

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 – Now
	<ul style="list-style-type: none">Ph.D. in Theoretical and Computational Chemistry<ul style="list-style-type: none">Adviser: Prof. Peng TaoCumulative GPA: 3.95 / 4.0	
	Georgia Tech , Atlanta, Georgia, USA	Aug 2020 – Now
	<ul style="list-style-type: none">M.S. in Computer Science<ul style="list-style-type: none">Specialization: Computing Systems	
	Beijing University of Chemical Technology , Beijing, China	Aug 2015 – Jun 2019
	<ul style="list-style-type: none">B.Eng. in Chemical Engineering<ul style="list-style-type: none">Cumulative GPA: 3.49 / 4.33	
RESEARCH EXPERIENCE	Center for Research Computing, Center for Drug Discovery, Design, and Delivery (CD4) Department of Chemistry, Southern Methodist University Graduate Research Assistant Focus: <ul style="list-style-type: none">Molecular dynamics of biomacromoleculesDecipher protein allostery through machine learning based methodsMachine learning and database based allostery development	Aug 2019 – Now
PUBLICATIONS	<ul style="list-style-type: none">[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. <i>Communications Chemistry</i>, 2020, 3, 134.[3] Hao Tian, Francesco Trozzi, Brian Zoltowski and Peng Tao. Deciphering the Allosteric Process of Phaeodactylum tricornutum Aureochrome 1a LOV Domain. <i>The Journal of Physical Chemistry B</i>, 2020, 124, 41, 8960–8972.[2] Hao Tian and Peng Tao. iVis Dimensionality Reduction Framework for Biomacromolecular Simulations. <i>Journal of Chemical Information and Modeling</i>, 2020.[1] Hao Tian and Peng Tao. Deciphering the Protein Motion of S1 Subunit in SARS-CoV-2 Spike Glycoprotein Through Integrated Computational Methods. <i>Journal of Biomolecular Structure and Dynamics</i>, 2020.	
PROJECTS	getarticle, an open source Github repository, star: 21, downloads: 4k <ul style="list-style-type: none">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, passer.smu.edu <ul style="list-style-type: none">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 network.	
AWARDS & SCHOLARSHIPS	Outstanding Teaching Assistant Southern Methodist University, Dallas, TX, USA, 2020	May 2020
	Meritorious Winner of Mathematical Contest in Modeling Beijing University of Chemical Technology, Beijing, China	Mar 2018
	Outstanding Undergraduate Beijing University of Chemical Technology, Beijing, China	Sep 2015

**LEADERSHIP &
SERVICES**

Diversify Protein Science

Member

Living Journal of Computational Molecular Sciences

Student reviewer

SKILLS

Scripting languages: Python, Java, Bash

Front end: HTML, CSS, JavaScript, jQuery

Back end: PHP

Machine learning packages: Scikit-learn, Keras, PyTorch

Source control management: Git

Others: \LaTeX

[Last updated on 2020-10-28]