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EDUCATION:

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

RESEARCH INTERESTS:

My research is focused on developing and applying translational bioinformatics methods to identify disease genes, pathways, and biomarkers with applications in cancers, neurodegenerative diseases, and other types of diseases.

RESEARCH EXPERIENCE:

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

- Translational bioinformatics research on neurodegenerative diseases and cancers
- Integrative multi-modal data analysis and machine learning approach for disease mechanistic study, disease subtyping and biomarker identification
- Software and pipeline development for integrative omic data mining, network analysis, and computational pathology image analysis

Research Scientist – Regenstrief Institute 2018- present

Assistant Research Professor – Department of Biomedical Informatics, OSU 2015-2017

- Developed network-based pan-cancer research program to understand cancer physiology and provide therapeutic targets
- Developed gene co-expression network guided tool for functional copy number variance discovery
- Mined condition-specific 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 various types of NGS data for cancer biomarker and 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 2004-2005
Department of Microbiology, The Ohio State University

- 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:

- Journal Associate Editor for *Frontiers in Genetics* 2021-present

- Journal Associate Editor for BMC Medical Genomics 2019-present
- 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
- Reviewer for various journals and conferences including
 - Nature Communications, Nature Microbiology
 - 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)

RESEARCH 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
- Various undergraduate/graduate courses guest lecturer, 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:

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

1. 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 transfer learning framework to infer impressions of cellular and patient phenotypes between patients and single cells”, *Genome Medicine*, accepted

2. 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)
3. 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)
4. 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.
5. 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*, preprint online 17 July 2021. |doi: 10.1016/j.gpb.2020.06.026.
6. 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.
7. 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.
8. 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”, *Nat. Comm.*, 12, 3445 (2021) |doi:10.1038/s41467-021-23774.w
9. 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.
10. 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.
11. 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”, *Sci. Rep.*, 2021 Jan. 11;11:353 |doi: 0.1038/s41598-020-79740-x.
12. 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.
13. 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.
14. 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.
 15. 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.
 16. 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.
 17. 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.
 18. 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/accel.13233.
 19. 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.
 20. 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/accel.13210. (*co-first author).
 21. 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.
 22. 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.
 23. 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.

24. 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.
25. 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.
26. 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.
27. 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.
28. 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)
29. 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.
30. 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.
31. 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.
32. 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.
33. 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.
34. 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.
35. 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.
36. S. Xiang, Z. Huang, H. Wang, Z. Han, C. Y. Yu, D. Ni, K. Huang, and **J. Zhang**, "Condition-Specific Gene Co-expression Network Mining Identified Key Pathways and Regulators in Alzheimer's Disease", *BMC Med. Genomics* 2018 Dec 31;11(Suppl 6):115. |doi: 10.1186/s12920-018-0431-1.
 37. W. Hankey, Z. Chen, M. Bergman, M. Fernandez, B. Hancioglu, X. Lan, A. Jegga, **J. Zhang**, V. Jin, B. Aronow, Q. Wang, and J. Groden, "Chromatin-associated APC Regulates Gene Expression in Collaboration with Canonical WNT Signaling and AP-1", *Oncotarget*, 2018 Jul 27;9(58):31214-31230.
 38. W. Hankey, M. McIlhatton, K. Ebede, B. Kennedy, B. Hancioglu, **J. Zhang**, G. Brock, K. Huang, and J. Groden, "Mutational Mechanisms That Activate Wnt Signaling and Predict Outcomes in Colorectal Cancer Patients", *Cancer Research*, 2018 Feb 1;78(3):617-630 |doi: 10.1158/0008-5472.CAN-17-1357.
 39. Z. Han, T. Johnson, **J. Zhang**, and K. Huang, "Functional Virtual Flow Cytometry – A Visual Analytic Approach for Characterizing Single Cell Gene Expression Patterns", *Biomed Res Int*. 2017;2017:3035481 |doi: 10.1155/2017/3035481. Erratum in: *Biomed Res Int*. 2017;9393251.
 40. J. Cheng*, **J. Zhang***, Y. Han, X. Wang, X. Ye, Y. Meng, A. Pawani, Z. Han, Q. Feng, and K. Huang, "Integrative Analysis of Histopathological Images and Genomic Data for Predicting Clear Cell Renal Cell Carcinoma Prognosis", *Cancer Res.*, 2017 Nov; 77(21): e91-e100. (*co-first authors)
 41. **J. Zhang**, and K. Huang, "Pan-cancer Analysis of Frequent DNA Co-methylation patterns Reveals Consistent Epigenetic Landscape Changes in Multiple Cancers", *BMC Genomics*, 2017 Jan 25;18(Suppl 1):1045 |doi: 10.1186/s12864-016-3259-0.
 42. J. R. Karras, M. Schrock, B. Batar, **J. Zhang**, K. La Perle, T. Druck, K. Huebner. "Fhit Loss-Associated Initiation and Progression of Neoplasia In Vitro". *Cancer Sci*. 2016, Nov; 107(11): 1590-1598.
 43. J. A. Deiuliis, R. Syed, D. Duggineni, J. Rutsky, P. Rengasamy, **Zhang J**, K. Huang, B. Needleman, D. Mikami, K. Perry, et al. "Visceral Adipose MicroRNA 223 Is Upregulated in Human and Murine Obesity and Modulates the Inflammatory Phenotype of Macrophages", *PLoS One* 2016 Nov 3; 11(11): e0165962.
 44. **J. Zhang**, Z. Abrams, J. D. Parvin, and K. Huang. "Integrative analysis of somatic mutations and transcriptomic data to functionally stratify breast cancer patients", *BMC Genomics*, Aug 22;17 Suppl 7:513. doi: 10.1186/s12864-016-2902-0.
 45. Z. Han, **J. Zhang**, G. Sun, G. Liu, K. Huang, "A Matrix Rank Based Concordance Index for Evaluating and Detecting Conditional Specific Co-expressed Gene Modules". *BMC Genomics*. 2016 Aug 22;17 Suppl 7: 519.
 46. **J. Zhang**, and K. Huang, "Normalized lmQCM: An Algorithm for Detecting Weak Quasi-Cliques in Weighted Graph with Applications in Gene Co-Expression Module Discovery in Cancers". *Cancer Inform*. 2016 Jul 24;13(Suppl 3):137-46.
 47. S. Shroff *, **J. Zhang***, and K. Huang, "Gene Co-Expression Analysis Predicts Genetic Variants Associated with Drug Responsiveness in Lung Cancer", *AMIA Joint Summits Transl*

- Sci Proc.* 2016 Jul 20; 2016: 32-41. (* equal contributions, Winner of the *Marco Ramoni Distinguished Paper award*)
48. C. Paisie, M. Schrock, J. Karras, **J. Zhang**, S. Miuma, I. Ouda, C. Waters, J. Saldivar, T. Druck, and K. Huebner, “Exome-wide Single-base Substitutions in Tissues and Derived Cell Lines of The Constitutive Fhit Knockout Mouse”, *Cancer Science*, 2016 Apr. 107(4): 528-35 |doi: 10.1111/cas.12887, 2016.
 49. P. Gasparini, M. Fassan, L. Cascione, G. Guler, S. Balci, C. Irkkan, C. Paisie, F. Lovat, C. Morrison, **J. Zhang**, A. Scarpa, C. M. Croce, C. L. Shapiro, and K. Huebner, “Androgen Receptor Status Is A Prognostic Marker in Non-basal Triple Negative Breast Cancers and Determines Novel Therapeutics Options”. *PLoS One*: Feb 5; 9(2): e88525, 2014 | doi: 10.1371/journal.pone.0088525.
 50. S. Miuma, J. C. Saldivar, J. Karras, C. E. Waters, Y. Wang, V. Jin, J. Sun, T. Druck, **J. Zhang**, K. Huebner, “Fhit Deficiency-induced Global Genome Instability Promotes Mutation and Clonal Expansion”, *PloS One*, Nov.14; 8(11): e80730, 2013 |doi: 10.1371/journal.pone.0080730
 51. T. Bailey, P. Krajewski, I. Ladunga, C. Lefebvre, Q. Li, T. Liu, P. Madrigal, C. Taslim, and **J. Zhang**, “Practical Guidelines for The Comprehensive Analysis of ChIP-seq Data”, *PloS Comp. Biol.* Nov 14, 2013, 9(11): e1003326 |doi: 10.1371/journal.pcbi.1003326
 52. J. Deiuliis, G. Mihai, **J. Zhang**, C. Taslim, J. Varghese, A. Maiseyeu, K. Huang, and S. Rajagopalan, “Renin-sensitive MicroRNAs Correlate with Atherosclerosis Plaque Progression”, *J. Hum Hypertens*, Apr 28(4): 251-258, 2014. |doi:10.1038/jhh.2013.97
 53. W. I. Towler, **J. Zhang**, D. J. R. Ransburgh, A. E. Toland, C. Ishioka, N. Chiba, and J. D. Parvin, “Analysis of BRCA1 Variants in Double Strand Break Repair by Homologous Recombination and Single Strand Annealing”, *Human Mutation*, 34(3): 439-45, 2013 |doi: 10.1002/humu.22251
 54. Y. Xiang, **J. Zhang**, and K. Huang, “Mining Tissue-tissue Gene Co-expression Network for Tumor Microenvironment Study and Biomarker Prediction”, *BMC Genomics*, 14(S5): S4, 2013 |doi: doi: 10.1186/1471-2164-14-S5-S4
 55. **J. Zhang**, S. Ni, Y. Xiang, J. D. Parvin, Y. Yang, Y. Zhou, and K. Huang, “Gene Co-Expression Analysis Predicts Chromosomal Aberration Loci Associated with Colon Cancer Metastasis”, Special Issue for ICIBM Conference, International Journal of Computational Biology and Drug Design, *Int J Comput Biol Drug Des.* 6(1-2): 60-71, 2013 | doi: 10.1504/IJCBDD.2013.052202.
 56. H. Liu*, **J. Zhang***, G. F. Heine, M. Arora, H. G. Ozer, R. Onti-Srinivasan, K. Huang and J. D. Parvin, “Chromatin Modification by SUMO-1 Stimulates The Promoters of Translation Machinery Genes”, *Nucl. Acids Res.*, 40(20): 10172-10186, 2012 | doi: 10.1093/nar/gks819. (* equal contributions)
 57. M. Arora*, **J. Zhang***, G. F. Heine, G. Ozer, H. Liu, K. Huang and J. D. Parvin, “Promoters Active in Interphase Are Bookmarked During Mitosis by Ubiquitination”, *Nucl. Acids Res.*, 40(20): 10187-10202, 2012 | doi: 10.1093/nar/gks820. (* equal contributions)
 58. **J. Zhang**, K. Lu, Y. Xiang, M. Islam, S. Kotian, Z. Kais, C. Lee, M. Arora, H. Liu, J. D. Parvin, and K. Huang, “Weighted Frequent Gene Co-expression Network Mining to Identify

- Genes Involved in Genome Stability”, *PLoS Comput. Biol.* 8(8): e1002656. doi:10.1371/journal.pcbi.1002656, 2012 | doi: 10.1371/journal.pcbi.1002656.
59. **J. Zhang**, J. D. Parvin, and K. Huang, “Redistribution of H3K4me2 on Neural Tissue Specific Genes During Mouse Brain Development”, *BMC Genomics*, 13 (suppl.8): S5, 2012 | doi: 10.1186/1471-2164-13-S8-S5.
 60. K. E. Wenzke, C. Cantemir-Stone, **J. Zhang**, C. B. Marsh, and K. Huang, “Identifying Common Genes and Networks in Multi-organ Fibrosis”, *AMIA Summits Transl. Proc.* 2012:106-15, 2012.
 61. **J. Zhang**, S. Ni, J. D. Parvin, Y. Yang, and K. Huang, “Predicting Parkinson’s Disease Related Genes Using Frequent Gene Co-expression Analysis”, *Proceedings of IEEE Bioinformatics and Biomedicine (BIBM)*, pp.1042-1044, 12-15 Nov. 2011.
 62. **J. Zhang**, T. Knobloch, J. D. Parvin, C. Weghorst, K. Huang, “Identifying Smoking Associated Gene Co-expression Networks Related to Oral Cancer Initiation”. *Proceedings of the IEEE Bioinformatics and Biomedicine (BIBM)*, Atlanta, 2011 |doi: /10.1109/BIBMW.2011.6112553.
 63. R. Li, W. E. Ackerman, T. L. Summerfield, L. Yu, P. Galati, **J. Zhang**, K. Huang, R. Romero, and D. Kniss, “Inflammatory Gene Regulatory Networks in Amnion Cells Following Cytokine Stimulation: Translational Systems Approach to Modeling Human Parturition”, *PLoS One*, 2011:6(6): e20560, 2011.
 64. P. R. Payne, K. Huang, K. Keen-Circle, A. Kundu, **J. Zhang**, and T. B. Borlawsky, “Multi-Dimensional Discovery of Biomarker and Phenotype Complexes”, *BMC Bioinformatics*, 11, Suppl 9: S3, 2010.
 65. H.-Y. Wu, **J. Zhang**, K. Huang, “Peak Detection on ChIP-Seq Data Using Wavelet Transformation”, *Proceedings of the Workshop on Data Mining in Next Generation Sequencing Data* in IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Hong Kong, 2010.
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PEER-REVIEWED CONFERENCES PRESENTATIONS, PUBLICATION AND ABSTRACTS:

1. J. Couetil, T. Johnson, **J. Zhang**, K. Huang, "DEGAS: Mapping clinical metrics to spatial transcriptomics with deep learning", International Society for Computational Biology (ISCB) Rocky Mountain Bioinformatics Conference 2021, Dec.2-4, Snowmass, CO.
2. J. Liu, D. Robertson H. Wu, **J. Zhang**, "Text mining and portal development for gene-specific publications on Alzheimer's disease", The 6th International Workshop on Semantics-Powered Health Data Analytics (SEPDA 2021).
3. X. Huang, J. Liu, N. Jury, C. Lasagna-Reeves, **J. Zhang**, "Understanding the Uncoupling of Tauopathy And Dementia Through Comparative Analysis of Subgroups of Atypical Alzheimer's Disease Patients", Alzheimer's Association International Conference, Jul 26-30. Denver, USA.

4. Z. Liu, W. Shao, **J. Zhang**, M. Zhang, K. Huang, “Transfer Learning via Optimal Transportation for Integrative Cancer Patient Stratification”, International Joint Conference on Artificial Intelligence (IJCAI) 2021, Aug 21st-26th, Montreal, Canada.
5. 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”, AAIC Neuroscience Next, Nov.9-11, 2020.
6. Z. Huang, W. Shao, Z. Han, P. Salama, **J. Zhang**, K. Huang, “Survival prognosis with multi-omics data in lung adenocarcinoma reveals important co-expression modules”, AI and Big Data in Cancer: From Innovation to Impact, Boston, Mar. 29-30, 2020.
7. S. Xiang, D. Ni, K. Huang, **J. Zhang**, “Mining of differentially co-expressed gene modules reveals perturbed functional network and key regulators in Alzheimer's disease brains”, *Alzheimer's and Dementia*, 2020 Dec Nov;16(S3): e047095. Doi: 10.1002/alz.047095.
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12. X. Zhan, Y. Liu, C. Y. Yu, T. Wang, **J. Zhang**, D. Ni and K. Huang, “A pan-kidney cancer study identifies subtype specific perturbations on pathways with potential drivers in renal cell carcinoma”, ICIBM, 2020
13. Z. Huang, P. Salama, W. Shao, **J. Zhang**, K. Huang, “Low-rank Reorganization via Proportional Hazards Non-negative Matrix Factorization Unveils Survival Associated Gene Clusters”, NeurIPS 2020 Meeting
14. Y. You, S. Xiang, A. Perkins, Y. You, E. Allman, P. Cisternas, A. Oblak, J.C. Troncoso, **J. Zhang** and C.A. Lasagna-Reeves, “The role of tau interactome in the neurotoxicity and propagation of tau oligomers in neurodegenerative tauopathies”, Society for Neuroscience Conference, San Francisco, 2019.
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27. C. Cantemir, N. Marzlin, **J. Zhang**, K. Wenzke, K. Huang, C. B. Marsh, “Unique Gene Signature For Multi-Organ Fibrosis”, American Thoracic Society 2012 International Conference, May 18-23, 2012 o San Francisco, California.
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RECENT GRANTS:

1. IUSCCC TMM Big Data Grant, AI-based characterization of the tumor microenvironment of melanoma (Role: PI, 07/2021-06/2022)
2. NIH U54 Pilot Integrate genomic data analysis of pediatric sarcomas to identify functional CNVs and driving regulators (Role: PI, 06/2019-05/2020)

2. NIA R01 Tau-seed protein interactome and its role in neurodegenerative tauopathies (Role: Co-I, 09/2020-08/2025)
3. NIA U54 Alzheimer's Disease Drug Discovery Center (Role: Co-I, 09/2019-08/2024)
4. American Cancer Society Internal Research Grant (Role: contact PI, 06/2018-05/2019)
5. NCI ITCR U01 Informatics Links between Histological Features and Genetics in Cancers (Role: co-I, 05/2015 – 04/2018)