Wubing Zhang

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Experience

08/2019-present	**Visiting scholar**, Dana-Farber Cancer Institute, USA Mentor: X. Shirley Liu

Education

09/2017-present	**Ph.D. in Bioinformatics,** School of Life Sciences and Technology, Tongji University, China Advisor: Chenfei Wang
09/2012-09/2017	**B.S. in Bioinformatics,** College of Bioinformatics Science and Technology, Harbin Medical University, China Advisor: Xiujie Chen

Peer-reviewed Publications

First/Co-first Author Articles

1. **Wubing Zhang***, Shourya S. Roy Burman*, Jiaye Chen, Katherine A. Donovan, Yang Cao, Boning Zhang, Zexian Zeng, Yi Zhang, Dian Li, Eric S. Fishcher, Collin Tokheim, X. Shirley Liu. Machine learning modeling of protein-intrinsic features predicts tractability of targeted protein degradation. ***Under review*** (2021).
2. Shengqing Gu*, **Wubing Zhang***, Xiaoqing Wang*, Peng Jiang*, Nicole Traugh, Ziyi Li, Clifford Meyer, Blair Stewig, Yingtian Xie, Xia Bu, Michael Manos, Alba Font-Tello, Evisa Gjini, Ana Lako, Klothilda Lim, Jake Conway, Alok Tewari, Zexian Zeng, Avinash Das Sahu, Collin Tokheim, Jason L. Weirather, Jingxin Fu, Yi Zhang, Benjamin Kroger, Jin Hua Liang, Paloma Cejas, Gordon J. Freeman, Scott J. Rodig, Henry Long, Benjamin E. Gewurz, F. Stephen Hodi, Myles Brown, X. Shirley Liu. Therapeutically increasing MHC-I expression potentiates immune checkpoint blockade. ***Cancer Discovery*** (2021).
3. Binbin Wang*, Mei Wang*, **Wubing Zhang***, Tengfei Xiao, Chen-Hao Chen, Alexander 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).
4. Lingxiang Wu*, Xiujie Chen*, Denan Zhang*, **Wubing Zhang***, Lei Liu, Hongzhe Ma, Jingbo Yang, Hongbo Xie, Bo Liu, Qing Jin. IGSA: Individual Gene Sets Analysis, including Enrichment and Clustering. ***PLoS One*** (2016).

Other Collaboration Articles

5. Tong Han, Xujun Wang, Sailing Shi, **Wubing Zhang**, Qiu Wu, Ziyi Li, Jingxin Fu, Rongbin Zheng, Peng Zhang, Chenfei Wang. Cancer Cells Resistance to IFN-γ via Double-Strand Break Repair Pathway. ***Under review.***
6. Avinash Das Sahu, Xiaoman Wang, Phillip Munson, Xiaoqing Wang, Shengqing Gu, Gege Qian,

Zexian Zeng, Chenfei Wang, Collin Tokheim, **Wubing Zhang**, Jingxin Fu, Jin Wang, Jan Klomp, Meriem Bourajjaj, Bas Jansen, Inge Leenders, Jaap Lemmers, Mark Musters, Sanne van Zanten, Laura van Zelst, Arthur Oubrie, Jenny Worthington, Myles Brown, Jun S. Liu, Dejan Juric, Cliff A. Meyer, X. Shirley Liu, David E. Fisher, Keith T. Flaherty. Transcriptional inhibition of tumor energy metabolism through a nuclear receptor activates immunity. ***Under review.***

7. Zexian Zeng, Cheryl Wong, Lin Yang, Nofal Ouardaoui, Dian Li, **Wubing Zhang**, Shengqing Gu, Yi Zhang, Yang Liu, Xiaoqing Wang, Jingxin Fu, Liye Zhou, Boning Zhang, Sarah Kim, Kathleen B. Yates, Myles Brown, Gordon J. Freeman, Ravindra Uppaluri, Robert Manguso, X. Shirley Liu. TISMO: syngeneic mouse tumor database to model tumor immunity and immunotherapy response. ***Nucleic Acids Research*** (2021)
8. Collin Tokheim, Xiaoqing Wang, Richard Timms, Boning Zhang, Elijah L. Mena, Binbin Wang, Cynthia Chen, Jun Ge, Jun Chu, **Wubing Zhang**, Stephen J. Elledge, Myles Brown, X. Shirley Liu. Systematic Characterization of Mutations Altering Protein Degradation in Human Cancers. ***Molecular Cell*** (2021).
9. Nathan D. Mathewson, Orr Ashenberg, Itay Tirosh, Simon Gritsch, Elizabeth M. Perez, Sascha Marx, Livnat Jerby-Arnon, Rony Chanoch-Myers, Toshiro Hara, Alyssa R. Richman, Yoshinaga Ito, Jason Pyrdol, Mirco Friedrich, Kathrin Schumann, Michael J. Poitras, Prafulla C. Gokhale, L. Nicolas Gonzalez Castro, Marni E. Shore, Christine M. Hebert, Brian Shaw, Heather L. Cahill, Matthew Drummond, **Wubing Zhang**, Olamide Olawoyin, Hiroaki Wakimoto, Orit Rozenblatt-Rosen, Priscilla K. Brastianos, X. Shirley Liu, Pamela S. Jones, Daniel P. Cahill, Matthew P. Frosch, David N. Louis, Gordon J. Freeman, Keith L. Ligon, Alexander Marson, E. Antonio Chiocca, David A. Reardon, Aviv Regev, Mario L. Suvà, Kai W. Wucherpfennig. Inhibitory CD161 Receptor Identified in Glioma-infiltrating T cells by Single Cell Analysis. ***Cell*** (2021).
10. 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).
11. Shengqing Gu, Xiaoqing Wang, Xihao Hu, Peng Jiang, Ziyi Li, Nicole Traugh, Xia Bu, Qin Tang, Chenfei Wang, Zexian Zeng, Jingxin Fu, Cliff Meyer, Yi Zhang, Paloma Cejas, Klothilda Lim, Jin Wang, **Wubing Zhang**, Collin Tokheim, Avinash Das Sahu, Xiaofang Xing, Benjamin Kroger, Zhangyi Ouyang, Henry Long, Gordon J. Freeman, Myles Brown & X. Shirley Liu. Clonal tracing reveals diverse patterns of response to immune checkpoint blockade. ***Genome Biology*** (2020).
12. Sailing Shi, Shengqing Gu, Tong Han, **Wubing Zhang**, Lei Huang, Ziyi Li, Deng Pan, Jingxin Fu, Jun Ge, Myles Brown, Peng Zhang, Peng Jiang, Kai W. Wucherpfennig, Xiaole Shirley Liu· Inhibition of MAN2A1 enhances tumor response to anti-PD-L1. **Clinical *Cancer Research*** (2020).
13. Xiaojing Liu, Tingting Liu, Yafang Shang, Pengfei Dai, **Wubing Zhang**, Brian J Lee, Min Huang, Dingpeng Yang, Qiu Wu, Liu Daisy Liu, Xiaoqi Zheng, Bo O Zhou, Junchao Dong, Leng-Siew Yeap, Jiazhi Hu, Tengfei Xiao, Shan Zha, Rafael Casellas, X. Shirley Liu, Fei-Long Meng. ERCC6L2 promotes DNA orientation-specific recombination in mammalian cells. ***Cell Research*** (2020).
14. Jingxin Fu, Karen Li, **Wubing Zhang**, Changxin Wan, Jing Zhang, Peng Jiang, X. Shirley Liu. Large-scale public data reuse to model immunotherapy response and resistance. ***Genome Medicine*** (2020).
15. Mei Wang, Qilong Chen, Hailing Liu, Hao Chen, Binbin Wang, **Wubing Zhang**, Ailu Mading, Wenjing Li, Shuangqi Li, Hang Liu, ZhongKai Gu, Shuxian Liu, Rui Guo, Wei Li, Tengfei Xiao, Feizhen Wu. CRISPR/Cas9 screens Reveal Dasatinib Targets of Inhibiting T cell Activation and Proliferation. *Preprint on* ***bioRxiv*** (2018).

Research Presentations

Poster Presentations

1. CSHL Meeting: Virtual Ubiquitin, Autophagy & Disease (04/27–30/2021)

   Title: "Protein intrinsic features predict tractability of targeted protein degradation"
2. AACR Meeting: Tumor immunology and immunotherapy, Boston, MA 02115 (11/17–20/2019)

   Title: "Decoupled regulation of MHC-I and PD-L1 provides insights into rational combination therapy with immune checkpoint blockade"
3. PQG Conference: Quantitative challenges in cancer immunology and immunotherapy, Harvard Medical School, Boston, MA 02115 (11/04–05/2019)

   Title: "Decoupled regulation of MHC-I and PD-L1 provides insights into rational combination therapy with immune checkpoint blockade"
4. CSHA Meeting: Scientific and Technical Advances in Cancer Immunology, Suzhou, China (06/08-12/2019)

   Title: "Data-driven identification of MHC-I modulation mechanism by conventional cancer therapies", **best poster award**
5. The 8th National Conference on Bioinformatics and Systems Biology of China and the 1st (Macao) International Bioinformatics Symposium, the University of Macau, Macau SAR, China (10/22-24/2018)

   Title: "TIDE: a web platform for evaluating tumor immune-suppressive function of user-defined gene sets"
6. Cold Spring Harbor Asia Meeting: The Systems Biology of Gene Regulation & Genome Editing conference, Suzhou, China (10/08-12/2018)

   Title: "Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute"

Oral Presentations

1. Dana Farber Targeted Protein Degradation Webinar (12/02/2021)

   Invited talk: Machine learning modeling of protein-intrinsic features predicts tractability of targeted protein degradation

Research Experience

Visiting Scholar, Dana-Farber Cancer Institute, X. Shirley Liu Lab (08/2019-present)

- **Predicting tractability of targeted protein degradation by machine learning modeling of features intrinsic to protein targets**
  - Developed a machine learning model (MAPD) to predict tractability of targeted protein degradation
  - Identified the ubiquitination potential as the most important feature in predicting protein degradability
  - Established a user-friend web platform (http://mapd.cistrome.org/) for prioritizing protein targets susceptible to targeted protein degradation
  - Developed an R package (https://liulab-dfci.github.io/MAPD/index.html) for extensive analysis of protein degradability
- **Therapeutically increasing MHC-I to potentiate immune checkpoint blockade**

  - Found a strong positive correlation between MHC-I and PD-L1 expression by analyzing TCGA and CCLE gene expression data
  - Identified TRAF3 as a negative regulator of MHC-I by analyzing dual-marker FACS-based CRISPR screens
  - Discovered that TRAF3 suppresses MHC-I expression through inhibiting the activity of NF-kB by integrative analysis of RNA-seq and ATAC-seq data
  - Studied the association of Traf3-knockout gene expression signature with MHC-I expression, immune cell infiltration, patient survival, and ICB response
  - Identified SMAC mimetics that phenocopy TRAF3 deficiency and up-regulate MHC-I through data mining in GEO
- **Model-based analysis of ubiquitin-proteasome system**
  - Developed integrative analysis pipeline for quantitative proteomics data
  - Studied the cis- and trans- effect of degron mutation on protein abundance
  - Studied the proteomic correlation with tumor immune microenvironment
- **Other collaborative projects**
  - Identified essential genes in antigen-specific and bystander T cell killing by analyzing CRISPR screens
  - Studied gene regulation in tumor microenvironment by analyzing single-cell sequencing data
  - Studied clinical relevance of CLEC2D and KLRB1 interaction based on gene expression signature-based analysis

<u>Graduate Research Assistant, Tongji University, Chenfei Wang Lab (10/2016-08/2019)</u>

- **Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute**
  - Developed an integrative analysis pipeline for pooled CRISPR screens
  - Incorporated functions for gene ID conversion, gene set enrichment analysis, and integration analysis of cancer genetic dependencies
- **Other collaborative projects**
  - Collected and analyzed CRISPR screens to identify genes regulating DNA damage response, T/NK cell immunity, and drug response
  - Studied the immune regulatory effect of small molecules by analyzing drug-induced transcriptomic response
  - Involved in the development of a computational pipeline for detecting protein targets from phage display data

<u>Undergraduate Research Assistant, Harbin Medical University, Xiujie Chen Lab (07/2015-10/2016)</u>

- **Individual Gene Sets Analysis (IGSA), including Enrichment and Clustering**
  - Developed a user-friendly application for gene set enrichment analysis and sample clustering
- **Computational drug repositioning based on the relationships between substructure–indication**
  - Built a computational model for drug repositioning by modeling drug-target interaction and drug indications

Honors and Awards

- Cold Spring Harbor Asia Conference Fellowship (2019)
- Taiyuan Scholarship, Tongji University (2018)
- Excellent Ph.D. Freshman Scholarship, Tongji University (2017)
- The Outstanding Graduates, Harbin Medical University (2017)
- Scholarship of China Telecom, China (2016)
- Outstanding Student (top 10), Harbin Medical University (2016)

- National Endeavor Scholarship (four-time awardee), Ministry of Education, China (2013-2017)

Teaching Activities

Teaching Assistant, Harvard Medical School (09/2020)
HMS Cancer Program, Cancer – Omics Specialty Track
This course provides a tutorial of useful tools and data resources in the DepMap portal.
Resource: https://www.youtube.com/watch?v=1knIFBXY9g0

Teaching Assistant, Tongji University (08/2018)
Bioinformatics training
This course covers a fundamental introduction of bioinformatics data (such as Microarrays, RNA-Seq, single-cell RNA-Seq, ChIP-Seq) and the application of probability and statistical tests.

Teaching Assistant, Harbin Institute of Technology (08/2017)
The Dragon Star Project course
This course introduces machine learning models and statistical tests in R programming.

Trainees

Name	Mentor period	Position in the lab	Current status
Jiaye Chen	2021	Graduate student	Graduate student at Harvard Medical School
Dian Li	2020-2021	Associate computational biologist	Graduate student at Washington University in St. Louis
Jun Ge	2018-2019	Graduate student	Graduate student at Tongji University
Yihan Xiao	2018-2019	Undergraduate student	Graduate student at Tongji University
Shuangyi Li	2018-2019	Undergraduate student	Graduate student at Tongji University

Professional Societies

2020–present	American Association for Cancer Research (AACR) Associate Member

Technical Skills

Machine learning
Bioinformatics
High-throughput data analysis
Programming languages: R, shell, python, mySQL, java, matlab, and perl
High-performance computing: R package development and shell workflow management
Code version control system: git
Code continuous integration: Travis CI

References

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