DAVID ZHAO

EDUCATION

University of Maryland, College Park   **Fall 2019 - Present**
B.Sc. in Biochemistry, Minor in Statistics   Expected Graduation Spring 2023
Cumulative GPA: 3.793 / 4.000

Relevant Coursework

- Biochemistry I, II & III
- Statistical Mechanics and Quantum Chemistry
- Applied Probability and Statistics I & II

- Fundamentals of Object-Oriented Programming
- Linear Algebra
- Calculus I, II & III

AWARDS & HONORS

AMGEN Scholar at the University of Tokyo
- Selected to contribute to a fully funded, independent research project at the University of Tokyo in the summer of 2023 from a pool of highly competitive undergraduate applicants pursuing careers in research.

Honors College, Integrated Life Sciences (ILS)
- The Integrated Life Sciences Program at the University of Maryland is a competitive, science-focused program designed for talented STEM students. ILS citation requirements include a significant 240-hour research requirement and a two-year commitment to accelerated coursework.

President's Freshman Merit Scholarship
- Recipients are identified through an evaluation of admission application materials to the University of Maryland including academic achievement, extracurriculars, awards, honors, and an essay.

RESEARCH EXPERIENCE

Research Intern, Ibex Biosciences   **December 2021 – Present**
- Explore efficacy of alternative eukaryotic transcription factors for induced pluripotent stem cell (iPSC) proliferation to avoid the risk of cancer associated with the Yamanaka factors.
- Analyze competing roles of the NF-κB protein family and the MAP-K pathway in generating pro-inflammatory cytokines, including TNF-α, through RT-PCR to assess synergistic or antagonistic effects between the two.
- Write programs and scripts in Java to analyze polypeptide sequences for amino acid residues and DNA nucleotides involved in site-directed mutagenesis of phosphorylatable proteins and for RT-PCR/qPCR data analysis.
- Transform astrocytes into neural progenitor cells through proprietary transcription factors for the regeneration of functioning neurons for the treatment of neurodegenerative diseases.

Undergraduate Researcher, Sunny Research Group, University of Maryland   **June 2021 – May 2022**
- Investigated role of branched chain amino acids (BCAAs) in oxidative metabolism and its connection to insulin resistance for the management of metabolic diseases such as non-alcoholic fatty liver disease (NAFLD) and type 2 diabetes mellitus.
- Interpreted gas chromatography mass spectrometry (GC-MS) peaks using Agilent MassHunter Quantitative Analysis software to assess abundance of key citric acid cycle intermediates and rates of ketogenesis.
- Quantitated carnitine palmitoyltransferase I (CPT1) mitochondrial membrane protein quantities in long chain fatty acid transport via western blotting and immunofluorescence analysis.
- Presented data for further discussion of findings to fellow researchers and faculty in the Department of Animal and Avian Sciences at the University of Maryland.

PROJECTS

Mission 14 to the International Space Station, National Center for Space Science Education (NCESSE)
- Formulate strategy to analyze replication rates of T4 *E.coli* bacteriophages in a microgravity environment via gene sequencing methods and real time polymerase chain reaction (qPCR).
- Arrange bacteriophage samples to be loaded aboard the ISS with guidance from NASA and the University of Maryland's Institute for Bioscience and Biotechnological Research (IBBR).

GC-MS Data Organization Tool – Java Program
- Developed Java program to analyze thousands of uniformly labeled Carbon-13 mass spectrometer peaks across multiple metabolic pathways, with isotope ratio and concentration calculation functionalities.

RT-PCR Data Processor – Java Program
- Developed Java Program to organize RT-PCR data produced by StepOne™ Real-Time PCR System software.
- Integrated Livak method for computational analysis of qPCR results.

Phosphorylation Site Indexer – Java Program
- Java program designed to index predicted phosphorylation sites in proteins for the identification of protein mutation sites. Can isolate open reading frames from a nucleotide sequence and identify the corresponding codon sequence for its respective amino acid and vice versa.
- Includes basic front-end functionality, allowing users to input a protein of interest and the indexes of interest.

LEADERSHIP & INVOLVEMENT

Student Volunteer, Food Recovery Network   **September 2019 – March 2020**
- Alleviated food insecurity issues and advocated for the accessibility and affordability of nutritious food for impoverished communities.
- Coordinated removal of excess dry foods from north and south campus diners at the University of Maryland at closing hours for food banks in the DC area.
- Refined teamwork and leadership skills with other campus students by communicating end-of-shift objectives, setting reasonable goals for food transported, and holding other volunteers accountable for their contributions.