Pin-Yao Huang, PhD
pyaohtw@gmail.com / 646-469-5628

- Experienced PhD scientist with expertise in **molecular genetics, genome engineering, and epigenetics**.
- Skilled in performing **CRISPR knockout and knockin** techniques in mammalian systems.
- Proficient in **optimizing experimental protocols** to simplify processes, reduce costs, and improve outcomes.
- Advanced **data analysis and batch processing**, using ChatGPT for coding tasks in Python and R.
- Proficient in using **electronic notebook Benchling** for experimental records and documentation.
- Committed to **continuous learning and applying new scientific knowledge** to drive advancements in research.
- **Collaborative** and eager to apply fundamental science to therapeutic applications, **contributing to team efforts** in optimizing efficiency and targeting specific cell types for the treatment of genetic diseases.

Proficiencies

Molecular Biology: Multi-fragment cloning strategies, RNA/DNA/protein extraction, genomic DNA PCR and NGS library preparation for INDEL analysis, qPCR, mRNA IVT synthesis, Western blotting, ELISA, protein purification, bimolecular fluorescence complementation, immunoprecipitation, chromatin immunoprecipitation (ChIP).

Cell Biology: DNA/RNA transfection using lipofectamine or lipid nanoparticles (LNP), genomic engineering (CRISPR/Cas9), maintenance of mESCs and other mammalian cell lines (HepG2, Hep3B, HEK293, human primary hepatocytes, Hepa1-6, AML12, mouse primary neurons), flow cytometry.

Computational Skills: Analysis of genomic sequencing data, interaction with high performance computing clusters, basic Python/R/Linux skills, AI-assisted code generation, Microsoft Office, Benchling, GraphPad, Adobe Illustrator.

Professional Experience

Sr. Scientist | Ionis Pharmaceuticals | 03/2023 - present

- **Led CRISPR-based transcriptional regulation project for therapeutic applications using RNA-LNP delivery**, targeting genes in liver and central nervous system (CNS) implicated in genetic diseases.
  - Researched literature to **design diverse CRISPR modules and strategically utilized genomic data** (e.g., histone modifications, CpG islands, RNA-seq) to determine gRNA targeting positions.
  - **Collaborated with interdisciplinary teams to screen gRNA targeting positions, chemistries, and LNP formulations**, aiming for optimal mRNA and gRNA delivery and editing efficiency in liver cells and mouse primary neurons. **Extended the study in vivo** to assess the efficacy of the selected approaches.
  - Performed molecular assays (RT-qPCR, Western blot, and 3' RNA-Seq) to assess the efficacy and off-target effects of CRISPR editing. **Streamlined NGS workflow for INDEL analysis**.
- Provided essential support to cross-functional teams.
  - Evaluated in vivo CRISPR editing efficiency through ELISA and INDEL analysis.
  - Participated in various working group meetings and offered insights to drive project advancement.

Postdoc | Dr. Danny Reinberg's lab, Howard Hughes Medical Institute, New York University | 11/2017 - 02/2023

- **Conducted a candidate-based screen to identify novel factors crucial for establishing chromatin boundaries during cell differentiation**, and utilized genetic validation approaches to **confirm the roles of 2 zinc-finger transcription factors identified in the screen**.
  - **Generated CRISPR knockout cell lines** from candidate screens and evaluated their functional phenotypes, particularly focusing on chromatin organization.
  - **Utilized CRISPR knock-in technology to introduce FLAG-HA tags into endogenous loci**, generating cell lines for subsequent protein purification and chromatin immunoprecipitation (ChIP) assays.
  - Conducted **comprehensive genomic analysis using Hi-C, ChIP-seq, and RNA-seq** to elucidate how the chromatin binding of the gene-of-interest affects genome organization and transcriptional regulation.
- Investigated the role of RNA in CTCF-mediated chromatin boundary formation using dCas9-targeted or dCas9-APX labeling-based approaches.

Education

PhD | Dr. Laurent Zimmerli's lab, National Taiwan University, Taiwan | Plant Biology | 2012 - 2017
- Employed genetic screens to uncover novel plant defense regulators.
- Discovered the transcription factor ERF19's role in negatively regulating Arabidopsis innate immunity.
- Further revealed that the NINJA co-repressor complex modulates the transcriptional activity of ERF19 through genetic and biochemical analyses.

MS | Dr. Laurent Zimmerli's lab, National Taiwan University, Taiwan | Plant Biology | 2010 - 2012
- Generated and analyzed 12 transgenic lines overexpressing cysteine-rich receptor-like kinases (CRKs), to elucidate their roles in plant defense, identifying 3 candidates with functional implications in innate immunity.
- Leveraged fundamental plant science to engineer disease-resistant crops, specifically demonstrating broad-spectrum resistance in tobacco plants overexpressing LecRK-VI.2. This protein boosts the innate immunity of transgenic plants, leading to enhanced resistance against 3 diverse bacterial pathogens.

BS | National Chiao Tung University, Taiwan | Biological Science and Technology | 2003 - 2007

Certificates

- Python for Non-Programmers | LinkedIn
- Career Essentials in Generative AI | Microsoft and LinkedIn

Awards

- Postdoctoral Research Abroad Program Fellowship | Ministry of Science and Technology, Taiwan (2016).
- Outstanding oral presentation award | 11th NTU-Kyoto U Symposium on Molecular and Cell Biology. Kyoto, Japan (2013).

Publications

Google Scholar Metrics: Total citations: 798 | - H-index: 8 |- i10-index: 8
- Ortabozkoyun, H.*, **Huang, P.Y.***, Cho, H., Tsirigos, A., Mazzoni, E.O., and Reinberg, D. (2023) Novel Chromatin Insulating Activities Uncovered upon Eliminating Known Insulators in vivo. bioRxiv.
- Ortabozkoyun-Kara, H., **Huang, P.Y.**, Cho, H., Narendra V., Leroy, G., Gonzalez-Buendia, E., Skok, J.A., Tsirigos, A., Mazzoni, E.O., and Reinberg, D. (2022) CRISPR and biochemical screens identify MAZ as a cofactor in CTCF-mediated insulation at Hox clusters. Nature Genetics. 54: 202-212.
- **Huang, P.Y.**, Zhang, J., Jiang, B., Chan C., Yu, J.H., Lu, Y. P., Chung, K., and Zimmerli, L. (2019). NINJA-associated ERF19 negatively regulates Arabidopsis pattern-triggered immunity. Journal of Experimental Botany. 10.1093/jxb/ery414.
- **Huang, P.Y.**, Catinot, J., and Zimmerli, L. (2016). Ethylene response factors in Arabidopsis immunity. Journal of Experimental Botany. 67: 1231-1241.
- Yeh, Y.H., Panzeri, D., Kadota, Y., Huang, Y.C., **Huang, P.Y.**, Tao, C.N., Roux, M., Chien, H.C., Chin, T.C., Chu, P.W., Zipfel, C., and Zimmerli, L. (2016) The Arabidopsis Malectin-Like/LRR-RLK IOS1 Is Critical for BAK1-Dependent and BAK1-Independent Pattern-Triggered Immunity. The Plant Cell. 28: 1701-1721.
- Catinot, J., Huang, J.B., **Huang, P.Y.**, Tseng, M.Y., Chen, Y.L., Gu, S.Y., Lo, W.S., Wang, L.C., Chen, Y.R., and Zimmerli, L. (2015) ETHYLENE RESPONSE FACTOR 96 positively regulates Arabidopsis resistance to necrotrophic pathogens by direct binding to GCC elements of jasmonate - and ethylene-responsive defence genes. Plant, Cell & Environment. 38: 2721-2734.
- Yeh, Y.H., Chang, Y.H., **Huang, P.Y.**, Huang, J.B., and Zimmerli, L. (2015) Enhanced Arabidopsis pattern-triggered immunity by overexpression of cysteine-rich receptor-like kinases. Frontiers in Plant Science. 6: 322.
- **Huang, P.Y.**, and Zimmerli, L. (2014). Enhancing crop innate immunity: new promising trends. Frontiers in Plant Science. 5: 624.
- **Huang, P.Y.**, Yeh, Y.H., Liu, A.C., Cheng, C.P., and Zimmerli, L. (2014) The Arabidopsis LecRK-VI.2 associates with the pattern-recognition receptor FLS2 and primes Nicotiana benthamiana pattern-triggered immunity. The Plant Journal. 79: 243-255.