Jie Zhang, Ph.D.

Department of Medical and Molecular Genetics 4846 Snowberry Bay Ct.

School of Medicine Carmel, IN 46033

Indiana University Phone: 614-216-9333 (cell)

410 W. 10th Street 317-274-2839 (office)

Indianapolis, OH 46202 Email: jizhan@iu.edu

# 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, neurological diseases, and other types of diseases.

# RESEARCH EXPERIENCE:

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

* Translational bioinformatics research on neurological diseases and cancers
* Integrative genomic analysis for precision medicine
* Software and visualization tools for mining gene expression networks and the associated genetic variations

**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 Group2002-2004

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:

* 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 chronical order):**

1. 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. Reports*, 2020 Oct. 22; 10(1), 18014. doi.org/10.1038/s41598-020-74917-w.
2. 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.
3. 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.
4. 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.
5. 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).
6. 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”, *Nature Communications*, (2020)11:1778 doi:10.1038/s41467-020-15671-5.
7. 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.
8. 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*, in press.
9. 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), doi:10.1016/j.ymeth.2020.04.008.
10. 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.
11. 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
12. 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.
13. 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)
14. 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.*2019 Jun 3; doi: 10.1109/TMI.2019.2920608. PubMed PMID: 31170067.
15. 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.
16. 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*, Aug 9; 18(8 suppl. 1): S37-S51. doi: 10.1074/mcp.RA118.001232.
17. 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.
18. 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.
19. 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.

# 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.

1. 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.
2. 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.
3. 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.
4. 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.

# 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;2017:9393251.

# J. Chen\*, 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 Research*, 2017 Nov; 77(21): e91-e100. (\*co-first authors)

# 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.

1. 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.
2. 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.
3. **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.
4. 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.
5. **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.
6. 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*)
7. 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.
8. 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.
9. 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
10. 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
11. J. Deiuliis, G. Mihai, **J. Zhang**, C. Taslim, J. Varghese, A. Maiseyeu, K. Huang, and S. Rajagopalan, “Renin-sensitive microRNAs correlate with atherosclerosis plague progression”, *J. Hum Hypertens*, Apr 28(4): 251-258, 2014.
12. 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.
13. 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.
14. **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.*](http://www.ncbi.nlm.nih.gov/pubmed/?term=Gene+co-expression+analysis+predicts+chromosomal+aberration+loci+associated+with+colon+cancer+metastasis) 6(1-2): 60-71, 2013.
15. 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. (\* equal contributions)
16. 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. (\* equal contributions)
17. **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.
18. **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.
19. 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.
20. **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.
21. **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.
22. 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.
23. 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.
24. 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.
25. **J. Zhang**, Y. Xiang, L. Ding, K. Keen-Circle, T. B. Borlawsky, H. G. Ozer, R. Jin, P. Payne, K. Huang, “Prognostic Biomarkers for Chronic Lymphocytic Leukemia Using Gene Co-expression Network Analysis”, *BMC Bioinformatics*, 11, Suppl: S5, 2010. (*AMIA Summit on Translational Bioinformatics Distinguished Paper Award*)
26. F. Rappaport, **J. Zhang**, M. H. Vos, R. B. Gennis, V. B. Borisov, “Heme-heme and heme-ligand interactions in the di-heme oxygen-reducing site of cytochrome bd from Escherichia coli revealed by nanosecond absorption spectroscopy”, *Biochim Biophys Acta.* 1797 (9): 1657-64, 2010.
27. **J. Zhang,** Y. Xiang, R. Jin, and K. Huang, “Using frequent co-expression network to identify gene clusters for breast cancer prognosis”, *IEEE Proceedings, International Joint Conferences on Bioinformatics, System Biology and Intelligent Computing*, 428-434, 2009.
28. A. M. Arutyunyan, V. B. Borisov, V. I. Novoderezhkin, J. Ghaim, **J. Zhang**, R. B. Gennis, and A. A. Konstantinov, “Strong excitonic interactions in the oxygen-reducing site of bd-type oxidase: the Fe-to-Fe distance between hemes d and b595 is 10 A”, *Biochemistry*, 2008; 47(6):1752-1759.
29. K. Yang, **J. Zhang**, A. S. Vakkasoglu, R. Hielscher, J. P. Osborne, J. Hemp, [H](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Miyoshi%20H%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus). Miyoshi, P. Hellwig, and R. B. Gennis, “Glutamate 107 in subunit I of the cytochrome bd quinol oxidase from Escherichia coli is protonated and near the heme d/heme b595 binuclear center”, *Biochemistry*, 2007; 46(11): 3270-3278.
30. I. Belevich, V. B. Borisov, **J. Zhang**, K. Young, A. A. Konstantinov, R. B. Gennis, and M. I. Verkhovsky, “Time-resolved electrometric and optical studies on cytochrome bd suggest a mechanism of electron-proton coupling in the di-heme active site”, *PNAS*, 2005; 102(10): 3657-3662.
31. **J. Zhang,** P. Hellwig, J. P. Osborne, and R. B. Gennis, “Arginine 391 in subunit I of the cytochrome *bd* quinol oxidase from *Escherichia coli* stabilizes the reduced form of the hemes and is essential for quinol oxidase activity”, *Journal of Biological Chemistry*, 2004; 279(52): 53980-53987.
32. **Zhang**, B. Barquera, and R. B. Gennis, “Gene fusions with β–lactamase show that the cytochrome *bd* quinol oxidase from *E. coli* has nine transmembrane helices with the O2 reactive site near the periplasmic surface”, *FEBS* *Letters*, 2004: 561(1-3): 58-62.
33. **J. Zhang**, J. P. Osborne, R. B. Gennis, and X. Wang, “Proton NMR study of the heme environment on bacterial quinol oxidases”, *Archives of Biochemistry and Biophysics*, 2004; 421(2): 186-191.
34. **J. Zhang**, W. Oettmeier, R. B. Gennis, and P. Hellwig, “FTIR spectroscopic evidence for the involvement of an acidic residue in quinone binding in cytochrome bd quinol oxidase of *Escherichia coli*”, *Biochemistry*, 2002: 41(14); 4612-4617.
35. V. B. Borisov, U. Liebl, F. Rappaport, J. Martin, **J. Zhang,** R. B. Gennis, A. A. Konstantinov, and M. H. Vos, “Interactions between heme d and heme b595 in quinol oxidase bd from *Escherichia coli*: A femtosecond photoselection study”, *Biochemistry*, 2002; 41(5): 1654-1662.
36. **J. Zhang**, P. Hellwig, J. P. Osborne, H. Huang, P. Moenne-Loccoz, A. A. Konstantinov, and R. B. Gennis, “Site-directed mutation of the highly conserved region near the Q-loop of the cytochrome bd quinol oxidase from *Escherichia coli* specifically perturbs heme b595”, *Biochemistry*, 2001; 40(29): 8548-8556.

**PEER-REVIEWED CONFERENCES PRESENTATIONS AND ABSTRACTS:**

1. Z. Liu, W. Shao, **J. Zhang**, M. Zhang, K. Huang, “Transfer Learning via Optimal Transportation for Integrative Cancer Patient Stratification”, Association for the Advancement of Artificial Intelligence (AAAI) 2021.
2. S. Xiang, D. Ni, K. Huang, **J. Zhang**, “Mining of differentially expressed gene modules reveals perturbed functional network and key regulators in Alzheimer's disease brains”, Alzheimer Association International Conference, Amsterdam, Jul. 26-30, 2020.
3. 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.
4. Y. Liu, C. Y. Yu, W. Shao, J. Hou, W. Feng, **J. Zhang**, X. Ye and 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 in Gene Co-expression module Discovery”,ICIBM, 2020
5. 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
6. 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
7. 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.
8. X. Taylor, P. Cisternas, Y. You, A. Perkins, S. Xiang, **J. Zhang**, A. Oblak, R. Vidal, C. Lasagna-Reeves, “Early Astrocytic Alterations and Loss of TREM2 are associated to Cerebral Amyloid Angiopathy”, Society for Neuroscience Conference, San Francisco, 2019
9. Z. Huang, T. Johnson, Z. Han, B. Helm, S. Cao, C. Zhang, P. Salama, M. Rizkalla, C. Yu, J. Cheng, S. Xiang, X. Zhan, **J. Zhang**, K. Huang, “Deep Learning-based Cancer Survival Prognosis from RNA-seq Data: Approaches and Evaluations”, ICIBM 2019, Columbus, OH.
10. B. Helm, X. Zhan, P. Pandya, K. Pollok, M. Murray, M. Marshall, M. Ferguson, Z. Han, J. Renbarger, K. Huang, **J. Zhang**, “Gene co-expression network reconstructed by gene fusion in alveolar rhabdomyosarcoma”, Gordon Research Conference on Cancer Genomics and Epigenetics, Lucca 2019.
11. T. Johnson, Z. Abrams, B. Helm, P. Neidecker, R. Machiraju, Y. Zhang, K. Huang, **J. Zhang**, “Integration of Mouse and Human Single-cell RNA Sequencing Infers Spatial Cell-type Composition in Human Brains”, RECOMP 2019, Washington DC.
12. J. Cheng, **J. Zhang**, Q. Feng, K. Huang, “Predicting Gastric Cancer Prognosis by Integrating Automated Histopathological Image Features and Genomic Data”, Bioimaging Informatics Conference, Banff, Canada, 2017.
13. **J. Zhang**, Z. Han, K. Huang, “Gene Co-expression Network Guided Functional CNV Discovery”, Cold Spring Harbor Asia AACR Joint Meeting - Big Data, Computation and Systems Biology in Cancer, Dec. 2015.
14. F. Cerciello, M. Sharpnack, A. Srivastava, S. G. Codreanu, L. Araujo, J. M. Amann1, **J. Zhang**, D. C. Liebler, C. A. Maher, R. Machiraju, K. Huang, K. R. Coombes,D. P. Carbone, “Correlation of gene and protein tissue expression for clinical treatment decisions in early stage lung cancers”, 14th Human Proteome Organization (HUPO) world congress, Vancouver, Sept., 2015
15. **J. Zhang**, T. Huang, R. Machiraju, K. Huang, “Estrogen Induced RNA Polymerase II Stalling in Breast Cancer Cell Line MCF7”, Z. Han, L. Tian, 10th International Symposium on Bioinformatics Research and Applications, Zhangjiajie, China, Jun.,2014
16. F. Cerciello, S. G. Codreanu, L. Araujo, J. M. Amann, N. S. Ranbaduge, O. E. Branson, A. S. Yilmaz, **J. Zhang**, D. C. Liebler, K. Huang, M. A. Freitas, K. R. Coombes, V. H. Wysocki, D. P. Carbone, “Integrated gene and protein tissue expression analysis for adjuvant treatment decisions in early stage lung cancer”. US HUPO 10th Annual Conference, Seattle, Apr. 2014.
17. A. S. Yilmaz, **J. Zhang**, L. Araujo, F. Cerciello, J. M. Amann, K. Huang, D. P. Carbone, “Search for prognostic and predictive gene signatures in early stage non-small cell lung cancer”, Ohio State University Comprehensive Cancer Center Annual Scientific Meeting, Columbus, Feb. 2014
18. **J. Zhang**, J. D. Parvin, K. Huang, “Brest Cancer patient stratification using somatic mutations and gene interaction networks”, Cold Spring Harbor Conference on Genome Informatics, Oct. 2013.
19. Y. Xiang\*, **J. Zhang\***, K. Huang, “Mining tissue-tissue gene co-expression network for tumor microenvironment study and biomarker prediction”, International Conference on Bioinformatics, 2013. (\*equal contributions).
20. H. Liu, **J. Zhang,** G. F. Heine, M. Arora, K. Huang,J. D. Parvin, “SUMOylation of chromatin in human genome through cell cycle”**,** [Ohio Collaborative Conference on Bioinformatics, 2010](http://www.ohiobioinformaticsconsortium.org/occbio/).
21. M. Arora, **J. Zhang,** G. F. Heine, H. Liu, K. Huang, J. D. Parvin, “Changes in chromatin ubiquitination in the human genome through cell cycle”, [Ohio Collaborative Conference on Bioinformatics, 2010](http://www.ohiobioinformaticsconsortium.org/occbio/)
22. **J. Zhang**, L. Ding, K. Keen-Circle, T. Borlawsky, Y. Xiang, H. G. Ozer, R. Jin, P. Payne, K. Huang, “Predicting Biomarkers for Chronic Lymphocytic Leukemia Using Gene Co-expression Network Analyses”, AMIA Annual Summit on Translational Bioinformatics, 2010.
23. K. Huang, R. Liu, **J. Zhang**, C. Zhang, “Tissue-Tissue Gene Co-expression Network for Tumor Microenvironment Study”, AMIA Annual Summit on Translational Bioinformatics, 2010.
24. K. Huang, J.Wu, **J. Zhang**, T. Huang, J. D. Parvin, GenomeScape: a universal 3D visualization tool for genomic data, AMIA Annual Summit on Translational Bioinformatics, San Francisco, March 2009.
25. Y. Xiang, **J. Zhang**, N. Ruan, R. Jin, J. D. Parvin, K. Huang. A study on frequent co-expression networks in cancers, AMIAAnnual Summit on Translational Bioinformatics, San Francisco, March 2009.
26. **J. Zhang**, P. Hellwig, J. P. Osborne, R. B. Gennis, “Mutations on the highly conserved arginine residue specifically perturbs the midpoint potential of heme b558 in cytochrome bd oxidase from *E. coli*”. Gordon Research Conference on Proton Pumping and Membrane Biology, USA, Feb. 2003.
27. Boehm, T. Mogi, **J. Zhang**, W. Mantele, R. B. Gennis and P. Hellwig, "FTIR spectroscopic evidence of the presence of acidic residues in the vicinity of the quinone and the oxygen binding site in cytochrome bd oxidase from *E. coli*", European BioEnergetics Conference, France, Sep. 2002.
28. **J. Zhang**, C. Rauch, P. Grodzinski, “Smaller, Faster, and More Convenient---PCR Optimization and Micro-PCR Development in Microfluidics Lab”, Motorola Intern/Co-op Presentation, Jul. 2001.
29. **J. Zhang**, J. P. Osborne, R. B. Gennis, “Mutation of highly conserved arginine residue may specifically perturb the quinol binding site of cytochrome bd oxidase in *Escherichia coli*”, Allerton Photosynthetic Conference, Oct. 2000.
30. **J. Zhang**, J. P. Osborne, P. Hellwig, R. B. Gennis, “Characterization of mutant E445A in cytochrome bd quinol oxidase in *Escherichia coli*”, Biochemistry Spring Conference, Apr. 1999.
31. **J. Zhang**, J. P. Osborne, R. B. Gennis, “Characterization of the highly conserved residues near the Q-loop of cytochrome bd oxidase in *Escherichia coli*”, Biochemistry Fall Conference, Oct. 1998.

## RECENT GRANTS:

1. American Cancer Society Internal Research Grant (Role: contact PI, Jun 2018-May 2019)
2. Informatics Links between Histological Features and Genetics in Cancers (Role: co-I with 20% effort, NCI ITCR U01, 05/2015 – 04/2018)

## REFERENCES:

Available upon request.