

Jia Qu

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EDUCATION

- **Biomedical Informatics** The Ohio State University
Biomedical Science Graduate Program Aug 2022 - May 2025
- **Pharmacology** China Pharmaceutical University
Master of Science Sep 2015 - Jun 2018
- **Pharmaceutical Analysis** China Pharmaceutical University
Bachelor of Science Sep 2011 - Jun 2015

WORK EXPERIENCE

- **Bioinformatician in NGS Data Analysis & Neuroscience Research** 2025 - Present
Ilaria Palmisano Lab, Department of Neuroscience The Ohio State University
 - **Bioinformatics & NGS Analysis:** Analyzed and managed large-scale genomic and transcriptomic datasets from human and animal studies, including in-house and publicly available datasets.
 - **Pipeline Development:** Developed and implemented reproducible computational pipelines for data preprocessing, quality control, statistical analysis, and downstream bioinformatics analyses.
 - **Computational Methods:** Applied statistical, machine learning, and bioinformatics methods to characterize biological patterns and extract interpretable features from high-dimensional datasets.
 - **Data Interpretation & Visualization:** Translated computational results into biological insights and prepared publication-quality visualizations and figures for scientific reports, manuscripts and grant submission.
- **Graduate Research Associate for Data Analysis & Computational Biology** 2022 - 2025
Qin Ma Lab, Department of Biomedical Informatics The Ohio State University
 - **Group Membership:** Member of the Center for AI & Bioinformatics in Immuno-Oncology (CATION), formerly the Immuno-Oncology Informatics Group (IOIG), Pelotonia Institute for Immuno-Oncology (PIIO).
 - **Bioinformatics Analysis:** Develop reproducible computational pipelines for omics data analysis and visualization.
 - **Computational Biology:** Apply statistical, machine learning, and integrative multi-omics approaches to investigate biological mechanisms, identify molecular signatures, and generate biologically interpretable insights.
- Translator - Life Sciences and Medical Translation Division, EC Innovations, Inc. 2019 - 2021
- Clinical research evaluation - Department of Clinical Evaluation, Tigermed CRO 2016 - 2019

SKILLS

- **NGS & Multi-omics Analysis:** Bulk RNA-seq, sc/snRNA-seq, Spatial Transcriptomics, ATAC-seq, ChIP-seq, Proteomics, Metabolomics, Multi-omics Integration
- **Bioinformatics & Statistics:** Data Processing and Quality Control, Differential Expression Analysis, Statistical Modeling, Dimensionality Reduction, Clustering, Machine Learning, Data Visualization
- **Programming & Computing:** Python, R, Linux, High-Performance Computing (HPC), Git/GitHub, Jupyter, SAS
- **AI Tools:** Claude Code (proficient), VS Code Copilot, and Large Language Models API calling, agentize personal workflow.
- **Visualization & Communication:** Adobe Illustrator, BioRender, PowerPoint, LaTeX, EndNote
- **Grant Writing & Preparation:** Grant proposal writing, methods section development, and preparation of administrative documents for grant submissions

PUBLICATIONS

- De Vitis E†, **Qu J†**, Carlino A, Collison B, Bellner M, Rincon Benavides M, Danzi MC, Shrestha B, Quach T, Higuera-Castro N, Wang Z, Palmisano I. Proteomic profiling of mouse visceral adipose secretome reveals an enhancement of axonal pro-regenerative factors under high-fat diet feeding. Submitted to *Science Advances* (†Co-first authors).
- Mota BC, Palmisano I, **Qu J**, Carlino A, Kocurova N, Abelleira-Hervas L, Crowley L, Morgan J, Garrido-Perez L, Aleksynas R, Velentza-Almpani E, Pickering C, Mazarakis ND, Sastre M. PGC-1 α gene therapy in aged mice results in improvements in cognition independent of changes in amyloid- β deposition. In preparation for submission to *Nature Aging*.
- Carlino A*, De Vitis E*, Collison B, Bellner M, **Qu J**, Zapata N, Whitehouse J, Gunsch G, Walker-Conway A, Quach T, Townsend K, Palmisano I. Enhanced Peripheral Nerve Regeneration in a Critical Window of Early-Intermediate Obesity. In preparation.
- Muller F, McLachlan E, Costa AC, **Qu J**, Shrestha B, Wang Z, De Virgiliis F, Hutson TH, Zhou L, Kong G,

Chadwick JS. CITED2 is a druggable epigenetic switch coupling neuronal maturation to regenerative decline [J]. EMBO Molecular Medicine. 2026,18(4):1174-1201.

- Taleb A, Ahmad KA, Ihsan AU, **Qu J**, Lin N, Hezam K, Koju N, Hui L, Ding Q. Antioxidant effects and mechanism of silymarin in oxidative stress-induced cardiovascular diseases [J]. Biomedicine & Pharmacotherapy. 2018,102:689-98.
- **Qu J**, Lin N, Zhou J, Ding Q. ROS-induced NLRP3 inflammasome activation and cardiovascular diseases [J]. Pharmacy Today. 2017(12):855-888.

CONFERENCE & SEMINAR PRESENTATIONS

- **High-fat diet feeding enhances axonal pro-regenerative factors within the mouse visceral adipose secretome** (Department of Neuroscience Research Day, 2026)
- **Proteomic profiling of mouse adipose secretome reveals axonal pro-regenerative factors enhanced under high-fat diet** (Chronic Brain Injury Program Research Day, 2026)
- **Proteomics reveals adipose tissue function distinguishing acute and chronic obesity** (Neuroscience Research Institute Annual Retreat, 2025)

RESEARCH PROJECTS

- **Enhanced peripheral nerve regeneration in a critical window of early-intermediate obesity** 2026
Analyzed metabolomics data from mouse and human subcutaneous and visceral adipose tissues to characterize obesity-associated metabolic alterations linked to neuropathy and peripheral nerve regeneration.
- **Cohesin-driven epigenomic regulation of axonal regenerative capacity in DRG neurons** 2026
Analyzed epigenomic profiles in dorsal root ganglion (DRG) using ATAC-seq and transcription factor footprinting to characterize injury-associated chromatin accessibility and regulatory programs underlying axon regeneration; contributed to grant preparation and submission.
- **Proteomic profiling of mouse visceral adipose secretome reveals an enhancement of axonal pro-regenerative factors under high-fat diet feeding** 2026
Integrated mouse visceral adipose secretome and extracellular-vesicle proteomics with mouse and human snRNA-seq to identify HFD-enriched metabolic and senescence-associated factors linked to enhanced peripheral nerve regeneration.
- **Single-cell and spatial profiling of GPCR expression heterogeneity in brain ependymal cells** 2025
Analyzed large-scale Allen Brain Atlas single-cell RNA-seq and MERFISH spatial transcriptomic datasets to characterize GPCR expression, co-expression patterns, and anatomical heterogeneity across multiciliated ependymal cell populations lining the dorsal third and lateral ventricles.
- **CITED2: a druggable epigenetic switch coupling neuronal maturation to regenerative decline** 2025
Integrated RNA-seq, chromatin accessibility (ATAC-seq), and histone acetylation (H3K9ac/H3K27ac) profiles to characterize transcriptional and epigenetic programs associated with neuronal maturation and axon regeneration.
- **Investigating tumor heterogeneity and discover potential insight for CTCL therapy** 2025
Analyzed GeoMx spatial transcriptomic data from chemotherapy-treated cutaneous T-cell lymphoma (CTCL) patients, identifying therapy-associated Th2 differentiation, TP53-regulated metabolic programs, and inflammatory pathways.
- **Enhancing clinical spatial transcriptomics data analysis to explore tumor heterogeneity** 2025
Developed and benchmarked a grid-search optimized RUV-4 batch-correction workflow for GeoMx Whole Transcriptome Atlas data, comparing performance with ComBat-seq, SVA, and limma while preserving biological variation.
- **Loss of chromosome Y and CD8+ T cell exhaustion in cancer** 2024
Integrated large-scale pan-cancer scRNA-seq datasets from atlases to identify LOY versus wild-type CD8+ T cells, followed by Seurat-based annotation and GSVA-based comparison of exhaustion-associated gene programs.
- **Establish a rare cell-related scRNA-seq database for systemic lupus erythematosus patients** 2024
Integrated PBMC scRNA-seq data from 240 systemic lupus erythematosus patients using Scanpy and applied cell-type annotation and graph-transformer-based multi-omics analysis to identify and characterize rare immune cell populations.
- **Integrative analysis for pooled CRISPR functional genetic screens** 2023
Analyzed pooled CRISPR knockout screens using FastQC and MAGeCK for sgRNA read mapping, count quantification, and differential enrichment testing across experimental conditions.
- **Multimodal biomarkers discovery for non-small cell lung cancer immunotherapy** 2023
Integrated multimodal NSCLC immunotherapy data from the LCMC3 study, including gene expression, WES, multiplex immunofluorescence, and immunophenotyping data, and developed an R-based workflow for patient metadata processing and flow-cytometry-based immune-cell annotation.
- **The role of transcription factor STAT1 in the antiviral immune response** 2022
Analyzed IFN-stimulated STAT1 ChIP-seq data using MOSAICS for peak calling, ChIPseeker for genomic annotation, clusterProfiler for pathway enrichment, and STRING for protein-protein interaction analysis.

- **Effects and mechanisms of tBHQ on NLRP3 inflammasome activation induced by AngII** *2016-2018*
Investigated AngII-induced ROS and NLRP3 inflammasome activation in human vascular endothelial cells using MTT, Western blot, ELISA, and RT-qPCR assays.
- **National science and technology major projects** *2013-2018*
In vitro cell and animal models for pharmacology and toxicology experiments. Evaluated candidate compounds in models of arrhythmia, hepatic injury, platelet aggregation, and hypertension.