Jie Zhang, Ph.D.

Associate Professor
Center for Computational Biology and Bioinformatics
Department of Medical and Molecular Genetics
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EDUCATION:

Ph. D.	Biochemistry, University of Illinois at Urbana-Champaign (UIUC) Dissertation: *Mutagenesis and spectroscopic studies on cytochrome bd quinol oxidase of Escherichia coli.*	1997 - 2002
B. S.	Bioscience and Biotechnology, Tsinghua University, China	1991 - 1996

RESEARCH INTERESTS:

My research is focused on developing and applying translational bioinformatic methods to identify disease genes, pathways, and biomarkers with applications in cancers, neurodegenerative diseases, and other types of human diseases. Our lab also focuses on bioinformatic data analysis tool development as well as applies computational pathology on histopathological image data for cancer diagnosis, subtyping and prognosis.

RESEARCH EXPERIENCE:

Associate Professor– Department of Medical and Molecular Genetics, IUSM	2024 - present
Adjunct Faculty – Department of Biostatistics and Health Data Science, IUSM	2019 - present
Adjunct Faculty – Department of Biomedical Engineering and Informatics, IUI	2018 - present
Research Scientist – Regenstrief Institute	2018- present
Core Faculty- Center for Computational Biology and Bioinformatics, IUSM	2017- present
Assistant Professor– Department of Medical and Molecular Genetics, IUSM	2017- 2024

Associate Professor -Department of Medical and Molecular Genetics, IUSM	2024- present
Assistant Professor– Department of Medical and Molecular Genetics, IUSM	2017- 2024

- Translational bioinformatics research on neurodegenerative diseases such as Alzheimer's disease, cerebral amyloid angiopathy dementia and Parkinson's disease for drug target/biomarker identification, patient stratification, and disease mechanism study

- Integrative multi-modal data analysis and machine learning approach for disease mechanistic study, disease subtyping and biomarker identification
- Computational pathological analysis with machine learning models on H&E images for cancer subtyping and metastasis prognosis
- Software and pipeline development for integrative omic data mining, network analysis, and computational pathology image analysis

Assistant Research Professor– Department of Biomedical Informatics, The Ohio State University 2015-2017

- Developed novel machine learning approaches for computational pathological image analysis with the application on cancer subtyping and prognosis as well as normal tissue phenotype-genotype study
- Developed frequent network-based approach to understand Alzheimer's disease and cancer etiology and progression
- Mined condition-specific gene networks to provide candidates for disease pathway study, biomarker identification and drug development
- Mined functional relationships of somatic mutated genes of cancer patients to assist patient stratification and biomarker discovery
- Integrated multi-omics data for Alzheimer's disease and cancer biomarker & drug discovery

Research Scientist – Department of Biomedical Informatics, OSU 2014-2015

- Developed various pipelines and algorithms for mining and analyzing large exome-seq data for cancer genetic variance discovery in breast and endometrial cancers.
- Mined gene co-expression networks for functional copy number variance discovery.
- Developed network approaches for integrating both genetic and phenotypic alterations for disease pathway discovery.
- Developed single cell RNA-seq data analysis pipeline for neural developmental and neurological disease studies.

Postdoctoral Researcher – OSUCCC Biomedical Informatics Shared Resources 2009-2014

- Analyzed next generation sequencing (NGS) data including ChIP-seq, RNA-seq, and exome sequencing.
- Developed frequent gene co-expression network mining pipeline on cancer microarray data to identify cancer prognosis biomarker candidates.

Volunteer Researcher - OSUCCC Biomedical Informatics Shared Resources 2008

- Identified co-expressed gene network in multiple types of cancers using microarray data. Simulated of genome mapping for bisulfite-seq experiments.

Postdoctoral Researcher - F. Robert Tabita Group Department of Microbiology, OSU 2024-2005

- Studied DNA binding property of the LysR family member CbbR protein using surface plasmon resonance (SPR).

Postdoctoral Research Associate - Robert B. Gennis Group 2002-2004
Department of Biochemistry, University of Illinois at Urbana-Champaign

Designed and generated protein-binding DNA aptamer to facilitate protein crystallization.

- Cloned and expressed hypothetical channel protein, studied its role in pathogenicity and drug resistance in *Salmonella enterica* Serovar *Typhimurium.*

Graduate Research Assistant - Robert B. Gennis Group 1997-2002
Department of Biochemistry, University of Illinois at Urbana-Champaign

- Structure and function relationship studies on cytochrome *bd* quinol oxidase in *E. coli* using spectroscopic and mutagenesis techniques.
- Developed expertise in enzyme functional analysis using a variety of spectroscopic instruments as well as expertise in molecular biology techniques.

PROFESSIONAL ACTIVITIES:

- Member, NIH NCI-ITCR Special Emphasis Panel 2023 - present
- Member, NIH Special Emphasis Panel ZRG1 PSE-H (55) 2022
- Member, NIH NIAID Special Emphasis Panel 2021
- Member, Treat-AD Pre-clinical Translational Science Grant Review 2021-present
- Associate Editor for Fronter in Genetics 2021-present
- Associate Editor for BMC Medical Genomics 2019-present
- Conference organizer for NCI ITCR 2024 Conference 2024
- Program Committee member for:
    - 2011 Bioinformatics and Biomedicine (BIBM) Next Generation Sequencing Workshop,
    - 2014, 2016, 2017 ACM conference on Bioinformatics Computational Biology and Health Informatics (ACM BCB),
    - 2015, 2016 International Conference on Intelligent Biology and Medicine (ICIBM)
    - 2018 International Conference on Genome Informatics (GIW)
    - 2018, 2019, 2020 AMIA Summit on Translational Bioinformatics
    - 2023 BIBM Conference
- Reviewer for various journals and conferences including
    - Nature Communications, Nature Microbiology, Nature Communications Biology
    - Scientific Reports
    - Bioinformatics
    - PLoS One, Frontier in Genetics
    - BMC Bioinformatics, BMC Medical Genomics, BMC Genomics
    - ACM conference on Bioinformatics Computational Biology and Health Informatics (ACM-BCB)
    - ACM/IEEE Transaction on Computational Biology and Bioinformatics, International Conference on Intelligent Computing (ICIC)

GRANT AWARDS:

1. NIGMS R01 Apply novel pathogenomic approaches to identify interpretable image QTLs for multiple normal tissues (Role: Contact PI, 09/01/2024-08/31/2026)
2. NIH R21 Identify and study the roles of key genes and proteins in subpopulations of Alzheimer’s disease patients with uncoupled neurofibrillary tangles (Role: Contact PI, 07/01/2022-06/30/2025)
3. NIH R01 DMS/NIGMS 1: Topological Study on Histological Images and Spatial Transcriptomics (Role: MPI, 09/01/2022 – 08/31/2026)
4. NCI ITCR A deep-transfer-learning framework to transfer clinical information to single cells and spatial locations in cancer tissues (Role: MPI, 07/01/2022 – 06/30/2025)
5. NIA U54 Alzheimer’s Disease Drug Discovery Center (Role: Co-I, 09/2019-08/2029)
6. NIH U54 Microphysiological systems to Advance Precision medicine for Alzheimer’s Disease and Related Dementias (Role: Co-I, to be started in Spring 2025 - 2030)
7. IUSCCC TMM Big Data Grant, AI-based characterization of the tumor microenvironment of melanoma (Role: PI, 07/2021-06/2022)
8. NIH U54 Pilot Integrate genomic data analysis of pediatric sarcomas to identify functional CNVs and driving regulators (Role: PI, 06/2019-05/2020)
9. NIA R01 Tau-seed protein interactome and its role in neurodegenerative tauopathies (Role: Co-I, 09/2020-08/2025)
10. American Cancer Society Internal Research Grant (Role: contact PI, 06/2018-05/2019)
11. NCI ITCR U01 Informatics Links between Histological Features and Genetics in Cancers (Role: Co-I, 05/2015 – 04/2018)

PAPER AWARDS:

- The Marco Ramoni Distinguished Paper Award (AMIA Summit on Translational Bioinformatics) - 2016
- Distinguished Paper Award (AMIA Summit on Translational Bioinformatics) – 2010

TEACHING EXPERIENCE:

• Director for graduate course G700 Heredity in Biomedical Science, IUSM	2019- present
• Guest lecturer for G852, G788, Q581, IUSM, IUB, IUPUI	2017- present
• Training sessions on various bioinformatics tools, OSU	2010 - 2017
• Lecturer for Mathematical Biology Institute Summer Program, OSU	2011, 2012
• Teaching assistant in Physical Biochemistry, UIUC	2000-2002
• Teaching assistant in Biochemistry, UIUC	1999
• Teaching assistant in Chemistry, UIUC	1997

PUBLICATIONS:

BOOK CHAPTER

1. **Epigenome-Wide Association Studies**, Chapter: Workflow to Mine Frequent DNA Co-methylation Clusters in DNA Methylome Data, Springer Nature, ISBN: 978-1-0716-1993-3, 2022.
2. **Practical Guide to ChIP-seq Data Analysis**, CRC Press, ISBN: 9780429487590, 2 November 2018.

PEER-REVIEWED JOURNAL PAPERS (in reversed chronical order):

1. X. Yang, D. Chatterjee, J. E. Couetil , Z. Liu , V. D Ardon , C. Chen , **J. Zhang** , K. Huang, T. S. Johnson, “Gradient boosting reveals spatially diverse cholesterol gene signatures in colon cancer”, *Frontiers in Genetics, accepted.*
2. W. Shao, M. Cheng, A. Lopez-Beltran, A. Osunkoya, **J. Zhang**, K. Huang, L. Cheng, “Beyond Deep Learning: A Novel Computational Pipeline Enables Reliable Diagnosis of Inverted Urothelial Papilloma and Distinguishes It from Urothelial Carcinoma”, *JCO Clinical Cancer Informatics*, 2025 Mar:9:e2400059| doi: 10.1200/CCI.24.00059.
3. X. Huang, **J. Zhang**, K. Huang, Y. Wang, “Inhomogeneous graph trend filtering via a ℓ_2 norm cardinality penalty”, *IEEE Transactions on Signal and Information Processing over Networks,* Mar 2025 | doi: 10.1109/TSIPN.2025.3553025.
4. X. Huang, A. Jannu, Z. Song, N. Jury-Garfe, C. Lasagna-Reeves, T. Johnson, K. Huang, **J. Zhang,** “Predicting Alzheimer’s Disease Subtypes and Understanding Their Molecular Characteristics in Living Patients with Transcriptomic Trajectory Profiling”, *Alzheimer's & Dementia,* 2025 Jan 15;21(1):e14241| doi: 10.1002/alz.14241.
5. N. Jury-Garfe, J. Redding-Ochoa, Y. You, P. Martínez, H. Karahan, E. Chimal-Juárez, T. S. Johnson, **J. Zhang**, S. Resnick, J. Kim, J. C. Troncoso, C. A. Lasagna-Reeves, “Enhanced microglial dynamics and paucity of tau seeding in the amyloid plaque microenvironment contributes to cognitive resilience in Alzheimer’s disease”, *Acta Neuropathol.*, 2024 Aug 5;148(1):15. doi: 10.1007/s00401-024-02775-1.
6. E. Ahat, Z. Shi, S. Chu, H. H. Bui, E. R. Mason, D. M. Soni, K. D. Roth, M. J. Chalmers, A. L. Oblak, **J. Zhang**, J. A. Gutierrez, T. Richardson, “SHIP1 modulation and proteome characterization of microglia”, *Journal of Proteomics*, 2024 May 20:302:105198|doi: 10.1016/j.jprot.2024.105198.
7. Liu, H. Wu, D. Robertson, **J. Zhang**, “Text mining and portal development for gene-specific publications on Alzheimer's disease and other neurodegenerative diseases”, *BMC Medical Informatics & Decision Making,* |Doi: 10.1186/s12911-024-02501-7.
8. X. Zhan, Y. Liu, A. J. Jannu, S. Huang, W. Wei, B. Ye, P. Pandya, K. Pollok, J. Renbarger, K. Huang, **J. Zhang**, “Identify the potential driver genes for gene fusion-negative rhabdomyosarcoma”, *Frontier in Oncology*, Volume 13 (2023) | doi:10.3389/fonc.2023.1080989.
9. Z. Huang, W. Shao, Z. Han, A. M. Alkashash, C. De la Sancha, A. V. Parwani, H. Nitta, Y. Hou, T. Wang, P. Salama, M. Rizkalla, **J. Zhang**, Kun Huang*, Z. Li*, “Artificial Intelligence

Reveals Features Associated with Breast Cancer Neoadjuvant Chemotherapy Response from Multi-stain Histopathologic Images", *NPJ Precision Oncology,* 7:14, (2023) |doi:10.1038/s41698-023-00352-5 (*co-corresponding author)

10. P. H. Pandya, A. J. Jannu, *et al*., J. Zhang*, K. E. Pollok*, "Integrative Multi-OMICs Identifies Therapeutic Response Biomarkers and Confirms Fidelity of Clinically Annotated, Serially Passaged Patient-Derived Xenografts Established from Primary and Metastatic Pediatric and AYA Solid Tumors", *Cancers*, 2023, 15(1), 259. |doi:10.3390/cancers15010259. (*co-corresponding author).
11. J. E. Couetil, Z. Liu, K. Huang, **J. Zhang***, A. Alomari*, "Predicting melanoma survival and metastasis with interpretable histopathological features of machine learning models", *Front. Med.*, Volume 9, 2022 | doi:10.3389/fmed.2022.1029227. (*co-corresponding author).
12. P. Martinez, H. Patel, Y. You, N. Jury, A. Perkins, A. Lee-Gosselin, X. Taylor, Y. You, G. V. Di Prisco, X. Huang, S. Dutta, A. Wijeratne, J. Redding-Ochoa, S. S. Shahid, J. F. Codocedo, S. Min, G. E. Landreth, A. L. Mosley, Y. Wu, D. McKinzie, J. Rochet, **J. Zhang**, B. K. Atwood, J. Troncoso, C. A. Lasagna-Reeves, "Bassoon contributes to tau-seed propagation and neurotoxicity", *Nature Neurosciences* (2022) |doi:10.1038/s41593-022-01191-6.
13. * L. Alsaleh, C. Li, J. Couetil, Z. Ye, K. Huang, **J. Zhang**, C. Chen, T. S. Johnson, "Spatial transcriptomic analysis reveals associations between genes and cellular topology in breast and prostate cancers", *Cancers,* 2022, 14(19), 4856 |doi:10.3390/cancers14194856.
14. Y. Liu, T. Wang, B. Duggan, M. Sharpnack, K. Huang, **J. Zhang**, X. Ye, T. S. Johnson, "SPCS: A Spatial and Pattern Combined Smoothing Method for Spatial Transcriptomic Expression", *Brief Bioinfor.* 2022 Apr 4; bbac116. |doi: 10.1093/bib/bbac116.
15. X. Taylor, P. Cisternas, N. Jury, P, Martinez, X. Huang, Y. You, J. Redding-Ochoa, R. Vidal, **J. Zhang**, J. Troncoso, Cristian A. Lasagna-Reeves, "Activated Endothelial Cells Induce a Distinct Type of Astrocytic Reactivity", *Communications Biology*, volume 5, Article number: 282 (2022)| doi: 10.1038/s42003-022-03237-8.
16. T. S. Johnson, Y. Liu, T. Wang, B. Duggan, X. Ye, **J. Zhang**, K. Huang, "SPCS: A Spatial and Pattern Combined Smoothing Method for Spatial Transcriptomic Expression", *Briefings in Bioinformatics*, 2022 Apr 4; bbac116 | doi: 10.1093/bib/bbac116.
17. Y. Wu, M. Cheng, S. Huang, Z. Pei, Y. Zuo, J. Liu, K. Yang, Q. Zhu, **J. Zhang**, H. Hong, D. Zhang, K. Huang, L. Cheng, W. Shao, "Recent Advances of Deep Learning for Computational Histopathology: Principles and Applications", *Cancers,* 2022, 14, 1199. | doi.org/10.3390/cancers14051199
18. T. S. Johnson, C. Y. Yu, Z. Huang, S. Xu, T. Wang, C. Dong, W. Shao, M. A. Zaid, Y. Wang, C. Bartlett, Y. Zhang, Y. Liu, K. Huang, and **J. Zhang**, "Diagnostic Evidence GAuge of Single cells (DEGAS): a flexible deep transfer learning framework for prioritizing cells in relation to disease", *Genome Medicine*, 14:11 (2022) |doi.org/10.1186/s13073-022-01012-2.
19. Z. Liu, T. S. Johnson, W. Shao, M. Zhang, **J. Zhang*** and K. Huang*, "Optimal transport- and kernel-based early detection of mild cognitive impairment patients based on magnetic resonance and positron emission tomography images", *Alzheimer's Research & Therapy,* (2022) 14:4 |doi.org/10.1186/s13195-021-00915-3. (*co-corresponding authors)
20. X. Huang, K. Huang, T. Johnson, M. Radovich, **J. Zhang*,** J. Ma, Y*. Wang*, "ParsVNN: Parsimony Visible Neural Networks for Uncovering Cancer-Specific and Drug-sensitive

Genes and Pathways", *Nucl. Acid Res. in Genomics and Bioinformatics*, Vol.3, Issue 4, Dec. 2021, lqab097 |doi.org/10.1093/nargab/lqab097. (*co-corresponding author)

21. Y. Liu, X. Ye, C. Y. Yu, W. Shao, J. Hou, W. Feng, **J. Zhang**, X. Ye, K. Huang, "TPSC: a module detection method based on topology potential and spectral clustering in weighted networks and its application in gene co-expression module discovery", *BMC Bioinformatics*, Vol. 22:111, 2021 |doi: 10.1186/s12859-021-03964-5.
22. Z. Lu, X. Zhan, Y. Wu, J. Cheng, W. Shao, D. Ni, Z. Han, **J. Zhang,** Q. Feng, K. Huang, "BrcaSeg: A Deep Learning Approach for Tissue Quantification and Genomic Correlations of Histopathological Images", *Genomics, Proteomics & Bioinformatics*, 2021 Dec;19(6):1032-1042. Epub 2021 Jul 17 |doi: 10.1016/j.gpb.2020.06.026.
23. W. Shao, T. Wang, Z. Huang, Z. Han, **J. Zhang**, K. Huang, "Weakly Supervised Deep Ordinal Cox Model for Survival Prediction from Whole-slide Pathological Images", *IEEE Transaction on Medical Imaging*, 2021, Jul 15; PP |doi: 10.1109/TMI.2021.3097319.
24. C. Xu, S. Sun, T. S. Johnson, R. Qi, S. Zhang, **J. Zhang**, K. Yang, "The glutathione peroxidase Gpx4 in Treg cells restrains lipid peroxidation and ferroptosis to sustain Treg activation and suppression of antitumor immunity", *Cell reports*, 35(11), 15 June 2021, 109235 | doi:10.1016/j.celrep.2021.109235.
25. T. Wang, W. Shao, Z. Huang, H. Tang, **J. Zhang**, Z. Ding, K. Huang, "MOGONET Integrates Multi-omics Data Using Graph Convolutional Networks Allowing Patient Classification and Biomarker Identification", *Nature Communications,* 12, 3445 (2021) |doi:10.1038/s41467-021-23774.w
26. Y. Liu, X. Ye, X. Zhan, C. Y. Yu, **J. Zhang**, K. Huang, "TPQCI: A Topology Potential-Based Method to Quantify Functional Influence of Copy Number Variations", *Methods*, S1046-2023(21)00107-9 (2021) |doi:10.1016/j.ymeth.2021.04.015.
27. S. Storey, Z. Zhang, Z. Luo, D. Von Ah, M. Metzger, **J. Zhang**, A. Jakka, K. Huang, "Association of Comorbid Diabetes with Clinical Outcomes and Healthcare Utilization in Colonrectal Cancer Survivors", *Oncol. Nurs. Forum,* 2021 Mar 1;48(2):195-206|doi: 10.1188/21.ONF.195-206.
28. T. S. Johnson, S. Xiang, T. Dong, M. Cheng, T. Wang, K. Yang, D. Ni, K. Huang, **J. Zhang**, "Combined Differential Expression and Differential Co-expression Analysis on Gene Networks Reveals Changes in Cell Population Largely Explain Core Microglia Genes' Up-expression in Alzheimer's Disease Brains", *Scientific Reports*, 2021 Jan. 11;11:353 |doi: 10.1038/s41598-020-79740-x.
29. S. K. Sieberts, J. Schaff, M. Duda, et al., **J. Zhang**, et al., L. Omberg, "Crowdsourcing Digital Health Measures to Predict Parkinson's Disease Severity: The Parkinson's Disease Digital Biomarker DREAM Challenge", *NPJ Digital Medicine*, 4(53), 2021.
30. J. Cheng, Y. Liu, W. Huang, W. Hong, L. Wang, X. Zhan, Z. Han, D. Ni, K. Huang, **J. Zhang**, "Computational Image Analysis Identifies Histopathological Image Features Associated with Somatic Mutations and Patient Survival in Gastric Adenocarcinoma", *Front. Oncol.,* 31 March 2021 | doi:10.3389/fonc.2021.623382.
31. Z. Huang, Z. Han, T. Wang, P. Salama, K. Huang, and **J. Zhang,** "TSUNAMI: Translational Bioinformatics Tool Suite for Network Analysis and Mining", *Genomics Proteomics and Bioinformatics*, Mar. 2021|doi: 10.1016/j.gpb.2019.05.006.

32. T. S. Johnson, S. Xiang, B. R. Helms, Z. B. Abrams, P. Neidecker, R. Machiraju, Y. Zhang, K. Huang, and **J. Zhang**, "Spatial Cell Type Composition in Human Normal and Alzheimer Brains is Revealed Using Integrated Mouse and Human Single Cell RNA Sequencing", *Sci. Rep.*, 2020 Oct. 22; 10(1), 18014 |doi:10.1038/s41598-020-74917-w.
33. V. S. Jadhavi, P. B. C. Lin, T. Pennington, G. V. Di Prisco, A. J. Jannu, G. Xu, M. Moutinho, **J. Zhang,** B. K. Atwood, S. S. Puntambekar, S. J. Bissel, A. L. Oblak, G. E. Landreth, B. T. Lamb, "Trem2 Y38C Mutation and Loss of Trem2 Impairs neuronal Synapses in Adult Mice", *Mol. Neurodegen.*, 15(62), 2020 |doi:10.1186/s13024-020-00409-0.
34. W. Shao, T. Wang, L. Sun, T. Dong, Z. Han, Z. Huang, **J. Zhang**, D. Zhang, and K. Huang, **"**Multi-task Multi-modal Learning for Joint Diagnosis and Prognosis of Human Cancers", *Med. Imaging Analysis*, 2020 Oct; 65:101795 |doi: 10.1016/j.media.2020.101795.
35. P. Cisternas, X. Taylor, A. Perkins, O. Maldonado, E. Allman, R. Cordova, Y. Marambio, B. Munoz, T. Pennington, S. Xiang, **J. Zhang**, R. Vidal, B. Atwood, and C. A. Lasagna-Reeves, "Vascular Amyloid Accumulation Alters The GABAergic synapse and Induces Hyperactivity in A Model of Cerebral Amyloid Angiopathy", *Aging Cell*, 2020 Sep 10; e13233 |doi: 10.1111/acel.13233.
36. X. Taylor, P. Cisternas, Y. You, Y. You, S. Xiang, **J. Zhang**, R. Vidal, and C. A. Lasagna-Reeves, "A1-Reactive Astrocytes and A Loss of TREM2 Are Associated with An Early State of Pathology in A Mouse Model of Cerebral Amyloid Angiopathy", *J. Neuroinflammation*, 2020 Jul 25;17(1):223 |doi: 10.1186/s12974-020-01900-7.
37. L. Sun*, **J. Zhang***, W. Chen*, Y. Chen, X. Zhang, M. Yang, M. Xiao, F. Ma, Y. Yao, M. Ye, Z. Zhang, K. Chen, F. Chen, Y. Ren, S. Ni, Xi Zhang, Z. Yan, Z. Sun, H. Zhou, H. Yang, S. Xie, M E. Haque, K. Huang, and Y. Yang, "Attenuation of SMARCA4 and ERK-ETS Signaling Suppress Dopaminergic Degeneration in Drosophila Parkinson's Disease Models", *Aging Cell*, 2020;19:e13210 |doi: 10.1111/acel.13210. (*co-first author).
38. J. Cheng, Z. Han, R. Mehra, W. Shao, M. Cheng, Q. Feng, D. Ni, K. Huang, L. Cheng, and **J. Zhang**, "Computational Analysis of Pathological Images Enables A Better Diagnosis of TFE3 Xp11.2 Translocation Renal Cell Carcinoma", *Nat. Comm.*, (2020)11:1778 |doi:10.1038/s41467-020-15671-5.
39. Z. Lu, S. Xu, W. Shao, Y. Wu, **J. Zhang**, Z. Han, Q. Feng, K. Huang, "Deep-Learning-Based Characterization of Tumor-Infiltrating Lymphocytes in Breast Cancers from Histopathology Images and Multiomics Data", *JCO Clin Cancer Inform.* 2020 May; 4:480-490 |doi: 10.1200/CCI.19.00126.
40. W. Shao, S. Xiang, Z. Zhang, K. Huang, **J. Zhang**, "Hyper-graph Based Sparse Canonical Correlation Analysis for The Diagnosis of Alzheimer's Disease from Multi-dimensional Genomic Data", *Methods*, 2020 Apr 28; S1046-2023(20)30021-9 |doi: 10.1016/j.ymeth.2020.04.008.
41. Z, Huang, T. Johnson, Z. Han, B.R. Helm, S. Cao, C. Zhang, P. Salama, M. Rizkalla, C. Y. Yu, J. Cheng, S. Xiang, X. Zhan, **J. Zhang**, and K. Huang, "Deep Learning-based Cancer Survival Prognosis from RNA-seq Data: Approaches and Evaluations", *BMC Medical Genomics*, **13**, 41 (2020) |doi:10.1186/s12920-020-0686-1.
42. W. Shao, Z. Han, J. Cheng, L. Cheng, T. Wang, L. Sun, Z. Lu, **J. Zhang**, D. Zhang, and K. Huang, "Integrative Analysis of Pathological Images and Multi-dimensional Genomic Data

for Early-stage Cancer Prognosis", *IEEE Trans Med Imaging.* vol. 39, no. 1, pp. 99-110, Jan. 2020 |doi: 10.1109/TMI.2019.2920608.

43. E. Kouba, A. Lopez-Beltran, R. Montironi, F. Massari, K. Huang, M. Santoni, M. Chovanec, M. Cheng, M. Scarpelli, **J. Zhang**, A. Cimadamore, and L. Cheng, "Liquid Biopsy in The Clinical Management of Bladder Cancer: Current Status and Future Developments", *Exp. rev. Mol. Diag.*, 17 Oct 2019 |doi: 10.1080/14737159.2019.1680284.
44. B. R. Helm, X. Zhan, P. H. Pandya, M. E. Murray, K. E. Pollok, J. L. Renbarger, M. J. Ferguson, Z. Han, Dong N, **J. Zhang**, and K. Huang, "Gene Co-expression Networks Restructured by Gene Fusion in Rhabdomyosarcoma Cancers", *Genes* (Basel). 2019 Aug 30;10(9). pii: E665 |doi: 10.3390/genes10090665.
45. T. Wang, T. S. Johnson, W. Shao, Z. Lu, B. R. Helm, **J. Zhang*,** and K. Huang*, "BERMUDA: A Novel Deep Transfer Learning Method for Single-cell RNA Sequencing Batch Correction Reveals Hidden High-resolution Cellular Subtypes", *Genome Biology*, (2019) 20:165 |doi: 10.1186/s13059-019-1764-6.(*co-correspondent author)
46. Y. Han; X. Ye, C. Wang, Y. Liu, S. Zhang, W. Feng, K. Huang, and **J. Zhang**, "Integration of Molecular Features with Clinical Information for Predicting Outcomes for Neuroblastoma Patients", *Biol. Direct,* 2019 Aug 23;14(1):16 |doi: 10.1186/s13062-019-0244-y.
47. X. Zhan, J. Cheng, Z. Huang, Z. Han, B. Helm, X. Liu, **J. Zhang**, T. Wang, D. Ni, and K. Huang, "Correlation Analysis of Histopathology and Proteogenomics Data for Breast Cancer", *Mol. & Cel. Proteomics*, 2019, Aug 9; 18(8 suppl. 1): S37-S51 |doi: 10.1074/mcp.RA118.001232.
48. T. Wang, **J. Zhang**, and K. Huang, "Generalized Gene Co-expression Analysis Via Subspace Clustering Using Low-rank Representation", *BMC Bioinformatics,* 20(Suppl. 7):196 |doi:10.1186/s12859-019-2733-5, 2019.
49. T. S. Johnson, T. Wang, Z. Huang, C. Y. Yu, Y. Wu, Y. Han, Y. Zhang, K. Huang, and **J. Zhang**, "LAmbDA: Label Ambiguous Domain Adaptation Dataset Integration Reduces Batch Effects and Improves Subtype Detection", *Bioinformatics*, 2019, Nov. 1; 35(22):4696-4706. |doi: 10.1093/bioinformatics/btz295.
50. Z. Huang, X. Zhan, S. Xiang, T. Johnson, B. Helm, C.Y. Yu, **J. Zhang**, P. Salama, M. Rizkalla, Z. Han, and K. Huang "SALMON: Survival Analysis Learning with Multi-Omics Neural Networks on Breast Cancer", *Front Genet.* 2019 Mar 8; 10:166. |doi: 10.3389/fgene.2019.00166.
51. T. Wang, T. Johnson, **J. Zhang**, and K. Huang, "Topological Methods for Visualization and Analysis of High Dimensional Single-Cell RNA Sequencing Data". *Pacific Symp Biocomput.* 2019; 24:350-361.
52. Y. Han, X. Ye, J. Cheng, W. Feng, S. Zhang, Z. Han, **J. Zhang**, and K. Huang, "Integrative Analysis Based on Survival Associated Co-expression Gene Modules for Predicting Neuroblastoma Patient's Survival Time", *Biol. Direct*, 2019 Feb 13;14(1):4. |doi: 10.1186/s13062-018-0229-2.
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