

# HU Zixin

School Address: 60 Nanyang Drive, School of Biological Sciences, Nanyang Technological University, Singapore, 637551

Tel: (+65) 83722728; (+86) 15979669089

Personal website: <https://zixinhu-apple-manzana.github.io>

Email: [zixin003@e.ntu.edu.sg](mailto:zixin003@e.ntu.edu.sg); Alternative Email: [huzx16@fudan.edu.cn](mailto:huzx16@fudan.edu.cn)

## EDUCATION

2020-2025: Ph.D., School of Biological Sciences, Nanyang Technological University, Singapore (cGPA: 4.88/5.0)

2016-2020: Bachelor of Science in Biological Science, School of Life Sciences, Fudan University, Shanghai, China

## AWARDS

2020-2024: Tier 3 Project Scholarship

2019-2020: First Prize of the Scholarship for Outstanding Students

2017-2018: Second Prize of Fosunpharma Scholarship

2017-2018: Professional Scholarship for undergraduate students

2016-2017: Second Prize of the Scholarship for Outstanding Students

## INTERESTS

**Research:** biomolecular modelling; molecular dynamics (MD) simulations; coarse-grained (CG) model; multiscale model; intrinsically disordered proteins (IDPs); liquid-liquid phase separation (LLPS); biomolecular assembly

**Personal:** reading; pop and folk music; watching videos of toucan, capybara, koala, and pika; waiting for Murakami Haruki to be awarded the Nobel Prize every October

## PERSONALITY

Independent; open-minded; resilient; systematic thinker; biology & math lover

## SKILLS

**Software:** LAMMPS, GROMACS, RoseTTA, PyMOL, VMD, Inkscape, Blender

**Programming Languages:** C++, Python, MATLAB, JAVA, Linux command

## RESEARCH EXPERIENCES

Ph.D. student      *Supervisors: Prof. Dr. Lanyuan Lu & Prof. Dr. Lars Nordenskiöld*

**Project 1:** (*independent, manuscript in preparation*)      *Time: 2024-now*

### **A Systematic Investigation on the LLPS propensity of IDPs**

We designed a systematic procedure to examine the consistency of the LLPS propensity of IDPs from simulation and experiment in a small database. We will further investigate the secret of LLPS propensity encoded in sequence.

**Project 2:** (*independent, published*)      *Time: 2021-2024*

### **Refined Bonded Terms in CG Model for IDPs Improve Backbone Conformations**

We implemented bonded potentials for IDPs into the coarse-grained model, the Mpipi model. Results show improvement in the secondary structure propensity (SSP) of IDPs and capture the transient secondary structure without compromising the performance on the radius of gyration ( $R_g$ ) and LLPS propensity.

**Project 3:** (*collaborative, published*)

*Time: 2020-2022*

**The Intrinsically Disordered Region of Coronins Fine Tunes Oligomerization and Actin Polymerization**

Coronin is a class of multi-domain protein (MDP). Experiments showed that IDR tunes the oligomerization in yeast coronin but not in mice coronin. We used the hybrid CG model (Gō-like & KH model) to investigate this effect.

research assistant

*Supervisor: Prof. Dr. Yuguang Mu*

**Project 4:** (*independent, finished*)

*Time: July-August 2019*

**Molecular Dynamic (MD) Simulation Study on Bacterial Transglycosylase**

Bacterial transglycosylase is an enzyme involved in the synthesis of glycan. In drug discovery, it is a hot spot for the design of antibiotics. We used MD simulation and docking to perform virtual screening on the drug database to get insights into potential hits. We ended up with several potential lead compounds.

undergraduate student

*Supervisor: Prof. Dr. Motoyuki Hattori*

**Project 5:** (*final year project*)

*Time: 2019-2020*

**Study on the Structure of the Soluble Domains of MRS2 in Plants**

MRS2 is a family of magnesium ion transporters. Mutations on MRS2 are reported to induce morphological changes in *Arabidopsis thaliana* and *Oryza sativa*. We aimed to solve the structure of the soluble domains of MRS2 to get a deeper understanding of it. Time constraints did not enable completion and structure determination.

**Project 6:** (*summer project*)

*Time: July-August 2018*

**Study on the Structure of CALHM1**

Calcium Homeostasis Modulator 1 (CALHM1) is a voltage-gated ion channel related to several neurological diseases and functions of type II bud cells. We aimed to solve the structure of full-length CALHM1 with cryo-EM for mechanism study. We purified CALHM1 from human cell membranes successfully. Structure determination was not feasible due to time constraints.

**CONFERENCES**

14-17 May 2024: Cellular mechanisms driven by phase separation (EMBL, Germany)

1-3 Mar 2023: Phase Separation Regulated Life, In and Outside of Cells (Singapore)

**PUBLICATIONS**

1. **Zixin Hu**, Tiedong Sun, Wenwen Chen, Lars Nordenskiöld, and Lanyuan Lu (2024) Refined Bonded Terms in Coarse-Grained Models for Intrinsically Disordered Proteins Improve Backbone Conformations *The Journal of Physical Chemistry B* (<https://pubs.acs.org/doi/10.1021/acs.jpcc.4c02823>)
2. Xiao Han<sup>1</sup>, **Zixin Hu**<sup>1</sup>, Wahyu Surya, Qianqian Ma, Feng Zhou, Lars Nordenskiöld, Jaume Torres, Lanyuan Lu, Yansong Miao\* (2023) The Intrinsically Disordered Region of Coronins Fine Tunes Oligomerization and Actin Polymerization. *Cell Report* (<https://doi.org/10.1016/j.celrep.2023.112594>)