

Assistant Professor, Department of Chemical Engineering,
National Taiwan University of Science and Technology (Taiwan Tech)

EDUCATION:

Ph.D., Chemical Engineering, Virginia Tech, Blacksburg, VA, USA May 2020
Advisor: Dr. Chang Lu Dissertation: **New microfluidic technologies for studying histone modification and long non-coding RNA bindings**

M.S., Chemical Engineering, National Chung Hsing University, Taiwan June 2011
Advisor: Dr. Sung-Chyr Lin Thesis: **Effects of PEGylation on enzyme activity**

B.S., Chemical Engineering and Chemistry (double majors), National Chung Hsing University, Taichung, Taiwan June 2009
Advisor: Dr. Sung-Chyr Lin Project: **Lipase-catalyzed transesterification of soy oil and isopropyl alcohol for the production of biodiesel in a batch reactor**

PROFESSIONAL EXPERIENCE:

Assistant Professor, Department of Chemical Engineering, Taiwan Tech Feb. 2023 – present

Postdoctoral Research Scholar, Stanford University School of Medicine, Sean N. Parker Center for Allergy & Asthma Research
Advisor: Dr. Maya Kasowski (MD, PhD) Sep. 2020 – July 2022

RESEARCH INTERESTS:

Biotechnology development, Genome-wide studies using next generation sequencing (NGS), Microfluidic technology, Bioinformatics, Single cell research, CRISPR-Cas9 gene editing, Epigenomic regulations, Gene expression, Transcriptomics, Long noncoding RNA (lncRNA) regulation, Histone modification, DNA methylation, Enzyme engineering

RESEARCH EXPERIENCE:

Stanford University School of Medicine, Stanford, CA, USA Sep. 2020 – July 2022
Postdoctoral Research Scholar

- Developing a new technology to profile chromatin accessibility (ACAT-seq) and gene expression (RNA-seq) in the same single cell.
- Conducting single-cell ATAC-seq with 10x Genomics microfluidics platform to explore the role of epigenetic regulation in anaplastic thyroid cancer and peanut allergy.
- Profiling drug resistance genes with genome-wide pooled lentiviral CRISPR-Cas9 screening technology.

Virginia Tech, Blacksburg, VA, USA
Graduate Research Assistant: development of low-input epigenomic assays that enable studies of scarce tissue samples from patients and small lab animals. Aug. 2015 – May 2020

- Designed a low-input microfluidic chromatin isolation by RNA purification coupled with sequencing (ChIRP-seq) system for long noncoding RNA (lncRNA) profiling. Our technology dramatically permits profiling genome-wide lncRNA binding using as few as 100K cells, compared to conventional ChIRP-seq assays requiring 100 million cells per assay.
- Developed a semi-automated version of microfluidic oscillatory washing based chromatin immunoprecipitation followed by sequencing (MOW-ChIP-seq) for studying genome-wide histone modifications. 8 parallel assays and 100 cells per assay in a semi-automated microfluidic platform (compared to conventional ChIP-seq conducted manually requiring 10 million cells) with 6 different histone marks were tested.
- Profiled cell-type-specific epigenomic changes associated with BRCA1 mutation in breast tissue using MOWChIP-seq. We studied four separate cell types isolated from breast tissues using FACS and discovered different epigenomic dynamics in these cell types.
- Used MOWChIP-seq to profile epigenomes in primary neurons and glial cells from human and mouse brains.
- Explored epigenomic regulation in mouse bone marrow derived macrophages with various stimulatory concentrations of LPS. Conducted both MOWChIP-seq and RNA-seq (SMART-seq2) for examining gene regulation and expression.
- Tested single-cell bisulfite sequencing for studying DNA methylation in single cells.

Nuclear, biological and chemical research center, Taoyuan, Taiwan Oct. 2011 – Sep. 2012
Corporal (military service)

- Designed headspace gas chromatography system to detect a leak of military oil storage tanks.
- Analyzed sewage disposal from military camps in Taiwan.

National Chung Hsing University, Taichung, Taiwan Sep. 2009 – June 2011
Graduate Research Assistant

- Investigated enzyme activity after PEGylation.

- Performed enzyme purification from recombinant *E. coli*.

National Chung Hsing University, Taichung, Taiwan

Sep. 2007 – June 2009

Research assistant

- Investigated biodiesel using lipase transesterification of soy oil and isopropyl alcohol in a batch reactor.

TECHNICAL SKILLS:

Data analysis and bioinformatics: Bowtie, MACS, DiffBind, ROSE

Technologies: Illumina sequencing, CRISPR-Cas9 gene-editing, Chromatin Immunoprecipitation followed by sequencing (ChIP-seq), scRNA-seq, scATAC-seq, RNA-seq (Smart-seq2), ATAC-seq, Single-Cell bisulfite sequencing, Chromatin isolation by RNA purification (ChIRP-seq), PCR, qPCR, RT-qPCR, Microfluidic device design, fabrication, and testing, Adenovirus transfection and infection, Bacterial transformation, Cell culture, *E. coli* culture, Mouse breeding and maintenance, Mouse brain dissection, Genotyping, Fermentation, Nickel-NTA chromatography, DNA and protein electrophoresis, SDS-PAGE, Western blot, Sonication, PEGylation of protein

Instrument: Fluorescence activated cell sorter (FACS), 10x Genomics single cell microfluidics platform, High performance liquid chromatography (HPLC), Gas chromatography-mass spectrometry (GC-MS), Nuclear magnetic resonance (NMR)

TEACHING EXPERIENCE:

Taiwan Tech, Taipei, Taiwan

CH4109701 Biochemistry

Feb. 2023 – June 2023

Virginia Tech, Blacksburg, VA, USA

CHE4104 Process Materials, Graduate Teaching Assistant

Aug. 2019 – Dec. 2019

CHE3144 Mass Transfer, Graduate Teaching Assistant

Jan. 2019 – May 2019

CHE4104 Process Materials, Graduate Teaching Assistant

Aug. 2015 – Dec. 2015

- Conducted office hours to mentor students with their homework and exams
- Proctored and graded exams and homework

HONORS AND AWARDS:

Honorary member of Phi Tau Phi Scholastic Honor Society

June 2011

Summa cum laude and Valedictorian

June 2011

Stanford University School of Medicine Dean's Postdoctoral Fellowship Award

June 2022

PUBLICATIONS:

Hsieh, Y.-P., Naler, L. B., Lu, C., "Microfluidic oscillatory hybridized ChIRP-seq assay to profile genome-wide lncRNA binding," In Preparation

Hsieh, Y.-P., Naler, L. B., Ma, S., Lu, C., "Cell-type-specific epigenomic variations associated with BRCA1 mutation in pre-cancer human breast tissues," *NAR genom. bioinform.* 4 (2022) lqac006.

Naler, L. B.[#], **Hsieh, Y.-P.**[#], Geng, S., Zhou, Z., Li, L., Lu, C., "Epigenomic and transcriptomic analyses reveal differences between low-grade inflammation and severe exhaustion in LPS-challenged murine monocytes," *Commun. Biol.* 5 (2022) No. 102. (co-first authors) (impact factor=6.268)

Murphy, T. W., **Hsieh, Y.-P.**, Zhu, B., Naler, L. B., Lu, C., "Microfluidic platform for next-generation sequencing library preparation with low-input samples," *Analytical Chemistry* 92 (2020) 2519-2526. (impact factor =6.986)

Zhu, B.[#], **Hsieh, Y.-P.**[#], Murphy, T. W., Zhang, Q., Naler, L. B., Lu, C., "MOWChIP-seq for low-input and multiplexed profiling of genome-wide histone modifications," *Nature Protocols* 14 (2019) 3366-3394. (co-first authors) (impact factor =10.419)

Zhang, X., Wang, Y., Chiang, H.-C., **Hsieh, Y.-P.**, Lu, C., Park, B. H., Jatoi, I., Jin, V. X., Hu, Y., Li, R., "BRCA1 mutations attenuated super-enhancer function and chromatin looping in haploinsufficient human breast epithelial cells," *Breast Cancer Research* 21 (2019) 51. (impact factor =4.988)

Zhang, R., Qi, C.-F., Hu, Y., Shan, Y., **Hsieh, Y.-P.**, Xu, F., Lu, G., Dai, J., Gupta, M., Gui, M., Peng, L., Yang, J., Xue, Q., Chen-Liang, R., Chen, K., Zhang, Y., Fung-Leung, W.-P., Mora, J. R., Li, L., Morse, H. C., Ozato, K., Heeger, P. S., Xiong, H., "T follicular helper cells restricted by IRF8 contribute to T cell-mediated inflammation," *Journal of autoimmunity* 96 (2019) 113-121. (impact factor =6.658)

Murphy, T. W., **Hsieh, Y.-P.**, Ma, S., Zhu, Y., Lu, C., "Microfluidic low-Input fluidized-bed enabled ChIP-seq device for automated and parallel analysis of histone modifications," *Analytical Chemistry* 90 (2018) 7666-7674. (impact factor =6.350)

Ma, S., **Hsieh, Y.-P.**, Ma, J., Lu, C., "Low-input and multiplexed microfluidic assay reveals epigenomic variation across cerebellum and prefrontal cortex," *Science Advances* 4 (2018) eaar8187. (impact factor =12.804)

Sun, C., **Hsieh, Y.-P.**, Ma, S., Geng, S., Cao, Z., Li, L., Lu, C., "Immunomagnetic separation of tumor initiating cells by screening two surface markers," **Scientific Reports** 7 (2017) 40632. (impact factor =4.122)

Hsieh, Y.-P., Lin, S.-C., "Effect of PEGylation on the activity and stability of horseradish peroxidase and L-N-carbamoylase in aqueous phases," **Process Biochemistry** 50 (2015) 1372-1378. (impact factor =2.529)

PRESENTATIONS:

Hsieh, Y.-P., Naler, L. B., Zhang, X., Murphy, T.W., Li, R., Lu, C., Profiling cell-type-specific epigenomic changes associated with BRCA1 mutation in breast tissues using a low-input microfluidic technology. **AIChE 2019**, Orlando, FL (Oral)