Curriculum Vitae

Basic Information

Name: Qiqi Xie, M.D.
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Current Position: Postdoctoral Research Associate, School of Information Sciences, University of Illinois Urbana-Champaign
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Education

Sep 2016 – July 2019	M.S. in Orthopedics, Lanzhou University, Gansu, China
Sep 2010 – July 2015	M.D., Nanchang University, Jiangxi, China

Honor & Awards

2011: National College English Competition Encouragement Award, Nanchang University
2012: The Second-Prize Scholarship, Nanchang University
2014: The Third-Prize Scholarship, Nanchang University
2016: The Third-Prize Scholarship, Lanzhou University
2018: The First-Prize Scholarship, Lanzhou University
2018: National Scholarships, Lanzhou University
2018: Outstanding Graduates, Lanzhou University

Research Experience

Aug 2025 – Present: Postdoctoral Research Associate
School of Information Sciences, University of Illinois Urbana-Champaign, USA
Supervisor: Dr. Haohan Wang

- Apply multi-agent artificial intelligence to solve complex biomedical problems.
- Analyze large-scale transcriptomics data to understand how cellular systems behave and interact, with a focus on disease modeling.

Dec 2023 – Aug 2025: Research Associate
Department of Medical & Molecular Genetics, Indiana University School of Medicine, USA
Supervisor: Dr. Jia Shen

- Lead a multi-omics integration project combining single-cell and spatial transcriptomic data from GBM and DIPG.
- Construct cellular atlases and perform GRN (gene regulatory network) inference to dissect tumor heterogeneity.
- Conduct integrative analyses and visualization for a wide range of lab projects, including: DIPG Reference Mapping, DIPG and GBM scRNA-seq GRN inference, H3K9me3 MTSig, ETV family TFs (ETV1/4/5), DNMT1, KBTBD2, KLHL4, MUC16, SUV39H1 (carNK, TMZ), ZFAS1 (ovarian cancer), and Heme project.
- Apply RNA-seq, ChIP-seq, and ATAC-seq to study SUV39H1/H3K9me3-mediated chromatin regulation in glioblastoma stem-like cells.

- Participate in collaborative projects with Liu Lab, Niu Lab, and assist ZFAS1 project.
- Contributed as first/co-first author to high-impact publications in JCI Insight and npj Precision Oncology.
- Collaborate with wet-lab scientists to validate computational predictions.

Aug 2019 – July 2023: Scientific Research Secretary

Affiliated Hospital of Qinghai University, China

Supervisor: Prof. Guoshuang Shen

- Organized and led internal training courses on clinical research and scientific methods for graduate and doctoral students.
- Initiated and coordinated research interest groups in internal medicine.
- Participated in multiple clinical research projects and contributed to project completion and reporting.
- Responsible for foundational research of the Breast Disease Diagnosis and Treatment Center.
- Managed clinical sample collection and biobank setup for the department.
- Acted as liaison between clinical and research teams, bridging patient data and basic experiments.

Sep 2016 – July 2019: Graduate Researcher

Department of Orthopedics, Second Hospital of Lanzhou University, China

Supervisor: Prof. Jing Wang

- Focused on signaling pathways in osteoporosis and pain (TRPM2-GSK3β, endocannabinoid systems).
- Conducted rodent behavioral tests and molecular experiments including IHC, WB, qPCR, and exosome analysis.
- Initiated bioinformatics analysis of gene expression in pain and skeletal diseases.
- Contributed as first/co-first author to multiple publications.

Research Skills

Bioinformatics & Programming

- Proficient in R and Python for advanced data analysis, statistical modeling, and customized pipelines
- Experienced with high-performance computing (HPC) environments and Linux shell scripting for parallelized, large-scale biological data analysis
- Single-cell and spatial transcriptomics: data integration, clustering, trajectory inference, GRN reconstruction, and cell-cell communication
- Clinical multi-omics analysis: integration of genomics, transcriptomics, epigenomics, and clinical metadata to identify disease biomarkers and therapeutic targets
- Epigenomics: ChIP-seq, ATAC-seq, CUT&Tag, scATAC-seq analysis
- Machine learning: survival analysis, feature selection, and classifier modeling (caret, scikit-learn, XGBoost)
- Predictive modeling: clinical prognostic model construction (e.g., nomograms, Cox/LASSO regression), validation, and visualization
- AI-driven protein structure prediction (AlphaFold) and application to structure-function studies
- Network pharmacology and drug-target interaction modeling
- Radiogenomics and digital pathology: quantitative imaging feature extraction and integration with omics data (pyradiomics)
- Reproducible workflows and version control: Snakemake, RMarkdown, Git/GitHub

Molecular & Cell Biology

- Rodent models of pain and skeletal disease: behavioral assessment, tissue collection
- Molecular techniques: qPCR, Western blotting, immunohistochemistry (IHC), immunofluorescence (IF),

exosome isolation

- Cell-based assays: primary and immortalized cell culture, viability and apoptosis assays
- Equipment expertise: micro-drop PCR system, automated protein expression quantification, high-content live cell imaging, Seahorse cell metabolic analyzer

Data Visualization & Tools

- GraphPad Prism, Cytoscape, ImageJ, Adobe Illustrator, Photoshop

Grants and Projects

- Participant, National Natural Science Foundation of China Grant (Osteoporosis and Pain Pathways), 2017–2018
- Contributor, Provincial Key Research Projects (Qinghai Province Clinical Tumor Research Center Construction)
- Contributor, Qinghai Province Research Achievement Transformation Program: Early Diagnosis and Treatment Technology Promotion in Breast Cancer
- Project participant: "Endogenous cannabinoids regulate astrocyte-mediated pain: the MAPK-Glu-Gln shuttle pathway"
- Project participant: "The mechanism of TRPM2-GSK3β Signaling Pathway in Diabetic Osteoporosis"
- Project participant: "The mechanism of exosome microRNAs in osteoporosis"
- Project participant: "The pain mechanism and treatment of spinal diseases"
- Project participant: "The mechanism of exosome microRNAs in breast cancer bone metastasis"

Academic Service

- Editorial Board Member, Scientific Reports
- Special Reviewer for over 100 SCI-indexed manuscripts in journals including Genomics, Journal of Neuroinflammation, Journal of Cancer, Frontiers in Cell and Developmental Biology, Immunobiology, and Diagnostics
- Appointed Ambassador, Bentham Science Publishers

Publications

A. First author, Co- first author and Corresponding author (*) publications:

1. **Xie, Q.**, Du, Y., Ghosh, S., Rajendran, S., Cohen-Gadol, A.A., Baizabal, J.-M., Nephew, K.P., Han, L., and Shen, J. (2025). Multi-omics analysis identifies glioblastoma dependency on H3K9me3 methyltransferase activity. npj Precis. Onc.
2. Li, C., **Xie, Q.**, Ghosh, S., Cao, B., Du, Y., Vo, G.V., Huang, T.Y., Spruck, C., Carpenter, R.L., Wang, Y.A., et al. (2025). SUV39H1 maintains cancer stem cell chromatin state and properties in glioblastoma. JCI Insight.
3. **Xie, Q.**, Ou-yang, W., Zhang, M., Wang, H., and Yue, Q. (2020). Decreased Expression of NUSAP1 Predicts Poor Overall Survival in Cervical Cancer. J. Cancer.
4. li, M., Yan, T., Cai, Y., Wei, Y., and **Xie, Q*.** (2023). Expression of matrix metalloproteinases and their association with clinical characteristics of solid tumors. Gene.
5. Deng, Y., Yuan, W., Ren, E., Wu, Z., Zhang, G., and **Xie, Q*.** (2021). A four-methylated LncRNA signature predicts survival of osteosarcoma patients based on machine learning. Genomics.
6. Ren, E., Deng, Y., Yuan, W., Wu, Z., Zhang, G., and **Xie, Q*.** (2021). An immune-related gene signature for determining Ewing sarcoma prognosis based on machine learning. J. Cancer Res. Clin. Oncol.
7. Zhang, G., Wu, Z., Li, C., Ren, E., Yuan, W., Deng, Y., and **Xie, Q*.** (2020). Development of a Machine Learning-Based Autophagy-Related lncRNA Signature to Improve Prognosis Prediction in Osteosarcoma Patients. Front.

Mol. Biosci.

8. Deng, Y., Ren, E., Yuan, W., Zhang, G., Wu, Z., and **Xie, Q*.** (2020). GRB10 and E2F3 as Diagnostic Markers of Osteoarthritis and Their Correlation with Immune Infiltration. Diagnostics.
9. Wu, Z., Deng, Y., Zhang, G., Ren, E., Yuan, W., and **Xie, Q*.** (2018). Development of a novel immune-related genes prognostic signature for osteosarcoma. Sci. Rep.
10. Ren, E., Deng, Y., Yuan, W., Zhang, G., Wu, Z., Li, C., and **Xie, Q*.** (2018). An Immune-Related Long Non-Coding RNA Signature to Predict the Prognosis of Ewing's Sarcoma Based on a Machine Learning Iterative Lasso Regression. Front. Cell Dev. Biol.
11. Wang, H., Zhang, M., **Xie, Q.**, Yu, J., Qi, Y., and Yue, Q. (2019). Identification of diagnostic markers for major depressive disorder by cross-validation of data from whole blood samples. PeerJ.
12. Wang, H., **Xie, Q.**, Ou‑Yang, W., and Zhang, M. (2019). Integrative analyses of genes associated with idiopathic pulmonary fibrosis. J. Cell. Biochem.
13. Zhang, N., Wang, H., **Xie, Q.**, Cao, H., Wu, F., Di Wu, D.B., Wan, Y., Ohtani, H., Zhang, Z., Zhou, P., et al. (2019). Identification of potential diagnostic and therapeutic target genes for lung squamous cell carcinoma. Oncol Lett.

B. In Preparation:

14. **Xie, Q.**, Li, C., Ghosh, S., Rajendran, S., Cohen-Gadol, A.A., Baizabal, J.-M., Nephew, K.P., Han, L., and Shen, J. (2025). Comprehensive machine-learning survival framework develops a consensus model in large-scale multicenter cohorts for high-grade glioma.
15. **Xie, Q.**, Li, C., Ghosh, S., Rajendran, S., Cohen-Gadol, A.A., Baizabal, J.-M., Nephew, K.P., Han, L., and Shen, J. (2025). A comprehensive spatio-cellular map of the diffuse intrinsic pontine glioma.
16. Cao, B., **Xie, Q.**, Li, C., Ghosh, S., Rajendran, S., Cohen-Gadol, A.A., Baizabal, J.-M., Nephew, K.P., Han, L., and Shen, J. (2025). Targeting SUV39H1 promotes glioblastoma-natural killer crosstalk.
17. Cao, B., **Xie, Q.**, Li, C., Ghosh, S., Rajendran, S., Cohen-Gadol, A.A., Baizabal, J.-M., Nephew, K.P., Han, L., and Shen, J. (2025). The role of KBTBD2 in glioblastoma stemells.
18. Wu, Z., **Xie, Q.**, Li, C., Ghosh, S., Nephew, K.P., Han, L., and Shen, J. (2025). FGF21-mediated upregulation of SIRT1 delays Intervertebral Disc Degeneration by promoting PINK1/Parkin dependent mitophagy through deacetylation of FOXO3.

C. Other cooperative publications:

19. Wang, S., Zhang, H., Geng, B., **Xie, Q.**, Li, W., Deng, Y., Shi, W., Pan, Y., Kang, X., and Wang, J. (2018). 2-arachidonyl glycerol modulates astrocytic glutamine synthetase via p38 and ERK1/2 pathways. J. Neuroinflamm.
20. Li, J., Shen, G., Liu, Z., Liu, Y., Wang, M., Zhao, F., Ren, D., **Xie, Q.**, Li, Z., Liu, Z., et al. (2023). Treatment‑related adverse events of antibody‑drug conjugates in clinical trials: A systematic review and meta‑analysis. Cancer Innovation.
21. Zhao, F., Li, E., Shen, G., Dong, Q., Ren, D., Wang, M., Zhao, Y., Liu, Z., Ma, J., **Xie, Q.**, et al. (2023). Correlation between mismatch repair and survival of patients with gastric cancer after 5-FU-based adjuvant chemotherapy. J. Gastroenterol.
22. Li, Z., **Xie, Q.**, Zhao, F., Huo, X., Ren, D., Liu, Z., Zhou, X., Shen, G., and Zhao, J. (2024). Exploring GZMK as a prognostic marker and predictor of immunotherapy response in breast cancer: unveiling novel insights into treatment outcomes. J. Cancer Res. Clin. Oncol.
23. Fang, Q., Shen, G., **Xie, Q.**, Guan, Y., Liu, X., Ren, D., Zhao, F., Liu, Z., Ma, F., and Zhao, J. (2024). Development of Tumor Markers for Breast Cancer Immunotherapy. Curr. Mol. Med.
24. Huo, X., Shen, G., Wang, T., Li, J., **Xie, Q.**, Liu, Z., Wang, M., Zhao, F., Ren, D., and Zhao, J. (2023). Treatment

options for patients with human epidermal growth factor 2-positive breast cancer brain metastases: A systematic review and meta-analysis. Front. Oncol.

25. Zhao, F., Shen, G., Dong, Q., Xin, Y., Huo, X., Wang, M., Liu, Z., Zhao, Y., Ren, D., **Xie, Q.**, et al. (2023). Impact of platinum-based chemotherapy on the prognosis of early triple-negative breast cancer: a systematic review and meta-analysis. Clin. Exp. Med.
26. Zhang, J., **Xie, Q.**, Huo, X., Liu, Z., Da, M., Yuan, M., Zhao, Y., and Shen, G. (2022). Impact of intestinal dysbiosis on breast cancer metastasis and progression. Front. Oncol.
27. Wu, Z., Chen, Y., Zhang, G., **Xie, Q.**, Wang, K., Yang, X., Liu, T.-C., Wang, Z., Zhao, G., and Zhang, H. (2022). SKI knockdown suppresses apoptosis and extracellular matrix degradation of nucleus pulposus cells via inhibition of the Wnt/β-catenin pathway and ameliorates disc degeneration. Apoptosis 27, 133–148.
28. Deng, Y., Yang, L., **Xie, Q.**, Yang, F., Li, G., Zhang, G., Li, S., Wu, Z., Wang, J., and Kang, X. (2020). Protein Kinase A is Involved in Neuropathic Pain by Activating the p38MAPK Pathway to Mediate Spinal Cord Cell Apoptosis. Mediators of Inflammation.
29. Wu, Z., **Xie, Q.**, Liu, T., Yang, X., Zhang, G., and Zhang, H. (2021). Role of the Wnt pathway in the formation, development, and degeneration of intervertebral discs. Pathology - Research and Practice.
30. Zhang, G., Deng, Y., **Xie, Q.**, Ren, E., Ma, Z., He, X., Gao, Y., and Kang, X. (2020). Sirtuins and intervertebral disc degeneration: Roles in inflammation, oxidative stress, and mitochondrial function. Clin. Chim. Acta.
31. Yuan, W., **Xie, Q.**, Wang, K., Shen, W., Feng, X., Liu, Z., Shi, J., Zhang, X., Zhang, K., Deng, Y., et al. (2017). Screening of osteoarthritis diagnostic markers based on immune-related genes and immune infiltration. Sci. Rep.

D. Publications in Chinese Core Journals

32. **Xie Q**, Li W, Shi W, Deng Y, Ren E, Ma J, Kang X, Wang J. Bioinformatics analysis of gene chip data related to early pathological pain induced by SNI rat model. Life Science Research. (article in chinese)
33. **Xie Q**, Li W, Shi W, Deng Y, Ren E, Ma J, Pan Y, Kang X, Wang J. Effects of diabetes on bone biomechanics in ovariectomized rats. Chinese Journal of Medical Physics. (article in chinese)
34. **Xie Q**, Li W, Shi W, Deng Y, Ren E, Ma J, Kang X, Wang J. Advances in application of gemstone energy spectrum CT in skeletal system. Life Science Research. (review in Chinese)
35. **Xie Q**, Li W, Shi W, Deng Y, Ren E, Ma J, Kang X, Wang J. Bioinformatics analysis of osteoarthritis expression profile microarray integration. Hua Zhong Ke Ji Da Xue Xue Bao Yi Xue Ban. (article in Chinese)
36. Li W, **Xie Q**, Ren E, Deng Y, Pan Y, Ma J, Kang X, Wang J. Selection of sites for detecting bone mineral density in diabetic osteoporosis rats by DXA. Chinese Journal of Medical Physics. (article in chinese)
37. Deng Y, **Xie Q**, Li W, Shi W, Ma J, Pan Y, Kang X, Wang J. Visual analysis of related literature on quantitative computed tomography in diagnosis of osteoporosis. Chinese Journal of Medical Physics. (article in chinese)
38. Dong Q, **Xie Q**, Hu J, Wang M, Yuan G and Pan Y. The expression and clinical significance of formyl peptide receptor 1 in glioma were analyzed based on bioinformatics. Cancer, aberration, mutation. (article in chinese)
39. Dong Q, **Xie Q**, Zhao R, Huang X, Li W, Zhang Y, Pan Y. The correlation between quantitative parameters of EDCT and bone biomechanics. Chinese Journal of Medical Physics. (article in chinese)
40. Huang X, **Xie Q**, Deng Y, Zhao R, Dong Q, Zhou J. Preliminary study on the evaluation of biomechanics by EDCT. Chinese Journal of Medical Physics. (article in chinese)
41. Li W, **Xie Q**, Shi W, Deng Y, Ma Y, Xie J, Kang X, Wang J. Progress in the study of skeletal endocrine function. Life science Research. (review in chinese)

Conferences

- Speaker, Chinese Orthopaedic Association Annual Congress, Xiamen, China (2018)

- Attendee, Annual Meeting of the Chinese Society of Clinical Oncology (CSCO), Guangzhou, China (2021)
- Participant, National Symposium on Cancer Systems Biology, Shanghai, China (2022)
- Attendee, Symposium on Single-Cell Sequencing and Spatial Transcriptomics, Hangzhou, China (2022)
- Participant, Precision Medicine and Tumor Immunotherapy Conference, Nanjing, China (2023)

Research Interests

Systems Oncology and AI-Augmented Biomedicine

- How do we computationally decode the spatial and temporal complexity of cancer?

I am broadly interested in leveraging high-dimensional single-cell, spatial transcriptomic, and clinical multi-omic data to model the regulatory and evolutionary dynamics of tumors. My goal is to answer fundamental questions in systems oncology: How do cancer cell states emerge and transition in space? Can we map chromatin architecture to functional plasticity in stem-like tumor subpopulations? Can disease-specific gene regulatory networks (GRNs) reveal therapeutic vulnerabilities or reprogramming routes? I am especially drawn to the intersection of cancer biology and computational science—where recent advances in machine learning and foundation models open up new avenues to integrate image, sequence, and spatial data in a biologically meaningful way.

Glioma Epigenetics, GRN Plasticity, and AI Modeling

- Can we predict—and ultimately perturb—cancer fate trajectories from multi-modal omics and imaging?

My recent work focuses on glioblastoma and diffuse intrinsic pontine glioma (DIPG), where I investigate the epigenetic regulation of stem-like states through multi-omic integration (RNA-seq, CUT&Tag, ATAC-seq, scRNA-seq, spatial transcriptomics). I am interested in how histone modifications like H3K9me3 (e.g., via SUV39H1) maintain chromatin rigidity and GRN topology in resistant subpopulations. Building on this, I aim to use machine learning to infer dynamic regulatory networks and develop predictive models that link spatial cell states to therapeutic outcomes. I also aspire to extend these approaches to AI-guided protein structure prediction, digital pathology, and network pharmacology to support precision oncology.

References

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