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## PEER-REVIEWED PUBLICATIONS

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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) RBPPBind: 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,  $\pi$ , 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

## WORKING PAPERS

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- 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