

## Curriculum Vitae

Yuji Zhang, Ph.D.

Associate Professor, Department of Epidemiology and Public Health  
University of Maryland School of Medicine

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### **Contact Information**

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Foreign Languages: Chinese

### **Education**

2000 B.S., Biomedical Engineering, Southeast University, China

2003 M.S., Bioinformatics, Southeast University, China

2010 Ph.D., Computer Engineering, Virginia Polytechnic Institute and State University

### **Post Graduate Education and Training**

2000-2003 Research Assistant, School of Biological Science & Medical Engineering,  
Southeast University

2003-2004 Research Assistant, Department of Zoology, University of Oklahoma

2005-2010 Research Assistant, Department of Oncology, Georgetown University Medical  
Center

2005-2010 Research Assistant, Department of Electrical and Computer Engineering, Virginia  
Polytechnic Institute and State University

### **Employment History**

#### **Academic Appointments**

2011-2014 Assistant Professor, Department of Health Sciences Research, Mayo Clinic  
College of Medicine and Science

2014-2018 Assistant Professor, Department of Epidemiology and Public Health, UMSOM

2014-present Member, Hormone Response Cancers Program, UMGCCC, UMMC

2014-present Member, Population Science Program, UMGCCC, UMMC

2014-present Member, Program in Oncology, UMSOM

2015-present Member, Program for Personalized and Genomic Medicine, UMSOM

2016-present Affiliate Faculty Member, Institute of Global Health, UMSOM

- 2016-present Adjunct Faculty Member, School of Public Health, University of Maryland College Park
- 2016-present Affiliate Faculty Member, Center for Health-related Informatics and Bioimaging, University of Maryland
- 2018-present Associate Professor, Department of Epidemiology and Public Health, UMSOM
- 2020 Awarded Tenure, Department of Epidemiology and Public Health, UMSOM

### **Professional Society Memberships**

- 2005-2021 Member, Institute of Electrical and Electronics Engineers (IEEE)
- 2008-present Member, Society of Women Engineers
- 2009-present General Member, the Bioinformatics Organization
- 2010-2014 Member, Human Genome Organization
- 2010-present General Member, American Association for Cancer Research (AACR)
- 2010-present Member, International Society of Computational Biology (ISCB)
- 2010-present Member, Sigma Xi, The Scientific Research Society
- 2010-present Regular Member, The American Society of Human Genetics (ASHG)
- 2014-present Regular Member, American Medical Informatics Association (AMIA)
- 2021-present Senior Member, Institute of Electrical and Electronics Engineers (IEEE)

### **Honors And Awards**

- 1996 First-class Prize, Jiangsu Physics Contest, China
- 2002 Excellent Student Fellowship, Southeast University, awarded for distinguished students university wide
- 2012 Travel Award, the 20<sup>th</sup> Annual International Conference on Intelligence Systems for Molecular Biology
- 2019 Merit Scholarship, Women in AMIA Leadership Program, American Medical Informatics Association
- 2020 Winner of WIA (Women in AMIA) Leadership 2020 Seed Grant, American Medical Informatics Association

### **Administrative Service**

#### **Institutional Service**

- 2016-present Study Section Member, the UMB-UMCP Research & Innovation Seed Grant Program
- 2016-present Departmental Representative, UMSOM Faculty Council
- 2016-present Member of Admissions Committee, Epidemiology and Public Health Graduate Program, UMSOM
- 2016-present Member, Consulting Core Service of Biostatistics and Bioinformatics, UMSOM
- 2019-present Invited grant reviewer, the Institute for Clinical and Translational Research (ICTR) Accelerated Translational Incubator Pilot (ATIP) Grant Program, UMB
- 2019-present Faculty Judge, The Graduate Research Conference (GRC), UMB

- 2019-present Faculty Judge, Annual Public Health Research Day @ Maryland, University of Maryland, College Park
- 2019-2020 Member, 2019-2020 Cancer Genetic Epidemiology Faculty Search Committee, University of Maryland School of Medicine
- 2020 Invited grant reviewer, COVID-19 response seed grant program, MPower Steering Council
- 2020-present Faculty Judge, 43rd Annual Medical Student Research Day Celebration, UMSOM
- 2020-present Member, Selection Committee of STAR-PREP Science Training for Advancing Biomedical Research Postbaccalaureate Program, University of Maryland School of Medicine
- 2020-present Member, Admissions Committee of Medical Students, UMSOM
- 2020-present Member, Admissions Committee of the Cellular and Molecular Biomedical Science (CMBS) MS Program, UMSOM
- 2021 Member, 2020 Faculty Search Committee, Department of Neurology, University of Maryland School of Medicine
- 2021-2022 Member, 2021-2022 Cancer Genetic Epidemiology Faculty Search Committee, University of Maryland School of Medicine

**Local and National Service**

- 2010-present Peer review of over 150 scientific papers for 32 international journals (i.e., approximately 15 papers/5 journals per year), including but not limited to: ACM-BCB 2018; Aids; AMIA 2019; BioData Mining; Bioinformatics; Biological Chemistry; Biomedical Engineering and Computational Biology; Biomedical Informatics Insights; BMC Bioinformatics; BMC Genomics; BMC Medical Genomics; BMC Supplements; Briefings in Bioinformatics; Canadian Journal of Cardiology; Cellular Physiology and Biochemistry; Computational and Structural Biotechnology Journal; Expert Review of Molecular Diagnostics; EURASIP Journal on Bioinformatics and Systems Biology; Gene; ICHI 2019; IEEE Signal Processing Letters; Integrative Bioinformatics; International Journal of Biomedical Science; JCO Clinical Cancer Informatics; Journal of Association for Information Science and Technology; Journal of Bioinformatics and Computational Biology; Journal of Biomedical Informatics; Journal of Biomedical Semantics; Journal of Integrative Bioinformatics; Mathematical Biosciences; Methods of Information in Medicine; Nature Communications; Onco Targets and Therapy; PLOS ONE; Systems and Synthetic Biology; Scientific Reports; SpringPlus; VDOS proceedings 2015-2020.
- 2012 Member, Technical Program Committee, the 3rd International Conference on Biomedical Ontology, Graz, Austria, July 21-25, 2012.
- 2012 Member, Technical Program Committee, the 21st ACM International Conference on Information and Knowledge Management (CIKM 2012), Maui, Hawaii, USA, Oct 29 – Nov 2, 2012.
- 2012-present Abstract Reviewer, *AMIA Annual Symposium*
- 2012-present Abstract Reviewer, *AMIA Annual Informatics Summit*
- 2012-present Editorial Board Member, *Mutation & Cancer Studies*

- 2013-present Member, Technical Program Committee, International Workshop on Vaccine and Drug Ontology Studies, in conjunction with the International Conference on Biomedical Ontology (ICBO)
- 2014-present Editorial Board Member, *Annals of Hematology & Oncology*
- 2014 Program Co-Chair, the first workshop on Translational biomedical and clinical informatics, in conjunction with the 8th International Conference on Systems Biology and the 4th Translational Bioinformatics Conference (ISB/TBC 2014), Qingdao, China, Oct 24-27, 2014.
- 2014 Program Co-Chair, Workshop on Data Mining in Biomedical informatics and Healthcare, in conjunction with the 18th Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD 2014), Taiwan, May 14, 2014.
- 2014 Local organizer and member, Technical Program Committee, International Symposium on Integrative Bioinformatics 2014, Newcastle University, UK, May 12-14, 2014.
- 2014-2015 Guest Editor, *BioData Mining*
- 2017 Program Co-Chair, the first workshop on Knowledge Discovery in Translational Biomedical Informatics, in conjunction with the IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2017, Kansas City, MO, USA, Nov 13-16, 2017.
- 2018 Member, Program Committee, The 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), Washington, DC, USA, Aug 29-Sep 1, 2018.
- 2018 Session Chair of the Drug Discovery and Docking, The 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), Washington, DC, USA, Aug 29-Sep 1, 2018.
- 2019 Reviewer, the Seventh IEEE International Conference on Healthcare Informatics (ICHI 2019), Xi'an, China, Jun 10-13, 2019.
- 2019 Member, Technical Program Committee, the 4th International Workshop on Semantics-Powered Data Mining and Analytics (SEPDA 2019), in conjunction with the 19th International Semantic Web Conference (ISWC 2019), Auckland, New Zealand, Oct 26-30, 2019.
- 2020 Member of External Advisory Committee, Kenley School, Abilene, TX, USA.
- 2020 Grant Reviewer of the Medical Research Council (MRC), United Kingdom.
- 2021 Member of the Awards Committee, Networks 2021: A Joint Sunbelt and NetSci conference, Washington, DC, USA, July 6-11, 2021.
- 2021- present Topic Editor, Editorial Board, *Genes*
- 2021-present IEEE Senior Member Review Panel
- 2021-present NSF Reviewer
- 2022-present Chair of Baltimore Section, IEEE Women in Engineering (WIE) Region 2

### **Teaching Service**

### **Student Teaching**

- 2012-2014 Lecturer, Introduction to Bioinformatics  
Mayo Clinic College of Medicine

2012-2014 Number of students: 20-28; hours of teaching: 1 hour/week; number of weeks: 12  
Lecturer, Introduction to Bioinformatics,  
Department of Computer Science, Winona State University

2014-present Number of students: 16-24; hours of teaching: 1 hour/week; number of weeks: 12  
Attending Biostatistician, Journal Club of Epidemiology  
Department of Epidemiology and Public Health, UMSOM

2015-2016 Number of students: 10-18; hours of teaching: 2 hours/semester  
Lecturer, Statistics for Molecular Biology  
Department of Epidemiology and Public Health, UMSOM

2018-present Number of students: 4-8; hours of teaching: 1 hour/week; number of weeks: 8  
Lecturer, Molecular Toxicology  
Department of Epidemiology and Public Health, UMSOM

2018-present Number of students: 8; hours of teaching: 4 hours/semester; number of weeks: 16  
Lecturer, Molecular Epidemiology  
Department of Epidemiology and Public Health, UMSOM

2020-present Number of students: 4; hours of teaching: 4 hours/semester; number of weeks: 12  
Lecturer, Cancer Epidemiology  
Department of Epidemiology and Public Health, UMSOM

2020-present Number of students: 12; hours of teaching: 4 hours/semester; number of weeks:  
12  
Lecturer, Cancer Epidemiology  
Department of Epidemiology and Public Health, UMSOM

2020-present Mentor, The Foundations of Research and Critical Thinking (FRCT), UMSOM

2021 Panel Member, IEEE Senior Member Review Panel

### **Mentoring**

2001 Research Mentor  
Qianru Yu, 4<sup>th</sup> year undergraduate student, 4 hours per week

2010-2014 Research supervisor  
Asha Nair, Post-graduate, Bioinformatics, 4 hours per week

2012 Research mentor  
Feichen Shen, Ph.D., Medical Informatics, 4 hours per week

2015-2018 Research Mentor  
Lei Wang, post-graduate, Bioinformatics, 6 hours per week

2015-2018 Member of Ph.D. dissertation committee  
Kara Moser, graduate student, Molecular Epidemiology, 10 hours per year

2016 Research Mentor  
Haichen Zhang, graduate student, Human Genetics, 4 hours per week

2016-2020 Member of Ph.D. dissertation committee  
Amol Carl Shetty, graduate student, Bioinformatics, 10 hours per year

2017-2020 Research Mentor  
Junxiang Wang, graduate student, Computer Science, 2 hours per week

2018-2021 Research Mentor  
Andrea Fava, Clinical Fellow, 2 hours per week

2018-2021 Member of Ph.D. dissertation committee  
Emily Stucke, graduate student, Molecular Epidemiology, 10 hours per year

2018-2021 Member of Ph.D. dissertation committee

2019 Haichen Zhang, graduate student, Molecular Epidemiology, 10 hours per year  
Research Mentor  
Yi-Ju Chen, graduate student, Master Program, 4 hours per week

2020-present Member of Ph.D. dissertation committee  
Elizabeth Humphries, graduate student, Molecular Epidemiology, 10 hours per year

2020-present Research Mentor  
Barry Bu, high school student, Wootton High School, 4 hours per week

2021 Rotation Research Mentor  
Denisha Odie, graduate student, MS in Cellular & Molecular Biomedical Science (CMBS), Graduate Program in Life Sciences (GPILS), 4 hours per week

2021 Rotation Research Mentor  
Victoria Baskerville, graduate student, MS in Cellular & Molecular Biomedical Science (CMBS), Graduate Program in Life Sciences (GPILS), 4 hours per week

2021-present Member of Ph.D. dissertation committee  
Lydia He, graduate student, Molecular Epidemiology, 10 hours per year

2021-present Research Mentor  
Matthew Koslow, Postdoctoral Fellow, 2 hours per week

## **Grant Support**

### **Active Grants:**

09/20/16 – 05/31/23 (Co-Inv 20%) PI: M. Terrin  
*“PCTC Administrative Coordinating Center”*  
NHLBI/NIH, U24 HL134763  
Annual Direct Costs: \$1,131,510  
Total Direct Costs: \$7,920,570  
*Lead Bioinformatician and Biostatistician*

03/01/18 – 02/28/23 (Co-Inv 8%) PI: V. Njar  
*“Development of next generation galeterone analogs for prostate cancer therapy”*  
NCI/NIH, R01 CA224696  
Annual Direct Costs: \$ 290,238  
Total Direct Costs: \$1,451,190  
*Lead Bioinformatician and Biostatistician*

03/15/19 – 02/28/24 (Collaborator) PI: M. Levine  
*“Active vaccination and passive antibody strategies to prevent disease caused by multidrug-resistant bacterial pathogens”*  
NIAID/NIH, U19 AI142725  
Annual Direct Costs: \$1,654,708  
Total Direct Costs: \$8,273,540  
*Bioinformatician and Biostatistician*

06/16/20 – 05/31/25 (Co-Inv 10%) PI: M. Terrin

- “CMCRC consortium-wide coordinating core”  
 NIAID/NIH, U19 AI150574  
 Annual Direct Costs: \$131,951  
 Total Direct Costs: \$659,755  
*Lead Bioinformatician and Biostatistician*
- 07/01/20 – 03/31/23 (Co-Inv 1%) PI: H. Huang  
 “Photodynamic priming for bidirectional modulation of drug transport across the blood-brain tumor barrier”  
 NIBIB/NIH, R21 EB028508  
 Annual Direct Costs: \$135,907  
 Total Direct Costs: \$407,721  
*Lead Bioinformatician and Biostatistician*
- 07/01/20 – 06/30/25 (Co-Inv 20%) PI: K. Cullen  
 “Cigarette Restitution Fund Program”  
 Maryland Department of Health and Mental Hygiene  
 Annual Direct Costs: \$ 10,400,000  
 Total Direct Costs: \$ 10,400,000  
*Lead Bioinformatician*
- 07/24/20 – 04/30/24 (Site-PI 5%) PI: X. Xu  
 “Discovering cardiomyopathy modifiers and therapies via zebrafish genetics”  
 NHLBI/NIH, R01 HL107304  
 Annual Direct Costs: \$328,617  
 Total Direct Costs: \$1,314,468  
*Lead Bioinformatician and Biostatistician*
- 04/01/21 – 03/31/26 (Co-Inv 3%) PI: H. Huang  
 “Addressing Chemoresistance in Pancreatic and Ovarian Cancers: Photodynamic Priming and Repurposing of Tetracyclines using Targeted Photo-Activable Multi-Inhibitor Liposome”  
 NIBIB/NIH, R01 CA260340  
 Annual Direct Costs: \$548,466  
 Total Direct Costs: \$2,742,330  
*Lead Bioinformatician and Biostatistician*
- 05/01/21 – 04/30/22 (Co-Inv 5%) PI: J Magaziner  
 “University of Maryland Claude D. Pepper Older Americans Independence Center (UM-OAIC)”  
 NHLBI/NIA, P30 AG028747 15S2  
 Annual Direct Costs: \$249,898  
 Total Direct Costs: \$249,898  
*Bioinformatician and Biostatistician*

06/01/21 – 05/31/26 (Co-Inv 20%) PI: S. Adebamowo  
*“CARDiometabolic Disorders IN African-ancestry PopuLations (CARDINAL) Study Site”*  
 NCI/NIH, U01 HG011717  
 Annual Direct Cost: \$790,000  
 Total Direct Costs: \$3,950,000  
*Lead Bioinformatician and Biostatistician*

07/01/21 – 06/30/26 (Co-Inv 5%) PI: H. Wang  
*“Novel noncanonical actions of CAR in human liver”*  
 NCI/NIH, R01 CA262084  
 Annual Direct Cost: \$250,000  
 Total Direct Costs: \$1,250,000  
*Lead Bioinformatician and Biostatistician*

08/01/21 – 07/31/26 (Co-Inv 5%) PI: K. Cullen  
*“University of Maryland Comprehensive Cancer Center Support Grant”*  
 NCI/NIH, P30 CA134274  
 Annual Direct Costs: \$1,500,000  
 Total Direct Costs: \$7,500,000  
*Lead Bioinformatician*

**Completed Grants:**

09/01/10-06/30/14 (Co-Inv 20%) PI: R. Diasio  
*“Mayo comprehensive cancer center grant”*  
 National Cancer Institute, P30 CA15083  
 Annual Direct Costs: \$5,115,009  
 Total Direct Costs: \$20,460,036  
*Bioinformatician and Biostatistician*

09/19/11-06/30/14 (Co-Inv 25%) PI: S. Thibodeau  
*“Prostate cancer susceptibility: the ICPCG study”*  
 National Cancer Institute, U01 CA89600  
 Annual Direct Costs: \$1,272,612  
 Total Direct Costs: \$8,908,284  
*Bioinformatician and Biostatistician*

09/19/11-06/30/14 (Co-Inv 10%) PI: S. Thibodeau  
*“Functional significance of prostate cancer risk-SNPs”*  
 National Cancer Institute, R01 CA151254  
 Annual Direct Costs: \$228,217  
 Total Direct Costs: \$684,651  
*Bioinformatician and Biostatistician*

09/31/12-06/30/14 (Site-PI 25%) PI: R. Rademakers



- “GGGGCC hexanucleotide repeat expansions in neurodegenerative disease”  
 National Institute of Neurological Disorder and Stroke, R01 NS80882  
 Annual Direct Costs: \$361,947  
 Total Direct Costs: \$1,809,735  
*Bioinformatician and Biostatistician*
- 01/01/13-07/31/14 (Co-Inv 5%) PI: J. Aaron  
 “Development of novel monocarboxylate transporter 1 inhibitors for the treatment of glioblastoma multiforme”  
 Minnesota Partnership for Biotechnology and Medical Genomics  
 Annual Direct Costs: \$116,393  
 Total Direct Costs: \$116,393  
*Bioinformatician and Biostatistician*
- 03/20/13-06/30/14 (Co-Inv 5%) PI: M. J. Ackerman  
 “Cardiac channel mutations in SIDS”  
 Eunice Kennedy Shriver National Institute of Child Health and Human Development, R01 HD42569  
 Annual Direct Costs: \$352,194  
 Total Direct Costs: \$1,760,970  
*Bioinformatician and Biostatistician*
- 07/01/13-06/30/14 (Co-Inv 15%) PI: T. Patel  
 “Extracellular non-coding RNA biomarkers of hepatocellular cancer”  
 National Institute of Health, UH2 TR000884  
 Annual Direct Costs: \$366,588  
 Total Direct Costs: \$366,588  
*Bioinformatician and Biostatistician*
- 09/30/14-09/29/15 (Co-Inv 5%) PI: T. MacVittie  
 “Medical countermeasures against radiological threats: product development support”  
 National Institute of Allergy and Infectious Disease, 272201000046C-14-0-1  
 Annual Direct Costs: \$1,334,877  
 Total Direct Costs: \$1,334,877  
*Bioinformatician and Biostatistician*
- 08/08/08 – 07/31/16 (Co-Inv 5%) PI: K. Cullen  
 “University of Maryland Comprehensive Cancer Center Support Grant”  
 National Cancer Institute, P30 CA134274  
 Annual Direct Costs: \$1,000,000

- Total Direct Costs: \$8,000,000  
*Bioinformatician and Biostatistician*
- 11/01/16 – 07/31/17 (Collaborator) PI: K. Barry  
*“DNA methylation at chromosome 8q24 and the risk of aggressive prostate cancer”*  
UMGCCC  
Annual Direct Costs: \$30,000  
Total Direct Costs: \$30,000  
*Bioinformatician and Biostatistician*
- 07/01/17 – 06/30/18 (Co-Inv 5%) PI: Y. Mei  
*“A blood test for the early detection of lung cancers based on newly-discovered sprRNAs”*  
The Maryland Innovation Initiative  
Annual Direct Costs: \$115,000  
Total Direct Costs: \$115,000  
*Bioinformatician and Biostatistician*
- 04/01/17 – 03/31/19 (Co-Inv 3%) PI: E. Davila  
*“Augmenting T cell activity to weak tumor antigens and reversing myeloid cell-mediated T cell inhibition”*  
National Cancer Institute, R01 CA207913  
Annual Direct Costs: \$235,681  
Total Direct Costs: \$1,178,405  
*Bioinformatician and Biostatistician*
- 08/01/18 – 05/31/19 (Co-Inv 2%) PI: X. Cao  
*“Novel method for enhancing cancer immunotherapy efficacy and minimizing toxicity”*  
TEDCO  
Annual Direct Costs: \$2,888  
Total Direct Costs: \$2,888  
*Bioinformatician and Biostatistician*
- 07/01/15 – 06/30/19 (Co-Inv 10%) PI: R. Gartenhaus  
*“Lymphoma development in the elderly: Perturbed posttranscriptional regulation”*  
VA Merit Research Award  
Annual Direct Costs: \$150,000  
Total Direct Costs: \$600,000  
*Bioinformatician and Biostatistician*
- 03/01/16 – 02/29/20 (Co-Inv 3%) PI: P. Yang  
*“Apoptotic mechanism of maternal diabetes-induced neural tube defects”*

NIDDK/NIH, R01 DK083243  
Annual Direct Costs: \$275,000  
Total Direct Costs: \$1,375,000  
*Bioinformatician and Biostatistician*

07/01/17 – 04/30/21 (Co-Inv 2%) PI: P. Yang  
“*MicroRNA-suppressed mitochondrial fusion in mediating the teratogenicity of maternal diabetes leading to heart defects*”  
NHLBI/NIH, R01 HL134368  
Annual Direct Costs: \$390,939  
Total Direct Costs: \$1,563,756  
*Lead Bioinformatician and Biostatistician*

04/01/18 – 03/31/21 (Co-Inv 5%) PI: J. Dorgan  
“*Early life exposures and breast density in young women*”  
NCI/NIH, R01 CA214783  
Annual Direct Costs: \$204,482  
Total Direct Costs: \$817,928  
*Lead Bioinformatician*

08/10/16 – 07/31/21 (Collaborator) PI: J. Qi  
“*Role of histone demethylase JMJD1A in the DNA damage response of prostate cancer cells*”  
NCI/NIH, R01 CA207118  
Annual Direct Costs: \$228,750  
Total Direct Costs: \$1,143,750  
*Bioinformatician and Biostatistician*

09/10/16 – 07/31/21 (Co-Inv 5%) PI: M. Petri  
“*Hopkins Lupus Cohort*”  
NIAMS/NIH, R01 AR069572  
Annual Direct Costs: \$447,131  
Total Direct Costs: \$2,235,655  
*Lead Bioinformatician*

### **Patents**

1. Kohli M, Oberg AL, Mahoney DW, Zenka RM, **Zhang Y**, Zhang S. Predicting responses to androgen deprivation therapy and methods for treating prostate cancer. Publication number: WO2013116742.

### **Publications**

#### **Peer-reviewed journal articles**

1. **Zhang Y**, Zhu J, Sun X, Lu Z. A method of oligonucleotide synthesis optimization. *Biotechnology*. 2002;12(4):26-28.
2. Ressonm HW\*, **Zhang Y\***, Xuan J, Wang Y, Clarke R. Inference of gene regulatory networks from time course gene expression data using neural networks and swarm intelligence. *Proceedings of 2006 IEEE Symposium on Computational Intelligence and Bioinformatics and Computational Biology (CIBCB '06)*. 2006 Sep 28;435-442. *(primary author to design the experiment, perform the analysis, and write the manuscript)*
3. Ressonm HW\*, **Zhang Y\***, Xuan J, Wang Y, Clarke R. Inferring network interactions using recurrent neural networks and swarm intelligence. *Proceedings of the 28th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBS 2006)*. 2006 Aug 30;4241-4244. *(primary author to design the experiment, perform the analysis, and write the manuscript)*
4. Ressonm HW\*, **Zhang Y\***, Xuan J, Wang Y, Clarke R. Integrating multi-source biological data for transcriptional regulatory module discovery. *Proceedings of IEEE/NIH Life Science Systems and Applications Workshop 2007 (LISA 2007)*. 2007 Nov 8;184-187. *(primary author to design the experiment, perform the analysis, and write the manuscript)*
5. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Ressonm HW. Network motif-based identification of transcription factor-target gene relationships by integrating multi-source biological data. *BMC Bioinformatics*. 2008 Apr 21;9(1):203.
6. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Ressonm HW. Reverse engineering module networks by PSO-RNN hybrid modeling. *Proceedings of the 2008 International Conference on Bioinformatics and Computational Biology (BIOCOMP 2008)*. 2008; 401–407.
7. **Zhang Y**, Xuan J, de Los Reyes BG, Clarke R, Ressonm HW. Network motif-based identification of breast cancer susceptibility genes. *Proceedings of the 30th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBS 2008)*. 2008 Aug 20;5696-5699.
8. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Ressonm HW. Reverse engineering module networks by PSO-RNN hybrid modeling. *BMC Genomics*. 2009 Jul 7;10(1):S15.
9. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Ressonm HW. Module-based biomarker discovery for breast cancer. *Proceedings of 2010 IEEE International Conference on Bioinformatics & Biomedicine*. 2010 Dec 18;352-356.
10. **Zhang Y**, Xuan J, de los Reyes BG, Clarke R, Ressonm HW. Reconstruction of gene regulatory modules in cancer cell cycle by multi-source data integration. *PLOS ONE*. 2010 Apr 21;5(4):e10268.
11. Sun Z, Baheti S, Middha S, Kanwar R, **Zhang Y**, Li X, Beutler AS, Klee E, Asmann YW, Thompson EA, Kocher JP. SAAP-RRBS: streamlined analysis and annotation pipeline for reduced representation bisulfite sequencing. *Bioinformatics*. 2012 Jan 15;28(2):277-278. *(participated in determining analytic method, running analyses, and providing statistical interpretation)*
12. Craig TA\*, **Zhang Y\***, McNulty MS, Middha S, Ketha H, Singh RJ, Magis AT, Funk C, Price ND, Ekker SC, Kumar R. Research resource: whole transcriptome RNA sequencing detects multiple 1alpha, 25-dihydroxyvitamin D(3)-sensitive metabolic pathways in developing zebrafish. *Molecular Endocrinology*. 2012 Jun 25;26(9):1630-1642. *(primary author to design the experiment, perform the analysis, and write the manuscript)*

13. Wang J, **Zhang Y\***, Marian C, Ressom HW. Identification of aberrant pathways and network activities from high-throughput data. *Briefings in Bioinformatics*. 2012 Jan 27;13(4):406-419. *(determined analytic method, provided statistical interpretation)*
14. Asmann YW, Middha S, Hossain A, Baheti S, Li Y, Chai HS, Sun Z, Duffy PH, Hadad AA, Nair A, Liu X, **Zhang Y**, Klee EW, Kalari KR, Kocher JP. TREAT: a bioinformatics tool for variant annotations and visualizations in targeted and exome sequencing data. *Bioinformatics*. 2012 Jan 15;28(2):277-278. *(determined analytic method, ran analyses, provided statistical interpretation)*
15. Tao C, **Zhang Y**, Jiang G, Bouamrane MM, Chute CG. Optimizing semantic MEDLINE for translational science studies using semantic web technologies. MIXHS '12 Proceedings of the 2nd international workshop on Managing interoperability and compleXity in health systems. 2012 Oct 29;53-58. *(determined analytic method, ran analyses, provided statistical interpretation)*
16. **Zhang Y**, Li D, Tao C, Shen F, Liu H. An integrative computational approach to identify disease-specific networks from PubMed literature information. *Proceedings of IEEE International Conference on Bioinformatics and Biomedicine 2013*. 2013 Dec 18;72-75.
17. Leonard B, Hart SN, Burns MB, Carpenter MA, Temiz NA, Rathore A, Isaksson Vogel R, Nikas JB, Law EK, Brown WL, Li Y, **Zhang Y**, Maurer MJ, Oberg AL, Cunningham JM, Shridhar V, Bell DA, April C, Bently D, Bibikova M, Cheetham RK, Fan JB, Grocock R, Humphray S, Kingsbury Z, Peden J, Chien J, Swisher EM, Hartmann LC, Kalli KR, Goode EL, Sicotte H, Kaufmann SH, & Harris RS APOBEC3B upregulation and genomic mutation patterns in serous ovarian carcinoma. *Cancer Research*. 2013 Dec 15;73(24):7222-7231. *(determined analytic method, ran analyses, provided statistical interpretation)*
18. Hart SN, Therneau TM, **Zhang Y**, Poland GA, Kocher JP. Calculating sample size estimates for RNA sequencing data. *Journal of Computational Biology*. 2013 Dec 1;20(12):970-978. *(determined analytic method, ran analyses, provided statistical interpretation)*
19. **Zhang Y**, Tao C, He Y, Kanjamala P, Liu H. Network-based analysis of vaccine-related associations reveals consistent knowledge with the vaccine ontology. *Journal of Biomedical Semantics*. 2013 Nov 11;4(1):33.
20. Sun Z, Asmann YW, Nair A, **Zhang Y**, Wang L, Kalari KR, Bhagwate AV, Baker TR, Carr, JM, Kocher JP, Perez EA, Thompson EA. Impact of library preparation on downstream analysis and interpretation of RNA-Seq data: comparison between Illumina PolyA and NuGEN Ovation protocol. *PLOS ONE*. 2013;8(8):e71745. *(determined analytic method, ran analyses, provided statistical interpretation)*
21. Pugazhenthii S, **Zhang Y**, Bouchard R, & Mahaffey G. Induction of an inflammatory loop by interleukin-1 beta and tumor necrosis factor-alpha involves NF- kappa B and STAT-1 in differentiated human neuroprogenitor cells. *PLOS ONE*. 2013;8(7): e69585. *(determined analytic method, ran analyses, provided statistical interpretation)*
22. **Zhang Y**, Tao C, He Y, Kanjamala P, Liu H. Analysis of vaccine-related networks using Semantic MEDLINE and the vaccine ontology. *CEUR Workshop Proceedings, 2013*; 1061.
23. **Zhang Y**, Xuan J, Clarke R, Ressom HW. Module-based breast cancer classification. *International Journal of Data Mining and Bioinformatics*. 2013;7(3):284-302.
24. **Zhang Y**, Tao C. Network analysis of cancer-focused association network reveals distinct network association patterns. *Cancer Informatics*. 2014;13(S3):45.
25. Tao C, Wu P, **Zhang Y**. Linked vaccine adverse event data representation from VAERS for biomedical informatics research. *Lecture Notes in Computer Science (including subseries*

- Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics). 2014 May 13;652-661.
26. Craig, TA\*, **Zhang Y\***, Magisc AT, Funk CC, Price ND, Ekker, SC, Kumar R. Detection of 1,25-Dihydroxyvitamin D-regulated miRNAs in zebrafish by whole transcriptome sequencing. *Zebrafish*. 2014 Jun1;11(3):207-218. (\*co-first authorship)
  27. **Zhang Y**, Tao C. Correction to "Network analysis of cancer-focused association network reveals distinct network association patterns". *Cancer Inform*. 2014;13(Suppl 3):89.
  28. **Zhang Y**, Tao C, Jiang G, Nair A, Su J, Chute CG, Liu H. Network-based analysis reveals distinct association patterns in a Semantic MEDLINE-based Drug-Disease-Gene network. *Journal of Biomedical Semantics*. 2014 Aug 6;5(1):33.
  29. **Zhang Y**. Network-based analysis of time series RNA-seq gene expression data by integrating the interactome and gene ontology information. *Proceedings of 2014 8th International Conference on Systems Biology (ISB)*. 2014 Oct 24;201-209.
  30. Zhu Q, Liu H, **Zhang Y**, Wang J. Evidence based computational drug repositioning candidate screening pipeline design: case study. *Proceedings of 2014 8th International Conference on Systems Biology (ISB)*. 2014 Oct 24;210-218. (*determined analytic method, ran analyses, provided statistical interpretation*)
  31. Wang L, Chen J, Wang C, Uusküla-Reimand L, Chen K, Medina-Rivera A, Young E, Zimmermann M, Yan H, Sun Z, **Zhang Y**, Wu S, Huang H, Wilson MD, Kocher JP, Li W. MACE: model based analysis of ChIP-exo. *Nucleic Acids Research*. 2014, Nov 10;42(20):e156-e156. (*determined analytic method, ran analyses, provided statistical interpretation*)
  32. Tao C, Yu P, Luo Y, **Zhang Y**. Linked vaccine adverse event data from VAERS for biomedical data analysis and longitudinal studies. *BioData Mining*. 2014 Dec 31;7(1):36.
  33. Shih Y, **Zhang Y**, Ding Y, Ross CA, Li H, Olson TM, Xu X. The Cardiac transcriptome and dilated cardiomyopathy genes in zebrafish. *Circulation: Cardiovascular Genetics*. 2015 Apr;8(2):261-269. (*primary author to determine analytic method, run analyses, and provide statistical interpretation*)
  34. Felts SJ, Van Keulen VP, Scheid AD, Allen KS, Bradshaw RK, Jen J, Peikert T, Middha S, **Zhang Y**, Block MS, Markovic SN, Pease LR. Gene expression patterns in CD4+ peripheral blood cells in healthy subjects and stage IV melanoma patients. *Cancer Immunology & Immunotherapy*. 2015 Nov 1;64(11):1437-1447. (*determined analytic method, ran analyses, provided statistical interpretation*)
  35. **Zhang Y**. Network analysis reveals stage-specific changes in zebrafish embryo development using time course whole transcriptome profiling and prior biological knowledge. *BioData Mining*. 2015 Aug 28;8(1):26.
  36. **Zhang Y**, Yu P, & Tao C. Identification of sex-associated network patterns in vaccine-adverse event association network in VAERS. *Journal of Biomedical Semantics*. 2015 Aug 19;6(1):33.
  37. Thibodeau SN, French AJ, McDonnell SK, Chevillie J, Middha S, Tillmans L, Riska S, Baheti S, Larson MC, Fogarty Z, **Zhang Y**, Larson N, Nair A, O'Brien D, Wang L, Schaid DJ. Identification of candidate genes for prostate cancer-risk SNPs utilizing a normal prostate tissue eQTL data set. *Nature Communications*. 2015 Nov 27;6:8653. (*determined analytic method, ran analyses, provided statistical interpretation*)
  38. **Zhang Y**, Zhu Q, Liu H. Next generation informatics for big data in precision medicine era. *BioData Mining*. 2015 Nov 3;8(1):34.

39. Kitange GJ, Mladek AC, Schroeder MA, Pokorny JC, Carlson BL, **Zhang Y**, Nair AA, Lee JH, Yan H, Decker PA, Zhang Z, Sarkaria JN. Retinoblastoma binding protein 4 modulates temozolomide sensitivity in glioblastoma by regulating DNA repair proteins. *Cell Reports*. 2016 Mar 22;14(11):2587-98. *(determined analytic method, ran analyses, provided statistical interpretation)*
40. Fan L, Peng G, Sahgal N, Fazli L, Gleave M, **Zhang Y**, Hussain A, Qi J. Regulation of c-Myc expression by the histone demethylase JMJD1A is essential for prostate cancer cell growth and survival. *Oncogene*. 2016 May 12;35(19):2441-52. *(determined analytic method, ran analyses, provided statistical interpretation)*
41. Dong D, **Zhang Y**, Reece EA, Wang L, Harman CR, Yang P. microRNA expression profiling and functional annotation analysis of their targets modulated by oxidative stress during embryonic heart development in diabetic mice. *Reproductive Toxicology*. 2016 Oct 31;11(65):365-374. *(determined analytic method, ran analyses, provided statistical interpretation)*
42. Jackson IL, **Zhang Y**, Bentzen S, Hu J, Zhang C, Katz BP, Vujaskovic Z. Pathophysiological mechanisms underlying phenotypic differences in pulmonary radioresponse among murine strains. *Scientific Reports*. 2016 Nov 15;6:36579. *(determined analytic method, ran analyses, provided statistical interpretation)*
43. Wang L, Ma X, Xu X, **Zhang Y**. Systematic identification and characterization of cardiac long intergenic noncoding RNAs in zebrafish. *Scientific Reports*. 2017 Apr 28;7(1):1250.
44. Kaczanowska S, Joseph AM, Guo J, Tsai AK, Lasola JJ, Younger K, **Zhang Y**, Gonzales CV, Davila E. A synthetic CD8 $\alpha$ :MyD88 coreceptor enhances CD8<sup>+</sup> T-cell responses to weakly immunogenic and lowly expressed tumor antigens. *Cancer Research*. 2017 Dec 15; 77(24):7049-7058. *(determined analytic method, ran analyses, provided statistical interpretation)*
45. Jackson IL, **Zhang Y**, Bentzen S, Hu J, Zhang C, Katz BP, Vujaskovic Z. Corrigendum: Pathophysiological mechanisms underlying phenotypic differences in pulmonary radioresponse. *Scientific Reports*. *Sci Rep*. 2017 May 4;7:46782. *(determined analytic method, ran analyses, provided statistical interpretation)*
46. **Zhang Y**, Shen F, Mojarad MR, Li D, Tao C, Yu Y, Liu S, Liu H. Systematic identification of latent disease-gene relationships from PubMed articles. *PLOS ONE*. 2018 Jan 16; 13(1): e0191568.
47. Scheid AD, Keulen V, Felts SJ, Neier SC, Middha S, Nair AA, Techentin RW, Gilbert BK, Jen J, Neuhauser C, **Zhang Y**, Pease LR. Gene expression signatures characterized by longitudinal stability and interindividual variability delineate baseline phenotypic groups with distinct responses to immune stimulation. *The Journal of Immunology*. 2018 Mar 1; 200(5):1917-1928. *(determined analytic method, ran analyses, provided statistical interpretation)*
48. Wang L, Felts SJ, Van Keulen VP, Scheid AD, Block MS, Markovic SN, Pease LR, **Zhang Y**. Integrative genome-wide analysis of long noncoding RNAs in diverse immune cell types of melanoma patients. *Cancer Research*. 2018 Aug 1;78(15):4411-4423.
49. Wang J, Zhao L, Ye Y, **Zhang Y**. Adverse event detection by integrating Twitter data and VAERS. *Journal of Biomedical Semantics*. 2018 Jun 20; 9:19.
50. Wang L, Felts SJ, Van Keulen VP, Pease LR, **Zhang Y**. Exploring the effect of library preparation on RNA sequencing experiments. *Genomics*. 2018 Dec 6; pii: S0888-7543(18)30367-7.

51. Zandberg DP, Tallon LJ, Nagaraj S, Sadzewicz LK, **Zhang Y**, Strome MB, Zhao XE, Vavikolanu K, Zhang X, Papadimitriou JC, Hubbard FA, Bentzen SM, Strome SE, Fraser CM. Intratumor genetic heterogeneity in squamous cell carcinoma of the oral cavity. *Head Neck*. 2019 Aug;41(8):2514-2524. *(determined analytic method, ran analyses, provided statistical interpretation)*
52. Petri M, Fu W, Ranger A, Allaire N, Cullen P, Magder LS, **Zhang Y**. Association between changes in gene signatures expression and disease activity among patients with systemic lupus erythematosus. *BMC Medical Genomics*. 2019 Jan 9;12(1):4.
53. Ramalingam S, Ramamurthy VP, Gediya LK, Murigi FN, Purushottamachar P, Huang W, Choi EY, **Zhang Y**, Vasaitis TS, Kane MA, Lapidus RG, Njar VCO. The novel mnk1/2 degrader and apoptosis inducer VNLG-152 potently inhibits TNBC tumor growth and metastasis. *Cancers (Basel)*. 2019 Mar 3;11(3). *(determined analytic method, ran analyses, provided statistical interpretation)*
54. Kohli M, Oberg AL, Mahoney DW, Riska SM, Sherwood R, **Zhang Y**, Zenka RM, Sahasrabudhe D, Qin R, Zhang S. Serum Proteomics on the basis of discovery of predictive biomarkers of response to androgen deprivation therapy in advanced prostate cancer. *Clinical Genitourinary Cancer*. 2019 Aug;17(4):248-253. *(determined analytic method, ran analyses, provided statistical interpretation)*
55. Ren JJ, Sun T, He Y, **Zhang Y**. A statistical analysis of vaccine-adverse event data. *BMC Medical Informatics and Decision Making*. 2019 May 28;19(1):101.
56. Hu G, **Zhang Y**, Gupta M. RIP sequencing in mantle cell lymphoma identifies functional long non-coding RNAs associated with translation machinery. *Blood Cancer Journal*. 2019; 9: 55. *(determined analytic method, ran analyses, provided statistical interpretation)*
57. Ding Y, Wang L, **Zhang Y**, Xu X. Haploinsufficiency of mechanistic target of rapamycin attenuates bag3 cardiomyopathy in adult zebrafish. *Disease Models & Mechanisms*. 2019 Oct 1; 12(10): dmm040154. *(determined analytic method, ran analyses, provided statistical and bioinformatics interpretation)*
58. Kwegyir-Afful A, Ramalingam S, Ramamurthy V, Purushottamachar P, Murigi F, Vasaitis T, Huang W, Kane M, **Zhang Y**, Ambulos N, Tiwari S, Srivastava P, Nnane I, Hussain A, Qiu Y, Weber D, Njar V. Galeterone and the next generation galeterone analogs, VNPP414 and VNPP433-3 $\beta$  exert potent therapeutic effects in castration-/drug-resistant prostate cancer preclinical models in vitro and in vivo. *Cancers (Basel)*. 2019 Oct 24;11(11):1637. *(determined analytic method, ran analyses, provided statistical interpretation)*
59. Dorgan JF, Jung S, Dallal CM, Zhan M, Stennett CA, **Zhang Y**, Eckert RL, Snetselaar LG, Van Horn L. Alcohol consumption and serum metabolite concentrations in young women. *Cancer Causes Control*. 2020 Feb;31(2):113-126. *(determined analytic method, ran analyses, provided statistical interpretation)*
60. Fava A, Buyon J, Mohan C, Zhang T, Belmont HM, Izmirly P, Clancy R, Trujillo JM, Fine D, **Zhang Y**, Magder L, Rao DA, Arazi A, Berthier CC, Davidson A, Diamond B, Hachon N, Wofsy D, Apruzzese W, the Accelerating Medicines Partnership in SLE network, Raychaudhuri S, Petri M. Integrated urine proteomics and renal single-cell genomics identify an IFN- $\gamma$  response gradient in lupus nephritis. *JCI Insight*. 2020; 5(12): e138345. *(determined analytic method, ran analyses, provided statistical interpretation)*
61. Geng D, Ciavattone N, Lasola JJ, Shrestha R, Sanchez A, Guo J, Vlk A, Younis R, Wang L, Brown A, **Zhang Y**, Velasco-Gonzalez C, Tan AC, Davila E. Induction of IRAK-M in melanoma induces caspase-3 dependent apoptosis by reducing TRAF6 and calpastatin levels.



- Communications Biology. 2020; 3:306. *(determined analytic method, ran analyses, provided statistical interpretation)*
62. Barry KH, Mohanty K, Erickson P, Rose G, Cellini A, Clark K, Ambulos N, Yin J, Yan L, Poulin M, Meyer A, **Zhang Y**, Bentzen S, Burke A, Hussain A, Berndt S. MYC DNA methylation in prostate tumor tissue is associated with tumor aggressiveness. *Genes*. 2020;12(1):12. *(determined analytic method, ran analyses, provided statistical interpretation)*
  63. Inglut CT, Gray K, Vig S, Jung J, Stabile J, **Zhang Y**, Stroka KM, Huang HC. Photodynamic priming modulates endothelial cell-cell junction phenotype for light-activated remote control of drug delivery. *IEEE Journal of Selected Topics in Quantum Electronics*. 2021;27(4):7200311. *(determined analytic method, ran analyses, provided statistical interpretation)*
  64. Ferraris D, Lapidus R, Truong P, Bollino D, Carter-Cooper B, Lee M, Chang E, LaRossa-Garcia M, Dash S, Gartenhaus R, Choi EY, Kipe O, Lam V, Mason K, Palmer R, Williams E, Ambulos N, Kamangar F, **Zhang Y**, Kapadia B, Jing Y, Emadi A. Pre-Clinical activity of amino-alcohol dimeric naphthoquinones as potential therapeutics for acute myeloid leukemia. *Anti-Cancer Agents in Medicinal Chemistry*. 2021 Jun 2. doi: 10.2174/1871520621666210602131558. Epub ahead of print. PMID: 34080968. *(determined analytic method, ran analyses, provided statistical interpretation)*
  65. Serfecz JC, Saadin A, Santiago CP, **Zhang Y**, Bentzen SM, Vogel SN, Feldman RA. C5a activates a pro-inflammatory gene expression profile in human gaucher iPSC-derived macrophages. *International Journal of Molecular Sciences*. 2021; 22(18): 9912. *(determined analytic method, ran analyses, provided statistical interpretation)*
  66. Basehore S, Bohlman S, Weber C, Swaminathan S, **Zhang Y**, Jang C, Arany Z, Clyne AM. Laminar flow on endothelial cells suppresses eNOS O-GlcNAcylation to promote eNOS activity. *Circulation Research*. 2021 Nov 12;129(11):1054-1066. *(determined analytic method, ran analyses, provided statistical interpretation)*
  67. Sorrin AJ, Liu C, Cicalo J, Reader J, Najafali D, **Zhang Y**, Roque DM, Huang HC. Photodynamic priming improves the anti-migratory activity of prostaglandin E receptor 4 antagonist in cancer cells. *Cancers* 2021, 13(21): 5259. *(determined analytic method, ran analyses, provided statistical interpretation)*
  68. Bu H, Ding Y, Li J, Zhu P, Shih YH, Wang M, **Zhang Y**, Lin X, Xu X. Inhibition of mTOR or MAPK ameliorates vmhcl/myh7 cardiomyopathy in zebrafish. *JCI Insight*. 2021 Dec 22;6(24):e154215. *(determined analytic method, ran analyses, provided statistical interpretation)*
  69. De Castro A, Pranda MA, Gray KM, Merlo-Coyne J, Girma N, Hurwitz M, **Zhang Y**, Stroka KM. Morphological phenotyping of organotropic brain- and bone-seeking triple negative metastatic breast tumor cells. *Frontiers in Cell and Developmental Biology*. 2022. *Front. Cell Dev. Biol.*. Published online 17 February 2022. (<https://doi.org/10.3389/fcell.2022.790410>)
  70. Nian Y, Du J, Bu L, Li F, Hu X, **Zhang Y**, Tao C. Knowledge Graph-based Neurodegenerative Diseases and Diet Relationship Discovery. *Proceedings of CIBB 2021*. (in press)

## **Book Chapters**

1. **Zhang Y**, Ressom HW, Kocher JPA: Reverse engineering gene regulatory networks by integrating multi-source biological data, Reverse Engineering - Recent Advances and Applications. Edited by Telea AC, InTech Press, 2012.
2. **Zhang Y**: Gene regulatory networks: real data sources and their analysis, Evolutionary Computation in Gene Regulatory Network Research. Edited by Iba H, Noman N, Wiley Press, 2016.

## **Major Invited Speeches**

### Local

1. **Zhang Y**, Network-based approaches in systems medicine: current applications and future directions, Hormone Response Program, UMGCCC, UMSOM, Baltimore, MD, USA, Nov 14, 2014.
2. **Zhang Y**, Integrative informatics approaches and their applications in “Big Data” medicine era, Institute of Genome Sciences, UMSOM, Baltimore, MD, USA, Aug 17, 2015.
3. **Zhang Y**, From big data to precision medicine: a data science perspective, IEEE R2 Women in Engineering (WIE) 2022 Kick-off Meeting, Feb 28, 2022.

### National

4. **Zhang Y**, Identification of association patterns in public literature using network-based computational approaches: case studies in vaccine research, CBIL Seminar, Department of Electrical and Computer Engineering, Virginia Tech, Arlington, VA, USA, Nov 19, 2014.
5. **Zhang Y**, Subnetwork association pattern identification in drug-disease-gene networks, Department of Computer Science, Virginia Tech, Arlington, VA, USA, Apr 14, 2015.
6. **Zhang Y**, From big data to precision medicine: a data science perspective, Hillman Cancer Center, University of Pittsburgh (Virtual), Jan 31, 2022.

### International

7. **Zhang Y**, Systematic computational approaches in precision medicine era, School of Biological Science & Medical Engineering, Southeast University, Nanjing, China, Sep 16, 2014.

## **Abstracts**

1. **Zhang Y**, Wang H. Comparative analysis of circadian clock genes in Zebrafish, Fugu and Tetraodon. The 6th International Meeting on Zebrafish Development and Genetics, Madison, Wisconsin, Jul 2004.
2. **Zhang Y**, Xuan J, Wang Y, Ressom HW. Inferring gene regulatory networks from time-series gene expression data using recurrent neural networks and swarm intelligence. Fifth Asia Pacific Bioinformatics Conference (APBC 2007), Hongkong, China, Jan 14-17, 2007.
3. **Zhang Y**, Xuan J, Wang Y, Clarke R, Ressom HW. Inferring gene regulatory networks from time-series gene expression data using integrative swarm Intelligence method. The 9th Annual Lombardi Research Fair, Washington, DC, Feb 2007.

4. **Zhang Y**, Xuan J, Wang Y, Clarke R, Ressom HW. Identification of network motifs in transcriptional regulators by integrating multi-source biological data. Pacific Symposium on Biocomputing 2008 (PSB 2008), Big Island, HI, Jan 4-8, 2008.
5. **Zhang Y**, Asmann YW, Middha S, Hossain A, Baheti S, Li Y, Chai HS, Sun Z, Duffy PH, Hadad AA, Nair A, Liu X, Klee EW, Kalari KR, Kocher JP. TREAT: a comprehensive open framework for targeted re-sequencing analysis. The Next-Gen Sequencing Congress, Boston, MA, Apr 26-27, 2011.
6. Sicotte H, Therneau T, **Zhang Y**, Prodduturi N, Wang C, Kocher JP. Integrative survival analysis of TCGA tumors using cross-validated cox models. TCGA 1st Annual Scientific Symposium: Research Through TCGA, National Harbor, MD, Nov 17-18, 2011.
7. **Zhang Y**, Kocher JP. Network-based analysis of genome-wide association studies in breast cancer. TCGA 1st Annual Scientific Symposium: Research Through TCGA, National Harbor, MD, Nov 17-18, 2011.
8. **Zhang Y**, Wang C, Sun Z, Middha S, Kumar R, Kocher JP. Dynamic network analysis reveals stage-specific changes in early zebrafish embryo development. The 20th Annual International Conference on Intelligent Systems for Molecular Biology, Long Beach CA. Jul 15-17 2012.
9. Nair A, Hart S, Sicotte H, Klee E, Sinnwell J, **Zhang Y**, Li Y, Wang C, Oberg A, Middha S, Kocher JP, Therneau T. Optimizing sequence yield & interpreting data quality for RNA-Seq. The 20th Annual International Conference on Intelligent Systems for Molecular Biology, Long Beach, CA, Jul 15-17, 2012.
10. Sun Z, Baheti S, Middha S, Kanwar R, **Zhang Y**, Li X, Beutler A, Klee E, Asmann YW, Aubrey T, Kocher JP. SAAP-RRBS: Streamlined Analysis and Annotation Pipeline for Reduced Representation Bisulfite Sequencing. The 20th Annual International Conference on Intelligent Systems for Molecular Biology, Long Beach, CA, Jul 15-17, 2012.
11. **Zhang Y**, Tao C, Jiang G, Chute CG. Toward identifying novel relationships among genes, drugs and diseases by utilizing heterogeneous research data from semantic MEDLINE. Individualizing Medicine 2012: Transforming Patient Care With Genomics, Rochester, MN, Oct 1-3, 2012.
12. Kohli M, Oberg AL, Mahoney DW, Riska SM, **Zhang Y**, Zenka RM, Sahasrabudhe DM, Qin R, Carlson R, Zhang S. Serum proteomics and ingenuity pathway analysis (IPA)-guided discovery of response markers to androgen ablation in prostate cancer. Markers in Cancer, Hollywood, FL, Oct 11-13, 2012.
13. Baker M, **Zhang Y**, Blitterswijk MV, DeJesus-Hernandez M, Boylan KB, Graff-Radford NR, Dickson DW, Rademakers R. Total transcriptome sequencing analyses in brain tissue of C9ORF72 expanded repeat carriers. The 20th Annual Meeting International Alliance of ALS/MND Associations and 23rd International Symposium on ALS/MND, Chicago, IL, Dec 2-7, 2012.
14. **Zhang Y**, Nair A, Middha S, Wang L, Sun Z, Asmann YW, Kocher JPA. A novel bioinformatics pipeline for identification and characterization of long non-coding RNAs in whole transcriptome sequencing data. The 14th annual Advances in Genome Biology and Technology meeting, Marco Island, FL, Feb 20-23, 2013.
15. **Zhang Y**, Tao C, Jiang G, Nair A, Su J, Liu H. Network-based analysis reveals distinct association patterns in a semantic MEDLINE-based drug-disease-gene network. Summit on Translational Bioinformatics, San Francisco, CA, Mar 18-22, 2013.

16. **Zhang Y**, Craig TA, Middha S, Ekker SC, Kumar R, Kocher JPA. Network-based analysis of time series gene expression data by integrating the interactome and Gene Ontology information. Individualizing Medicine 2013: From Promise to Practice, Rochester, MN, Sep 30-Oct 2, 2013.
17. **Zhang Y**, Tao C, He Y, Kanjamala P, Liu H. Analysis of vaccine-related networks using semantic MEDLINE and the Vaccine Ontology. Individualizing Medicine 2013: From Promise to Practice, Rochester, MN, Sep 30-Oct 2, 2013.
18. Nair A, **Zhang Y**, Bhavsar J, Middha S, Kocher JPA. Identification of expressed long intergenic non-coding RNA (lincRNA) using RNA-Seq technology. Individualizing Medicine 2013: From Promise to Practice, Rochester, MN, Sep 30-Oct 2, 2013.
19. Lee A, **Zhang Y**, Rossmannith A, Kohli M. Differential miRNA expression profiles in castrate resistant prostate cancer and potential utility in predicting docetaxel response. Individualizing Medicine 2013: From Promise to Practice, Rochester, MN, Sep 30-Oct 2, 2013.
20. **Zhang Y**, French AJ, Nair A, McDonnell S, Middha S, Riska S, Fogarty Z, Schaid D, Thibodeau SN. Identification of tissue-specific long intergenic non-coding RNAs in normal prostate tissue. The American Society of Human Genetics Annual Meeting 2013, Boston, MA, Oct 22-26 2013.
21. **Zhang Y**, Roberts L, Patel T. Systematic identification of long intergenic non-coding RNAs expressed in hepatocellular carcinoma. NIH Extracellular RNA Communication Consortium 2nd Investigators' Meeting, Bethesda, MD, May 14-15, 2014.
22. **Zhang Y**. ICQ-lincRNA: A bioinformatics tool for Identification, characterization and quantification of long intergenic non-coding RNAs in RNA-Seq data. Systems Biology of Gene Regulation and Genome Editing Conference, Cold Spring Harbor Asia, Suzhou, China, Sep 9-12, 2014.
23. **Zhang Y**, Yu P, & Tao, C. Network Analysis Identifies sex-associated patterns in VAERS RDF graph. The Workshop of Vaccine and Drug Ontology Studies (VDOS 2014), in conjunction with the International Conference on Biomedical Ontologies (ICBO), Houston, TX, Oct 6-9, 2014.
24. **Zhang Y**, McDonnell S, French AJ, Cheville J, Middha S, Riska S, Baheti S, Fogarty Z, Tillmans L, Larson M, Larson N, Nair A, O'Brien D, Davila J, Wang L, Cunningham JM, Schaid D, Thibodeau SN. Identification of large intergenic non-coding genes as candidate targets for prostate cancer risk-SNPs utilizing a normal prostate tissue eQTL dataset. The 64th American Society of Human Genetics Annual Meeting, San Diego, CA, Oct 18-22, 2014.
25. **Zhang Y**. Systematic Identification of long intergenic non-coding RNAs in human normal prostate tissue. 2015 Advances in Genome Biology and Technology Meeting, Marco Island, FL, Feb 25-28, 2015.
26. Jackson IL, **Zhang Y**, Bentzen S, Vujaskovic Z. Interrogating pulmonary sensitivity to radiation using gene expression microarrays. The 60th Annual Meeting of the Radiation Research Society, Las Vegas, NV, Sep 21-24, 2015.
27. Wang L, Shih Y, Xu X, **Zhang Y**. Dilated cardiomyopathy-associated long intergenic non-coding RNAs in zebrafish cardiac transcriptome. American Society of Human Genetics Annual Meeting 2015 (ASHG 2015), Baltimore, MD, Oct 6-10, 2015.

28. Jackson IL, **Zhang Y**, Bentzen S, Vujaskovic Z. Using gene expression signatures to elucidate the mechanisms regulating pulmonary sensitivity to radiation. American Society for Radiation Oncology (ASTRO) 5th Annual Meeting, San Antonio, TX, Oct 18-21, 2015.
29. **Zhang Y**. Regulation of the immune response by long non-coding RNAs in healthy subjects and stage IV melanoma patients. 2016 Advances in Genome Biology and Technology (AGBT) Meeting, Marco Island, FL, Feb 10-13, 2016.
30. Felts S, **Zhang Y**, Pease L. Transcriptomic fingerprints reveal an immune phenotype shared by melanoma patients and a subset of healthy people. FOCIS 2016 Annual Meeting, Boston, MA, June 22-25, 2016.
31. **Zhang Y**, Du J, Tao C. Co-occurrence analysis of adverse events for Typhoid fever vaccines. Joint International Conference on Biological Ontology and BioCreative (2016), Corvallis, OR, Aug 1-4, 2016.
32. **Zhang Y**. Regulation of the immune response by long non-coding RNAs in healthy subjects and stage IV melanoma patients. American Society of Human Genetics Annual Meeting 2016 (ASHG 2016), Vancouver, Canada, Oct 18-22, 2016.
33. **Zhang Y**. Systematic identification and characterization of cardiac long intergenic noncoding RNAs in zebrafish. 2017 Advances in Genome Biology and Technology (AGBT) Meeting, Hollywood, FL, Feb 13-16, 2017.
34. **Zhang Y**. Integrative genome-wide analysis of long noncoding RNAs in diverse immune cell types of melanoma patients. American Society of Human Genetics Annual Meeting 2018 (ASHG 2018), San Diego, FL, Oct 16-20, 2018.
35. Barry KH, Mohanty K, Rose G, Cellini A, Ambulos N, Yin J, Yan L, Poulin M, Meyer A, **Zhang Y**, Bentzen S, Burke A, Hussain A, Berndt SI. MYC DNA methylation in prostate tumor tissue is associated with tumor aggressiveness. AACR Annual Meeting 2019, Atlanta, GA, Mar 29 – Apr 3, 2019.
36. Fava A, **Zhang Y**, Hacoheh N, Arazi A, Berthier C, Rao D, Brenner M, Wofsy D, Davidson A, Kretzler M, Hildeman D, Woodle S, Diamond B, Petri M. Single cell RNA expression in lupus nephritis comparing African American and Caucasian patients identifies differential expression of Type I Interferon pathway. The 13th International Lupus Conference (Lupus 2019), San Francisco, CA, Apr 5-8, 2019.
37. Barry KH, Mohanty K, Rose G, Cellini A, Ambulos N, Yin J, Yan L, Poulin M, Meyer A, **Zhang Y**, Bentzen S, Burke A, Hussain A, Berndt SI. MYC DNA methylation in prostate tumor tissue is associated with tumor aggressiveness. The American Association for Cancer Research Annual Meeting 2019, Atlanta, GA, Mar 29-Apr 3, 2019.
38. Fava A, **Zhang Y**, Hacoheh N, Arazi A, Berthier C, Rao D, Brenner M, Wofsy D, Davidson A, Kretzler M, Hildeman D, Woodle S, Diamond B, Petri M. Toward a liquid biopsy for lupus nephritis: urine proteomic analysis of SLE identifies inflammatory and macrophage signatures. The 2019 ACR/ARP Annual Meeting, Atlanta, GA, November 8–13, 2019.
39. Fava A, **Zhang Y**, Hacoheh N, Arazi A, Berthier C, Rao D, Brenner M, Wofsy D, Davidson A, Kretzler M, Hildeman D, Woodle S, Diamond B, Petri M. Renal single cell genomics links Type II Interferon and lupus nephritis in African Americans. The 2019 ACR/ARP Annual Meeting, Atlanta, GA, November 8–13, 2019.
40. Bu L, Du J, Tao C, **Zhang Y**. Knowledge graph for Alzheimer’s Disease: literature mining from clinical studies. The AMIA 2020 Virtual Annual Symposium, November 14-18, 2020.

41. Timofte I, **Zhang Y**, et al. Prognostic biomarkers of disease severity for patients infected with coronavirus COVID19 in elderly patients. 2021 OAIC ANNUAL MEETING (Virtual), April 28-30, 2021.
42. **Zhang Y**. Investigating potential druggability of long non-coding RNAs for novel treatment of Alzheimer's Disease. AAIC® Satellite Symposium (Virtual), May 12-13, 2021.
43. Du J, **Zhang Y**, Bu L, Li F, Tao C. Building an Alzheimer's Disease knowledge graph (ADKG) by extracting and synthesizing scientific evidence from biomedical literature and human-curated knowledge base. AAIC® Satellite Symposium (Virtual), May 12-13, 2021.
44. **Zhang Y**, Tao C. Investigating potential druggability of long non-coding RNAs for novel treatment of Alzheimer's Disease. The 15<sup>th</sup> Clinical Trials on Alzheimer's Disease (CTAD), November 9-12, 2021.
45. **Zhang Y**. Exploiting novel long noncoding RNAs as pharmacological targets for treating Alzheimer's Disease using an integrative informatics approach. 2022 Advances in Genome Biology and Technology (AGBT) Meeting, Orlando, FL, February 28-March 3, 2022.
46. DeCastro A, **Zhang Y**, Stroka KM. Morphological Phenotyping of Organotropic Brain- and Bone-seeking Triple Negative Metastatic Breast Tumor Cells. AACR 2022. (accepted)