Hongbo Liu, Ph.D.

Assistant Professor
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Highlights

- \>15 years of experience in bioinformatics, epigenomics, population genetics, and single-cell omics
- \>50 publications (including >20 top-tier journal articles, e.g. *Nature Genetics, NAR, JASN*)
- \>2500 citations (Google Scholar h-index: 26)
- \>15 years of research experience in epigenomics data (WGBS, RRBS, EPIC array, ChIP-seq, ATAC-seq, etc)
- Rich experience in population genetics (GWAS, meQTL, eQTL, Mendelian randomization, gene prioritization, etc)
- Rich experience in single-cell omics (scRNA-seq, snATAC-seq, single-cell Multiome, spatial transcriptomics, etc)
- Editorial Board Member for *Briefings in Functional Genomics*
- Guest Associate Editor for *Frontiers in Genetics*
- Reviewer for >20 journals including *Nucleic Acids Research, Human Molecular Genetics*
- Developed >10 highly accessed bioinformatics tools or platforms
- National Scholarship for Doctoral Students, Ministry of Education of China

Academic Experience

- 2024 –   *Assistant Professor*
      Department of Biomedical Genetics and University of Rochester Aging Institute
      University of Rochester Medical Center, University of Rochester, Rochester, NY, USA
- 2023 – 2024   *Research Associate*
      Department of Medicine, University of Pennsylvania, Philadelphia, PA, USA
- 2018 – 2023   *Postdoctoral Fellow*
      Department of Genetics, University of Pennsylvania, Philadelphia, PA, USA
- 2016 – 2018   *Postdoctoral Fellow*
      Department of Epigenetics, Van Andel Institute, Grand Rapids, MI, USA
- 2015 – 2016   *Associate Professor*
      College of Bioinformatics Science and Technology, Harbin Medical University, Harbin, China
- 2010 – 2012   *Research Assistant*
      College of Bioinformatics Science and Technology, Harbin Medical University, Harbin, China

Education

- 2012 – 2015   Ph.D., Harbin Institute of Technology, Harbin, China (Research Advisor: Prof. Qiong Wu)
- 2007 – 2010   MS, Harbin Medical University, Harbin, China (Research Advisor: Prof. Yan Zhang)
- 2003 – 2007   BS, Qufu Normal University, Qufu, China

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Honors and Awards

- 2022   Poster Prize in the Penn-Stanford CVI Symposium at the University of Pennsylvania
- 2019   Poster Prize in the Epigenetics Symposium at the Franklin Institute
- 2017   Science and Technology Award, Heilongjiang Province People's Government
- 2014   National Scholarship for Doctoral Students, Ministry of Education of China
- 2012   Science and Technology Award, Education Department of Heilongjiang Province
- 2011   Science and Technology Award, Science and Technology Department of Heilongjiang Province
- 2010   Outstanding Master's Degree Graduates, Heilongjiang Province Office of Education

Research Interests

- Genetic Architecture of Complex Diseases
  - *Techniques:* GWAS, meQTL, eQTL, fine-mapping, colocalization, Mendelian randomization, etc
- Cell Type-Specific Epigenetic Regulatory Elements
  - *Techniques:* WGBS, Shannon entropy-based bioinformatic tools, ChromHMM, etc
- Epigenetic Dynamics in Mammalian Development
  - *Techniques:* WGBS, Epigenetic clocks, enhancers, etc
- Epigenetic Regulation of Age-Related Chronic Diseases
  - *Techniques:* EPIC array, WGBS, ChIP-seq, ATAC-seq, RNA-seq, etc
- Cellular Origins of Age-Related Chronic Diseases
  - *Techniques:* snRNA-seq, snATAC-seq, Chromium Single Cell Multiome, etc

Publications

(* denotes equal contributors; # denotes corresponding author; grey numbers denote primary publications, defined as those on which I am a first author and/or co-first author and/or corresponding author)

1. **H. Liu**, T. Doke, D. Guo, X. Sheng, Z. Ma, J. Park, H. M. T. Vy, G. N. Nadkarni, A. Abedini, Z. Miao, M. Palmer, B. F. Voight, H. Li, C. D. Brown, M. D. Ritchie, Y. Shu and K. Susztak#. (2022) Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. *Nature Genetics*, **54**, 950-962.

2. P. Dhillon*, K. A. Mulholland*, H. Hu, J. Park, X. Sheng, A. Abedini, **H. Liu**, A. Vassalotti, J. Wu and K. Susztak#. (2023) Increased levels of endogenous retroviruses trigger fibroinflammation and play a role in kidney disease development. *Nature Communications*, **14**, 559.

3. N. Sandholm*, J. B. Cole*, V. Nair, X. Sheng, **H. Liu**, E. Ahlqvist, N. van Zuydam, E. H. Dahlstrom, D. Fermin, L. J. Smyth, R. M. Salem, C. Forsblom, E. Valo, V. Harjutsalo, E. P. Brennan, G. J. McKay, D. Andrews, R. Doyle, H. C. Looker, R. G. Nelson, C. Palmer, A. J. McKnight, C. Godson, A. P. Maxwell, L. Groop, M. I. McCarthy, M. Kretzler, K. Susztak, J. N. Hirschhorn, J. C. Florez# and P. H. Groop#. (2022) Genome-wide meta-analysis and omics integration identifies novel genes associated with diabetic kidney disease. *Diabetologia*, **65**, 1495-1509.

4. X. Liang, T. Aranyi, J. Zhou, Y. Guan, H. Hu, **H. Liu** and K. Susztak#. (2022) Tet2- and Tet3- Mediated Cytosine Hydroxymethylation in Six2 Progenitor Cells in Mice Is Critical for Nephron Progenitor Differentiation and Nephron Endowment. *Journal of the American Society of Nephrology*.

5. A. Tin*#, P. Schlosser*, P. R. Matias-Garcia, C. H. L. Thio, R. Joehanes, **H. Liu**, Z. Yu, A. Weihs, A. Hoppmann, F. Grundner-Culemann, J. L. Min, V. L. H. Kuhns, A. A. Adeyemo, C. Agyemang, J. Arnlov, N. A. Aziz, A. Baccarelli, M. Bochud, H. Brenner, J. Bressler, M. M. B. Breteler, C. Carmeli, L. Chaker, J. Coresh, T. Corre, A. Correa, S. R. Cox, G. E. Delgado, K. U. Eckardt, A. B. Ekici, K. Endlich, J. S. Floyd, E. Fraszczyk, X. Gao, X. Gao, A. C. Gelber, M. Ghanbari, S. Ghasemi, C. Gieger, P. Greenland, M. L. Grove, S. E. Harris, G. Hemani, P. Henneman, C. Herder, S. Horvath, L. Hou, M. A. Hurme, S. J. Hwang, S. L. R. Kardia, S. Kasela, M. E. Kleber, W. Koenig, J. S. Kooner, F. Kronenberg, B. Kuhnel, C. Ladd-Acosta, T. Lehtimaki, L. Lind, D. Liu, D. M. Lloyd-Jones, S. Lorkowski, A. T. Lu, R. E. Marioni, W. Marz, D. L. McCartney, K. A. C. Meeks, L. Milani, P. P. Mishra, M. Nauck, C. Nowak, A. Peters, H. Prokisch, B. M. Psaty, O. T. Raitakari, S. M. Ratliff, A. P. Reiner, B. Schottker, J. Schwartz, S. Sedaghat, J. A. Smith, N. Sotoodehnia, H. R. Stocker, S. Stringhini, J. Sundstrom, B. R. Swenson, J. B. J. van Meurs, J. V. van Vliet-Ostaptchouk, A. Venema, U. Volker, J. Winkelmann, B. H. R. Wolffenbuttel, W. Zhao, Y. Zheng, M. Loh, H. Snieder, M. Waldenberger, D. Levy, S. Akilesh, O. M. Woodward, K. Susztak, A. Teumer and A. Kottgen#. (2021) Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. *Nature Communications*, **12**, 7173.

6. L. J. Smyth#, J. Kilner, V. Nair, **H. Liu**, E. Brennan, K. Kerr, N. Sandholm, J. Cole, E. Dahlstrom, A. Syreeni, R. M. Salem, R. G. Nelson, H. C. Looker, C. Wooster, K. Anderson, G. J. McKay, F. Kee, I. Young, D. Andrews, C. Forsblom, J. N. Hirschhorn, C. Godson, P. H. Groop, A. P. Maxwell, K. Susztak, M. Kretzler, J. C. Florez and A. J. McKnight. (2021)

Assessment of differentially methylated loci in individuals with end- stage kidney disease attributed to diabetic kidney disease: an exploratory study. *Clinical Epigenetics*, **13**, 99.

7. X. Sheng*, Y. Guan*, Z. Ma, J. Wu, **H. Liu**, C. Qiu, S. Vitale, Z. Miao, M. J. Seasock, M. Palmer, M. K. Shin, K. L. Duffin, S. S. Pullen, T. L. Edwards, J. N. Hellwege, A. M. Hung, M. Li, B. F. Voight, T. M. Coffman, C. D. Brown and K. Susztak#. (2021) Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. *Nature Genetics*, **53**, 1322-1333.

8. P. Schlosser*#, A. Tin*, P. R. Matias-Garcia, C. H. L. Thio, R. Joehanes, **H. Liu**, A. Weihs, Z. Yu, A. Hoppmann, F. Grundner-Culemann, J. L. Min, A. A. Adeyemo, C. Agyemang, J. Arnlov, N. A. Aziz, A. Baccarelli, M. Bochud, H. Brenner, M. M. B. Breteler, C. Carmeli, L. Chaker, J. C. Chambers, S. A. Cole, J. Coresh, T. Corre, A. Correa, S. R. Cox, N. de Klein, G. E. Delgado, A. Domingo-Relloso, K. U. Eckardt, A. B. Ekici, K. Endlich, K. L. Evans, J. S. Floyd, M. Fornage, L. Franke, E. Fraszczyk, X. Gao, X. Gao, M. Ghanbari, S. Ghasemi, C. Gieger, P. Greenland, M. L. Grove, S. E. Harris, G. Hemani, P. Henneman, C. Herder, S. Horvath, L. Hou, M. A. Hurme, S. J. Hwang, M. R. Jarvelin, S. L. R. Kardia, S. Kasela, M. E. Kleber, W. Koenig, J. S. Kooner, H. Kramer, F. Kronenberg, B. Kuhnel, T. Lehtimaki, L. Lind, D. Liu, Y. Liu, D. M. Lloyd-Jones, K. Lohman, S. Lorkowski, A. T. Lu, R. E. Marioni, W. Marz, D. L. McCartney, K. A. C. Meeks, L. Milani, P. P. Mishra, M. Nauck, A. Navas-Acien, C. Nowak, A. Peters, H. Prokisch, B. M. Psaty, O. T. Raitakari, S. M. Ratliff, A. P. Reiner, S. E. Rosas, B. Schottker, J. Schwartz, S. Sedaghat, J. A. Smith, N. Sotoodehnia, H. R. Stocker, S. Stringhini, J. Sundstrom, B. R. Swenson, M. Tellez-Plaza, J. B. J. van Meurs, J. V. van Vliet-Ostaptchouk, A. Venema, N. Verweij, R. M. Walker, M. Wielscher, J. Winkelmann, B. H. R. Wolffenbuttel, W. Zhao, Y. Zheng, M. Loh, H. Snieder, D. Levy, M. Waldenberger, K. Susztak, A. Kottgen and A. Teumer#. (2021) Meta-analyses identify DNA methylation associated with kidney function and damage. *Nature Communications*, **12**, 7174.

9. G. Z. Quinn, A. Abedini, **H. Liu**, Z. Ma, A. Cucchiara, A. Havasi, J. Hill, M. B. Palmer# and K. Susztak#. (2021) Renal Histologic Analysis Provides Complementary Information to Kidney Function Measurement for Patients with Early Diabetic or Hypertensive Disease. *Journal of the American Society of Nephrology*, **32**, 2863-2876.

10. Z. Miao*, M. S. Balzer*, Z. Ma, **H. Liu**, J. Wu, R. Shrestha, T. Aranyi, A. Kwan, A. Kondo, M. Pontoglio, J. Kim, M. Li, K. H. Kaestner and K. Susztak#. (2021) Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets. *Nature Communications*, **12**, 2277.

11. Y. Guan*, X. Liang*, Z. Ma, H. Hu, **H. Liu**, Z. Miao, A. Linkermann, J. N. Hellwege, B. F. Voight and K. Susztak#. (2021) A single genetic locus controls both expression of DPEP1/CHMP1A and kidney disease development via ferroptosis. *Nature Communications*, **12**, 5078.

12. T. Doke, S. Huang, C. Qiu, X. Sheng, M. Seasock, **H. Liu**, Z. Ma, M. Palmer and K. Susztak#. (2021) Genome-wide association studies identify the role of caspase-9 in kidney disease. *Science Advances*, **7**, eabi8051.

13. T. Doke, S. Huang, C. Qiu, **H. Liu**, Y. Guan, H. Hu, Z. Ma, J. Wu, Z. Miao, X. Sheng, J. Zhou, A. Cao, J. Li, L. Kaufman, A. Hung, C. D. Brown, R. Pestell and K. Susztak#. (2021) Transcriptome-wide association analysis identifies DACH1 as a kidney disease risk gene that contributes to fibrosis. *Journal of Clinical Investigation*, **131**.

14. P. Dhillon*, J. Park*#, C. Hurtado Del Pozo, L. Li, T. Doke, S. Huang, J. Zhao, H. M. Kang, R. Shrestra, M. S. Balzer, S. Chatterjee, P. Prado, S. Y. Han, **H. Liu**, X. Sheng, P. Dierickx, K. Batmanov, J. P. Romero, F. Prosper, M. Li, L. Pei, J. Kim, N. Montserrat# and K. Susztak#. (2021) The Nuclear Receptor ESRRA Protects from Kidney Disease by Coupling Metabolism and Differentiation. *Cell Metabolism*, **33**, 379-394.e378.

15. A. Abedini*, Y. O. Zhu*, S. Chatterjee*, G. Halasz, K. Devalaraja-Narashimha, R. Shrestha, S. Balzer M, J. Park, T. Zhou, Z. Ma, K. M. Sullivan, H. Hu, X. Sheng, **H. Liu**, Y. Wei, C. M. Boustany-Kari, U. Patel, S. Almaani, M. Palmer, R. Townsend, S. Blady, J. Hogan, L. Morton and K. Susztak#. (2021) Urinary Single-Cell Profiling Captures the Cellular Diversity of the Kidney. *Journal of the American Society of Nephrology*, **32**, 614-627.

16. X. Sheng, C. Qiu, **H. Liu**, C. Gluck, J. Y. Hsu, J. He, C. Y. Hsu, D. Sha, M. R. Weir, T. Isakova, D. Raj, H. Rincon-Choles, H. I. Feldman, R. Townsend, H. Li and K. Susztak#. (2020) Systematic integrated analysis of genetic and epigenetic variation in diabetic kidney disease. *Proceedings of the National Academy of Sciences*, **117**, 29013-29024.

17. Y. Guan*, **H. Liu***, Z. Ma, S. Y. Li, J. Park, X. Sheng and K. Susztak#. (2020) Dnmt3a and Dnmt3b-Decommissioned Fetal Enhancers are Linked to Kidney Disease. *Journal of the American Society of Nephrology*, **31**, 765-782.

18. S. Xu*, **H. Liu***, L. Wan*, W. Zhang, Q. Wang, S. Zhang, S. Shang, Y. Zhang# and D. Pang#. (2019) The MS-lincRNA landscape reveals a novel lincRNA BCLIN25 that contributes to tumorigenesis by upregulating ERBB2 expression via epigenetic modification and RNA-RNA interactions in breast cancer. *Cell Death & Disease*, **10**, 920.

19. Y. He*#, J. Shi*, Q. T. Nguyen*, E. You, **H. Liu**, X. Ren, Z. Wu, J. Li, W. Qiu, S. K. Khoo, T. Yang, W. Yi#, F. Sun, Z. Xi, X. Huang, K. Melcher, B. Min# and H. E. Xu#. (2019) Development of highly potent glucocorticoids for steroid-resistant severe asthma. *Proceedings of the National Academy of Sciences*, **116**, 6932-6937.

20. Y. Guan, **H. Liu** and K. Susztak#. (2019) Long-Range Chromatin Interactions in the Kidney. *Journal of the American Society of Nephrology*, **30**, 367-369.

21. S. Zhang, Y. Wang, Y. Gu, J. Zhu, C. Ci, Z. Guo, C. Chen, Y. Wei, W. Lv, **H. Liu**, D. Zhang and Y. Zhang#. (2018) Specific breast cancer prognosis-subtype distinctions based on DNA methylation patterns. *Molecular Oncology*, **12**, 1047-1060.

22. Y. Xiong*, Y. Wei*, Y. Gu*, S. Zhang, J. Lyu, B. Zhang, C. Chen, J. Zhu, Y. Wang, **H. Liu#** and Y. Zhang#. (2017) DiseaseMeth version 2.0: a major expansion and update of the human disease methylation database. *Nucleic Acids Research*, **45**, D888-d895.

23. Y. Wen*, Y. Wei*, S. Zhang, S. Li, **H. Liu**, F. Wang, Y. Zhao, D. Zhang# and Y. Zhang#. (2017) Cell subpopulation deconvolution reveals breast cancer heterogeneity based on DNA methylation signature. *Briefings in Bioinformatics*, **18**, 426-440.

24. H. Wang*, W. Yan*, S. Zhang*, Y. Gu, Y. Wang, Y. Wei, **H. Liu**, F. Wang, Q. Wu and Y. Zhang#. (2017) Survival differences of CIMP subtypes integrated with CNA information in human breast cancer. *Oncotarget*, **8**, 48807-48819.

25. Y. Wei*, S. Zhang*, S. Shang*, B. Zhang, S. Li, X. Wang, F. Wang, J. Su, Q. Wu, **H. Liu#** and Y. Zhang#. (2016) SEA: a super-enhancer archive. *Nucleic Acids Research*, **44**, D172-179.

26. Y. Wang*, J. Zhang*, X. Xiao*, **H. Liu**, F. Wang, S. Li, Y. Wen, Y. Wei, J. Su, Y. Zhang# and Y. Zhang#. (2016) The identification of age-associated cancer markers by an integrative analysis of dynamic DNA methylation changes. *Scientific Reports*, **6**, 22722.

27. **H. Liu#**, S. Li, X. Wang, J. Zhu, Y. Wei, Y. Wang, Y. Wen, L. Wang, Y. Huang, B. Zhang, S. Shang and Y. Zhang#. (2016) DNA methylation dynamics: identification and functional annotation. *Brief Funct Genomics*, **15**, 470-484.

28. **H. Liu*#**, X. Liu*, S. Zhang*, J. Lv, S. Li, S. Shang, S. Jia, Y. Wei, F. Wang, J. Su, Q. Wu and Y. Zhang#. (2016) Systematic identification and annotation of human methylation marks based on bisulfite sequencing methylomes reveals distinct roles of cell type- specific hypomethylation in the regulation of cell identity genes. *Nucleic Acids Research*, **44**, 75-94.

29. H. Liu*, J. Lyu*, **H. Liu***, Y. Gao, J. Guo, H. He, Z. Han, Y. Zhang and Q. Wu#. (2016) Computational identification of putative lincRNAs in mouse embryonic stem cell. *Scientific Reports*, **6**, 34892.

30. W. Li, H. Liu, M. Yu, X. Zhang, Y. Zhang, **H. Liu**, J. X. Wilson and G. Huang#. (2016) Folic Acid Alters Methylation Profile of JAK-STAT and Long-Term Depression Signaling Pathways in Alzheimer's Disease Models. *Molecular Neurobiology*, **53**, 6548-6556.

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32. C. Zhang*, H. Zhao*, J. Li, **H. Liu**, F. Wang, Y. Wei, J. Su, D. Zhang, T. Liu# and Y. Zhang#. (2015) The identification of specific methylation patterns across different cancers. *PLoS One*, **10**, e0120361.

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34. H. Yan*, D. Zhang*, **H. Liu**, Y. Wei, J. Lv, F. Wang, C. Zhang, Q. Wu, J. Su# and Y. Zhang#. (2015) Chromatin modifications and genomic contexts linked to dynamic DNA methylation patterns across human cell types. *Scientific Reports*, **5**, 8410.

35. F. Wang*, S. Zhang*, **H. Liu**, Y. Wei, Y. Wang, X. Han, J. Su, D. Zhang, B. Xie# and Y. Zhang#. (2015) CellMethy: Identification of a focal concordantly methylated pattern of CpGs revealed wide differences between normal and cancer tissues. *Scientific Reports*, **5**, 18037.

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37. Y. Wei, J. Su, **H. Liu**, J. Lv, F. Wang, H. Yan, Y. Wen, H. Liu, Q. Wu# and Y. Zhang#. (2014) MetaImprint: an information repository of mammalian imprinted genes. *Development*, **141**, 2516-2523.

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40. **H. Liu***, R. Zhu*, J. Lv, H. He, L. Yang, Z. Huang, J. Su, Y. Zhang, S. Yu and Q. Wu#. (2014) DevMouse, the mouse developmental methylome database and analysis tools. *Database (Oxford)*, **2014**, bat084.

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42. X. Xiao, Z. Li, **H. Liu**, J. Su, F. Wang, X. Wu, H. Liu, Q. Wu and Y. Zhang#. (2013) Genome-wide identification of Polycomb target genes in human embryonic stem cells. *Gene*, **518**, 425-430.

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47. **H. Liu***, Y. Chen*, J. Lv, H. Liu, R. Zhu, J. Su, X. Liu, Y. Zhang# and Q. Wu#. (2013) Quantitative epigenetic co-variation in CpG islands and co-regulation of developmental genes. *Scientific Reports*, **3**, 2576.

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Bioinformatic Tools or Platforms

- SMART   A Python package for deep analysis of DNA methylation by whole genome bisulfite sequencing
  http://fame.edbc.org/smart
- QDMR   A Java Package for identifying differentially methylated regions across large-scale datasets
  http://fame.edbc.org/qdmr
- QDCMR   A Java package for quantifying chromatin modification difference from ChIP-seq data
  https://github.com/hbliu/QDCMR
- SEA   A comprehensive online archive and analysis platform for super-enhancers for 11 species
  http://sea.edbc.org
- DiseaseMeth   A web-based resource and analysis platform for abnormal DNA methylation of human diseases
  http://diseasemeth.edbc.org
- MethyMarks   A web-based resource platform for tissue-specific methylation marks in human
  http://fame.edbc.org/methymark
- EpiDiff   Epigenetic Difference Analysis Tool based on adapting Shannon entropy
  https://www.edbc.org/db/EpiDiff
- Kidney_Epi_Pri A pipeline for prioritization of disease-causal genes by integrating GWAS with the epigenome
  https://github.com/hbliu/Kidney_Epi_Pri
- eGFR_GWAS   eGFRcrea GWAS and Prioritization Atlas based on 1.5 million individuals
  https://susztaklab.com/GWAS
- Kidney_meQTL   Human kidney methylation QTL atlas based on 443 human kidneys
  https://susztaklab.com/Kidney_meQTL
- Kidney_eQTL   Human kidney expression QTL atlas based on 686 human kidneys
  https://susztaklab.com/Kidney_eQTL

- HKOCA   Human kidney open chromatin atlas based on 57,282 cells from 12 cell types of human kidneys
              https://susztaklab.com/Human_snATAC

Grants

- 2015 – 2017   National Natural Science Foundation of China, #61403112 (PI: Hongbo Liu)
- 2012 – 2014   Foundation of Education Department of Heilongjiang Province, #12521270 (PI: Hongbo Liu)

Courses Taught

- 2015 – 2016   Computational Epigenetics (Harbin Medical University)
- 2015 – 2016   Biomolecular Network Analysis (Harbin Medical University)
- 2015 – 2016   Combinatorics and Graph Theory (Harbin Medical University)
- 2011 – 2012   Database Principles and Applications (Harbin Medical University)
- 2010 – 2011   System Biology (Harbin Medical University)

Undergraduate Students Trained (Harbin Medical University)

- 2015 – 2016   Shanshan Zhang (current position: Graduate student at Case Western Reserve University)
- 2014 – 2015   Shipeng Shang (current position: Assistant professor at Qingdao University)
- 2013 – 2014   Yunzhen Wei (current position: Assistant professor at Guangdong Medical University)
- 2012 – 2014   Rangfei Zhu (current position: CEO of Hangzhou Mugu Technology Co., Ltd)

Computing Skills

R, Java, Python, C, HTML, Javascript, Linux shell, SQL.

Scientific Society Member

- 2018 – present   American Association for Cancer Research (AACR)
- 2019 – present   American Society of Nephrology (ASN)
- 2022 – present   The American Society of Human Genetics (ASHG)

Journal Editorial Boards

- 2016 – present   *Briefings in Functional Genomics* (Editorial Board)
- 2018 – 2019   *Frontiers in Genetics* (Guest Associate Editor)

Reviewer

Science Translational Medicine	Human Molecular Genetics
Nucleic Acids Research	Quantitative Biology
Journal of the American Society of Nephrology	Genes
Aging	Briefings in Functional Genomics
Molecular Therapy - Nucleic Acids	Frontiers in Oncology
Briefings in Bioinformatics	Frontiers in Aging Neuroscience
Frontiers in Genetics	PLOS ONE
Frontiers in Cell and Developmental Biology	Current Bioinformatics
Oncotarget	The International Journal of Molecular Sciences
Methods	Cell & Bioscience
Healthcare	The Journal of Clinical Endocrinology & Metabolism

Invited Talks

- 10/07/2022   *Lightning round presenter*, 7th Annual MidAtlantic Bioinformatics Conference (Philadelphia, PA)
- 08/08/2022   *Invited speaker*, International Conference on Intelligent Biology and Medicine (Philadelphia, PA)
- 05/19/2022   *Invited speaker*, Chinese Genomics Meet-up online (CGM online)
- 04/25/2022   *Invited speaker*, Penn Genetics 2022 Global Scientific Symposium (Philadelphia, PA)
- 04/14/2022   *Invited speaker*, University of Science and Technology of China (Hefei, China)
- 03/06/2019   *Invited speaker*, Keystone symposia: Unraveling the Secrets of Kidney Disease (BC, Canada)
- 07/10/2016   *Invited speaker*, The International Symposium on the Frontier of Big Data in Science (Baotou, China)

Poster Presentation

- 10/24/2022   *Poster presenter and award*, The Penn-Stanford CVI Symposium (Philadelphia, PA)
- 06/02/2022   *Poster presenter*, Upenn Department of Medicine 2022 Research Day, (Philadelphia, PA)
- 06/02/2022   *Poster presenter*, HUP/CHOP Renal Research Symposium (Philadelphia, PA)
- 03/15/2022   *Poster presenter*, Penn IDOM Spring Symposium (Philadelphia, PA)
- 12/16/2019   *Poster presenter and award*, Fox Chase Cancer Center Epigenetics Symposium (Philadelphia, PA)
- 11/05/2019   *Poster presenter*, Kidney Week 2019, American Society of Nephrology (Washington DC)
- 03/19/2019   *Poster presenter*, Penn IDOM Spring Symposium (Philadelphia, PA)
- 12/17/2015   *Poster presenter*, 8th International Stem Cell and Regenerative Medicine Forum (Guangzhou, China)