

# Hao Tian

3215 Daniel Ave, Dallas, TX, 75205, USA  
haot@smu.edu • +1 (682) 347-6392 • <https://htian1997.github.io>

## EDUCATION

**Southern Methodist University**, Dallas, Texas, USA

Aug 2019 – May 2023 (expected)

- Ph.D. in Theoretical and Computational Chemistry
- Adviser: Prof. Peng Tao
- Topic: Understanding protein allostery through molecular dynamics and artificial intelligence
- GPA: 3.97 / 4.0

**Georgia Tech**, Atlanta, Georgia, USA

Aug 2020 – May 2022 (expected)

- M.S. in Computer Science
- Specialization: Computing Systems
- GPA: 4.0 / 4.0

**Beijing University of Chemical Technology**, Beijing, China

Aug 2015 – Jun 2019

- B.Eng. in Chemical Engineering
- GPA: 3.49 / 4.33

## PUBLICATIONS

- [5] Hao Tian, Xi Jiang and Peng Tao. PASSer: Prediction of Allosteric Sites Server. *Machine Learning: Science and Technology*, 2021.
- [4] Zilin Song, Hongyu Zhou, Hao Tian, Xinlei Wang and Peng Tao. Unraveling the energetic significance of chemical events in enzyme catalysis via machine-learning based regression approach. *Communications Chemistry*, 2020, 3, 134.
- [3] Hao Tian, Francesco Trozzi, Brian Zoltowski and Peng Tao. Deciphering the Allosteric Process of Phaeodactylum tricornutum Aureochrome 1a LOV Domain. *The Journal of Physical Chemistry B*, 2020, 124, 41, 8960–8972.
- [2] Hao Tian and Peng Tao. iVis Dimensionality Reduction Framework for Biomacromolecular Simulations. *Journal of Chemical Information and Modeling*, 2020, 60, 10, 4569-4581.
- [1] Hao Tian and Peng Tao. Deciphering the Protein Motion of S1 Subunit in SARS-CoV-2 Spike Glycoprotein Through Integrated Computational Methods. *Journal of Biomolecular Structure and Dynamics*, 2020.

## CODING PROJECTS

getarticle, an open source Github repository, star: 22, downloads: 6k

- A package based on SciHub and Google Scholar that can download articles given DOI, website address or keywords;
- Imported in Python or used as command line.

PASSer: Protein Allosteric Sites Server, <https://passer.smu.edu>

- A web server to predict allosteric sites given protein PDB ID or PDB file;
- Implemented using Django framework and JSmol;
- Learn both physical properties through XGBoost model and pocket topology through graph convolutional neural network.

## AWARDS & SCHOLARSHIPS

**Outstanding Teaching Assistant**

May 2020

Southern Methodist University

**Meritorious Winner of Mathematical Contest in Modeling**

Mar 2018

Beijing University of Chemical Technology

**Outstanding Undergraduate**

Sep 2015

Beijing University of Chemical Technology

## INVITED TALKS

**Machine Learning Framework for Deciphering the Allosteric Process of Circadian Clock Protein**

Dec 2020

Department of Chemistry and Biochemistry, The University of Oklahoma

## **SKILLS**

Programming languages: Python, Java, Bash, JavaScript, PHP, SQL

Skill stacks: HTML, CSS, jQuery, Git

Machine learning packages: Scikit-learn, Keras, PyTorch

*[Last updated on 2021-03-02]*