

Wen-Wei Liang, Ph.D.

101 6th Ave, New York, NY
wliang@nygenome.org
(314) 540-1364

Molecular geneticist and genomicist aiming to unravel the epigenetic mechanisms governing tumor heterogeneity through integrated experimental and computational approaches.

EDUCATION

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| Washington University in St. Louis | Ph.D. in Molecular Genetics and Genomics | 2014–2020 |
| National Yang-Ming University, Taiwan | M.S. in Microbiology and Immunology | 2009–2011 |
| National Tsing-Hua University, Taiwan | B.S. in Life Science | 2005–2009 |

FELLOWSHIPS

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| Taiwan Ministry of Education - Washington University in St. Louis Fellow (\$732,000) | 2014–2018 |
| Washington University in St. Louis Precision Medicine Pathway Fellow (\$5,000) | 2015–2016 |
| Taiwan Ministry of Education Fellowship to Study Abroad (\$10,000) | 2007–2008 |

RESEARCH EXPERIENCES

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| New York University & New York Genome Center | New York, NY |
| Postdoctoral research associate, Laboratory of Neville Sanjana | 2021–Present |

- **Transcriptome-scale RNA-targeting CRISPR screens reveal essential lncRNAs in human cells:** Conducted Cas13 pooled screens and perturbation assays, coupled with single-cell RNA sequencing, to identify and characterize hundreds of lncRNAs crucial for cell proliferation and their mechanistic roles.
- **Targeting onco-lncRNAs as a strategy against cancer:** Conducted integrative bioinformatic analyses alongside *in vitro* and *in vivo* pooled screens to identify lncRNAs driving tumor progression in BRCA xenograft and organoid models.

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| Washington University in St. Louis | St. Louis, MO |
| Ph.D. student and postdoctoral research associate, Laboratory of Li Ding | 2015–2021 |

- **Epigenetic regulation during cancer transitions across 11 tumour types:** Utilized snATAC sequencing, single-cell RNA sequencing, and bulk whole-exome sequencing data from the Human Tumor Atlas Network (HTAN) to profile over a million cells or nuclei. Identified cancer-specific accessible region dynamics correlating with gene expression, uncovering novel regulatory regions and their target genes.
- **Integrative multi-omic cancer profiling reveals DNA methylation patterns associated with therapeutic vulnerability and cell-of-origin:** Leveraged DNA methylation, RNA sequencing, and proteomic data from the Clinical Proteogenomic Tumor Analysis Consortium (CPTAC) to elucidate how epigenetic changes in cancer cells influence gene expression, protein levels, tumor characteristics, and therapeutic responses.
- **Driver fusions and their implications in the development and treatment of human cancers:** Conducted comprehensive analysis of gene fusions in over 9,000 tumors across 33 cancer types from The Cancer Genome Atlas (TCGA), uncovering how these fusions drive the expression of oncogenes, tumor suppressor genes, and kinases. Identified druggable fusions in 6.0% of cases, highlighting their potential as targets for precision therapies.

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| Academia Sinica | Taipei, Taiwan |
| Master's student and research assistant, Laboratory of Soo-Chen Cheng | 2009–2014 |

- **A novel mechanism for Prp5 function in prespliceosome formation and proofreading the branch site sequence:** Identified the role of Prp5 in spliceosome assembly and branch site proofreading, showing how Prp5's interactions with U2 snRNA and subsequent release facilitate accurate spliceosome assembly.

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| National Tsing-Hua University | Hsinchu, Taiwan |
| Undergraduate student, Laboratory of Chung-Yu Lan | 2008–2009 |

- Investigated the reactions of the iron-responsive element under virulence gene expression in *Candida albicans*.

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| Linköping University | Linköping, Sweden |
| Visiting student, Laboratory of Jordi Altimiras | 2007–2008 |

- Analyzed G-protein coupled receptor-dependent contractility in chicken heart tissue.

PUBLICATIONS

First authorship (* Equal contribution)

1. **Liang, W.-W.** *, Müller, S. *, Hart, S. K., Wessels, H.-H., Méndez-Mancilla, A., Sookdeo, A., Choi, O., Caragine, C, Corman, A, Lu, L., Kolumba, O., Williams, B. & Sanjana, N. E. Transcriptome-scale RNA-targeting CRISPR screens reveal essential lncRNAs in human cells. *Accepted in Cell* (2024).
2. **Liang, W.-W.**, Wendl, M. C., Wyczalkowski, M. A., Chen, F. & Ding, L. Emerging roles of epigenetic drivers in regulating cancer transitions. *Revision in Nature Review Genetics* (2024).
3. **Liang, W.-W.**, Lu, R. J.-H., Jayasinghe, R. G., Foltz, S. M., Porta-Pardo, E., Geffen, Y., Wendl, M. C., Lazcano, R., Kolodziejczak, I., Song, Y., *et al.* Integrative multi-omic cancer profiling reveals DNA methylation patterns associated with therapeutic vulnerability and cell-of-origin. *Cancer Cell* 41, 1567–1585.e7 (2023). (**Featured in The Scientist magazine**).
4. Terekhanova, N. V. *, Karpova, A. *, **Liang, W.-W.** *, Strzalkowski, A., Chen, S., Li, Y., Southard-Smith, A. N., Iglesia, M. D., Wendl, M. C., Jayasinghe, R. G., *et al.* Epigenetic regulation during cancer transitions across 11 tumour types. *Nature* 623, 432–441 (2023). (**Spotlighted in Nature Genetics and Trends in Genetics**).
5. Gao, Q. *, **Liang, W.-W.** *, Foltz, S. M. *, Mutharasu, G., Jayasinghe, R. G., Cao, S., Liao, W.-W., Reynolds, S. M., Wyczalkowski, M. A., Yao, L., *et al.* Driver fusions and their implications in the development and treatment of human cancers. *Cell Rep.* 23, 227–238.e3 (2018). (**Best of Cell Reports 2018**).
6. **Liang, W.-W.** & Cheng, S.-C. A novel mechanism for Prp5 function in prespliceosome formation and proofreading the branch site sequence. *Genes Dev.* 29, 81–93 (2015).

Co-authorship

7. Li, Y., Dou, Y., Da Veiga Leprevost, F., Geffen, Y., Calinawan, A. P., Aguet, F., Akiyama, Y., Anand, S., Birger, C., Cao, S., *et al.* Proteogenomic data and resources for pan-cancer analysis. *Cancer Cell* 41, 1397–1406 (2023).
8. Carrot-Zhang, J., Yao, X., Devarakonda, S., Deshpande, A., Damrauer, J. S., Silva, T. C., Wong, C. K., Choi, H. Y., Felau, I., Robertson, A. G., *et al.* Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. *Cell Rep.* 34, 108707 (2021).
9. Huang, C., Chen, L., Savage, S. R., Eguez, R. V., Dou, Y., Li, Y., da Veiga Leprevost, F., Jaehnig, E. J., Lei, J. T., Wen, B., *et al.* Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. *Cancer Cell* 39, 361–379.e16 (2021).
10. Wang, L.-B., Karpova, A., Gritsenko, M. A., Kyle, J. E., Cao, S., Li, Y., Rykunov, D., Colaprico, A., Rothstein, J. H., Hong, R., *et al.* Proteogenomic and metabolomic characterization of human glioblastoma. *Cancer Cell* (2021).
11. Bailey, M. H., Meyerson, W. U., Dursi, L. J., Wang, L.-B., Dong, G., **Liang, W.-W.**, Weerasinghe, A., Li, S., Kelso, S., MC3 Working Group, *et al.* Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nat. Commun.* 11, 4748 (2020).
12. Gillette, M. A., Satpathy, S., Cao, S., Dhanasekaran, S. M., Vasaikar, S. V., Krug, K., Petralia, F., Li, Y., **Liang, W.-W.**, Reva, B., *et al.* Proteogenomic characterization reveals therapeutic vulnerabilities in lung adenocarcinoma. *Cell* 182, 200–225.e35 (2020).
13. Bailey, M. H., Tokheim, C., Porta-Pardo, E., Sengupta, S., Bertrand, D., Weerasinghe, A., Colaprico, A., Wendl, M. C., Kim, J., Reardon, B., *et al.* Comprehensive characterization of cancer driver genes and mutations. *Cell* 173, 371–385.e18 (2018).
14. Jayasinghe, R. G., Cao, S., Gao, Q., Wendl, M. C., Vo, N. S., Reynolds, S. M., Zhao, Y., Climente-González, H., Chai, S., Wang, F., *et al.* Systematic analysis of splice-site-creating mutations in cancer. *Cell Rep.* 23, 270–281.e3 (2018).
15. Sanchez-Vega, F., Mina, M., Armenia, J., Chatila, W. K., Luna, A., La, K. C., Dimitriadoy, S., Liu, D. L., Kantheti, H. S., Saghafein, S., *et al.* Oncogenic signaling pathways in the cancer genome atlas. *Cell* 173, 321–337.e10 (2018).
16. Foltz, S. M., **Liang, W.-W.**, Xie, M. & Ding, L. MIRMMR: binary classification of microsatellite instability using methylation and mutations. *Bioinformatics* 33, 3799–3801 (2017).
17. Niu, B., Scott, A. D., Sengupta, S., Bailey, M. H., Batra, P., Ning, J., Wyczalkowski, M. A., **Liang, W.-W.**, Zhang, Q., McLellan, M. D., *et al.* Protein-structure-guided discovery of functional mutations across 19 cancer types. *Nat. Genet.* 48, 827–837 (2016).

HONORS & AWARDS

- Best of Cell Reports 2018 2018
- Outstanding Merit Research Award National Yang-Ming University 2011
- Dean's List, Department of Life Science, National Tsing-Hua University 2007
- Outstanding student from Low-income, Lu Feng-Zhang Memorial Scholarship 2006

SELECTED TALKS

- CSHL Meeting: The Biology of Genomes** Cold Spring Harbor Laboratory, NY, 2024
NYC RNA Symposium Rockefeller University, NY, 2024
Transcriptome-scale RNA-targeting CRISPR screens reveal essential lncRNAs in human cells
- The CPTAC Annual Scientific Symposium** Virtual, 2021
The CPTAC Site Visit – NYU-WU-BYU PGDAC New York University, NY, 2019
Multiomic profiling reveals tumorigenic DNA methylation associated with therapeutic vulnerability and cell-of-origin
- CSHL Meeting: Eukaryotic mRNA Processing** Cold Spring Harbor Laboratory, NY, 2013
Taiwan Yeast Meeting Taiwan, 2013
A novel mechanism for Prp5 function in prespliceosome formation and proofreading the branch site sequence

TEACHING & MENTORING

- Simons foundation-NYU biology summer undergraduate research program, New York, NY**
Offer high-quality research training and opportunities that are often inaccessible to underrepresented students.
- **Sebastián H. Díaz-Rodríguez**, Undergraduate at University of Puerto Rico-Río Piedras Summer 2024
- Laboratory of Neville Sanjana, New York University, New York, NY**
- **Breanna Williams**, Master's student at NYU, Recipient of the Wasserman Center Internship Grant 2022–2023
Current - Research technician at Memorial Sloan Kettering Cancer Center
 - **Olivia Choi**, Undergraduate at NYU, Recipient of the NYU Dean's Undergraduate Research Fund 2022–2024
Current - Ph.D. student at John Hopkins University
- Laboratory of Li Ding, Washington University in St. Louis, St. Louis, MO**
- **Carolyn Lou**, Undergraduate at WashU 2015–2017
Current - Associate Director in Pfizer Biostatistics
 - **Terrence Tsou**, Undergraduate at WashU 2017–2019
Current - Medical student at John Hopkins University
 - **Rita Jui-Hsien Lu**, Graduate research technician at WashU 2019–2020
Current - Bioinformatician at Mount Sinai medical school
- Department of Biology, Washington University in St. Louis, St. Louis, MO** Spring 2016
Delivered lectures, provided assistance in molecular biology experiments, and assessed student performance as a teaching assistance in the Microbiology Laboratory course (Biol 3491) for over 30 undergraduate students.

SERVICE & OUTREACH

- Postdoc Seminar Series, New York Genome Center, New York, NY** 2021–Present
Organized monthly seminars featuring presentations by postdoctoral researchers.
- Café Philo at NY, New York, NY** 2024
Delivered a talk introducing the human genome and genome editing to a general audience of over 30 participants.
- Biology Club, Rutgers University-Camden, Camden, NJ** 2022
Participated as a panelist to discuss career development opportunities in science and technology with over 20 students.
- Midwest Taiwanese Biotechnology Association, Chicago, IL** 2017–2021
Co-founded the association, served in various leadership roles including Finance (2018), Promotion (2019), and President (2021), and organized events to foster dialogue among more than 300 young scientists across Midwest cities.