Weizhe Ding

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Educational Background

B.S., Biotechnology, School of Life Science, Liaoning University, China

Sept. 2018 - Jul. 2022

GPA: 3.32/4

Honors: Won the Individual Scholarship of Liaoning University in September 2020

Core Subjects: Advanced Mathematics, Biostatistics, Bioinformatics, Biochemistry

Scientific Research Experiences

State Key Laboratory of Molecular Reaction Dynamics

Dalian Institute of Chemical Physics, Chinese Academy of Sciences

Dec. 2020 - Mar. 2021

With Professor Guohui Li Dalian

- Investigated the application of machine learning and deep learning in kinases for the past ten years, and classified
 papers according to kinase inhibitors, phosphorylation sites, protein-ligand affinity, molecular dynamics simulation,
 and bioinformatics. An English review paper is expected to be published.
- Summarized the protein three-dimensional structure database information, and used Python and server (Linux) to download all pdb files automatically.

Key Laboratory of Nutrition, Metabolism and Food Safety

Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences

Aug. 2020 - Aug. 2021

With Professor Xu Lin Shanghai

- By joining the kechuang project which was funded by Chinese Academy of Sciences with CNY 40,000,
 meta-analysis research between plant-based dietary patterns and type 2 diabetes has been completed.
- By using Pubmed, Web of Science, and Cochrane to retrieve relevant literature for the past ten years, several
 papers have been concluded which determined by title, summary, and content. Stata and R have been used to
 analyze the data further and a paper has been expected to be published.

Key Laboratory of Growth Regulation and Translational Research of Zhejiang Province

Westlake University Jul. 2020 - Aug. 2020

With Professor Ju-Sheng Zheng

Hangzhou

Participated in the research between gut microflora and nutritional distribution of the persons who received
 treatment of drug addiction, and mainly took responsibilities for psychological and dietary questionnaire design.

- Assisted in the construction of a type 2 diabetes candidate inhibitors database, and mainly used Python to automatically download the mol2 files of target molecules.
- Participated in the research of CMPF metabolic mechanism, and took responsibilities for collating data of LC-MS.

Pathogen Discovery and Big Data Center

Institut Pasteur of Shanghai, Chinese Academy of Sciences

Apr. 2020 - Jul. 2020

With Associate Professor Yihong Hu

Shanghai

- Finished a review of B cell immortalization as co-authors and expected to be published sooner.
- Independently completed a meta-analysis on the drug resistance of AIDS in Henan Province. After collecting and
 analyzing relevant Chinese papers in the past ten years with R, the relevance between drug resistance and the
 time of drug-taking has been confirmed and the paper is expected to be published.

Project Experiences

School of Life Sciences, Liaoning University

Sept. 2020 - Present

With Vice Dean, Professor Xiangyu Cao

Shenyang

- Completed the subject between natural active product and α-amylase. After a virtual screening of Dalbergia odorifera, eriodictyol has been determined as the best natural active component and molecular docking, molecular dynamics simulation and spectroscopy were used for further analysis. This paper has already under review and is expected to be published in *International Journal of Biological Macromolecule*.
- Participated in the research on the mechanism of Costunolide-Induced MCF-7 Cells Apoptosis by finished molecular docking and paper's revision. This paper has been published on *Chemistry and Biodiversity*.
- Co-published patents as "Application of Eriocitrin in the preparation of drugs for inhibiting cardiovascular diseases"
 and "Application of Lentinus edodes mycelium polysaccharide in preparation of drugs to inhibit amylase activity".

School of Pharmaceutical Sciences, Liaoning University

Sept. 2020 - Present

With Dean, Professor Hongsheng Liu

Shenyang

- Participate in the Innovation and Entrepreneurship Training Program for College Students and mainly found candidate compounds as herg inhibitors by using virtual screening and molecular dynamic simulation.
- By developing a new network similarity integration algorithm that predicts the interaction between lncRNA and miRNA, a paper has been published in *Journal of Mudanjiang Medical College*.
- Designed a subject on the molecular dynamics fingerprint (MDFP). After calculating the candidate molecular data with molecular dynamics simulation and Rdkit, the best features of MDFP and 2D/3D fingerprints have been determined by machine learning and a paper is expected to be published sooner.

Papers

- Jingjing Zhang¹, Weizhe Ding¹, Zhipeng Tang et al. Eriodictyol as α-amylase inhibitors: virtual screening, molecular docking, molecular dynamic simulation and spectroscopy, *Int J Biol Macromol*. Under Review (¹co-first author)
 IF=5.162
- 2. Weizhe Ding*, Li Zhang*#, Yang Nan, et al. Combining Multi-Dimensional Molecular Fingerprints to Predict hERG Cardiotoxicity of Compounds. bioRxiv (*co-first author, #Corresponding author)
- 3. **Weizhe Ding**, Yang Nan, Shujuan Wu et al. Prediction of potential IncRNA-miRNA interactions through a Network similarity integration method, *Journal of Mudanjiang Medical College*. In Press
- Dan Liu, Meng Zeng, Jing-Wen Pi, Mei-Jia Liu, Wei-Zhe Ding, et al. Exploring the Potential Mechanism of Costunolide-Induced MCF-7 Cells Apoptosis by Multi-Spectroscopy, Molecular Docking and Cell Experiments, Chem. Biodiversity. 18 (2021) e2001069 IF=2.039

Activities

1. Ernst & Young (China)	Campus Ambassador		Apr. 2020 - Apr. 2021
2. KPMG (China)	Campus Ambassador		Dec. 2019 - Mar. 2021
3. Post-Graduation Charity Foundation (NPO)		Co-founder	Jan. 2019 - Mar. 2019
4. 2018 Innovation and Entrepreneurship Training Program		Second Prize	Sept. 2018 - Jul. 2020
Won the Second Prize at a provincial level			

Language Proficiency and Skills

Language Proficiency:

CET-6: 571 / 710

IELTS: 6.0 / 9.0

Skills: Gromacs, Shell, Python, R, Linux, Stata, Microsoft Office