YUMENG ZHANG

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This is Yumeng, currently a graduate student in UMass Amherst Chemistry Department. I am studying how to use MD simulations to study the biological systems. I also worked on the methodologies that can help improve the efficiency and accuracy of MD simulations.

EDUCATION

PhD   (In Progress)   Sep 2019 -
University of Massachusetts, Amherst
Chemistry Department
[Chen Lab](#)

BS   Wuhan University, China   May 2019
Major: Chemistry

HONORS AND AWARDS

Freshman Scholarship of Wuhan University   2015

2nd Class Freshman Scholarship of Wuhan University   2016

RESEARCH INTERESTS

Studying the biological systems via MD simulations. We try to use either coarse-grained model or atomistic samplings to study the dynamics between proteins. Integrating with the experimental approaches, we want to characterize the mechanism of several significant bio-systems:
- SPIN&MPO
- CypD&p53-NTD
- KCNQ
- Proteases in nanopore

Methodology. We want to develop new methods to achieve higher efficiency in samplings with accuracy, like coarse-grained model and enhanced sampling method.
- HyRes II force field
- REST3

TEACHING EXPERIENCE

CHEM111 TA in UMass Amherst Chemistry department.   2019-2020

PUBLICATIONS

1. X. Gong#, Y. Zhang# and J. Chen, "Advanced Sampling Methods for Multiscale Simulation of Disordered Proteins and Dynamic Interactions" *Biomolecules*, 11, 1416 (2021) (Invited Review). MDPI

2. J. Zhao, X. Liu, A. Blayney, Y. Zhang, L. Gandy, F. Zhang, R. J. Linhardt, J. Chen, C. Baines, S. N. Loh and C. Wang, "Intrinsically disordered N-terminal domain (NTD) of p53 interacts with mitochondrial PTP regulator Cyclophilin D" *J. Mol. Biol.* 434, 167552 (2022). JMB

CO-WORKERS

- Chen Lab
- Wang Lab
- Geisbrecht Lab

SKILLS

Programming: Python

OTHER

Hobbies: Games.
Cat-oholic.