CD4<sup>+</sup> T cells.” *Immunity* 30, 155–167 (2009). (cited > 1000)
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<sup>§</sup>, PENG Peizhi. “Experimental study of the relationship between NMR relaxation time and the concentration of solutions.” *Physics Bulletin* (ISSN 0509-4038) 2005 (10), 30–32 (2005). (In Chinese)
48. ZANG Chongzhi, ZHANG Jietian<sup>§</sup>, PENG Peizhi. “Discussion of data processing method for measuring NMR relaxation time.” *Physics Experimentation* (ISSN 1005-4642) 25(5), 45–47 (2005). (In Chinese)
49. ZANG Chongzhi, PENG Peizhi, ZHANG Jietian<sup>§</sup>, LU Sihua. “Teaching experimentation of MRI.” *Physics Experimentation* (ISSN 1005-4642) 24(8), 3–7 (2004). (In Chinese)

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

50. 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).

51. 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).
52. 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).
53. 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).
54. 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).
55. 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).
56. 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).
57. 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).
58. 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).
59. 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).

60. Chongzhi Zang, Dustin E. Schones, Chen Zeng, Kairong Cui, Keji Zhao, Weiqun Peng. “Genome-wide identification of ChIP-Seq enriched regions based on a statistical model.” In: *Proceedings of the 7th Asia-Pacific Bioinformatics Conference*, edited by Michael Q. Zhang, Michael S. Waterman, Xuegong Zhang. Beijing: Tsinghua University Press, 835 (2009).

## SOFTWARE AND RESOURCES

1. SICER: Spatial-clustering approach for the Identification of ChIP-Enriched Regions, a ChIP-Seq data analysis method and software package. <http://home.gwu.edu/~wpeng/Software.htm>
2. RECOGNICER: Recursive Coarse-Graining approach for the Identification of ChIP-Enriched Regions, a ChIP-Seq ultra-broad peak calling method. <https://github.com/zanglab/recognicer>
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. 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 R35 GM133712 PI: Zang 09/01/2019–07/31/2024  
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: MPI
3. Virginia Commonwealth Health Research Board PI: Zang 11/01/2020–10/31/2022  
Aberrant CTCF binding as an epigenetic signature of cancer  
Role: PI
4. NIH R01 HL148239 PI: Miller 06/01/2019–04/30/2024  
Cis-regulatory architecture of coronary vascular wall loci  
Role: Co-Investigator

- Completed Research Support**

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multi-modal single cell transcriptome and epigenome data  
Role: Co-PI

15. 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
16. 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 BIOC8145: Functional Analysis of Genomes BIMS7100: Research Ethics BIOL4910: Undergraduate Research CHEM3951: Undergraduate Research	Lecture Lectures 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

1. Center for Cancer Genomics, Department of Biochemistry and Molecular Genetics, Northwestern University. 12/09/2020
2. 14th International Bioinformatics Workshop (IBW 2019), Beijing, China. 08/03/2019
3. State Key Laboratory of Cardiovascular Disease, Peking Union Medical College. Beijing, China. 07/31/2019
4. School of Mathematics, Shandong University. Jinan, China. 07/29/2019
5. Department of Cognitive Science, University of California, San Diego, CA. 12/20/2018
6. Biomedical Pioneering Innovation Center, Peking University. Beijing, China. 8/21/2018
7. Department of Pathology, University of Virginia. Charlottesville, VA. 12/19/2017
8. Department of Biostatistics, Virginia Commonwealth University. Richmond, VA. 11/3/2017

9. Center for Quantitative Biology, Peking University. Beijing, China. 09/29/2017
10. Institute of Biophysics, Chinese Academy of Sciences. Beijing, China. 09/28/2017
11. Beijing Institute for Scientific and Engineering Computing, Beijing University of Technology. Beijing, China. 09/27/2017
12. Center for Statistical Science, Tsinghua University. Beijing, China. 09/25/2017
13. Department of Physics, Fudan University. Shanghai, China. 09/23/2017
14. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Shanghai, China. 09/18/2017
15. School of Life Sciences, Peking University. Beijing, China. 06/08/2016
16. Workshop on Analysis of ChIP-Seq Data, National Cancer Institute, National Institutes of Health. Bethesda, MD. 05/17/2016
17. Laboratory of Genome Integrity, National Cancer Institute, National Institutes of Health. Bethesda, MD. 04/07/2016
18. 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–)  
 Qingying Chen, PhD (UVA, 01/2021–)  
 William F. Lamberti, PhD (UVA, 01/2021–)

### *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 (Biomedical Engineering, UVA, 08/2018–12/2019)  
 Mengxue Tian (PhD in Biomedical Sciences, UVA, 07/2020–)  
 Hongpan Zhang (PhD in Biomedical Sciences, UVA, 07/2020–)  
 Audrey Putelo (PhD in Biomedical Sciences, UVA. Rotation 07/2020–08/2020)  
 Jose Verdezoto (PhD in Biomedical Sciences, UVA, Rotation 10/2020–11/2020)  
 Jamel Simpson (PhD in Biomedical Sciences, UVA, Rotation 1/2021–2/2021)

### *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, 01/2017–10/2020)  
 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–)  
 Yang Yu (PhD in Biology, UVA, 12/2019–)

## **PROFESSIONAL SERVICES**

<i>Ad hoc grant reviewer</i>	Research Councils UK (RCUK) (2017) Netherlands Organisation for Scientific Research (NWO) (2017)
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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 Lab, 2020–2021

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

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

*Admissions Committee*, Biomedical Sciences (BIMS) PhD Program, UVA, 2020–2021

Updated: December 2020