

# Wen-Wei Liang, Ph.D.

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

## EDUCATION

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

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

<b>New York University &amp; New York Genome Center</b>	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.

<b>Washington University in St. Louis</b>	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 of 206 samples across 11 cancer types 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 of 687 samples across 7 cancer types 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.

<b>Academia Sinica</b>	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.

<b>National Tsing-Hua University</b>	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*.

<b>Linköping University</b>	Linköping, Sweden
Visiting student, Laboratory of Jordi Altimiras	2007–2008

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

## PUBLICATIONS

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### 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. Li, Y., Porta-Pardo, E., Tokheim, C., Bailey, M. H., Yaron, T. M., Stathias, V., Geffen, Y., Imbach, K. J., Cao, S., Anand, S., *et al.* Pan-cancer proteogenomics connects oncogenic drivers to functional states. *Cell* 186, 3921–3944.e25 (2023).
9. 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).
10. Huang, C., Chen, L., Savage, S. R., Eguev, 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).
11. 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).
12. 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).
13. 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).
14. Cao, S., Wylie, K. M., Wyczalkowski, M. A., Karpova, A., Ley, J., Sun, S., Mashl, R. J., **Liang, W.-W.**, Wang, X., Johnson, K., *et al.* Dynamic host immune response in virus-associated cancers. *Commun. Biol.* 2, 109 (2019).
15. 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).
16. Jayasinghe, R. G., Cao, S., Gao, Q., Wendl, M. C., Vo, N. S., Reynolds, S. M., Zhao, Y., Clemente-González, H., Chai, S., Wang, F., *et al.* Systematic analysis of splice-site-creating mutations in cancer. *Cell Rep.* 23, 270–281.e3 (2018).
17. Sanchez-Vega, F., Mina, M., Armenia, J., Chatila, W. K., Luna, A., La, K. C., Dimitriadou, S., Liu, D. L., Kantheti, H. S., Saghafeina, S., *et al.* Oncogenic signaling pathways in the cancer genome atlas. *Cell* 173, 321–337.e10 (2018).

18. 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).
19. 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

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

## TEACHING & MENTORING

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

## SERVICE & OUTREACH

<b>Postdoc Seminar Series, New York Genome Center, New York, NY</b>	2021–Present
Organized monthly seminars featuring presentations by postdoctoral researchers.	
<b>Café Philo at NY, New York, NY</b>	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.