Wei Li, Ph.D.

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EMPLOYMENT

2025 -	Associate Professor (with tenure) University of Maryland-Institute for Health Computing (IHC) Department of Pharmacology & Physiology; Institute for Genome Sciences (IGS); Mariene and Stewart Greenebaum Comprehensive Cancer Center (UMGCCC) University of Maryland School of Medicine
2018 – 2025	Principal Investigator Center for Genetic Medicine Research; Center for Cancer and Immunology Research Children's National Hospital 7144 13th Pl NW, Washington DC 20012
2024 – 2025	Associate Professor (with tenure) Department of Genomics and Precision Medicine; Department of Pediatrics (secondary); Department of Biochemistry and Molecular Medicine (tertiary) School of Medicine and Health Sciences, George Washington University, Washington, DC
2018 – 2024	Assistant Professor George Washington University, Washington, DC
2012 – 2018	Postdoctoral Fellow Department of Biostatistics and Computational Biology (now Department of Data Science) Dana-Farber Cancer Institute, Harvard T.H. Chan School of Public Health Boston, MA 02215 Advisor: X. Shirley Liu
2011	Research Intern Bioinformatics Division, Novartis Institutes for Biomedical Research (NIBR) Emeryville, CA 94608

EDUCATION

2008-2012	Ph.D. in Computer Science and Engineering, University of California, Riverside • Advisor: Tao Jiang
2006-2008	Master in Computer Science, Tsinghua University, Beijing, China • Advisor: Yannan Zhao
2002-2006	Bachelor in Computer Science, Tsinghua University, Beijing, China

HONORS AND DISTINCTIONS

[1] Mrs. Mary Elizabeth McGehee Joyce Chair in Genetic Research, Children’s National Hospital. 2024 – 2025
[2] Research Starter Award, Pharmaceutical Research and Manufacturers of America Foundation (PhRMA), 2019
[3] APBC 2015 Best Paper Award, 2015
[4] IEEE ICCABS Conference Travel Award, 2012

[5] Graduate Division Fellowship Award, University of California, Riverside, 2008-2009
[6] Director, Tsinghua University Military Band Freshman Division, 2006-2007
[7] Tsinghua University Student Art Group Fellowship, 2005
[8] Tsinghua University Academic Career Fellowship, 2004
[9] Deputy Director, Tsinghua University Military Band, 2004-2005
[10] Freshman Excellence Scholarship, Tsinghua University, 2002
[11] Highest ranking student in Guangdong Province College Entrance Exam (equivalent to SAT College Admission Exam; ranked 1st/~163,000)

PUBLICATIONS

***First/Co-first author**. **#Corresponding/Co-corresponding author**.

Selected papers

[1] Bicna Song, Dingyu Liu, Weiwei Dai, Natalie McMyn, Qingyang Wang, Dapeng Yang, Adam Krejci, Anatoly Vasilyev, Nicole Untermoser, Anke Loregger, Dongyuan Song, Breanna Williams, Bess Rosen, Xiaolong Cheng, Lumen Chao, Hanuman Kale, Hao Zhang, Yarui Diao, Tilmann Bürckstümmer, Jenet M. Siliciano, Jingyi Jessica Li, Robert Siliciano, Danwei Huangfu, **Wei Li**. Decoding Heterogenous Single-cell Perturbation Responses. Nature Cell Biology 27, 493–504 (2025). https://www.nature.com/articles/s41556-025-01626-9

[2] Bicna Song, **Wei Li.** Factoring Single Cell Perturbations. Nature Methods 2023. https://doi.org/10.1038/s41592-023-02002-x.

[3] Zexu Li*, Zihan Li*, Xiaolong Cheng*, Shengnan Wang, Xiaofeng Wang, Shixin Ma, Zhiyan Lu, Han Zhang, Wenchang Zhao, Zhisong Chen, Yingjia Yao, Cheng Zhang, Lumen Chao, **Wei Li#,** Teng Fei#. Intrinsic targeting of host RNA by Cas13 constrains its utility. Nature Biomedical Engineering 2024; 8, 177-192. https://doi.org/10.1038/s41551-023-01109-y

[4] Xiaolong Cheng*, Zexu Li*, Rrocheng Shan, Zihan Li, Shengnan Wang, Wenchang Zhou, Han Zhang, Lumen Chao, Jian Peng, Teng Fei#, **Wei Li#.** Modeling CRISPR-Cas13d on-target and off-target effects using machine learning approaches. Nature Communications 2023, 14 (1), 752. http://deepcas13.weililab.org

[5] Weiwei Dai, Fengting Wu, Victoria E. Walker-Sperling, Bicna Song, Joseph Varriale, Hao Zhang, Dan H. Barouch, Janet D. Siliciano, **Wei Li#**, Robert F. Siliciano#. Genome-wide CRISPR screens identify combinations of candidate latency reversing agents for targeting the latent HIV-1 reservoir. Science Translational Medicine 2022, 14 (667) eabh3351.

[6] Christoph Bock, Paul Datlinger, Florence Chardon, Matthew A Coelho, Matthew B Dong, Keith A Lawson, Tian Lu, Laetitia Maroc, Thomas M Norman, Bicna Song, Geoff Stanley, Sidi Chen, Mathew Garnett, **Wei Li**, Jason Moffat, Lei S Qi, Rebecca S Shapiro, Jay Shendure, Jonathan S Weissman, Xiaowei Zhuang. High-content CRISPR screening. Nature Reviews Methods Primers 2022, 2(1) 1-23.

[7] Zexu Li*, Yingjia Yao*, Xiaolong Cheng*, Qing Chen, Wenchang Zhao, Shixin Ma, Zihan Li, Hu Zhou, **Wei Li#**, Teng Fei#. A Computational Framework of Host-Based Drug Repositioning for Broad-Spectrum Antivirals against RNA Viruses. *iScience* 2021, 24(3) 102148.

[8] Yingbo Cui*, Xiaolong Cheng*, Qing Chen, Bicna Song, Anthony Chiu, Yuan Gao, Tyson Dawson, Lumen Chao, Wubing Zhang, Dian Li, Zexiang Zeng, Jijun Yu, Zexu Li, Teng Fei, Shaoliang Peng, **Wei Li#**. CRISP-view: a database of functional genetic screens spanning multiple phenotypes. *Nucleic Acids Research* 2021, 49 (D1) D848-854. http://crispview.weililab.org

[9] Yinghua Li*, Bo Li*, **Wei Li*,** Yuan Wang, Seçkin Akgül, Daniel M. Treisman, Kevin A Heist, Brianna Pierce, Benjamin Hoff, Cheng-Ying Ho, David O Ferguson, Alnawaz Rehemtulla, Siyuan Zheng, Brian D Ross, Jun Z. Li, Yuan Zhu. Murine models of IDH-wild-type glioblastoma exhibit spatial segregation of tumor initiation and manifestation during evolution. *Nature Communications* 2020; 11, 3669.

[10] Lin Yang*, Yuqing Zhu*, Hua Yu*, Xiaolong Cheng, Sitong Chen, Yulan Chu, He Huang, Jin Zhang#, **Wei Li#.** scMAGeCK links genotypes with multiple phenotypes in single-cell CRISPR screens. Genome Biology 2020, 21 (1) 1-14. https://bitbucket.org/weililab/scmageck

[11] Binbin Wang*, Mei Wang*, Wubing Zhang*, Tengfei Xiao, Chen-Hao Chen, Alexander Wu, Feizhen Wu, Nicole Traugh, Xiaoqing Wang, Ziyi Li, Shenglin Mei, Yingbo Cui, Sailing Shi, Jesse Jonathan Lipp, Matthias Hinterndorfer, Johannes Zuber, Myles Brown, **Wei Li#**, X. Shirley Liu#. Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute. *Nature Protocols* 2019; 14, 756–780.

[12] Teng Fei*, **Wei Li*,** Jingyu Amy 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. *PNAS* 2019; 116 (50), 25186-25195.

[13] Tengfei Xiao*, **Wei Li***, Xiaoqing Wang, Han Xu, Qiu Wu, Peng Jiang, Jixin Yang, Teng Fei, Chongzhi Zang, Qi Liao, Jonathan Rennhack, Eran Andrechek, Rinath M. Jeselsohn, X. Shirley Liu, Myles Brown. Estrogen-regulated Feedback Loop Limits the Efficacy of Estrogen Receptor-targeted Breast Cancer Therapy. *PNAS* 2018; 115 (31), 7869-7878.

[14] Chen-Hao Chen*, Tengfei Xiao*, Han Xu, Peng Jiang, Cliff Meyer, **Wei Li#,** Myles Brown#, X. Shirley Liu#. Improved design and analysis of CRISPR Knockout Screens. *Bioinformatics* 2018; 34 (23), 4095-4101.

[15] Qingyi Cao, Jian Ma, Chen-Hao Chen, Han Xu, Zhi Chen#, **Wei Li#**, X. Shirley Liu#. CRISPR-FOCUS: a web server for designing focused CRISPR screening experiments. *PLoS ONE* 2017; 12(9): e0184281.

[16] Shiyou Zhu*, **Wei Li***, Jingze Liu, Chen-Hao Chen, Qi Liao, Han Xu, Tengfei Xiao, Zhongzheng Cao, Jingyu Peng, Pengfei Yuan, Myles Brown, Xiaole Shirley Liu & Wensheng Wei. CRISPR/Cas9-mediated genomic deletion screening for long non-coding RNAs using paired-gRNAs. *Nature Biotechnology* 2016; 34:1279-1286.

[17] **Wei Li***, Johannes Koster*, Tengfei Xiao, Han Xu, Chen-Hao Chen, Jun S. Liu, Myles Brown, Xiaole S. Liu. Quality control, modeling and visualization of genome-wide CRISPR screens using MAGeCK-VISPR. *Genome Biology* 2015; 16:281.

[18] **Wei Li***, Han Xu*, Tengfei Xiao, Le Cong, Feng Zhang, Jun S. Liu, Myles Brown, X. Shirley Liu. MAGeCK enables robust identification of essential genes from genome-scale CRISPR-Cas9 knockout screens. *Genome Biology* 2014; 15:554. http://mageck.sourceforge.net. ***Citation: >2500; >200,000 software downloads***

[19] Masruba Tasnim, Shining Ma, Ei-Wen Yang, Tao Jiang# and **Wei Li#**. Accurate Inference of Isoforms from Multiple Sample RNA-Seq Data. *BMC Genomics* 2015; 16 (S2):S15. Also appear in 2015 *Asian Pacific Bioinformatics Conference* (*APBC* 2015). **APBC 2015 Best Paper Award.**

[20] **Wei Li*#** and Tao Jiang. Transcriptome Assembly and Isoform Expression Level Estimation from Biased RNA-Seq Reads. *Bioinformatics* 2012; 28(22):2914-2921.

[21] **Wei Li**, Jianxing Feng, Tao Jiang. IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly. *Journal of Computational Biology* 2011; 18(11):1693-1707. Also appear in the *Research in Computational Molecular Biology* (*RECOMB* 2011).

Submitted and preprint manuscripts

[22] **Wei Li**. Adapting Blockchain Technology for Scientific Computing. arXiv:1804.08230 [cs.CR] (2018).

[23] Alexander Wu, Tengfei Xiao, Teng Fei, Shirley X Liu, **Wei Li**. Reducing False Positives in CRISPR/Cas9 Screens from Copy Number Variations. *bioRxiv* 247031, 2018; https://doi.org/10.1101/247031.

Other journal papers and conference proceedings

[24] Anja Deutzmann, Delaney K Sullivan, Renumathy Dhanasekaran, **Wei Li**, Xinyu Chen, Ling Tong, Wadie D Mahauad-Fernandez, John Bell, Adriane Mosley, Angela N Koehler, Yulin Li, Dean W Felsher. Nuclear to cytoplasmic transport is a druggable dependency in MYC-driven hepatocellular carcinoma. Nature Communications 2024, 15 (963).

[25] Haihui Pan, Xiaolong Cheng, Pedro Felipe Gardeazábal Rodríguez, Xiaowen Zhang, Inhee Chung, Victor X Jin, **Wei Li**, Yanfen Hu, Rong Li. An essential signaling function of cytoplasmic NELFB is independent of RNA polymerase II pausing. J Biol Chem 2023, 299(11):105259.

[26] Jianting Shi, Xun Wu, Ziyi Wang, Fang Li, Yujiao Meng, Rebecca M Moore, Jian Cui, Chenyi Xue,

Katherine R Croce, Arif Yurdagul, John G Doench, **Wei Li,** Konstantinos S Zarbalis, Ira Tabas, Ai Yamamoto, Hanrui Zhang. A Genome-wide CRISPR Screen Identifies WDFY3 as a Novel Regulator of Macrophage Efferocytosis. Nature Communications 2022, 13 (1), 1-19.

[27] Xiaolin Wei, Yu Xiang, Derek T Peters, Choiselle Marius, Tongyu Sun, Ruocheng Shan, Jianhong Ou, Xin Lin, Feng Yue, **Wei Li**, Kevin W Southerland, Yarui Diao. HiCAR is a robust and sensitive method to analyze open-chromatin-associated genome organization. *Molecular Cell* 2022; 82 (6) 1225-1238.e6.

[28] Xiaoqing Wang, Collin Tokheim, Shengqing Stan Gu, Binbin Wang, Qin Tang, Yihao Li, Nicole Traugh, Zexian Zeng, Yi Zhang, Ziyi Li, Boning Zhang, Jingxin Fu, Tengfei Xiao, **Wei Li,** Clifford A Meyer, Jun Chu, Peng Jiang, Paloma Cejas, Klothilda Lim, Henry Long, Myles Brown, X Shirley Liu. In vivo CRISPR screens identify the E3 ligase Cop1 as a modulator of macrophage infiltration and cancer immunotherapy target. *Cell* 2021, 184 (21), 5357-5374. e22

[29] Shaokun Shu, Hua-Jun Wu, Y Ge Jennifer, Rhamy Zeid, Isaac S Harris, Bojana Jovanović, Katherine Murphy, Binbin Wang, Xintao Qiu, Jennifer E Endress, Jaime Reyes, Klothilda Lim, Alba Font-Tello, Sudeepa Syamala, Tengfei Xiao, Chandra Sekhar Reddy Chilamakuri, Evangelia K Papachristou, Clive D'Santos, Jayati Anand, Kunihiko Hinohara, **Wei Li,** Thomas O McDonald, Adrienne Luoma, Rebecca J Modiste, Quang-De Nguyen, Brittany Michel, Paloma Cejas, Cigall Kadoch, Jacob D Jaffe, Kai W Wucherpfennig, Jun Qi, X Shirley Liu, Henry Long, Myles Brown, Jason S Carroll, Joan S Brugge, James Bradner, Franziska Michor, Kornelia Polyak. Synthetic lethal and resistance interactions with BET bromodomain inhibitors in triple-negative breast cancer. *Molecular Cell* 2020; 78 (6) 1096-1113.

[30] Sitong Chen, Lin Yang, **Wei Li**. CRISPR Screening "Big Data" Informs Novel Therapeutic Solutions. *The CRISPR Journal 2019;* 2 (3), 152-154.

[31] Yuwei Zhang, Yang Tao, Huihui Ji, **Wei Li**, Xingli Guo, Derry Minyao Ng, Maria Haleem, Yang Xi, Changzheng Dong, Jinshu Zhao, Lina Zhang, Xiaohong Zhang, Yangyang Xie, Xiaoyu Dai, Qi Liao. Genome-wide identification of the essential protein-coding genes and long noncoding RNAs for human pan-cancer. *Bioinformatics* 2019; btz230.

[32] Shiyou Zhu, Zhongzheng Cao, Zhiheng Liu, Yuan He, Yinan Wang, Pengfei Yuan, **Wei Li,** Feng Tian, Ying Bao and Wensheng Wei. Guide RNAs with embedded barcodes boost CRISPR-pooled screens. *Genome Biology* 2019; 20:20.

[33] Laura Cato, Jonas de Tribolet-Hardy, Irene Lee, Jaice T. Rottenberg, Ilsa Coleman, Diana Melchers, René Houtman, Tengfei Xiao, **Wei Li**, Takuma Uo, Shihua Sun, Nane C. Kuzni, Bettina Göppert, Fatma Ozgun, Martin E. van Royen, Adriaan B. Houtsmuller, Raga Vadhi, Prakash K. Rao, Lewyn Li, Steven P. Balk, Robert B. Den, Bruce Trock, R. Jeffrey Karnes, Robert Jenkins, Eric Klein, Elai Davicioni, Friederike J. Gruhl, Henry W. Long, X. Shirley Liu, Andrew C. B. Cato, Nathan A. Lack, Peter S. Nelson, Stephen R. Plymate, Anna C. Groner, Myles Brown. ARv7 represses tumor suppressor genes in castration-resistant prostate cancer. *Cancer Cell* 2019; 35 (3), 401-413.

[34] Björn Grüning, Ryan Dale, Andreas Sjödin, Jillian Rowe, Brad A. Chapman, Christopher H. Tomkins-Tinch, Renan Valieris, The Bioconda Team, Johannes Köster. Bioconda: sustainable and comprehensive software distribution for the life sciences. *Nature Methods* 2018; 15, 475–476.

[35] Diana Miao, Claire A Margolis, Wenhua Gao, Martin H Voss, **Wei Li,** Dylan J Martini, Craig Norton, Dominick Bossé, Stephanie M Wankowicz, Dana Cullen, Christine Horak, Megan Wind-Rotolo, Adam Tracy, Marios Giannakis, Frank Stephen Hodi, Charles G Drake, Mark W Ball, Mohamad E Allaf, Alexandra Snyder, Matthew D Hellmann, Thai Ho, Robert J Motzer, Sabina Signoretti, William G Kaelin, Toni K Choueiri, Eliezer M Van Allen. Genomic correlates of response to immune checkpoint therapies in clear cell renal cell carcinoma. *Science* 2018; 359 (6377), 801-806.

[36] Rinath Jeselsohn, Johann S Bergholz, Matthew Pun, MacIntosh Cornwell, Weihan Liu, Agostina Nardone, Tengfei Xiao, **Wei Li**, Xintao Qiu, Gilles Buchwalter, Ariel Feiglin, Kayley Abell-Hart, Teng Fei, Prakash Rao, Henry Long, Nicholas Kwiatkowski, Tinghu Zhang, Nathanael Gray, Diane Melchers, Rene Houtman, X Shirley Liu, Ofir Cohen, Nikhil Wagle, Eric P Winer, Jean Zhao, Myles Brown. Allele-Specific Chromatin Recruitment and Therapeutic Vulnerabilities of ESR1 Activating Mutations. *Cancer Cell* 2018; 33 (2) 173-186.

[37] Mulin Jun Li, Jian Zhang, Qian Liang, Chenghao Xuan, Jiexing Wu, Peng Jiang, **Wei Li,** Yun Zhu, Panwen Wang, Daniel Fernandez, Yujun Shen, Yiwen Chen, Jean-Pierre A. Kocher, Ying Yu, Pak

Chung Sham, Junwen Wang, Jun S. Liu, X. Shirley Liu; Exploring genetic associations with ceRNA regulation in the human genome. *Nucleic Acids Res* 2017; 45 (10) 5653-5665.

[38] Teng Fei, Yiwen Chen, Tengfei Xiao, **Wei Li**, Laura Cato, Peng Zhang, Maura B. Cotter, Michaela Bowden, Rosina T. Lis, Shuang G. Zhao, Qiu Wu, Felix Y. Feng, Massimo Loda, Housheng Hansen He, X. Shirley Liu, Myles Brown. HNRNPL and its RNA Targets Regulate Prostate Cancer Growth. *PNAS* 2017; 114 (26), E5207-E5215.

[39] Wenhua Gao, **Wei Li,** Tengfei Xiao, Shirley Liu, William G. Kaelin, Jr., M.D. Inactivation of the PBRM1 Tumor Suppressor Gene Amplifies the HIF-Response in VHL-/- Clear Cell Renal Carcinoma. *PNAS* 2017; 114(5) 1027-1032.

[40] Jian Ma, Johannes Köster, Qian Qin, Shengen Hu, **Wei Li**, Chenhao Chen, Qingyi Cao, Jinzeng Wang, Shenglin Mei, Qi Liu, Han Xu, and Xiaole Shirley Liu. CRISPR-DO for genome-wide CRISPR design and optimization. *Bioinformatics* 2016; 32 (21) 3336-3338.

[41] Shom Goel, Qi Wang, April C. Watt, Sara M. Tolaney, Deborah A. Dillon, **Wei Li**, Susanne Ramm, Adam C. Palmer, Haluk Yuzugullu, Kwok-Kin Wong, X. Shirley Liu, Piotr Sicinski, Eric P. Winer, Ian E. Krop, Jean J. Zhao. Overcoming Therapeutic Resistance in HER2-Positive Breast Cancers With CDK4/6 Inhibitors. *Cancer Cell* 2016; 29(3):255-269.

[42] Peng Jiang, Hongfang Wang, **Wei Li**, Chongzhi Zang, Bo Li, Yinling Wong, Cliff Meyer, Jun S. Liu, Jon Aster, X. Shirley Liu. Network analysis of gene essentiality in functional genomic screens. *Genome Biology* 2015; 16:239.

[43] Han Xu, Chen-Hao Chen, **Wei Li**, Cliff Meyer, Tengfei Xiao, Le Cong, Feng Zhang, Jun S. Liu, Myles Brown, X. Shirley Liu. Sequence determinants of improved CRISPR sgRNA design. *Genome Research 2015*; 25(8):1147-57.

[44] Xuesong Zhao, Tatyana Ponomaryov, Kimberly J. Ornell, Pengcheng Zhou, Sukriti K. Dabral, Ekaterina Pak, **Wei Li**, Scott X. Atwood, Ramon J. Whitson, Anne Lynn S. Chang, Jiang Li, Anthony E. Oro, Jennifer A. Chan, Joseph F. Kelleher, and Rosalind A. Segal. RAS/MAPK activation drives resistance to Smo inhibition, metastasis and tumor evolution in Shh pathway-dependent tumors. *Cancer Research* 2015; 75(17):3623-35.

[45] Xiaoqi Zheng, Qian Zhao, Hua-Jun Wu, **Wei Li**, et al. MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. *Genome Biology* 2014; 15:419.

[46] Paul M. Ruegger, Elizabeth Bent, **Wei Li**, Daniel R. Jeske, Xinping Cui, Jonathan Braun, Tao Jiang, James Borneman. Improving Oligonucleotide Fingerprinting of rRNA Genes by Implementation of Polony Microarray Technology. *Journal of Microbiological Methods* 2012; 90(3):235-240.

[47] **Wei Li**, *et al*. Workshop: Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. *IEEE 2nd Computational Advances in Bio and Medical Sciences* (*ICCABS* 2012), pp. 1

[48] Jianxing Feng, **Wei Li**, Tao Jiang. Inference of isoforms from short sequence reads. *Journal of Computational Biology* 2011, 18(3):305-321. Also appear in the *Research in Computational Molecular Biology* (*RECOMB* 2010).

[49] **Wei Li**, *et al*. Workshop: Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges. *IEEE 1st Computational Advances in Bio and Medical Sciences* (*ICCABS* 2011), pp. 271

[50] **Wei Li**, Paul Ruegger, James Borneman, Tao Jiang. Polony Identification Using the EM Algorithm Based on a Gaussian Mixture Model. *IEEE International Conference on BioInformatics and BioEngineering* (*BIBE* 2010), 220-225.

[51] **Wei Li**, et al. SVM feature selection and sample regression for Chinese medicine research. 2008 *International Conference on Information and Automation* (*ICIA* 2008), pp. 1773.

[52] **Wei Li**, et al. COX-2 activity prediction in Chinese medicine using neural network based ensemble learning methods. *International Joint Conference on Neural Networks* (*IJCNN* 2008), pp. 1853.

PATENTS

[1] Generation of alemtuzumab-resistant multivirus-specific T cells and uses thereof. Michael Keller, Cecilia Motta, Susan Conway, Pamela Chansky, Catherine Bollard, **Wei Li**, Allistair Abraham. 63/818,840. 558522US.

[2] Compositions and Methods for Making and Decoding Paired-Guide RNA Libraries and Uses Thereof.

Jingyu Amy Peng, Tengfei Xiao, **Wei Li,** X. Shirley Liu, Myles Brown. WO2019023291A3.

[3] Biomarkers predictive of endocrine resistance in breast cancer. X. Shirley Liu, Myles Brown, **Wei Li,** Tengfei Xiao. US Patent App. 16/315,861.

PRESENTATIONS

[1] Decoding Heterogenous Single-cell Perturbation Responses from Perturb-seq.
- *ELLIS Health Workshop: Cell Perturbation Modeling (Virtual). European Laboratory for Learning and Intelligent Systems (ELLIS), 2024*

[2] Modeling key mutational events in NF1-driven tumorigenesis using Perturb-seq and AI-driven in silico perturbation prediction methods.
- *Brain Tumor Initiative (BTI) 1st Annual Meeting, Detroit MI, 2024*

[3] Predicting CRISPR-Cas13 On-target Efficiencies and Intrinsic RNA Off-targets.
- *American Society of Gene and Cell Therapy (ASGCT) annual meeting, Baltimore MD 2024*

[4] Decoding Heterogenous Single-cell Perturbation Responses with Perturbation-response Score
- *IGVF Scientific Seminar, 2023*
- *STATGEN2024, Pittsburgh PA, 2024*
- *SCBA Annual Scientific Symposium, College Park MD, 2024*

[5] From Gene Editing to Genome Function
- *Icahn School of Medicine, Mount Sinai Hospital, New York NY 2023*
- *University of Maryland Medical School, Baltimore MD 2024*
- *DC-CFAR Advanced Technology Core Annual Research Day, Washington, DC, 2024*

[6] Best practice for perturb-seq data analysis and integration
- Workshop by European Molecular Biology Laboratory – European Bioinformatics Institute (EMBL-EBI), Boston MA, June 2023

[7] Understanding the efficiencies and specificities of CRISPR-Cas13 RNA-editing enzymes
- Young Bioinformatics PI (YBP) Symposium, 2022

[8] Big Data and Gene Editing Approaches to Understand Human Genome.
- *GWU Inter-department Seminar Series (Virtual) 2022*
- 6th International Big Data Forum (BDF), Beijing, China (Virtual) 2021.

[9] Gene Editing and Machine Learning Approaches to Understand Human Genome.
- Indiana University, CBB program (Virtual) 2021;
- Center for Genetic Medicine Research Seminar (Virtual), 2021.

[10] CRISPR, Single-cell and Big Data Approaches to Understand Human Genome.
- *Drug Resistance and Sensitivity Network (DRSN), NCI Cancer Moonshot, single-cell working group (Virtual) 2022.*
- Tavros Therapeutics, inc (Virtual) 2021.

[11] Single-cell and Big Data Approaches for CRISPR Screening.
- Abbvie Inc (Virtual) 2020;
- Center for Genetic Medicine Research Seminar (Virtual). 2020.

[12] Linking genotypes with multiple phenotypes in single-cell CRISPR screens.
- Young Bioinformatics PI meeting (YBP 2019);
- Tsinghua University (Beijing) August 2019;
- Cold Spring Harbor Laboratory symposium: “Genome Engineering: The CRISPR/Cas9 Revolution”, Sept. 2019;

[13] *Identification of Essential Sites in the CTCF and FOXA1 Cistromes*.
- Cold Spring Harbor Laboratory symposium: “Genome Engineering: The CRISPR/Cas9 Revolution”, August 2018;
- SCBA DC Annual Scientific Symposium, March 2018.

[14] *Genome-wide CRISPR Screens Identified Drivers of Endocrine Resistance and Synthetic Lethal Vulnerabilities in Breast Cancer*.
- CSH-Asia Conference: Precision Cancer Biology: From Targeted to Immune Therapies conference (Suzhou, China), September 2017;

- AACR Precision Medicine Series: Opportunities and Challenges of Exploiting Synthetic Lethality in Cancer (San Diego, USA). January 2017;
- Cold Spring Harbor Laboratory symposium: “Genome Engineering: The CRISPR/Cas9 Revolution”, August 2016.

[15] *Genome-wide CRISPR Screens: Algorithms and Applications to Cancer Therapy Resistance*

- Children’s National Medical Center (Washington DC), August 2017;
- University of Texas Health San Antonio, May 2017;
- University of Arizona, April 2017;
- University of Illinois Urbana Champaign, March 2017;
- McGill University, February 2017;
- University of Pittsburgh, May 2016.

[16] *Computational Algorithms for CRISPR Screens and A Study of Breast Cancer Hormone Independence.*

- Workshop of CRISPR Congress 2016, Boston, MA

[17] *Quality Control, Modeling and Visualization of Genome-wide CRISPR Screens Using MAGeCK-VISPR*.

- Frontiers in CRISPR Symposium: New Development and Applications of CRISPR-Cas9 for Genome-Editing. Boston, MA, January 2016;
- Cold Spring Harbor Laboratory symposium: “Genome Engineering: The CRISPR/Cas9 Revolution”, September 2015;
- Genomics GetTogether Seminar, Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, July 2015.

[18] *Introduction to CRISPR Screens*.

- Seminar in Longwood Translational Medicine China Initiative. October 2015.

[19] *Identification of cell-type specific essential genes using MAGeCK-VISPR*.

- Center for Functional Cancer Epigenetics Scientific Retreat, Dana-Farber Cancer Institute, August 2015.

[20] *CRISPR MAGeCK and Other Tricks.*

- Cell Circuits and Epigenomics Program Seminar. Broad Institute of Harvard and MIT. June 2015.

[21] *Computational Analysis of Genome-Scale CRISPR-Cas9 Knockout Screening Experiments*

- Center for Functional Cancer Epigenetics Seminar, Dana-Farber Cancer Institute, Mar. 2014.

[22] *Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges.*

- Computational Biology and Bioinformatics program, Yale University, June 2012;
- Dana-Farber Cancer Institute, June 2012;
- Harvard University, May 2012;
- IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2011). Orlando, FL. February 2011.

[23] *Transcriptome Assembly and Isoform Expression Level Estimation from Biased RNA-Seq Reads.*

- IEEE ICCABS 2012. Las Vegas, NV. March 2012.

[24] *IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly.*

- 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2011). Vancouver, Canada, March 2012.

[25] *Polony Identification Using the EM Algorithm Based on a Gaussian Mixture Model.*

- 10th IEEE BIBE 2010. Philadelphia, PA, May 2010.

[26] *COX-2 Activity Prediction in Chinese Medicine Using Neural Network Based Ensemble Learning Methods.*

- The 2008 International Joint Conference on Neural Networks (IJCNN 2008). Hong Kong, May 2008.

EDUCATIONAL ACHIEVEMENTS

2022-	Lecturer, GWU. Computational Biology and Bioinformatics: Principles and Practices (GENO8232)
2020-	Guest lecturer, GWU. Computational Biology (PUBH6885).

2016	Guest lecturer, Harvard University. Introduction to Computational Biology and Bioinformatics (STAT115).
2011	Teaching Assistant, University of California, Riverside. Machine Learning (CS229).
2010	Teaching Assistant, University of California, Riverside. The Theory of Automata and Formal Languages (CS150).
2008-2009	Teaching Assistant, Tsinghua University. Robot Soccer: Theory and Practice

GRANTS

[1] NIH/NCI R01 (CA266432; PI: Wu). *Molecular Function and Mechanism of ARID4B in ERalpha Signaling and Breast Cancer.* 2022-2027. Role: co-I.

[2] NIH/NHLBI R01 (HL168174; PI: Zhang, Li, Marcora). *Integrative genomic and functional genomic studies to connect variant to function for CAD GWAS loci.* 2023-2027. Role: MPI.

[3] Pilot award, District of Columbia Intellectual and Developmental Disabilities Research Center (DC-IDDRC). *Establishing Core Resources for Variant Classification in Neurodevelopmental Disorders.* Role: PI (with Dr. Irene Zohn)

[4] Gilbert Family Foundation (GFF) award. Develop a strategical platform to interrogate multi-omics data from NF1-associated tumors (PI: Zhu, Li, Baranov). Role: MPI

COMPLETED GRANTS

[1] District of Columbia Center for AIDS Research (DC-CFAR), Transitional Investigator Award 2023. *Mechanism of Action of CYLD and YPEL5 As Novel Drug Targets for HIV-1 Latency Reversal*. Role: PI.

[2] Pilot award, Virginia-Tech and Children's National Hospital (VT-CNH) Research Collaborations on AI. 2024. Role: PI (with Dr. Jia-Ray Yu)

[3] NIH/NHGRI R01 (HG010753; PI: Li). *Modeling Functional Elements Using CRISPR Screening*. 2019 – 2025. Role: PI

[4] NIH/NHGRI R01 Supplement (3R01-HG010753-05S1). *Modeling Heterogenous Outcomes in Functional Genetic Screens Using Single-cell Genomics as Readouts.* 2023-2025. Role: PI

[5] Pilot award, Center for Genetic Medicine Research. *Defining novel targetable mechanisms of disease for viral bronchioltics using CRISPR screens and human infant airway epithelial models.* 2021, Role: PI (with Dr. Gustavo Nino).

[6] COVID-19 High Performance Computing (HPC) consortium award. Functional Genetics and Machine Learning Approaches for COVID19 Drug Repurposing. 2021, Role: PI.

[7] COVID-19 High Performance Computing (HPC) consortium award. *Target Identification for Broad Antiviral Therapy using Functional Genetic Screening Datasets.* 2020. Role: PI.

[8] 2019 Research Starter Grant in Informatics, Pharmaceutical Research and Manufacturers of America Foundation (PhRMA). *Identification of Cancer Essential Genes and Drug Targets from CRISPR Screens. 2019,* Role: PI.

[9] Board of Visitors Award, Children's National Medical Center. *Identifying Drug Targets to Selectively Kill Brain Tumors.* 2019, Role: PI.

TRAINEES

- Postdoc/Scientist
    - Xiaolong Cheng, postdoc, 2019 – 2023
    - Bic-Na Song, postdoc, 2019 – current
    - Lumen Chao, postdoc/scientist, 2020 – current
    - Kai Wang, postdoc, 2021 – 2024
    - Vipin Menon, postdoc, 2024 – current
    - Yangqi Su, postdoc, 2025 – current
- Graduate students

    - Pamela Chansky, GWU IBS Ph.D. student. 2022 – current
- Technician
    - Qing Chen, 2019 – 2020
- Master student:
    - Lin Yang, 2019 – 2020, GWU (Biochemistry and Molecular Biology).
    - Sitong Chen, 2019 – 2020, GWU (Biochemistry and Molecular Biology).
    - Chia-Han Lee, 2019 – 2020, GWU (Biochemistry and Molecular Biology).
    - Yuan Gao, 2020 – 2021, GWU (Biochemistry and Molecular Biology).
    - Ruocheng Shan, 2020 – 2021, GWU (Computer Science).
    - Wei Shao, 2020 – 2021, GWU (Biochemistry and Molecular Biology).
    - Junyan (Jeremy) Li, 2022 – 2023, GWU (Biochemistry and Molecular Biology)
    - Quan Yuan, 2022 – 2024, GWU (Biochemistry and Molecular Biology)
    - Li-Ting Wang, 2023 – 2024, GWU (Biochemistry and Molecular Biology)
    - Julia Zhu, 2023 – 2024, GWU (Biochemistry and Molecular Biology)
- Interns
    - Anthony Chiu, 2020 (GWU MD student, received GWU Gill Fellowship for internship)
    - Abnihav Adhikari, 2020-2021 (Thomas Jefferson High School).
    - Mozhan Haghighatian, 2021 (Undergraduate at University of Maryland, College Park)
    - Rod Rahmjoo, 2022 – current (Master student at University of Maryland, College Park)
    - Daniel Zheng, 2022 – current (Polytechnic School Pasadena)
    - Isabelle Yang, 2022 (Montgomery Blair High School)
    - Diana Zhu, 2024 (Undergraduate at University of Maryland, College Park)

MEMBERSHIPS AND SERVICES

- Founding director, Gene Editing Core, Children's National Hospital, 2023 - 2025
    - Found and directed the newly established gene editing core to provide gene-editing services
    - Services: CRISPR screen, Perturb-seq, gene knockin/knockout, bioinformatics analysis, consulting and grant writing, etc.
    - Website: https://weililab.org/gecore/
- NIH Study Section Reviewer
    - ZRG1 MGG-R (90) S, Molecular Genetics and Genomics, 2025
    - ZRG1 F07C-H (20), Fellowships in Infectious Diseases and Immunology, 2025
    - ZRG1 MGG-M (70) R, SCGE Phase II, 2024
    - Genomics, Computational Biology and Technology (GCAT), 2023
- Affiliate member, NIH IGVF (Impact of Genomic Variation on Function) Consortium, 2023 -
- Affiliate member, NIH MorPhiC (Molecular Phenotypes of Null Alleles in Cells) Consortium, 2024 -
- Bioinformatics/Machine Learning leader, Advanced Technology Core, DC-CFAR (District of Columbia Center for AIDS Research)
- Referee, Computational Biology and Bioinformatics, Regeneron Science Talent Search (STS), 2024
- Program Committee (PC) member:
    - IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM), 2022,2024
    - International Conference for Genome Informatics (GIW) and Australian Bioinformatics & Computational Biology Society (ABACBS) Conference, 2019
    - International Conference for Genome Informatics (GIW), 2022
- Vice President, Harvard Medical School Chinese Scholars and Scientists Association (HMS-CSSA, http://hms-cssa.org), 2014-2018
    - Organized and hosted Cancer Epigenetics Mini-symposium, Single Cell Genomics Mini-symposium (2015), CRISPR screening Mini-symposium (2015);

  - Organized 2015, 2016 and 2017 Harvard Chinese Life Science Annual Symposium, a whole-day seminar attracting > 500 participants every year;
- Founding member & associate director, Longwood Translational Medicine China Initiative (LTMCI, http://www.lwtransmed.org/), 2013-2016
  - Co-founder of the organization to facilitate the increasing collaboration among doctors and scientists from China and US. Organized over 40 seminars in 3 years
- Dissertation committee and thesis readers
  - Konstantinos Karagiannis, PhD, GWU IBS program, 2019
  - Hongyu Liu, GWU (Biochemistry and Molecular Biology), 2020
  - Xiang Li, PhD, GWU Department of Physics, 2021
  - Turkey Alsaeedy, GWU (Biochemistry and Molecular Biology), 2021
  - Christian Dillard; Evgenia Ulianova; GWU (Biochemistry and Molecular Biology), 2022
  - Ganna Reint, PhD, Department of Biosciences, University of Oslo, Norway, 2022
  - Jonathan Lotempio, GWU IBS program, 2022
  - Nathaniel Stearrett, PhD, GWU IBS program, 2023
  - Yueshan Zhao, University of Pittsburgh School of Pharmacy, 2023
  - Claudia Melo; Woudasie Admasu; Sarah Tiufekchiev; Tommy Voigt; GW IBS program 2024
  - Shuyue Wang, Texas MD Anderson Cancer Center, 2024
- Consultant
  - Tavros Therapeutics (paid), 2021
- Member of IEEE, ICSB, AACR, ASGCT.
- Reviewer: Cell, Nature, Science, Nature Biotechnology, Genome Research, Genome Biology, PLoS Computational Biology, Nucleic Acid Research, Bioinformatics, Biostatistics, BMC Bioinformatics, BMC Genomics, BMC Cancer, Epigenetics and Chromatin, PLoS ONE, Journal of Computational Biology, ISMB/ECCB, RECOMB, WABI.
- Editorial Board, Computational and Structural Biology Journal (CSBJ; 2023 – current)
- Editorial Board, Journal of Translational Genetics and Genomics (2023 – current)
- Associate Editor, Frontiers in Oncology, Cancer Genetics; Genome Editing in Cancer and Immunology; (2022 – current)
- Academic editor and member of the Editorial Board, PLoS Computational Biology (2023 – current)