

Tzu-Tang Lin

b03601046@gmail.com | [linkedin.com/in/tzutang-lin/](https://www.linkedin.com/in/tzutang-lin/) | github.com/LinTzuTang |
intzutang.github.io/ | scholar.google.com/citations?user=2Yxesf0AAAAJ

PROFESSIONAL SUMMARY

AI × Bioinformatics researcher with 7+ years across drug discovery, genomics, and biomedical AI. Skilled in RNA–small molecule modeling, functional peptide/protein design, NGS/GWAS, and EHR applications. Skilled in leading end-to-end research pipelines—from dataset curation to deep learning model development—and collaborating with academia, hospitals, and industry partners.

PROFESSIONAL EXPERIENCE

Research Assistant — University of Florida, College of Pharmacy May 2024 – Aug 2025

- Built a cross-domain multimodal contrastive framework for RNA–ligand affinity, integrating RiNALMo & SMI-TED LLMs plus 3D structure into CLIP-based foundation models; Test RMSE 1.68 vs 1.85 benchmark.
- Applied biomolecule GNNs (GIGN), 3D-CNNs, and a custom representation module for fine-tuning and transfer learning.
- Curated RNA–small molecule datasets (PDB, PDBbind, HARIBOSS); automated ligand-pocket detection, structure-based clustering (RNA3DB, RAlign), and feature extraction (RDKit, Biopython, PyMOL).
- Performed 10M-scale virtual screening (RNAmigos), docking score evaluation (AutoDock Vina), and decoy generation (DeepCoy).
- Explored generative AI protein design with RFdiffusion, AlphaFold, and ProteinMPNN.

Research Assistant — Virginia Tech, Dept. of Computer Science Aug 2023 – Apr 2024

- Conducted metagenomic analysis of wastewater treatment plants for ARGs/AMPs using Diamond BLAST, Minimap2, MEGAHIT, MetaSPAdes, Kraken2 and related tools.
- Built PathoVF, a pathogen/virulence-factor predictor using multi-modal DNA encodings and protein LLMs (ProtBERT, ESM-1b).

Data Scientist — Cathay Financial Holdings, Data Science R&D Lab Dec 2022 – May 2023

- Improved ICU sepsis early-warning and drug recommendations via Feature Tokenizer Transformer (FT-Transformer) on EHR data; achieving accuracy 0.915.
- Contributed to FinTech AI projects: signature recognition, synthetic banking data (Generative AI), and a federated-learning financial AI agent; deployed at scale on AWS EC2/SageMaker/S3.
- Achieved Bronze (Top 9%) in Kaggle Novozymes Enzyme Stability Prediction Challenge (solo).

Research Assistant / Bioinformatics Engineer — Academia Sinica, Institute of Information Science Jun 2019 – Dec 2022

- Developed an AI-driven antimicrobial peptide platform; curated datasets and applied CNN, LSTM, Doc2Vec, and WGAN-gp for prediction and generation.
 - Designed two peptides with in vitro activity against cancer and antibiotic-resistant bacteria (MIC 2–45 µg/mL).
 - Packaged models into AI4AXP web platform (antibacterial, antifungal, anticancer, antiviral, hemolysis).
 - Invited to Healthcare+ Expo Taiwan (2021, 2022); won the 20th National Innovation Award (2023) for 'AI Fleming'.
- Analyzed Taiwan Biobank genomes; developed DL models for disease phenotypes from SNPs for precision medicine.
- Performed GWAS on aquatic species using PLINK, GATK, DeepVariant; transferred patented know-how for aquaculture SNP microarray design.

Research Intern — Academia Sinica, Institute of Information Science Jul 2018 – Jun 2019

- Proposed PC6 physicochemical protein encoding; integrated into AI4AMP deep-learning predictor surpassing prior SOTA.

EDUCATION

University of Florida — PhD Program in Pharmaceutical Sciences (Withdrawn) | May 2024 – Aug 2025 | AI Drug Discovery (AIDD)

National Taiwan University — B.S. in Agronomy | Sep 2015 – Jun 2019 | Specialization: Experimental Design & Biostatistics

SELECTED PUBLICATIONS

1. **Lin, T.-T.**, Yang, L.-Y., Lin, C.-Y., Wang, C.-T., Lai, C.-W., Ko, C.-F., Shih, Y.-H., Chen, S.-H. (2023). Intelligent De Novo Design of Novel Antimicrobial Peptides against Antibiotic-Resistant Bacteria Strains. *International Journal of Molecular Sciences*, 24(7), 6788.
2. **Lin, T.-T.**, Sun, Y.-Y., Cheng, W.-C., Lu, I.-H., Chen, S.-H., Lin, C.-Y. (2022). AI4AVP: An Antiviral Peptides Predictor in Deep Learning Approach with Generative Adversarial Network Data Augmentation. *Bioinformatics Advances*, 2(1), vbac080.
3. **Lin, T.-T.**, Yang, L.-Y., Lu, I.-H., Cheng, W.-C., Hsu, Z.-R., Chen, S.-H., Lin, C.-Y. (2021). AI4AMP: An Antimicrobial Peptide Predictor Using Physicochemical Property-Based Encoding Method and Deep Learning. *mSystems*, 6(3), e00299-21.

Full list: Google Scholar (link above)

PATENTS

Lin, C.-Y., Chen, S.-H., Lu, I.-H., **Lin, T.-T.**, Hsieh, P.-H., Cheng, H.-C. (2020). 'Optimizing the SNP (Single-Nucleotide Polymorphism) microarray probes design and construction of the analytic pipeline for SNP calling and Genotyping based on the Whole Genome Assembly'. 05T-1091014.

LEADERSHIP

Instructor, Cathay General Hospital Data Science Workshop (2023)

Supervised 4 summer interns, Academia Sinica (2019–2022)

Peer reviewer, Briefings in Bioinformatics (2022)

TECHNICAL SKILLS

Programming & AI: Python, R, PyTorch, TensorFlow, Keras, Scikit-learn, Hugging Face, SQL

Cloud & Tools: AWS (EC2, SageMaker, S3), Docker, Git, Conda, Jupyter, Linux, VS Code, MySQL

Bioinformatics & Databases: RDKit, Biopython, PyMOL, AlphaFold, PLINK, GATK, BWA-MEM, DeepVariant, SAM/BAM/BCFtools, Kraken2, Diamond BLAST, MEGAHIT, CD-HIT, Minimap2, Fastp, RCSB PDB, PDBbind, UniProt, NCBI