

QIU, XINRU

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Education

PhD University of California, Riverside (UCR) – Riverside, CA Genetics, Genomics, and Bioinformatics (GGB) Committee: Adam Godzik (chair), Meera Nair, Zhenyu Jia	June 2023
MS University of Southern California (USC) – Los Angeles, CA Pharmaceutical Sciences Advisor: Wei-Chiang Shen	May 2015
BS Jilin University (JLU) – Changchun, China Pharmacy	June 2013

Professional Experience

University of California, Riverside – Riverside, CA Postdoctoral Researcher, Advisor: Adam Godzik Conducting advanced research in computational biology, with focus on AI-driven protein engineering and single-cell foundation models.	July 2023 – Present
<ul style="list-style-type: none"> • Generative AI-Driven Discovery and Protein Engineering for PET Plastic Degradation: Selected as a finalist for INNOVAR Entrepreneurship Program funding. Leveraging RFDiffusion, ProteinMPNN, AlphaFold2, and ESMFold for enzyme modification. Developed automated workflows for computational protein design. • Single-cell Transcriptomics Analysis of Sex-specific Immune Responses: Contributed to grant proposal through experimental design and preliminary data generation. Implemented comprehensive analysis pipeline using Seurat, scVelo, Monocle3, CellRank2, SCENIC and CellChat. Developed integrated R/Python workflows for population dynamics modeling and gene regulatory network inference. • Decoding Immune Cell State Transitions with Foundation Models: Evaluated foundation models (Geneformer, scPRINT, UCE, CellPLM, scGPT) for immune cell state analysis. Developed specialized attention mechanisms for temporal immune response analysis. Enhanced resolution of cell subtypes and rare population clustering. 	
University of California, Riverside – Riverside, CA Ph.D. Research Assistant, Advisor: Adam Godzik	Aug 2018 – June 2023
<ul style="list-style-type: none"> • Platelet Transcriptional Profiling in Inflammatory Diseases: Investigated platelet transcriptional changes in COVID-19, sepsis, and systemic lupus erythematosus using single-cell transcriptional profiling coupled with machine learning techniques. Identified distinct platelet subpopulations associated with disease severity and outcomes. Revealed that platelet transcriptional changes can exacerbate endothelial damage and affect lymphocyte function. Expanded understanding of platelets' role in inflammatory and immune responses and identified potential new therapeutic targets for diseases characterized by platelet dysfunction. • Sepsis Biomarker Discovery: Identified molecular biomarkers and pathways in sepsis disease progression using single-cell RNA sequencing and advanced bioinformatics techniques. Implemented Cell Ranger pipeline and applied tools including Seurat, Scanpy, SingleR, scCATCH, and Monocle. Discovered novel biomarkers associated with sepsis progression and elucidated key cellular pathways involved in sepsis pathogenesis. Findings contribute to potential improvements in sepsis diagnosis and treatment strategies. • Post-COVID Risk Factor Analysis: Uncovered risk factors for post-COVID conditions through SARS-CoV-2 variant analysis. Utilized IRMA and SPAdes pipelines for assembly, with Trimmomatic for read trimming. Employed BV-BRC, Genome Detective, and Coronavirus3D tools for variant identification. Conducted correlation studies, univariate logistic regression, ROC Curve, and AUC analyses. Identified specific SARS-CoV-2 variants associated with higher risk of post-COVID conditions and determined key clinical and demographic risk factors for long-term COVID-19 effects. Findings contribute to improved risk assessment and management strategies for COVID-19 patients. 	
Illumina – San Diego, CA Bioinformatics Intern – Doctoral Leveraged analytical ability and examined data from databases like PharmVar, PharmGKB, and CPIC. Partnered with cross-functional and cross-cultural teams.	Jun 2022 to Sep 2022

- Established end-to-end workflow for creating PGx research reports by utilizing Illumina DRAGEN Bio-IT platform, Typescript, Node.js, and HTML.

Vantari Genetics – Irvine, CA

2015 to 2018

Clinical Genomics Scientist

Contributed to the development and implementation of Next-Generation Sequencing (NGS) pipelines for hereditary cancer testing, with a focus on variant classification and interpretation.

- **NGS Pipeline Development:** Worked closely with the Bioinformatics Pipeline Engineer to create integrated workflows for variant discovery and interpretation. Contributed to pipeline validation efforts, ensuring accuracy and reliability of genetic testing results.
- **Variant Classification and Interpretation:** Conducted NGS hereditary cancer multigene tests, interpreting complex genetic data. Classified genetic variants following ACMG guidelines, ensuring consistency and accuracy in reporting. Developed and implemented standardized workflows and SOPs for variant classification, improving efficiency and reducing error rates.
- **Data Analysis and Reporting:** Analyzed data from key genomic databases including RefSeq, UCSC Genome Browser, ClinVar, HGMD, TCGA, ENCODE, UniProt, GEO, Ensembl, COSMIC, and dbSNP. Prepared concise, clinically relevant patient reports based on genetic findings and current literature.
- **Training and Knowledge Sharing:** Organized and conducted training sessions for new hires on NGS technologies and variant interpretation. Contributed to the development of educational materials for both internal use and client education.

University of Southern California – Los Angeles, CA

2014 to 2015

Research Assistant

- **Protein Expression and Purification:** Expressed and purified a cell-penetrating peptide using standard molecular biology techniques.
- **Molecular Biology Techniques:** Utilized PCR, gel electrophoresis, and Western blotting for protein and peptide characterization.
- **Data Analysis:** Analyzed experimental data using basic statistical methods and created visualizations.
- **Scientific Communication:** Contributed to weekly lab meetings and assisted in manuscript preparation.
- **Laboratory Management:** Maintained detailed lab notes and helped draft protocols for common procedures.

Honors and Awards

- Higher Education Emergency Relief Funds (HEERF) Dissertation Year Fellowship (\$7,200), 2022
- Annual GGB Symposium Best Poster Award, 2022
- Trainee Poster Award, American Association of Immunologists (AAI), 2022
- 4th Annual Ultimate Biomed Retreat Award for "Best Poster", UCR, 2022
- Student Award of Excellence (2,000 RMB, awarded to one student per class), JLU, 2012
- Student Award of Excellence (2,000 RMB, awarded to one student per class), JLU, 2011
- National English Competition for College Students Grand Prize, China, 2010
- National Fellowship (8,000 RMB), Ministry of Education, China, 2010
- Outstanding Student Award (2,000 RMB, awarded to one student per class), JLU, 2009

Teaching Experience

National Institute of Allergy and Infectious Diseases (NIAID), NIH – Seattle, WA

December 2024

Workshop on Computational Modeling of Proteins for Infectious Disease

- Led hands-on workshop for infectious disease researchers, providing instruction on computational protein modeling techniques and tools.
- Designed and delivered practical demonstrations of protein structure prediction and analysis tools for biomedical applications.

University of California, Riverside – Riverside, CA

Sep 2023 to Dec 2024

Adam Godzik, School of Medicine Division of Biomedical Sciences

- Taught 'BMSC 202 - Molecular Basis of Disease' at the Master's level to a cohort of 25 students. Course content

included in-depth analysis of disease etiology at the molecular level, with a focus on contemporary discoveries and diverse methodological applications.

- Designed and implemented practical R coding exercises to improve students' programming skills.

University of California, Riverside – Riverside, CA

Sep 2021 to Dec 2021

Ayala Rao, Department of Plant Pathology & Microbiology

- Taught 'BIOL107A - Molecular Biology,' an undergraduate course with an enrollment of 160 students. Topics included genetics, recombinant DNA technology, molecular cloning, and virology.
- Composed and administered quizzes and examinations to assess academic performance.
- Conducted weekly group discussions to enhance collaborative learning and critical thinking.
- Held regular office hours and provided supplemental educational materials to support student learning.

University of California, Riverside – Riverside, CA

Mar 2021 to June 2021

James Burnette, Department of Evolution, Ecology and Organismal Biology

- Taught 'BIOL020- Dynamic Genome' an undergraduate course with an average attendance of 60 students per quarter, encompassing plant and animal genomics, bioinformatics tools, and genomic databases.
- Constructed and graded quizzes, exams, and homework to evaluate student comprehension.
- Collaborated with a team of four teaching assistants to streamline lab sessions and grading processes.

Undergraduate Students Advised

- Keita Ichii, 2023 Winter, Spring, Fall
- Abraham Takkouche, 2023 Winter, Spring, Fall
- Jacob Sola, 2023 Winter, Spring, Fall
- Jasmine Nguyen, 2022 Spring
- Britney Margheim, 2019 Fall
- Mabel Shehada, 2019 Fall
- Dev Tanna, 2019 Fall

Publications

Journal Publications and Preprints

1. **Qiu, Xinru**, Meera G. Nair, Lukasz Jaroszewski, and Adam Godzik. "Deciphering Abnormal Platelet Subpopulations in COVID-19, Sepsis and Systemic Lupus Erythematosus through Machine Learning and Single-Cell Transcriptomics." *International Journal of Molecular Sciences* 25, no. 11 (2024): 5941.
2. **Qiu, Xinru**, Han Li, Greg Ver Steeg, and Adam Godzik. "Advances in AI for Protein Structure Prediction: Implications for Cancer Drug Discovery and Development." *Biomolecules* 14, no. 3 (2024): 339.
3. **Qiu, Xinru**, Jiang Li, Jeff Bonenfant, Lukasz Jaroszewski, Aarti Mittal, Walter Klein, Adam Godzik, and Meera G. Nair. "Dynamic changes in human single-cell transcriptional signatures during fatal sepsis." *Journal of Leukocyte Biology* 110, no. 6 (2021): 1253-1268.
4. Vizcarra, Edward A., Arzu Ulu, Tyler A. Landrith, **Xinru Qiu**, Adam Godzik, and Emma H. Wilson. "Group 1 metabotropic glutamate receptor expression defines a T cell memory population during chronic Toxoplasma infection that enhances IFN-gamma and perforin production in the CNS." *Brain, Behavior, and Immunity* 114 (2023): 131-143.
5. Takkouche, Abraham, **Xinru Qiu**, Mayya Sedova, Lukasz Jaroszewski, and Adam Godzik. "Unusual structural and functional features of TplRR/BspA-like LRR proteins." *Journal of Structural Biology* 215, no. 3 (2023): 108011.
6. Li, Jiang, Rebecca E. Ruggiero-Ruff, Yuxin He, **Xinru Qiu**, Nancy Lainez, Pedro Villa, Adam Godzik, Djurdjica Coss, and Meera G. Nair. "Sexual dimorphism in obesity is governed by RELM α regulation of adipose macrophages and eosinophils." *Elife* 12 (2023): e86001.
7. Bergersen, Kristina V., Kathy Pham, Jiang Li, Michael T. Ulrich, Patrick Merrill, Yuxin He, Sumaya Alaama, **Xinru Qiu**, Indira S. Harahap-Carrillo, Keita Ichii, Shyleen Frost, Marcus Kaul, Adam Godzik, Erica C. Heinrich, and Meera G. Nair. "Health disparities in COVID-19: Immune and vascular changes are linked to disease severity and persist in a high-risk population in Riverside County, California." (2023).

8. Alisoltani, Arghavan, **Xinru Qiu**, Lukasz Jaroszewski, Mayya Sedova, Mallika Iyer, and Adam Godzik. "Gender differences in smoking-induced changes in the tumor immune microenvironment." Archives of Biochemistry and Biophysics 739 (2023): 109579.
9. Bonenfant, Jeffrey, Jiang Li, Luqman Nasouf, Joseph Miller, Tammy Lowe, Lukasz Jaroszewski, **Xinru Qiu** et al. "Resistin Concentration in Early Sepsis and All-Cause Mortality at a Safety-Net Hospital in Riverside County." Journal of Inflammation Research 15 (2022): 3925.
10. Zhou, Wan Lin, Lin Lin Li, **Xin Ru Qiu**, Qi An, and Mei Hua Li. "Effects of combining insulin-like growth factor 1 and platelet-derived growth factor on osteogenesis around dental implants." Chin J Dent Res 20, no. 2 (2017): 105-109.
11. Li, Mei-hua, Yi-shu Wang, Hong-lan Zhou, Ya-juan Li, **Xin-ru Qiu**, Xue-yao Wang, and Yu-yang Zhao. "Inhibitory effects of mistletoe alkali on salivary adenoid cystic carcinoma cells." Chemical Research in Chinese Universities 29, no. 2 (2013): 275-279.
12. Mei-hua, Li, Zhou Hong-lan, Wang Wei, and **Qiu Xin-ru**. "Inhibition of salidroside on salivary gland adenoid cystic carcinoma." Chemical Research in Chinese Universities 26, no. 6 (2010): 969-973.

PhD Dissertation

Qiu, Xinru. Exploring Immune Cell Heterogeneity Through Single-Cell RNA Sequencing Analysis. University of California, Riverside, 2023.

Master Thesis

Qiu, Xinru. pH-Sensitive Cytotoxicity of a Cell Penetrating Peptide Fused with a Histidine-Glutamate Co-oligopeptide. University of Southern California, 2015.

Presentations and Invited Talks

- Poster, RNA and AI Symposium 2024, San Diego, CA Oct 2024
Single-Cell Analysis of Platelet Heterogeneity in COVID-19 and Sepsis Using Foundation Models
- Poster, La Jolla Immunology Conference, San Diego, CA Oct 2024
Deciphering Abnormal Platelet Subpopulations in Inflammatory Diseases through Machine Learning and Single-Cell Transcriptomics
- Poster, RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges, Los Angeles, CA Nov 2023
Deciphering Abnormal Platelet Subpopulations in Inflammatory Diseases through Machine Learning and Single-Cell Transcriptomics
- Poster, Predictive Modeling in Biology & Medicine Con., Riverside, CA Nov 2023
Deciphering Abnormal Platelet Subpopulations in Inflammatory Diseases through Machine Learning and Single-Cell Transcriptomics
- Poster, Inaugural Symposium Center for RNA Biology, Riverside, CA Nov 2022
Single-cell analysis identifies specific platelet subpopulations in COVID-19, sepsis, and systemic lupus erythematosus drive the disease severity
- Poster, 2022 UCR GGB Symposium, Riverside, CA Oct 2022
Single-cell analysis identifies specific platelet subpopulations in COVID-19, sepsis, and systemic lupus erythematosus drive the disease severity
- Poster, 5th Annual Ultimate Biomed Retreat, Riverside, CA Oct 2022
Single-cell analysis identifies specific platelet subpopulations in COVID-19, sepsis, and systemic lupus erythematosus drive the disease severity

- Poster, MolMed mini symposium, Riverside, CA May 2022
Dynamic changes in human single-cell transcriptional signatures during fatal sepsis
- Poster, AAI IMMUNOLOGY2022, Portland, OR May 2022
Dynamic changes in human single-cell transcriptional signatures during fatal sepsis
- Poster, 4th Annual Ultimate Biomed Retreat, Zoom Nov 2021
Dynamic changes in human single-cell transcriptional signatures during fatal sepsis
- Talk, 2021 UCR GGB Symposium, Zoom Oct 2021
Dynamic changes in human single-cell transcriptional signatures during fatal sepsis
- Talk and Poster, UC Irvine 2020 Immunology Fair, Zoom Dec 2020
Analysis of Single Cell Expression Data from Sepsis Patients: A Pilot Study
- Talk, 3rd Annual Ultimate Biomed Retreat, Zoom Oct 2020
Analysis of Single Cell Expression Data from Sepsis Patients: A Pilot Study
- Talk and Poster, 2020 UCR GGB Symposium, Zoom Oct 2020
Analysis of Single Cell Expression Data from Sepsis Patients: A Pilot Study
- Talk and Poster, 2019 UCR GGB Symposium, Riverside, CA Sep 2019
Mutations at protein-protein interfaces effect on drug resistance in cancer
- Poster, Inaugural MolMed Symposium, Riverside, CA Mar 2019
Mutations at protein-protein interfaces effect on drug resistance in cancer

Reports by Media

- Report by news.ucr.edu <https://shorturl.at/brvL4>
Article title: Protein found to protect females against obesity.
Featured in UCR's Top Stories of 2023 <https://shorturl.at/kvzV2>
- Report by news.ucr.edu <https://shorturl.at/szNW>
Article title: How sepsis need not be fatal.

Professional Affiliations

GGB Graduate Student Association, University of California, Riverside 2021-2022
Secretary

- Co-organized program symposiums and seminars, developing the program, inviting speakers, coordinating logistics, and ensuring that the events ran smoothly.
- Organized and hosted Ph.D. candidate qualifying exam information seminar, developing the content and structure of the seminar, leveraged my expertise in the field to provide valuable insights and information about the qualifying exam process.
- Working with the GSA President in facilitating monthly board meetings, coordinating with members of the board to ensure their attendance, preparing meeting materials, and taking minutes during the meeting to capture key decisions and action items.

Professional Service

Journal Reviews

- Advanced Science (Wiley)
- Big Data and Cognitive Computing (MDPI)
- Biology - MDPI
- BioMedInformatics (MDPI)
- Biomolecules (MDPI)
- Communications Biology (Nature)
- Data (MDPI)
- Frontiers in Genetics (Frontiers)
- Genes (MDPI)
- Genomics (Elsevier)
- Inflammation (Springer)
- International Journal of Environmental Research and Public Health (MDPI)
- Heliyon (Cell Press)
- Journal of Clinical Medicine (MDPI)
- Journal of Molecular Biology (Elsevier)
- Journal of Personalized Medicine (MDPI)
- Mathematics (MDPI)
- Molecular Immunology (Elsevier)
- Scientific Reports (Nature)

Conference Reviews

- Generative and Experimental Perspectives for Biomolecular Design (GEM) workshop at International Conference on Learning Representations (ICLR) 2024
- AI4Science workshop at International Conference on Machine Learning (ICML) 2024

Grant Reviews

- UCR Minigrants for Undergraduate Research & Creative Activities

Professional Memberships

- **Member**, The International Society of Computational Biology (ISCB)
- **Member**, Human Cell Atlas (HCA)
- **Member**, The American Association of Immunologists (AAI)

Languages

English: Fluent

Chinese - Mandarin: Native Language

Technical Skills and Tools

- **Programming Languages:** Python, R, Java, JavaScript, HTML, SQL, Bash, Git
- **Operating Systems and Cloud Computing Platforms:** Unix, Linux, Windows, MacOS, Google Cloud Platform
- **High-Performance Computing (HPC):** Experience with HPC clusters for large-scale computational tasks. Implemented parallel processing techniques to optimize resource usage and accelerate data analysis pipelines. Experienced in scaling bioinformatics workflows for HPC environments.
- **Machine Learning & Data Analysis Tools:**
 - Libraries: Pandas, NumPy, SciPy, TensorFlow, PyTorch, Scikit-learn, Keras, Hugging Face Transformers, Bioconductor, Tidyverse, RDKit
 - Models & Techniques: Classification and Regression (Linear & Logistic Regression, Random Forest, XGBoost, SVM, Naive Bayes, Decision Trees, Gradient Boosting, Elastic Net); Clustering (K-means, Hierarchical Clustering); Dimensionality Reduction (PCA, LDA, t-SNE, UMAP); Sequence Modeling and Analysis (Hidden Markov Models, RNNs, LSTM); Deep Learning (CNNs, Autoencoders, Diffusion Models, Transformers); Model Evaluation and Selection (ROC, AUC, Cross-Validation, Grid Search and Randomized Search for Hyperparameter Optimization); Ensemble Methods (Bagging, Boosting)
 - Visualization Tools: ggplot2, Plotly, Seaborn, Matplotlib, Shiny, Tableau, BioRender
- **Bioinformatics Tools and Pipelines:**
 - Sequence Alignment: BLAST, Bowtie, BWA, STAR, HISAT2, Tophat2
 - Genomic Annotation: ANNOVAR, VEP, SnpEff
 - Variant Calling: GATK, SAMtools, bcftools, Picard
 - Transcriptomics: Cufflinks, Kallisto, Salmon, DESeq, edgeR, limma
 - Single-Cell Analysis: CellRanger, Seurat, SCANPY, Monocle, SingleR, PAGA
 - Pathway Analysis: clusterProfiler, ReactomePA, GSVA
 - Structural Biology Tools: AlphaFold2 and ESMFold for protein structure prediction and analysis; PyMOL and Chimera for molecular visualization
- **Databases:**
 - Genomic Databases: 1000 Genomes Browser, dbSNP, gnomAD, HGMD, COSMIC, ClinVar
 - Transcriptomic Databases: GEO, SRA, ENCODE, ArrayExpress
 - Pathway & Protein Databases: KEGG, Reactome, IPA, Gene Ontology (GO), PANTHER; SWISS-PROT, Protein Data Bank (PDB), STRING, UniProt
 - Genome Browsers: UCSC Genome Browser, Ensembl, Integrative Genomics Viewer (IGV)