Wen-Wei Liang, Ph.D.

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

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

Experience

New York Genome Center & New York University — New York, NY
Postdoctoral research associate, Laboratory of Neville Sanjana — 2021–Present
Washington University in St. Louis — St. Louis, MO
Postdoctoral research associate, Laboratory of Li Ding — 2020–2021

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. *In press at 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. *Invited at Nature Reviews 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., 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). ***(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., 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., Fenyö, 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. [*], Eguez, R. V., Dou, Y., Li, Y., da Veiga Leprevost, F., Jaehnig, E. J., Lei, J. T., Wen, B., Schnaubelt, M., Krug, K., Song, X., Cieślik, 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. [+], Vasaikar, 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., Fenyö, D., Miner, J. H., Walter, M. J., Cancer Genome Atlas Research Network, Vincent, B., Eyras, 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., Dimitriadoy, S., Liu, D. L., Kantheti, H. S., Saghafinia, 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).

Research Projects

New York Genome Center & New York University — 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.

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 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.

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.

Selected Talks

Transcriptome-scale RNA-targeting CRISPR screens reveal essential lncRNAs in human cells
CSHL Meeting: The Biology of Genomes Cold Spring Harbor Laboratory, NY, 2024
NYC RNA Symposium Rockefeller University, NY, 2024
The MacMillan Center for the Study of the Non-Coding Cancer Genome New York Genome Center, NY, 2024

Multiomic 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
Taiwan Yeast Meeting Taiwan, 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 to Study Abroad ($10,000) 2007–2008

Honors & Awards

- 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 Low-income, Lu Feng-Zhang Memorial Scholarship 2006

Teaching & Mentoring

Simons foundation-NYU biology summer undergraduate research program, New York, NY
Mentored 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

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 John 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 John Hopkins University

- **Rita Jui-Hsien Lu**, Research technician 2019–2020
  Current - Senior bioinformatician at Mount Sinai medical scool

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 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.

References

Dr. Li Ding (Ph.D. mentor)
Distinguished Professor
Department of Medicine and Genetics
Washington University in St. Louis
lding@wustl.edu

Dr. Ben Raphael (Collaborator)
Professor
Department of Computer Science
Princeton University
braphael@princeton.edu

Dr. Neville Sanjana (Postdoctoral mentor)
Associate Professor
Department of Biology
New York Genome Center and New York University
sanjana-office@nyu.edu