

ZIYUE CHENG

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GitHub: [Justype](#)

Education

McMaster University	Hamilton, ON, Canada
Ph.D. in Biochemistry and Biomedical Science	<i>Jan. 2025 – Current</i>
New York University	New York, NY, USA
M.S. in Biology, Computational Biology Track, GPA 4.0/4.0	<i>Sep. 2022 – May 2024</i>
Huazhong Agricultural University, HZAU	Wuhan, Hubei, China
B.S. in Veterinary Medicine, GPA 3.5/4.0	<i>Sep. 2017 – Jun. 2022</i>

Research Experience

Hong Han , McMaster University	<i>2024 – Current</i>
<ul style="list-style-type: none">Studying tumor microenvironment with single cell sequencing and spatial transcriptomicsStudying alternative splicing using RNA-seq, scRNA-seq, and long read sequencingDeveloping a pipeline with bash, Python, and R to analyze plate-based scRNA-seq data	
Christine Vogel , New York University	<i>2023 – 2024</i>
<ul style="list-style-type: none">Studied ribosome pattern of start-stop (a regulatory element on 5' untranslated region)Developed a pipeline with R and bash scripts to analyze ribosome footprint data on HPCPerformed statistical analysis within and between datasets	
Qigai He , Huazhong Agricultural University	<i>2021 – 2022</i>
<ul style="list-style-type: none">Studied Epidemiologic investigation on different genotypes of porcine circovirusesUsed TaqMan qPCR to compare the amount of each virus.Used sanger sequencing and phylogenetic tree to determine the variant type.	

Honors & Awards

2023	Biology Master's Research Grant	<i>New York University</i>
2020	Arctic Code Vault Contributor	<i>GitHub</i>
2019	Outstanding Individual in International Exchange	<i>HZAU and Massey University</i>

Skills

Bioinformatics	<ul style="list-style-type: none">RNA-seq, scRNA-seq, ribosome footprinting, whole genome sequencingStatistical analysis with R, Plotting with ggplot2R packages: DESeq2, Seurat, clusterProfilerMachine learning with Python scikit-learn
Biology	<ul style="list-style-type: none">Cell Culture, DNA/RNA extractionPCR, RT-PCR, real-time PCR
Programming	<ul style="list-style-type: none">Python, R/Tidyverse, HTML/JavaScript, SQL, MySQL/MariaDBDeveloping cross-platform and Windows applications with C#

Teaching Experience

Protein Structure and Enzyme Function BIOCHEM2BB3 McMaster University
Undergraduate Course TA *Winter 2025*

- Led tutorial groups and guided student research projects (NMR, cryo-EM, X-ray crystallography).
- Conducted Q&A sessions and graded assignments to support student learning.

Biological Databases & Datamining BIOL-GA 1009 New York University
Graduate Course TA *Spring 2024*

- Taught Database, SQL, and Machine Learning with R and Python.
- Graded homework and answered questions during class and office hours.

Programming for Biologists BIOL-GA 1007 New York University
Graduate Course TA *Fall 2023*

- Taught Basic concepts of Python, regular expression, Pandas, SciPy, and plots.
- Graded homework and introduced new concepts and answered questions during office hours.

Publication

- Justin Rendleman, Solomon Haizel, Shaohuan Wu, Junjie Liu, Xinyi Ge, Huijing Zou, Mahabub Pasha Mohammad, Matthew Pressler, Shuvadeep Maity, **Ziyue Cheng**, Vladislava Hronová, Zhaofeng Gao, Anna Herrmannová, Amy Lei, Kristina Allgoewer, Daniel Sultanov, Will Edward Hinckley, Krzysztof J. Szkop, Ivan Topisirovic, Ola Larsson, Maria Hatzoglou, Leoš Shivaya Valášek, Christine Vogel. *Regulatory start-stop elements in 5' untranslated regions pervasively modulate translation* [Preprint]. bioRxiv 2021.07.26.453809 Update 2023; doi: <https://doi.org/10.1101/2021.07.26.453809>