



¹Mathematics, ³Biochemistry & Molecular Biology, and ⁴Electrical & Computer Engineering, Michigan State University

²Department of Pharmaceutical Sciences, University of Maryland

Drug discovery is critical to modern healthcare but is hindered by traditional methods like molecular docking, free energy perturbation, and empirical modeling, which are time-consuming, costly, and often limited in scope. Deep learning has emerged as a transformative tool, enabling accurate predictions of protein structures and complex patterns while driving a shift toward data-driven approaches. Transformer-based models like ChatGPT demonstrate the promise of self-supervised learning, addressing the scarcity of labeled data in drug discovery. However, challenges remain in adapting these models to capture stereochemical intricacies in protein-ligand interactions. Addressing these limitations could revolutionize drug discovery, making it faster, more accurate, and cost-effective.

1. [Chen, Dong](#), et al. "Multiscale topology-enabled structure-to-sequence transformer for protein–ligand interaction predictions." *Nature Machine Intelligence* 6.7 (2024): 799-810.
2. [Chen, Dong](#), et al. "Persistent hyperdigraph homology and persistent hyperdigraph Laplacians." *Foundations of Data Science* 5.4 (2023): 558.
3. [Chen, Dong](#), et al. "Drug Resistance Predictions Based on a Directed Flag Transformer." *Advanced Science* (2025).