

Wei Li, Ph.D.

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EMPLOYMENT

- 2018- Principal Investigator
Center for Genetic Medicine Research & Center for Cancer and Immunology Research
Children's National Hospital
7144 13th PI, Washington DC 20010
Assistant Professor
Department of Genomics and Precision Medicine & Department of Pediatrics
School of Medicine and Health Sciences
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] Research Starter Award, Pharmaceutical Research and Manufacturers of America Foundation (PhRMA), 2019
- [2] APBC 2015 Best paper award, 2015
- [3] IEEE ICCABS conference Travel Award, 2012
- [4] Graduate Division Fellowship Award, University of California, Riverside, 2008-2009
- [5] Director, Tsinghua University Military Band Freshman Division, 2006-2007
- [6] Tsinghua University Student Art Group Fellowship, 2005
- [7] Tsinghua University Academic Career Fellowship, 2004
- [8] Deputy Director, Tsinghua University Military Band, 2004-2005
- [9] Freshman Excellence Scholarship, Tsinghua University, 2002
- [10] 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] 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.
- [2] 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.
- [3] 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.weillab.org>
- [4] 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.
- [5] 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/weillab/scmageck>
- [6] 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 Hinterdorfer, Johannes Zuber, Myles Brown, **Wei Li**[#], X. Shirley Liu[#]. Integrative analysis of pooled CRISPR genetic screens using MAGECKFlute. *Nature Protocols* 2019; 14, 756–780.
- [7] 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.
- [8] 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.
- [9] 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.
- [10] 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.
- [11] Shiyong 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.
- [12] **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.
- [13] **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: >1000; >100,000 software downloads**
- [14] 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.**
- [15] **Wei Li**^{**} and Tao Jiang. Transcriptome Assembly and Isoform Expression Level Estimation from Biased RNA-Seq Reads. *Bioinformatics* 2012; 28(22):2914-2921.

- [16] **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)*. **Citation: 179**

Submitted and preprint manuscripts

- [17] Xiaolong Cheng*, Zexu Li*, Rrocheng Shan, Ziyi Li, Lumen Chao, Jian Peng, Teng Fei#, **Wei Li**#. Modeling CRISPR-Cas13d on-target and off-target effects using machine learning approaches. Under review in Nature Communications. Also at BioRxiv 2021, 458773. <https://doi.org/10.1101/2021.09.02.458773>.
- [18] Weiwei Dai, Fengting Wu, Victoria E. Walker-Sperling, Bicna Song, Joseph Varriale, Hao Zhang, Janet D. Siliciano, Dan H. Barouch, **Wei Li**#, Robert F. Siliciano#. Targeting the latent HIV-1 reservoir with synergistic combinations of latency reversing agents identified in genome-wide CRISPR screens. Under review, Science Translational Medicine.
- [19] 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. Under review in Nature Communications. Also at BioRxiv 2022, 477299. <https://doi.org/10.1101/2022.01.21.477299>.
- [20] **Wei Li**. Adapting Blockchain Technology for Scientific Computing. arXiv:1804.08230 [cs.CR] (2018).
- [21] 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

- [22] 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.
- [23] 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 Wucherpfnig, 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.
- [24] Sitong Chen, Lin Yang, **Wei Li**. CRISPR Screening “Big Data” Informs Novel Therapeutic Solutions. *The CRISPR Journal* 2019; 2 (3), 152-154.
- [25] 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.
- [26] Shiyong 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.
- [27] 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.

- [28] 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.
- [29] 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.
- [30] 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.
- [31] 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.
- [32] 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.
- [33] 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.
- [34] 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.
- [35] 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 Scinski, 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.
- [36] 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.
- [37] 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.
- [38] 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.
- [39] 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.
- [40] 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.
- [41] **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

- [42] 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)*.
- [43] **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
- [44] **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.
- [45] **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.
- [46] **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] 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. Submitted.
- [2] 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] *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.
- [2] *Gene Editing and Machine Learning Approaches to Understand Human Genome.*
@Indiana University, CBB program (Virtual) 2021; @Center for Genetic Medicine Research Seminar (Virtual), 2021.
- [3] *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.
- [4] *Single-cell and Big Data Approaches for CRISPR Screening.*
@Abbvie Inc (Virtual) 2020; @Center for Genetic Medicine Research Seminar (Virtual). 2020.
- [5] *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;
- [6] *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.
- [7] *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.
- [8] *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.
- [9] *Computational Algorithms for CRISPR Screens and A Study of Breast Cancer Hormone Independence.*
@Workshop of CRISPR Congress 2016, Boston, MA

- [10] *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.
- [11] *Introduction to CRISPR Screens.*
 @Seminar in Longwood Translational Medicine China Initiative. October 2015.
- [12] *Identification of cell-type specific essential genes using MAGeCK-VISPR.*
 @Center for Functional Cancer Epigenetics Scientific Retreat, Dana-Farber Cancer Institute, August 2015.
- [13] *CRISPR MAGeCK and Other Tricks.*
 @Cell Circuits and Epigenomics Program Seminar. Broad Institute of Harvard and MIT. June 2015.
- [14] *Computational Analysis of Genome-Scale CRISPR-Cas9 Knockout Screening Experiments.*
 @Center for Functional Cancer Epigenetics Seminar, Dana-Farber Cancer Institute, Mar. 2014.
- [15] *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 (ICCBAS 2011). Orlando, FL. February 2011.
- [16] *Transcriptome Assembly and Isoform Expression Level Estimation from Biased RNA-Seq Reads.*
 @IEEE ICCABS 2012. Las Vegas, NV. March 2012.
- [17] *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.
- [18] *Polony Identification Using the EM Algorithm Based on a Gaussian Mixture Model.*
 @10th IEEE BIBE 2010. Philadelphia, PA, May 2010.
- [19] *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

2020	Guest lecturer, George Washington University. 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/NHGRI R01 (HG010753). *Modeling Functional Elements Using CRISPR Screening.*
 2019 - 2024 Role: PI. DC: \$1.25M
- [2] 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.*
 2019-2020 Role: PI. DC: \$100,000
- [3] Board of Visitors Award, Children’s National Medical Center. *Identifying Drug Targets to Selectively Kill Brain Tumors.*
 2019 – 2020 Role: PI. DC: \$25,000
- [4] COVID-19 High Performance Computing (HPC) consortium award. *Target Identification for Broad Antiviral Therapy using Functional Genetic Screening Datasets.*

- 2020 – 2021 Role: PI. \$40,000 AWS credit.
- [5] Pilot award, Center for Genetic Medicine Research. *Defining novel targetable mechanisms of disease for viral bronchiolitis using CRISPR screens and human infant airway epithelial models.*
2021 Role: PI (with Dr. Gustavo Nino). DC: \$20,000.
- [6] COVID-19 High Performance Computing (HPC) consortium award. Functional Genetics and Machine Learning Approaches for COVID19 Drug Repurposing.
2021 Role: PI. \$200,000 AWS credit.

TRAINEES

- Postdoc
 - Xiaolong Cheng, postdoc, 2019 – current
 - Bic-Na Song, postdoc, 2019 – current
 - Lumen Chao, postdoc, 2020 – current
 - Kai Wang, postdoc, 2021 – current
- Technician
 - Qing Chen, 2019 – 2020, now GWU PhD student
- Master student:
 - Lin Yang, 2019 – 2020, GWU (Biochemistry and Molecular Biology). Now a computational associate at Dana-Farber Cancer Institute/Harvard School of Public Health.
 - Sitong Chen, 2019 – 2020, GWU (Biochemistry and Molecular Biology). Now a statistician at University of Miami.
 - Chia-Han Lee, 2019 – 2020, GWU (Biochemistry and Molecular Biology). Now a staff scientist at NIH.
 - Yuan Gao, 2020 – 2021, GWU (Biochemistry and Molecular Biology). Now a Ph.D. student at University of Maryland, College Park.
 - Ruocheng Shan, 2020 – 2021, GWU (Computer Science). Now a Ph.D. student at GWU.
 - Wei Shao, 2020 – 2021, GWU (Biochemistry and Molecular Biology). Now a Ph.D. student at the University of California, Irvine.
- Interns
 - Mozhan Haghghatian, 2021—current (Undergraduate at University of Maryland, College Park)
 - Anthony Chiu, 2020 (GWU MD student, received GWU Gill Fellowship for intership)
 - Abnihav Adhikari, Thomas Jefferson High School, 2020-2021. Now an undergraduate at University of Washington

MEMBERSHIPS AND SERVICES

- Program Committee (PC) member:
 - International Conference for Genome Informatics (GIW) and Australian Bioinformatics & Computational Biology Society (ABACBS) Conference, 2019
- 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
 - Konstantinos Karagiannis, PhD, GWU IBS program, 2019
 - Xiang Li, PhD, GWU Department of Physics, 2021
 - Ganna Reint, PhD, Department of Biosciences, University of Oslo, Norway, 2022
- Thesis reader
 - Turkey Alsaedy, GWU (Biochemistry and Molecular Biology), 2021
 - Hongyu Liu, GWU (Biochemistry and Molecular Biology), 2020
- Member of IEEE, ICSB, AACR.
- Reviewer: Cell, 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.
- Guest editor: PLoS Computational Biology