

# Hsuan-Chun Lin, Ph.D.

(216) 712-2555

hsuanchunlin@outlook.com

Github: hsuanchunlin

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- Ph.D. in biochemistry with 3 years postdoc experience on RNA HPLC, LC-MS, mass spectrometry method development and RNA/protein purification.
  - 7 high-impact publications and 10 conference presentations of research results.
  - Optimized the accuracy and efficiency of RNA kinetic isotope effect measurements for drug discovery 10-fold by introducing HPLC, LC-MS, mass spectrometry, FRET, stopped-flow, CD spectroscopy, and micro-plate assay.
  - Accelerated NGS and gene therapy data analysis and visualization pipeline 10-fold faster by using Python, pandas, matplotlib, R, C++, scikit-learn, statistical modeling, data visualization, and machine learning.
  - Developed novel next-generation sequencing (NGS) methods to increase over 4,000-time efficiency in research of RNA/DNA-protein interaction.
  - 7 cross-functional biochemical projects, resulting in 4 scientific collaborations with \$2,540,000 funding.

## SKILLS

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<b>Experienced with</b>	<b>Design and produce plasmid DNA, in vitro transcription, RNA/Protein Purification, nucleic acid analysis, FPLC, HPLC, Mass Spectroscopy, LC-MS, Origin, Biochemistry, Molecular Biology, RNA, Protein Purification, Next-generation sequencing (NGS) methods development, RNA-Seq</b>
<b>Programming Languages</b>	Python, R, Perl, Matlab, SQL, C++, L <sup>A</sup> T <sub>E</sub> X, Markdown
<b>Miscellaneous</b>	SQL, git

## EXPERIENCE

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### Postdoctoral Associate

**Feb 2017 — Dec 2019**

*Department of Chemistry, University of Florida*

*Gainesville FL, USA*

- Managed 4 projects, published 1 article in Journal of the American Chemical Society (in Press 2023), and presented in 2018 national ACS meeting.
- Optimized the accuracy and efficiency of RNA kinetic isotope effect measurements for drug discovery 10-fold by introducing HPLC, LC-MS, mass spectrometry, FRET, stopped-flow, CD spectroscopy, and micro-plate assay.
- Accelerated NGS data analysis pipeline 10-fold faster by using Unix/Linux shell commands, Python, R, C++, Pandas, scikit-learn, MATLAB, statistical modeling, data visualization, and machine learning algorithms.

### Graduate Research Assistant

**Aug 2011 — Jan 2017**

*Case Western Reserve University,*

*Cleveland OH, USA*

- Led 3 projects, presented in 7 national/regional conferences and published 5 papers on top peer reviewed journals.
- Performed large scale RNA synthesis from plasmid design, in vitro transcription to RNA isolation.
- Developed and implemented High Throughput Kinetics and Equilibrium binding assays (HTS-KIN/EQ) by employing Illumina next generation sequencing to increase the pace of RNA/DNA -protein research more than 4000 times.
- Applied Machine learning algorithms (e.g. , k-mean, random forest, neural network, novel linear regression models, PCA, and t-SNE) to predict and visualize the rules of biomolecule interactions and accelerate the data driven experimental design 30-fold faster than current methods.

### Research Assistant

**Jun 2009 — July 2011**

*Kaohsiung Medical University,*

*Kaohsiung Taiwan*

- Developed and optimized BMP-2 gene therapy for osteonecrosis by applying micro-CT, immunohistochemistry, Western blot, ELISA, and real-time PCR.

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## HANDS-ON EXPERIENCE

Jan 2020 — present  
Orlando FL, USA

- Build CycleGAN voice converter and miRNA generator from scratch by Tensorflow 2.0 and Keras.
- Apply Natural language processing, Embedding, LSTM, and Transformer models to generate texts, categorize articles, and visualize the rules of RNA-Protein interactions.

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## EDUCATION

<b>Ph.D. in Biochemistry</b> , Case Western Reserve University, Cleveland OH, USA	<b>2011 — 2017</b>
<b>M.S. in Biochemistry and Molecular Biology</b> , National Cheng Kung University, Tainan Taiwan	<b>2005 — 2007</b>
<b>B.S. in Chemistry</b> , National Taiwan University, Taipei Taiwan	<b>2001 — 2005</b>

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## PUBLICATIONS

1. Benjamin Weissman, Şölen Ekesan, Hsuan-Chun Lin, Shahbaz Gardezi, Nansheng Li, Timothy J. Giese, Erika McCarthy, Michael E Harris, Darrin M York, and Joseph A Piccirilli, A dissociative transition state in Hepatitis Delta Virus ribozyme catalysis. **J. Am. Chem. Soc.** 2023.
2. Jain, N.\*; Lin, H. C.\*; Morgan, C. E.; Harris, M. E.; Tolbert, B. S., Rules of RNA specificity of hnRNP A1 revealed by global and quantitative analysis of its affinity distribution. **Proc. Natl. Acad. Sci. U.S.A** 2017.  
N.J. and H.-C.L. contributed equally to this work.
3. Lin, H. C.; Zhao, J.; Niland, C. N.; Tran, B.; Jankowsky, E.; Harris, M. E., Analysis of the RNA Binding Specificity Landscape of C5 Protein Reveals Structure and Sequence Preferences that Direct RNase P Specificity. **Cell Chem. Biol** 2016, 23 (10), 1271-1281.
4. Lin, H. C., Yandek, L.E., Gjermeni, I. & Harris, M.E. Determination of relative rate constants for in vitro RNA processing reactions by internal competition. **Anal. Biochem.** 467, 54-61 (2014).
5. Niland, C. N.; Zhao, J.; Lin, H. C.; Anderson, D. R.; Jankowsky, E.; Harris, M. E., Determination of the Specificity Landscape for Ribonuclease P Processing of Precursor tRNA 5' Leader Sequences. **ACS Chem. Biol** 2016, 11 (8), 2285-92.
6. Yandek, L.E., Lin, H. C. & Harris, M.E. Alternative substrate kinetics of Escherichia coli ribonuclease P: determination of relative rate constants by internal competition. **J. Biol. Chem** 288, 8342-8354 (2013).
7. Chang, P.C., Wu, H.L., Lin, H. C., Wang, K.C. & Shi, G.Y. Human plasminogen kringle 1-5 reduces atherosclerosis and neointima formation in mice by suppressing the inflammatory signaling pathway. **J Thromb Haemost** 8, 194-201 (2010).

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## CONFERENCE TALKS

1. Hsuan-Chun Lin, Benjamin Weissman, Syed Shahbaz Gardezi, Vernon Anderson, Darrin York, Joseph Piccirilli, Michael Harris 2018 ACS National meeting New Orleans, March 22-26  
*Kinetic isotope effects on catalysis by the HDV ribozyme-precise determination of isotope ratios using electrospray ionization time-of-flight mass spectrometry*
2. Hsuan-Chun Lin, 2014 Rustbelt RNA meeting Pittsburgh, October 17-18  
*Next-generation tools for RNA enzymology: Determination of rate and equilibrium constants for large populations of RNA substrate variants using high throughput sequencing.*

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## PROFESSIONAL REFERENCES

**Tony Pastore** - Postdoctoral Associate at University of Texas Medical Branch at Galveston

**Contact:** [ajpastor@utmb.edu](mailto:ajpastor@utmb.edu) - (407) 536-3907

**Raul Jobava** - Postdoctoral Associate at Yale University

**Contact:** [raul.jobava@yale.edu](mailto:raul.jobava@yale.edu) - (216) 278-8250

**Ching-Yuan Chang** - Data Analyst at University of Florida

**Contact:** [c.chang@ufl.edu](mailto:c.chang@ufl.edu) - (352) 278-2664