

CURRICULUM VITAE

Chongzhi Zang, PhD

Assistant Professor
University of Virginia
P.O. Box 800717, Charlottesville, VA 22908, USA
+1-908-838-5158 (cell) | 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</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 (03/2017–08/2019)
07/2010 – 10/2016	Harvard University/Dana-Farber Cancer Institute , 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	National Institutes of Health , 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	The George Washington University , 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 <i>Undergraduate Research Assistant</i> , High-field Physics Group (L05) (Thesis Advisor: Jie Zhang, PhD)

PUBLICATIONS

Peer-reviewed Journal Articles

Total citations > 11,000; H-index = 29 (Google Scholar)

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

1. 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).
2. Naomi D. Atkin, Heather M. Raimer, Zhenjia Wang, **Chongzhi Zang**, Yuh-Hwa Wang. "Assessing AML susceptibility in rearrangement-driven patients by DNA breakage at topoisomerase II and CTCF/cohesin binding sites." *Genes, Chromosomes and Cancer*, doi:10.1002/gcc.22993 (2021).
3. Zhenjia Wang, Yifang Zhang, **Chongzhi Zang**. "BART3D: Inferring transcriptional regulators from differential Hi-C data." *Bioinformatics*, doi:10.1093/bioinformatics/btab173 (2021).
4. 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*, doi:10.1093/nargab/lqab022 (2021).
5. Zachary V. Thomas, Zhenjia Wang, **Chongzhi Zang**. "BART Cancer: a web resource for transcriptional regulators in cancer genomes." *NAR Cancer*, doi:10.1093/narcan/zcab011 (2021).
6. 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*, doi:10.1038/s41375-020-01116-x (2021).
7. **Chongzhi Zang**§, Yiren Wang, Weiqun Peng§. "RECOGNICER: a coarse-graining approach for identifying broad domains from ChIP-seq data." *Quantitative Biology* 8, 359–368 (2020).
8. 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).
9. 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).
10. The ENCODE Project Consortium (including **Chongzhi Zang**), Jill E. Moore*, Michael J.

Purcaro*, Henry E. Pratt*, Charles B. Epstein*, Noam Shores*, Jessika Adrian*, Trupti Kauli*, 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[§], 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).

11. **The ENCODE Project Consortium** (including **Chongzhi Zang**), 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).
12. 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 Harman, 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).
13. 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* 18, 1262–1277 (2021). doi:10.1038/s41423-020-0436-5 (2020).
14. 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).
15. 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* 36, 1663–1667 (2020).
16. 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).

17. 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).
18. 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).
19. 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).
20. 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).
21. 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).
22. 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).
23. 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).
24. 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).
25. 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).
26. 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).

27. 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).
28. **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).
29. **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).
30. 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).
31. 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).
32. 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).
33. 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).
34. 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. 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[§]. "Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases." **The American Journal of Human Genetics** 95, 535–552 (2014).
35. 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).
36. 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).

37. 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).
38. 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).
39. 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).
40. 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).
41. 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).
42. 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).
43. 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).
44. 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).
45. 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)

46. 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)
47. 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).
48. **Chongzhi Zang**, Dustin E. Schones, Chen Zeng, Kairong Cui, Keji Zhao, Weiqun Peng. “A clustering approach for identification of enriched domains from histone modification ChIP-Seq data.” **Bioinformatics** 25, 1952–1958 (2009). (cited > 900)
49. 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)
50. Kairong Cui*, **Chongzhi Zang***, Tae-Young Roh, Dustin E. Schones, Richard W. Childs, Weiqun Peng, Keji Zhao. “Chromatin signatures in multipotent hematopoietic stem cells indicate the fate of bivalent genes during differentiation.” **Cell Stem Cell** 4, 80–93 (2009). (cited > 600)
51. 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)
52. 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)
53. **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)
54. **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)
55. **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 Papers/Abstracts

56. 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).
57. 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).
58. 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).
59. 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).
60. **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).
61. 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).
62. 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).
63. 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).
64. 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).
65. 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).

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

SOFTWARE AND RESOURCES

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

HONORS AND AWARDS

- University of Virginia Research Excellence Award 2020

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

RESEARCH SUPPORT

Current Research Support

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

8. NIH R01 HL148239 PI: Miller 06/01/2019–04/30/2024
Cis-regulatory architecture of coronary vascular wall loci
Role: Co-Investigator
9. DOD/CDMRP Impact Award PI: Mohi 09/01/2019–06/30/2022
Targeted therapies for myeloproliferative neoplasms
Role: Co-Investigator
10. NIH R01 HL149893 PI: Mohi 01/01/2020–12/31/2023
The role of PTPN11 in myelofibrosis
Role: Co-Investigator
11. NIH 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
12. 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
13. NIH R01 GM132138 PI: Li 09/01/2019–07/31/2023
Genome-wide investigation of cis-splicing between adjacent genes
Role: Collaborator

Completed Research Support

14. NIH/NCI K22 CA204439 PI: Zang 09/01/2017–08/31/2019*
Quantitative modeling for chromatin regulation of gene expression in cancer
Role: PI
* Funded for 3 years but Year 03 fund was relinquished on 08/31/2019 due to Dr. Zang's funding of NIGMS MIRA (R35) award.
15. Phi Beta Psi Charity Trust Research Grant PI: Zang 08/15/2018–08/14/2020
Integrative modeling of multi-source genomic data for functional gene regulation in colorectal cancer
Role: PI
16. NIH/NIEHS R01 ES024727 PI: Cuddapah 02/01/2017–06/30/2020
Epigenetic reprogramming by nickel through chromatin domain disruption
Role: Subcontract PI
17. 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
18. 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

19. 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
20. 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: Recent Advances in Public Health Genomics BIOC8145: Bioinformatics & Functional Analysis of Genomes BIMS6000: Core Course in Integrative Biosciences: Genome Architecture & Dynamics BIMS7100: Research Ethics BIOL4910: Undergraduate Research CHEM3951: Undergraduate Research	Co-instructor Co-instructor Co-instructor Co-instructor Discussion Leader Mentor Mentor
04/2021	New York University EHSC-GA-2050: Epigenetics and Environmental Diseases	Guest Lecture
05/2016	NIH/NCI Bioinformatics Workshop	Guest Instructor
11/2014	NIH/NCI Bioinformatics Workshop	Guest Instructor
09/2005–05/2008	The George Washington University Physics 001, Physics 002 Astronomy 001, Astronomy 002	Teaching Assistant Lab & Recitation Lab Instructor

INVITED TALKS

1. Department of Environmental Medicine, New York University. New York, NY. 05/11/2021
2. Child Health Research Center, University of Virginia. Charlottesville, VA. 04/23/2021
3. Foundation of Biomedical Data Science Seminar Series, University of Virginia School of Data Science. Charlottesville, VA. 04/02/2021
4. Computational Biology and Bioinformatics Seminar Series, Duke University. Durham, NC. 03/29/2021
5. Center for Cancer Genomics, Department of Biochemistry and Molecular Genetics, Northwestern University. Chicago, IL. 12/09/2020
6. 14th International Bioinformatics Workshop (IBW 2019), Beijing, China. 08/03/2019
7. State Key Laboratory of Cardiovascular Disease, Peking Union Medical College. Beijing, China. 07/31/2019
8. School of Mathematics, Shandong University. Jinan, China. 07/29/2019

9. Department of Cognitive Science, University of California, San Diego, CA. 12/20/2018
10. Biomedical Pioneering Innovation Center, Peking University. Beijing, China. 8/21/2018
11. Department of Pathology, University of Virginia. Charlottesville, VA. 12/19/2017
12. Department of Biostatistics, Virginia Commonwealth University. Richmond, VA. 11/3/2017
13. Center for Quantitative Biology, Peking University. Beijing, China. 09/29/2017
14. Institute of Biophysics, Chinese Academy of Sciences. Beijing, China. 09/28/2017
15. Beijing Institute for Scientific and Engineering Computing, Beijing University of Technology. Beijing, China. 09/27/2017
16. Center for Statistical Science, Tsinghua University. Beijing, China. 09/25/2017
17. Department of Physics, Fudan University. Shanghai, China. 09/23/2017
18. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Shanghai, China. 09/18/2017
19. School of Life Sciences, Peking University. Beijing, China. 06/08/2016
20. Workshop on Analysis of ChIP-Seq Data, National Cancer Institute, National Institutes of Health. Bethesda, MD. 05/17/2016
21. Laboratory of Genome Integrity, National Cancer Institute, National Institutes of Health. Bethesda, MD. 04/07/2016
22. Department of Immunobiology, Yale University. New Haven, CT. 03/11/2016
23. University of Virginia. Charlottesville, VA. 02/05/2016
24. The Wistar Institute. Philadelphia, PA. 01/29/2016
25. Academy of Mathematics and Systems Science, Chinese Academy of Sciences. Beijing, China. 01/07/2016
26. Peking University Third Hospital. Beijing, China. 01/05/2016
27. Peking University Medical Center. Beijing, China. 01/04/2016
28. University of Illinois College of Medicine, Peoria, IL. 12/17/2015
29. The Stadtman Symposium, National Institutes of Health. Bethesda, MD. 12/10/2015
30. National Heart, Lung, and Blood Institute, National Institutes of Health. Bethesda, MD. 11/20/2015
31. University of Nevada School of Medicine, Reno, NV. 10/06/2015
32. College of Pharmacy, University of Rhode Island. Kingston, RI. 06/24/2015
33. Uniformed Services University of the Health Sciences. Bethesda, MD. 05/29/2015
34. Department of Electrical & Computer Engineering, University of Nebraska, Lincoln, NE. 02/18/2015
35. National Human Genome Research Institute, National Institutes of Health. Bethesda, MD. 02/04/2015
36. National Cancer Institute, National Institutes of Health. Bethesda, MD. 12/19/2014
37. Cancer epigenetics symposium, Harvard Medical School. Boston, MA. 12/14/2014
38. Biophysics Seminar, The George Washington University. Washington, DC. 10/02/2014
39. Workshop on big data analysis in biomedical research, Harvard Medical School. Boston, MA. 06/24/2014
40. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological

Sciences, Chinese Academy of Sciences. Shanghai, China. 11/28/2013

41. Institute of Systems Biomedicine, Shanghai Jiao Tong University. Shanghai, China. 11/26/2013
42. Computational Biology and Bioinformatics Organization, Broad Institute. Boston, MA. 10/16/2013
43. Megakaryocyte and Platelet Biology Joint Meeting, Boston Children's Hospital. Boston, MA. 09/12/2012
44. Department of Animal and Avian Sciences, College of Agriculture and Natural Resources, University of Maryland, College Park, MD. 09/28/2009

CONTRIBUTED PRESENTATIONS

1. 2021 NHLBI Systems Biology Symposium (Virtual), 05/2021. (3 *Posters by lab members*)
2. American Association for Cancer Research (AACR) Annual Meeting (Virtual), 04/2021. (*Poster*)
3. American Physical Society (APS) March Meeting (Virtual), 03/2021. (*Talk*)
4. American Association for Cancer Research (AACR) Annual Meeting (Virtual), 06/2020. (*Poster*)
5. iPoLS 2020: International Physics of Living Systems Annual Meeting (Virtual), 06/2020. (*Poster*)
6. Keystone Meeting on Cancer Epigenetics. Keystone, CO, 01/2020. (*Poster*)
7. Physics Meets Biology 2019, Institute of Physics, University of Oxford. Oxford, UK, 09/2019. (*Poster*)
8. RECOMB 2019: 23rd Annual International Conference on Research in Computational Molecular Biology. Washington, DC, 05/2019 (5 *Posters by lab members*)
9. Gordon Research Conference on Cancer Genetics and Epigenetics. Lucca, Italy, 04/2019. (*Poster*)
10. American Association for Cancer Research (AACR) Annual Meeting. Atlanta, GA, 04/2019. (*Poster*)
11. American Physical Society (APS) March Meeting. Boston, MA, 03/2019. (*Talk*)
12. ISMB 2018: Conference on Intelligent Systems for Molecular Biology. Chicago, IL, 07/2018. (*Poster*)
13. Biophysics of Epigenetic and Chromatin Dynamics Workshop, Higgs Centre for Theoretical Physics, University of Edinburgh. Edinburgh, UK, 04/2018. (*Poster*)
14. American Physical Society (APS) March Meeting. Los Angeles, CA, 03/2018. (*Talk*)
15. Keystone Meeting on Cancer Epigenetics. Breckenridge, CO, 02/2018. (*Poster*)
16. Cold Spring Harbor Asia Meeting on Precision Cancer Biology. Suzhou, China, 09/2017. (*Poster*)
17. Keystone Meeting on Epigenetics and Human Disease. Seattle, WA, 01/2017. (*Poster*)
18. NCI Symposium on Chromosome Biology. Bethesda, MD, 11/2016. (*Poster*)
19. ENCODE Consortium Meeting. San Diego, CA, 06/2016. (*Poster*)

20. AACR Special Conference on Chromatin and Epigenetics in Cancer. Atlanta, GA, 09/2015. (*Poster*)
21. Keystone Meeting on Cancer Epigenetics. Santa Fe, NM, 02/2014. (*Poster*)
22. NCI Symposium on Chromosome Biology. Bethesda, MD, 04/2013. (*Poster*)
23. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2012. (*Poster*)
24. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2010. (*Poster*)
25. The 7th Asia Pacific Bioinformatics Conference. Beijing, China, 01/2009. (*Best Poster Award Winner*)
26. American Physical Society (APS) March Meeting. New Orleans, LA, 03/2008. (*Talk*)

MENTEES AND STUDENTS

Postdoctoral Associates Mentored

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

Graduate Students Mentored

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

PhD Committee Service

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

Undergraduate Student Research Supervised

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

Visiting Students/Scholars

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)

PROFESSIONAL SERVICE

<i>Ad hoc grant reviewer</i>	Medical Research Council, Research Councils UK (RCUK) (2017) Netherlands Organisation for Scientific Research (NWO) (2017) NIH Center for Scientific Review (CSR): ZRG1 PSE-B (04) Special Emphasis Panel (2020) ZMH1 ERB-M (06) Special Emphasis Panel (2020) ZRG1 CB-K (55) Special Emphasis Panel (2021) Inova Translational Research Funding Program (2018) UVA internal review committee for Virginia CHRB awards (2021) UVA Carter Immunology Center internal review committee (2021)
<i>Ad hoc journal reviewer</i>	<i>Nature Biotechnology</i> <i>Nature Genetics</i> <i>Nature Methods</i> <i>Nature Communications</i> <i>Genome Research</i> <i>Genome Biology</i> <i>EMBO Journal</i> <i>Nucleic Acids Research</i> <i>Cancer Research</i> <i>Cellular and Molecular Life Sciences</i> <i>Bioinformatics</i> <i>Briefings in 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>PLOS One</i> <i>Quantitative Biology</i> <i>IEEE/ACM Transactions on Computational Biology & Bioinformatics</i> <i>Computational Statistics and Data Analysis</i> <i>Biomolecules</i> <i>Frontiers of Medicine</i> <i>Frontiers in Oncology</i>
<i>Guest Editor</i>	<i>PLOS Computational Biology</i>
<i>Topical Advisory Board</i>	<i>Epigenomes</i>
<i>Faculty Mentor</i>	Biomedical Data Science Innovation Lab: Challenges in Brain Analytics and Integration, 2020–2021

<i>Co-Chair</i>	AACR Annual Meeting Minisymposium: Transcriptional Gene Regulation in Cancer, 2020
<i>Planning Committee</i>	Emerging Scholars in Genome Sciences Symposium, UVA, 2020– <i>Committee Chair</i> , 2021
<i>Admissions Committee</i>	Biomedical Sciences (BIMS) PhD Program, UVA, 2020–2021

Updated: September 2021