

# ZIYUE CHENG

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GitHub: [Justype](#)

## Education

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

## Research Experience

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

## 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"><li>RNA-seq, scRNA-seq, ribosome footprinting, whole genome sequencing</li><li>Statistical analysis with R, Plotting with ggplot2</li><li>R packages: DESeq2, Seurat, clusterProfiler</li><li>Machine learning with Python scikit-learn</li></ul>
Biology	<ul style="list-style-type: none"><li>Cell Culture, DNA/RNA extraction</li><li>PCR, RT-PCR, real-time PCR</li></ul>
Programming	<ul style="list-style-type: none"><li>Python, R/Tidyverse, HTML/JavaScript, SQL, MySQL/MariaDB</li><li>Developing cross-platform and Windows applications with C#</li></ul>

## Teaching Experience

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

Taught Basic concepts of Python, regular expression, Pandas, SciPy, and plots.

Graded homework and introduced new concepts and answered questions during class and office hours.

**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 class and office hours.

## Posters / Publication

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- 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>