

Wen-Wei Liang, Ph.D.

Genome engineer and computational biologist exploring the roles of long noncoding RNAs in tumor progression via high-throughput approaches.

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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

Experience

New York Genome Center & New York University	New York, NY
Postdoctoral research associate, Laboratory of Dr. Neville Sanjana	2021–Present
Washington University in St. Louis	St. Louis, MO
Postdoctoral research associate, Laboratory of Dr. Li Ding	2020–2021
Academia Sinica	Taipei, Taiwan
Research assistant, Laboratory of Dr. Soo-Chen Cheng	2011–2014

Publications

First authorship (* Equal contribution)

1. **Liang, W.-W.** *, Mueller, S. J. *, Hart, S. K., Wessels, H.-H., Méndez-Mancilla, A., Sookdeo, A., Choi, O., Caragine, C. M., Corman, A., Lu, L., Kolumba, O., Williams, B. & Sanjana, N. E. Essential lncRNAs in the human transcriptome. *Cell Genom.*, 101253 (2026). (*Corrected version of Liang et al., Cell (2024)*).
2. **Liang, W.-W.** *, Müller, S. *, Hart, S. K., Wessels, H.-H., Méndez-Mancilla, A., Sookdeo, A., Choi, O., Caragine, C. M., Corman, A., Lu, L., Kolumba, O., Williams, B. & Sanjana, N. E. RETRACTED: transcriptome-scale RNA-targeting CRISPR screens reveal essential lncRNAs in human cells. *Cell* 187, 7637–7654.e29 (2024). (*Retracted by authors due to gRNA off-targeting issues; see retraction notice at [https://www.cell.com/cell/fulltext/S0092-8674\(25\)01367-4](https://www.cell.com/cell/fulltext/S0092-8674(25)01367-4)*).
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., Govindan, A., Demicco, E. G., Li, X., Li, Y., Sethuraman, S., Payne, S. H., Fenyö, D., Rodriguez, H., Wiznerowicz, M., Shen, H., Mani, D. R., Rodland, K. D., Lazar, A. J., Robles, A. I., Ding, L. & Clinical Proteomic Tumor Analysis Consortium. Integrative multi-omic cancer profiling reveals DNA methylation patterns associated with therapeutic vulnerability and cell-of-origin. *Cancer Cell* 41, 1567–1585.e7 (2023).
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., Liu, J., Song, Y., Cao, S., Houston, A., Liu, X., Wyczalkowski, M. A., Lu, R. J.-H., Caravan, W., Shinkle, A., Naser Al Deen, N., Herndon, J. M., Mudd, J., Ma, C., Sarkar, H., Sato, K., Ibrahim, O. M., Mo, C.-K., Chasnoff, S. E., Porta-Pardo, E., Held, J. M., Pachynski, R., Schwarz, J. K., Gillanders, W. E., Kim, A. H., Vij, R., 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., Yu, L., Sun, S. Q., Fusion Analysis Working Group, Cancer Genome Atlas Research Network, Chen, K., Lazar, A. J., Fields, R. C., Wendl, M. C., Van Tine, B. A., Vij, R., Chen, F., Nykter, M., Shmulevich, I. & Ding, L. 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 (*,+ Equal contribution)

7. Li, Y. *, Dou, Y. *, Da Veiga Leprevost, F. *, Geffen, Y. *, Calinawan, A. P. *, Aguet, F., Akiyama, Y., Anand, S., Birger, C., Cao, S., Chaudhary, R., Chilappagari, P., Cieslik, M., Colaprico, A., Zhou, D. C., Day, C., Domagalski, M. J., Esai Selvan, M., Fenyő, D., Foltz, S. M., Francis, A., Gonzalez-Robles, T., Gümüş, Z. H., Heiman, D., Holck, M., Hong, R., Hu, Y., Jaehnig, E. J., Ji, J., Jiang, W., Katsnelson, L., Ketchum, K. A., Klein, R. J., Lei, J. T., **Liang, W.-W.**, 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., Akiyama, Y., Liu, W., Wyczalkowski, M. A., Song, Y., Storrs, E. P., Wendl, M. C., Zhang, W., Sibai, M., Ruiz-Serra, V., **Liang, W.-W.**, Terekhanova, N. V., Rodrigues, F. M., Clauser, K. R., Heiman, D. I., Zhang, Q., Aguet, F., Calinawan, A. P., Dhanasekaran, S. M., Birger, C., Satpathy, S., Zhou, D. C., Wang, L.-B., Baral, J., Johnson, J. L., Huntsman, E. M., 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., Castro, M. A. A., Bao, L., Rheinbay, E., Liu, E. M., Trieu, T., Haan, D., Yau, C., Hinoue, T., Liu, Y., Shapira, O., Kumar, K., Mungall, K. L., Zhang, H., Lee, J. J.-K., Berger, A., Gao, G. F., Zhitomirsky, B., **Liang, W.-W.**, Zhou, M., Moorthi, S., Berger, A. H., Collisson, E. A., Zody, M. C., Ding, L., Cherniack, A. D., 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. *, Egue, R. V., Dou, Y., Li, Y., da Veiga Leprevost, F., Jaehnig, E. J., Lei, J. T., Wen, B., Schnaubelt, M., Krug, K., Song, X., Cieřlik, M., Chang, H.-Y., Wyczalkowski, M. A., Li, K., Colaprico, A., Li, Q. K., Clark, D. J., Hu, Y., Cao, L., Pan, J., Wang, Y., Cho, K.-C., Shi, Z., Liao, Y., Jiang, W., Anurag, M., Ji, J., Yoo, S., Zhou, D. C., **Liang, W.-W.**, Wendl, M., Vats, P., 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. *, Stathias, V. *, Cornwell, M. *, Petralia, F. *, Wu, Y., Reva, B., Krug, K., Pugliese, P., Kawaler, E., Olsen, L. K., **Liang, W.-W.**, Song, X., Dou, Y., Wendl, M. C., Caravan, W., Liu, W., Cui Zhou, D., Ji, J., Tsai, C.-F., Petyuk, V. A., Moon, J., Ma, W., Chu, R. K., Weitz, K. K., Moore, R. J., Monroe, M. E., 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, PCAWG novel somatic mutation calling methods working group, Saksena, G., Ellrott, K., Wendl, M. C., Wheeler, D. A., Getz, G., Simpson, J. T., Gerstein, M. B., Ding, L. & PCAWG Consortium. 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. *, Vasaiakar, S. V. *, Krug, K. *, Petralia, F. *, Li, Y., **Liang, W.-W.**, Reva, B., Krek, A., Ji, J., Song, X., Liu, W., Hong, R., Yao, L., Blumenberg, L., Savage, S. R., Wendl, M. C., Wen, B., Li, K., Tang, L. C., MacMullan, M. A.,

- Avanessian, S. C., Kane, M. H., Newton, C. J., Cornwell, M., Kothadia, R. B., Ma, W., Yoo, S., Mannan, R., Vats, P., Kumar-Sinha, C., Kawaler, E. A., Omelchenko, T., *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., DiPersio, J. F., Gay, H., Ratner, L., Chen, F., Adkins, D. R. & Ding, L. 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., Ng, P. K.-S., Jeong, K. J., Cao, S., Wang, Z., Gao, J., Gao, Q., Wang, F., Liu, E. M., Mularoni, L., Rubio-Perez, C., Nagarajan, N., Cortés-Ciriano, I., Zhou, D. C., **Liang, W.-W.**, Hess, J. M., Yellapantula, V. D., Tamborero, D., Gonzalez-Perez, A., Suphavilai, C., Ko, J. Y., Khurana, E., Park, P. J., Van Allen, E. M., Liang, H., MC3 Working Group, *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., Climente-González, H., Chai, S., Wang, F., Varghese, R., Huang, M., **Liang, W.-W.**, Wyczalkowski, M. A., Sengupta, S., Li, Z., Payne, S. H., Fenyő, D., Miner, J. H., Walter, M. J., Cancer Genome Atlas Research Network, Vincent, B., Eyra, E., Chen, K., Shmulevich, I., Chen, F. & Ding, L. 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., Chakravarty, D., Daian, F., Gao, Q., Bailey, M. H., **Liang, W.-W.**, Foltz, S. M., Shmulevich, I., Ding, L., Heins, Z., Ochoa, A., Gross, B., Gao, J., Zhang, H., Kundra, R., Kandoth, C., Bahceci, I., Dervishi, L., Dogrusoz, U., Zhou, W., Shen, H., Laird, P. W., Way, G. P., Greene, C. S., Liang, H., Xiao, Y., *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., Sun, S. Q., Tripathi, P., Lou, C., Ye, K., Mashl, R. J., Wallis, J., Wendl, M. C., Chen, F. & Ding, L. Protein-structure-guided discovery of functional mutations across 19 cancer types. *Nat. Genet.* 48, 827–837 (2016).

Selected and Invited Talks

Transcriptome-scale RNA-targeting CRISPR screens reveal essential lncRNAs in human cells

Feigin Rising Stars Symposium (*Invited*)

Baylor College of Medicine, TX, 2026

Salk Rising Stars Symposium

The Salk Institute, SD, 2025

STATGEN 2025: Statistics in Genomics and Genetics (*Invited*)

University of Minnesota, MN, 2025

CSHL Meeting: The Biology of Genomes

Cold Spring Harbor Laboratory, NY, 2024

NYC RNA Symposium

Rockefeller University, NY, 2024

Genome Engineering Seminar Series at Harvard Medical School (*Invited*)

Virtual, 2024

Multomic profiling reveals tumorigenic DNA methylation associated with therapeutic vulnerability and cell-of-origin

The CPTAC Annual Scientific Symposium

Virtual, 2021

The CPTAC Site Visit – NYU-WU-BYU PGDAC

New York University, NY, 2019

A novel mechanism for Prp5 function in prespliceosome formation and proofreading the branch site sequence

CSHL Meeting: Eukaryotic mRNA Processing

Cold Spring Harbor Laboratory, NY, 2013

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 (\$10,000)	2007–2008

Honors & Awards

- Invited to Feigin Rising Stars Symposium, Baylor College of Medicine 2026
- Outstanding postdoctoral fellow, Rising Stars Symposium, The Salk Institute 2025
- Travel Award, STATGEN 2025: Statistics in Genomics and Genetics 2025
- Outstanding Contribution Award, New York Genome Center 2024
- NYU Postdoctoral Travel Grant Award, New York University 2024
- Best of *Cell Reports* 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 a low-income background, Lu Feng-Zhang Memorial Scholarship 2006

Teaching & Mentoring

Simons Foundation–NYU Biology Summer Undergraduate Research Program, New York, NY

Mentored an underrepresented student on a project focused on identifying long noncoding RNAs essential for macrophage differentiation and polarization using *in vitro* CRISPR pooled screening.

- **Sebastián H. Díaz-Rodríguez**, Undergraduate at University of Puerto Rico–Río Piedras Summer 2024
Current - Undergraduate, NIH-funded Research Initiative for Scientific Enhancement (RISE) scholar

Laboratory of Neville Sanjana, New York University, New York, NY

- **Breanna Williams**, Master's student, Recipient of the Wasserman Center Internship Grant 2022–2023
Current - Research technician at Memorial Sloan Kettering Cancer Center
- **Olivia Choi**, Undergraduate, Recipient of the NYU Dean's Undergraduate Research Fund 2022–2024
Current - Ph.D. student at Johns Hopkins University

Laboratory of Li Ding, Washington University in St. Louis, St. Louis, MO

- **Carolyn Lou**, Undergraduate 2015–2017
Current - Associate Director at Pfizer Biostatistics
- **Terrence Tsou**, Undergraduate 2017–2019
Current - Medical student at Johns Hopkins University
- **Rita Jui-Hsien Lu**, Research technician 2019–2020
Current - Senior 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 assistant 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 and coordinated 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 this 501(c)(3) nonprofit organization with over 2,000 members, served in various leadership roles including Finance (2018), Promotion (2019), and President (2021), and organized events to foster dialogue among young scientists across Midwest cities.
- Institute of Molecular Biology, Academia Sinica, Taiwan** 2014–2018
Served as a panelist to discuss how to apply for PhD programs in the United States with over 20 undergraduates.

Research Projects

- New York Genome Center & New York University** New York, NY
Postdoctoral research associate, Laboratory of Dr. Neville Sanjana 2021–Present
- ***Essential lncRNAs in the human transcriptome***: Conducted Cas13 pooled screens and perturbation assays, coupled with single-cell RNA sequencing, to identify and characterize about 5,500 lncRNAs crucial for cell proliferation and their mechanistic roles.
 - ***Targeting onco-lncRNAs as a strategy against cancer***: Conducted integrative analyses alongside *in vitro* and *in vivo* pooled screens to identify lncRNAs driving tumor progression in BRCA organoids.
- Washington University in St. Louis** St. Louis, MO
Ph.D. student and postdoctoral research associate, Laboratory of Dr. Li Ding 2015–2021
- ***Epigenetic regulation during cancer transitions across 11 tumour types***: Integrated snATAC-seq, single-cell RNA-seq, and whole-exome sequencing across 206 samples from 11 cancer types in HTAN, profiling over one million cells and nuclei to identify cancer-specific regulatory elements linked to gene expression.
 - ***Integrative multi-omic cancer profiling reveals DNA methylation patterns associated with therapeutic vulnerability and cell-of-origin***: Integrated DNA methylation, RNA-seq, and proteomic data from 687 samples across 7 cancer types in CPTAC to define how aberrant methylation shapes gene expression, tumor features, and therapeutic vulnerability.
 - ***Driver fusions and their implications in the development and treatment of human cancers***: Analyzed gene fusions in over 9,000 tumors across 33 TCGA cancer types, revealing their effects on oncogenes, tumor suppressors, and kinases, and identifying druggable fusions in 6.0% of cases.
- Academia Sinica** Taipei, Taiwan
Master's student and research assistant, Laboratory of Dr. 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.
- National Tsing-Hua University** Hsinchu, Taiwan
Undergraduate student, Laboratory of Dr. Chung-Yu Lan 2008–2009
- Investigated the reactions of the iron-responsive element under virulence gene expression in *C. albicans*.