Yi-Hsuan Lin, PhD

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HIGHLIGHTS

- **10+ years** of research experience in **theoretical biophysics**, **computational biology**, and **bioinformatics**
- **10+ years** of coding experience in **C/C++** and **Python** for scientific computing
- **20** scientific papers in peer-reviewed journals cumulatively cited **over 2000** times

EDUCATION

Ph.D., Physics, The Ohio State University, Ohio, USA 2015
B.Sc., Physics, University of Illinois at Urbana-Champaign, Illinois, USA (GPA 3.74, High Distinction) 2009

EXPERIENCE

HTuO Biosciences, Vancouver, BC, Canada

Research & Development Lead Nov 2022 – present
Molecular Modelling Lead Jan 2021 – Nov 2022

- Establish the physics principles of a proprietary molecular dynamics force field for pharmaceutical applications
- Develop a molecular mechanism platform based on the proprietary force field
- Design and implement free energy simulation methods for protein-ligand binding systems
- Incorporate machine learning to parametrize force fields and optimize their simulation performance
- Implement mathematical physics to validate stability of various simulation methods

Sustainability.Exchange, Toronto, ON, Canada

Data Scientist Jun 2020 – Oct 2020

- Applied supervised machine learning algorithms and Bayesian statistics to build models for time series forecasting of environmental, social and corporate governance (ESG) financial data.

University of Toronto & Hospital for Sick Children, Toronto, ON, Canada

Postdoctoral Fellow Jul 2015 – Jul 2021

- Developing theoretical and computational methods for investigating biological liquid-liquid phase separation
- Collaborating with experimentalists and computational biologists to test the above-mentioned physics theory
- Published peer-reviewed papers and mentored junior scientists
- Project: *Theories for sequence-dependent phase behaviors of biomolecular condensates*

SKILLS

- **Programming:** C/C++, Python, Cython, Matlab/Octave, Mathematica, Julia, SQL
- **Tools:** Numpy, Scipy, Pandas/Polars, Matplotlib, Scikit-Learn, PyTorch, PyMC, SQLite, MPI, Git
- **Math/Stat:** Numerical Analysis, Bayesian Statistics, Linear Algebra, Stochastic Calculus, Differential Equation
- **Modelings:** Theoretical Physics, Molecular Biophysics, Bioinformatics, Monte Carlo Simulation, Molecular Dynamics Simulation, Machine Learning, Deep Learning, Data Visualization

HONORS AND AWARDS

Postdoctoral Award, Intrinsically Disordered Protein Subgroup, Biophysical Society (USA) 2019
Connell Award for Postdoctoral Fellow, Department of Biochemistry, University of Toronto 2018
Scholarship for Study Abroad, Taiwan Ministry of Education 2007–2013
Gold Medal, The 36th International Physics Olympiad 2005

PUBLICATIONS

20. Fayet A, Ayoub A, Fejes A, Janežič M, **Lin Y-H**, Moitessier A, Moitessier N, Neal M, Pottel J, Rostaing O, Weiser B, Zoldan J, and Burai-Patrascu M (2025) The Sixth CACHE Challenge – A Comprehensive Drug Discovery Workflow to Discover Potential Inhibitors of the Triple Tudor Domain of SETDB1. *ChemRxiv*, DOI:10.26434/chemrxiv-2025-jrtx9
19. **Lin Y-H**, Kim TH, Das S, Pal T, Wessén J, Rangadurai AK, Kay LE, Forman-Kay JD, and Chan HS (2024) Electrostatics of salt-dependent reentrant Phase behaviors highlights diverse roles of ATP in biomolecular condensates. *eLife* **13**:RP100284
18. **Lin Y-H**, Wessén J, Pal T, Das S, and Chan HS (2023) Numerical techniques for applications of analytical theories to sequence-dependent phase separations of intrinsically disordered proteins. In *Phase-Separated Biomolecular Condensates: Methods and Protocols* **2563** 51-94
17. Gaither J*, **Lin Y-H***, and Bundschuh R (2022) RBPBind: quantitative prediction of protein-RNA interactions. *J Mol Biol* **434** 167515 (*equal contribution)
16. **Lin Y-H**, Wu H, Jia B, Zhang M, and Chan HS (2022) Assembly of model postsynaptic densities involves interactions auxiliary to stoichiometric binding. *Biophys J* **121** 151–171
15. Wessén J, Pal T, Das S, **Lin Y-H**, and Chan HS (2021) A simple explicit-solvent model of polyampholyte phase behaviors and its ramifications for dielectric effects in biomolecular condensates. *J Phys Chem B* **125** 4337–4358
14. Das S, **Lin Y-H**, Vernon RM, Forman-Kay JD, and Chan HS (2020) Comparative roles of charge, π, and hydrophobic interactions in sequence-dependent phase separation of intrinsically disordered proteins. *Proc Natl Acad Sci USA* **117** 28795–28805
13. Amin AN*, **Lin Y-H***, Das S, and Chan HS (2020) Analytical theory for sequence-specific binary fuzzy complexes of charged intrinsically disordered proteins. *J Phys Chem B* **124** 6709–6720 (*equal contribution)
12. **Lin Y-H**, Brady JP, Chan HS, and Ghosh K (2020) A unified analytical theory of heteropolymers for sequence-specific phase behaviors of polyelectrolytes and polyampholytes. *J Chem Phys* **152** 045102
11. Cinar H, Oliva R, **Lin Y-H**, Chen X, Zhang M, Chan HS, and Winter RHA (2020) Pressure sensitivity of SynGAP/PSD-95 condensates as a model for postsynaptic densities and its biophysical and neurological ramifications. *Chem Eur J* **26** 11024–11031
10. Das S, Amin AN, **Lin Y-H**, and Chan HS (2018) Coarse-grained residue-based models of disordered protein condensates: utility and limitations of simple charge pattern parameters. *Phys Chem Chem Phys* **20** 28558–28574
9. **Lin Y-H**, Forman-Kay JD, and Chan HS (2018) Theories for sequence-dependent phase behaviors of biomolecular condensates. *Biochemistry* **57** 2499–2508
8. Das S, Eisen A, **Lin Y-H**, and Chan HS (2018) A lattice model of charge-pattern-dependent polyampholyte phase separation. *J Phys Chem B* **122** 5418–5431
7. **Lin Y-H**, Brady JP, Forman-Kay JD, and Chan HS (2017) Charge pattern matching as a "fuzzy" mode of molecular recognition for the functional phase separations of intrinsically disordered proteins. *New J Phys* **19** 115003
6. Brady JP, Farber PJ, Sekhar A, **Lin Y-H**, Huang R, Bah A, Nott TJ, Chan HS, Baldwin AJ, Forman-Kay JD, and Kay LE (2017) Structural and hydrodynamic properties of an intrinsically disordered region of a germ-cell specific protein upon phase separation. *Proc Natl Acad Sci USA* **114** E8194–E8203
5. **Lin Y-H** and Chan HS (2017) Phase separation and single-chain compactness of charged disordered proteins are strongly correlated. *Biophys J* **112** 2043–2046
4. **Lin Y-H**, Song J,Forman-Kay JD, and Chan HS (2017) Random-phase-approximation theory for sequence-dependent, biologically functional liquid-liquid phase separation of intrinsically disordered proteins. *J Mol Liq* **228** 176–193
3. **Lin Y-H**, Forman-Kay JD, and Chan HS (2016) Sequence-specific polyampholyte phase separation in membraneless organelles. *Phys Rev Lett* **117** 178101
2. **Lin Y-H** and Bundschuh R (2015) RNA structure generates natural cooperativity between single-stranded RNA binding proteins targeting 5' and 3'UTRs. *Nucleic Acids Res* **43** 1160–1169
1. **Lin Y-H** and Bundschuh R (2013) Interplay between single-stranded binding proteins on RNA secondary structure. *Phys Rev E* **88** 052707