

# Hongbo Liu, Ph.D.

---

## Appointment

Assistant Professor, Department of Biomedical Genetics  
Member, University of Rochester Aging Institute  
University of Rochester Medical Center  
University of Rochester



## Contact Information

Lab Website: <https://hbliulab.org>

E-mail: [Hongbo\\_Liu@URMC.Rochester.edu](mailto:Hongbo_Liu@URMC.Rochester.edu)

Address: Department of Biomedical Genetics (KMRB#2-9834), 601 Elmwood Ave, Rochester, NY 14642

## Education and Training

- |               |   |                                |
|---------------|---|--------------------------------|
| • 2018 – 2023 | Postdoctoral Fellow (mentor: Dr. Katalin Susztak)     | University of Pennsylvania     |
| • 2016 – 2018 | Postdoctoral Fellow (mentor: Dr. Hui Shen)            | Van Andel Institute            |
| • 2012 – 2015 | Ph.D., Biomedical Engineering (advisor: Dr. Qiong Wu) | Harbin Institute of Technology |
| • 2007 – 2010 | MSc, Biomedical Engineering (advisor: Dr. Yan Zhang)  | Harbin Medical University      |
| • 2003 – 2007 | B.S., Information and Computing Science               | Qufu Normal University         |

## Professional Experience

- |                  |                     |   |
|------------------|---------------------|---|
| • 2024 – present | Assistant Professor | Department of Biomedical Genetics, University of Rochester        |
| • 2024 – present | Member              | University of Rochester Aging Institute                           |
| • 2023 – 2024    | Research Associate  | Department of Medicine, University of Pennsylvania                |
| • 2015 – 2016    | Associate Professor | College of Bioinformatics Sci. & Tech., Harbin Medical University |
| • 2010 – 2012    | Research Assistant  | College of Bioinformatics Sci. & Tech., Harbin Medical University |

## 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. Reverse chronological order)

1. **Hongbo Liu**<sup>#</sup>, Amin Abedini, Eunji Ha, Ziyuan Ma, Xin Sheng, Bernhard Dumoulin, Chengxiang Qiu, Tamas Aranyi, Shen Li, Nicole Dittrich, Hua-Chang Chen, Ran Tao, Der-Cherng Tarn, Feng-Jen Hsieh, Shih-Ann Chen, Shun-Fa Yang, Mei-Yueh Lee, Pui-Yan Kwok, Jer-Yuarn Wu, Chien-Hsiun Chen, Atlas Khan, Nita A. Limdi, Wei-Qi Wei, Theresa L. Walunas, Elizabeth W. Karlson, Eimear E. Kenny, Yuan Luo, Leah Kottyan, John J. Connolly, Gail P. Jarvik, Chunhua Weng, Ning Shang, Joanne B. Cole, Josep M. Mercader, Ravi Mandla, Timothy D. Majarian, Jose C. Florez, Mary E. Haas, Luca A. Lotta, Theodore G. Drivas, Ha My T. Vy, Girish N. Nadkarni, Laura K. Wiley, Melissa P. Wilson, Christopher R. Gignoux, Humaira Rasheed, Laurent F. Thomas, Bjørn Olav Åsvold, Ben M. Brumpton, Stein I. Hallan, Kristian Hveem, Jie Zheng, Jacklyn N. Hellwege, Matthew Zawistowski, Sebastian Zöllner, Nora Franceschini, Hailong Hu, Jianfu Zhou, Krzysztof Kiryluk, Marylyn D. Ritchie, Matthew Palmer, Todd L. Edwards, Benjamin F. Voight, Adriana M. Hung and Katalin Susztak<sup>#</sup>. Kidney multiome-based genetic scorecard reveals convergent coding and regulatory variants, *Science*, 387, eadp4753. (2025)
2. Shen Li, **Hongbo Liu**, Hailong Hu, Eunji Ha, Praveena Prasad, Brenita C. Jenkins, Ujjalkumar Subhash Das, Sarmistha Mukherjee, Kyosuke Shishikura, Renming Hu, Daniel J. Rader, Liming Pei, Joseph A. Baur, Megan L. Matthews, Garret A. FitzGerald, Melanie R. McReynolds and Katalin Susztak<sup>#</sup>. Human genetics identify convergent signals in mitochondrial LACTB-mediated lipid metabolism in cardiovascular-kidney-metabolic syndrome, *Cell Metabolism*, 37, 154-168 e157. (2025)
3. Teresa K. Chen<sup>#</sup>, Aditya L. Surapaneni, Insa M. Schmidt, Sushrut S. Waikar, Josef Coresh, **Hongbo Liu**, Katalin Susztak, Eugene P. Rhee, Celina Liu, Pascal Schlosser and Morgan E. Grams. Proteomics and Incident Kidney Failure in Individuals With CKD: The African American Study of Kidney Disease and Hypertension and the Boston Kidney Biopsy Cohort, *Kidney Medicine*, 6, 100921. (2024)

## Hongbo Liu, Ph.D.

4. Xiujie Liang, **Hongbo Liu**, Hailong Hu, Eunji Ha, Jianfu Zhou, Amin Abedini, Andrea Sanchez-Navarro, Konstantin A. Klotzer and Katalin Susztak<sup>#</sup>. TET2 germline variants promote kidney disease by impairing DNA repair and activating cytosolic nucleotide sensors, *Nature Communications*, 15, 9621. (2024)
5. Tanya J. Major\*, Riku Takei\*, Hirotaka Matsuo\*, Megan P. Leask\*, Nicholas A. Sumpter\*, Ruth K. Topless\*, Yuya Shirai\*, Wei Wang\*, Murray J. Cadzow, Amanda J. Phipps-Green, Zhiqiang Li, Aichang Ji, Marilyn E. Merriman, Emily Morice, Eric E. Kelley, Wen-Hua Wei, Sally P. A. McCormick, Matthew J. Bixley, Richard J. Reynolds, Kenneth G. Saag, Tayaza Fadason, Evgenia Golovina, Justin M. O'Sullivan, Lisa K. Stamp, Nicola Dalbeth, Abhishek Abhishek, Michael Doherty, Edward Roddy, Lennart T. H. Jacobsson, Meliha C. Kapetanovic, Olle Melander, Mariano Andres, Fernando Perez-Ruiz, Rosa J. Torres, Timothy Radstake, Timothy L. Jansen, Matthijs Janssen, Leo A. B. Joosten, Ruiqi Liu, Orsolya I. Gaal, Tania O. Crisan, Simona Rednic, Fina Kurreeman, Tom W. J. Huizinga, Rene Toes, Frederic Liote, Pascal Richette, Thomas Bardin, Hang Korng Ea, Tristan Pascart, Geraldine M. McCarthy, Laura Helbert, Blanka Stiburkova, Anne- K. Tausche, Till Uhlig, Veronique Vitart, Thibaud S. Boutin, Caroline Hayward, Philip L. Riches, Stuart H. Ralston, Archie Campbell, Thomas M. MacDonald, Akiyoshi Nakayama, Tappei Takada, Masahiro Nakatochi, Seiko Shimizu, Yusuke Kawamura, Yu Toyoda, Hirofumi Nakaoka, Ken Yamamoto, Keitaro Matsuo, Nariyoshi Shinomiya, Kimiyoshi Ichida, Chaeyoung Lee, Linda A. Bradbury, Matthew A. Brown, Philip C. Robinson, Russell R. C. Buchanan, Catherine L. Hill, Susan Lester, Malcolm D. Smith, Maureen Rischmueller, Hyon K. Choi, Eli A. Stahl, Jeff N. Miner, Daniel H. Solomon, Jing Cui, Kathleen M. Giacomini, Deanna J. Brackman, Eric M. Jorgenson, **Hongbo Liu**, Katalin Susztak, Suyash Shringarpure, Alexander So, Yukinori Okada, Changgui Li, Yongyong Shi and Tony R. Merriman<sup>#</sup>. A genome-wide association analysis reveals new pathogenic pathways in gout, *Nature Genetics*, 56, 2392-2406. (2024)
6. Amin Abedini\*, Jonathan Levinsohn\*, Konstantin A. Klotzer, Bernhard Dumoulin, Ziyuan Ma, Julia Frederick, Poonam Dhillon, Michael S. Balzer, Rojesh Shrestha, **Hongbo Liu**, Steven Vitale, Andi M. Bergeson, Kishor Devalaraja-Narashimha, Paola Grandi, Tanmoy Bhattacharyya, Erding Hu, Steven S. Pullen, Carine M. Boustany-Kari, Paolo Guarnieri, Anil Karihaloo, Daniel Traum, Hanying Yan, Kyle Coleman, Matthew Palmer, Lea Sarov-Blat, Lori Morton, Christopher A. Hunter, Klaus H. Kaestner, Mingyao Li and Katalin Susztak<sup>#</sup>. Single-cell multi-omic and spatial profiling of human kidneys implicates the fibrotic microenvironment in kidney disease progression, *Nature Genetics*, 56, 1712-1724. (2024)
7. Edward D. Siew<sup>\*\*</sup>, Jacklyn N. Hellwege\*, Adriana M. Hung, Bethany C. Birkelo, Andrew J. Vincz, Sharidan K. Parr, Jason Denton, Robert A. Greevy, Cassianne Robinson-Cohen, **Hongbo Liu**, Katalin Susztak, Michael E. Matheny and Digna R. Velez Edwards. Genome-wide association study of hospitalized patients and acute kidney injury, *Kidney International*, 106, 291-301. (2024)
8. Abel Fothi, **Hongbo Liu**, Katalin Susztak and Tamas Aranyi<sup>#</sup>. Improve-RRBS: a novel tool to correct the 3' trimming of reduced representation sequencing reads, *Bioinformatics Advances*, 4, vbae076. (2024)
9. Yu Yan, **Hongbo Liu**, Amin Abedini, Xin Sheng, Matthew Palmer, Hongzhe Li and Katalin Susztak<sup>#</sup>. Unraveling the epigenetic code: human kidney DNA methylation and chromatin dynamics in renal disease development, *Nature Communications*, 15, 873. (2024)
10. Amin Abedini, Andrea Sanchez-Navarro, Junnan Wu, Konstantin A. Klotzer, Ziyuan Ma, Bibek Poudel, Tomohito Doke, Michael S. Balzer, Julia Frederick, Hana Cernecka, **Hongbo Liu**, Xiujie Liang, Steven Vitale, Peter Kolkhof and Katalin Susztak<sup>#</sup>. Single-cell transcriptomics and chromatin accessibility profiling elucidate the kidney-protective mechanism of mineralocorticoid receptor antagonists, *The Journal of Clinical Investigation*, 134, (2024)
11. Dhanunjay Mukhi, Lingzhi Li, **Hongbo Liu**, Tomohito Doke, Lakshmi P. Kolligundla, Eunji Ha, Konstantin Klotzer, Amin Abedini, Sarmistha Mukherjee, Junnan Wu, Poonam Dhillon, Hailong Hu, Dongyin Guan, Katsuhiko Funai, Kahealani Uehara, Paul M. Titchenell, Joseph A. Baur, Kathryn E. Wellen and Katalin Susztak<sup>#</sup>. ACSS2 gene variants determine kidney disease risk by controlling de novo lipogenesis in kidney tubules, *The Journal of Clinical Investigation*, 134, (2023)
12. Jianfu Zhou, Amin Abedini, Michael S. Balzer, Rojesh Shrestha, Poonam Dhillon, **Hongbo Liu**, Hailong Hu and Katalin Susztak<sup>#</sup>. Unified Mouse and Human Kidney Single-Cell Expression Atlas Reveal Commonalities and Differences in Disease States, *Journal of the American Society of Nephrology*, 34, 1843-1862. (2023)
13. Farah Lizotte, Marina Rousseau, Benoit Denhez, Dominique Levesque, Andreanne Guay, **Hongbo Liu**, Julie Moreau, Sarah Higgins, Robert Sabbagh, Katalin Susztak, Francois-Michel Boisvert, Anne Marie Cote and Pedro Gerald<sup>#</sup>. Deletion of protein tyrosine phosphatase SHP-1 restores SUMOylation of podocin and reverses the progression of diabetic kidney disease, *Kidney International*, 104, 787-802. (2023)
14. Pascal Schlosser<sup>#</sup>, Jingning Zhang, **Hongbo Liu**, Aditya L. Surapaneni, Eugene P. Rhee, Dan E. Arking, Bing Yu, Eric Boerwinkle, Paul A. Welling, Nilanjan Chatterjee, Katalin Susztak, Josef Coresh and Morgan E. Grams.

## Hongbo Liu, Ph.D.

- Transcriptome- and proteome-wide association studies nominate determinants of kidney function and damage, *Genome Biology*, 24, 150. (2023)
15. Kelly Yichen Li, Claudia Ha Ting Tam, **Hongbo Liu**, Samantha Day, Cadmon King Poo Lim, Wing Yee So, Chuiguo Huang, Guozhi Jiang, Mai Shi, Heung Man Lee, Hui-Yao Lan, Cheuk-Chun Szeto, Robert L. Hanson, Robert G. Nelson, Katalin Susztak, Juliana C. N. Chan, Kevin Y. Yip<sup>#</sup> and Ronald C. W. Ma<sup>#</sup>. DNA methylation markers for kidney function and progression of diabetic kidney disease, *Nature Communications*, 14, 2543. (2023)
  16. Daigoro Hirohama, Amin Abedini, Salina Moon, Aditya Surapaneni, Simon T. Dillon, Allison Vassalotti, **Hongbo Liu**, Tomohito Doke, Victor Martinez, Zaipul Md Dom, Anil Karihaloo, Matthew B. Palmer, Josef Coresh, Morgan E. Grams, Monika A. Niewczas<sup>#</sup> and Katalin Susztak<sup>#</sup>. Unbiased Human Kidney Tissue Proteomics Identifies Matrix Metalloproteinase 7 as a Kidney Disease Biomarker, *Journal of the American Society of Nephrology*, 34, 1279-1291. (2023)
  17. Poonam Dhillon\*, Kelly Ann Mulholland\*, Hailong Hu, Jihwan Park, Xin Sheng, Amin Abedini, **Hongbo Liu**, Allison Vassalotti, Junnan Wu and Katalin Susztak<sup>#</sup>. Increased levels of endogenous retroviruses trigger fibroinflammation and play a role in kidney disease development, *Nature Communications*, 14, 559. (2023)
  18. Xiujie Liang, Tamas Aranyi, Jianfu Zhou, Yuting Guan, Hailong Hu, **Hongbo Liu** and Katalin Susztak<sup>#</sup>. 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*, 34, 572-589. (2023)
  19. **Hongbo Liu**, Tomohito Doke, Dong Guo, Xin Sheng, Ziyuan Ma, Joseph Park, Ha My T. Vy, Girish N. Nadkarni, Amin Abedini, Zhen Miao, Matthew Palmer, Benjamin F. Voight, Hongzhe Li, Christopher D. Brown, Marylyn D. Ritchie, Yan Shu and Katalin Susztak<sup>#</sup>. Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease, *Nature Genetics*, 54, 950-962. (2022)
  20. Niina Sandholm\*, Joanne B. Cole\*, Viji Nair, Xin Sheng, **Hongbo Liu**, Emma Ahlqvist, Natalie van Zuydam, Emma H. Dahlstrom, Damian Fermin, Laura J. Smyth, Rany M. Salem, Carol Forsblom, Erkka Valo, Valma Harjutsalo, Eoin P. Brennan, Gareth J. McKay, Darrell Andrews, Ross Doyle, Helen C. Looker, Robert G. Nelson, Colin Palmer, Amy Jayne McKnight, Catherine Godson, Alexander P. Maxwell, Leif Groop, Mark I. McCarthy, Matthias Kretzler, Katalin Susztak, Joel N. Hirschhorn<sup>#</sup>, Jose C. Florez and Per-Henrik Groop<sup>#</sup>. Genome-wide meta-analysis and omics integration identifies novel genes associated with diabetic kidney disease, *Diabetologia*, 65, 1495-1509. (2022)
  21. Pascal Schlosser<sup>\*\*</sup>, Adrienne Tin\*, Pamela R. Matias-Garcia, Chris H. L. Thio, Roby Joehanes, **Hongbo Liu**, Antoine Weihs, Zhi Yu, Anselm Hoppmann, Franziska Grundner-Culemann, Josine L. Min, Adebowale A. Adeyemo, Charles Agyemang, Johan Arnlov, Nasir A. Aziz, Andrea Baccarelli, Murielle Bochud, Hermann Brenner, Monique M. B. Breteler, Cristian Carmeli, Layal Chaker, John C. Chambers, Shelley A. Cole, Josef Coresh, Tanguy Corre, Adolfo Correa, Simon R. Cox, Niek de Klein, Graciela E. Delgado, Arce Domingo-Relloso, Kai-Uwe Eckardt, Arif B. Ekici, Karlhans Endlich, Kathryn L. Evans, James S. Floyd, Myriam Fornage, Lude Franke, Eliza Fraszczyk, Xu Gao, Xin Gao, Mohsen Ghanbari, Sahar Ghasemi, Christian Gieger, Philip Greenland, Megan L. Grove, Sarah E. Harris, Gibran Hemani, Peter Henneman, Christian Herder, Steve Horvath, Lifang Hou, Mikko A. Hurme, Shih-Jen Hwang, Marjo-Riitta Jarvelin, Sharon L. R. Kardia, Silva Kasela, Marcus E. Kleber, Wolfgang Koenig, Jaspal S. Kooner, Holly Kramer, Florian Kronenberg, Brigitte Kuhnel, Terho Lehtimaki, Lars Lind, Dan Liu, Yongmei Liu, Donald M. Lloyd-Jones, Kurt Lohman, Stefan Lorkowski, Ake T. Lu, Riccardo E. Marioni, Winfried Marz, Daniel L. McCartney, Karlijn A. C. Meeks, Lili Milani, Pashupati P. Mishra, Matthias Nauck, Ana Navas-Acien, Christoph Nowak, Annette Peters, Holger Prokisch, Bruce M. Psaty, Olli T. Raitakari, Scott M. Ratliff, Alex P. Reiner, Sylvia E. Rosas, Ben Schottker, Joel Schwartz, Sanaz Sedaghat, Jennifer A. Smith, Nona Sotoodehnia, Hannah R. Stocker, Silvia Stringhini, Johan Sundstrom, Brenton R. Swenson, Maria Tellez-Plaza, Joyce B. J. van Meurs, Jana V. van Vliet-Ostaptchouk, Andrea Venema, Niek Verweij, Rosie M. Walker, Matthias Wielscher, Juliane Winkelmann, Bruce H. R. Wolffenbuttel, Wei Zhao, Yinan Zheng, Marie Loh, Harold Snieder, Daniel Levy, Melanie Waldenberger, Katalin Susztak, Anna Kottgen and Alexander Teumer<sup>#</sup>. Meta-analyses identify DNA methylation associated with kidney function and damage, *Nature Communications*, 12, 7174. (2021)
  22. Adrienne Tin<sup>\*\*</sup>, Pascal Schlosser\*, Pamela R. Matias-Garcia, Chris H. L. Thio, Roby Joehanes, **Hongbo Liu**, Zhi Yu, Antoine Weihs, Anselm Hoppmann, Franziska Grundner-Culemann, Josine L. Min, Victoria L. Halperin Kuhns, Adebowale A. Adeyemo, Charles Agyemang, Johan Arnlov, Nasir A. Aziz, Andrea Baccarelli, Murielle Bochud, Hermann Brenner, Jan Bressler, Monique M. B. Breteler, Cristian Carmeli, Layal Chaker, Josef Coresh, Tanguy Corre, Adolfo Correa, Simon R. Cox, Graciela E. Delgado, Kai-Uwe Eckardt, Arif B. Ekici, Karlhans Endlich, James S. Floyd, Eliza Fraszczyk, Xu Gao, Xin Gao, Allan C. Gelber, Mohsen Ghanbari, Sahar Ghasemi, Christian Gieger, Philip Greenland, Megan L. Grove, Sarah E. Harris, Gibran Hemani, Peter Henneman, Christian Herder, Steve Horvath, Lifang Hou, Mikko A. Hurme, Shih-Jen Hwang, Sharon L. R. Kardia, Silva Kasela, Marcus E. Kleber, Wolfgang Koenig, Jaspal S. Kooner, Florian Kronenberg, Brigitte Kuhnel, Christine Ladd-Acosta, Terho Lehtimaki, Lars Lind, Dan Liu, Donald M. Lloyd-Jones, Stefan Lorkowski, Ake T. Lu, Riccardo E. Marioni, Winfried Marz, Daniel L.

## Hongbo Liu, Ph.D.

- McCartney, Karlijn A. C. Meeks, Lili Milani, Pashupati P. Mishra, Matthias Nauck, Christoph Nowak, Annette Peters, Holger Prokisch, Bruce M. Psaty, Olli T. Raitakari, Scott M. Ratliff, Alex P. Reiner, Ben Schottker, Joel Schwartz, Sanaz Sedaghat, Jennifer A. Smith, Nona Sotoodehnia, Hannah R. Stocker, Silvia Stringhini, Johan Sundstrom, Brenton R. Swenson, Joyce B. J. van Meurs, Jana V. van Vliet-Ostaptchouk, Andrea Venema, Uwe Volker, Juliane Winkelmann, Bruce H. R. Wolffenbuttel, Wei Zhao, Yinan Zheng, Marie Loh, Harold Snieder, Melanie Waldenberger, Daniel Levy, Shreeram Akilesh, Owen M. Woodward, Katalin Susztak, Alexander Teumer and Anna Kottgen<sup>#</sup>. Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus, *Nature Communications*, 12, 7173. (2021)
23. Tomohito Doke, Shizheng Huang, Chengxiang Qiu, Xin Sheng, Matthew Seasock, **Hongbo Liu**, Ziyuan Ma, Matthew Palmer and Katalin Susztak<sup>#</sup>. Genome-wide association studies identify the role of caspase-9 in kidney disease, *Science Advances*, 7, eabi8051. (2021)
24. Yuting Guan\*, Xiujie Liang\*, Ziyuan Ma, Hailong Hu, **Hongbo Liu**, Zhen Miao, Andreas Linkermann, Jacklyn N. Hellwege, Benjamin F. Voight and Katalin Susztak<sup>#</sup>. A single genetic locus controls both expression of DPEP1/CHMP1A and kidney disease development via ferroptosis, *Nature Communications*, 12, 5078. (2021)
25. Xin Sheng\*, Yuting Guan\*, Ziyuan Ma, Junnan Wu, **Hongbo Liu**, Chengxiang Qiu, Steven Vitale, Zhen Miao, Matthew J. Seasock, Matthew Palmer, Myung K. Shin, Kevin L. Duffin, Steven S. Pullen, Todd L. Edwards, Jacklyn N. Hellwege, Adriana M. Hung, Mingyao Li, Benjamin F. Voight, Thomas M. Coffman, Christopher D. Brown and Katalin Susztak<sup>#</sup>. 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. (2021)
26. Ghazal Z. Quinn, Amin Abedini, **Hongbo Liu**, Ziyuan Ma, Andrew Cucchiara, Andrea Havasi, Jon Hill, Matthew B. Palmer and Katalin Susztak<sup>#</sup>. 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. (2021)
27. Tomohito Doke, Shizheng Huang, Chengxiang Qiu, **Hongbo Liu**, Yuting Guan, Hailong Hu, Ziyuan Ma, Junnan Wu, Zhen Miao, Xin Sheng, Jianfu Zhou, Aili Cao, Jianhua Li, Lewis Kaufman, Adriana Hung, Christopher D. Brown, Richard Pestell and Katalin Susztak<sup>#</sup>. Transcriptome-wide association analysis identifies DACH1 as a kidney disease risk gene that contributes to fibrosis, *The Journal of Clinical Investigation*, 131, (2021)
28. L. J. Smyth<sup>#</sup>, 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. Assessment of differentially methylated loci in individuals with end-stage kidney disease attributed to diabetic kidney disease: an exploratory study, *Clinical Epigenetics*, 13, 99. (2021)
29. Zhen Miao\*, Michael S. Balzer\*, Ziyuan Ma, **Hongbo Liu**, Junnan Wu, Rojesh Shrestha, Tamas Aranyi, Amy Kwan, Ayano Kondo, Marco Pontoglio, Junhyong Kim, Mingyao Li, Klaus H. Kaestner and Katalin Susztak<sup>#</sup>. Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets, *Nature Communications*, 12, 2277. (2021)
30. Amin Abedini\*, Yuan O. Zhu\*, Shatakshee Chatterjee, Gabor Halasz, Kishor Devalaraja-Narashimha, Rojesh Shrestha, Michael S Balzer, Jihwan Park, Tong Zhou, Ziyuan Ma, Katie Marie Sullivan, Hailong Hu, Xin Sheng, **Hongbo Liu**, Yi Wei, Carine M. Boustany-Kari, Uptal Patel, Salem Almaani, Matthew Palmer, Raymond Townsend, Shira Blady, Jonathan Hogan, Lori Morton and Katalin Susztak<sup>#</sup>. Urinary Single-Cell Profiling Captures the Cellular Diversity of the Kidney, *Journal of the American Society of Nephrology*, 32, 614-627. (2021)
31. Poonam Dhillon\*, Jihwan Park\*<sup>#</sup>, Carmen Hurtado Del Pozo, Lingzhi Li, Tomohito Doke, Shizheng Huang, Juanjuan Zhao, Hyun Mi Kang, Rojesh Shrestha, Michael S. Balzer, Shatakshee Chatterjee, Patricia Prado, Seung Yub Han, **Hongbo Liu**, Xin Sheng, Pieterjan Dierickx, Kirill Batmanov, Juan P. Romero, Felipe Prosper, Mingyao Li, Liming Pei, Junhyong Kim, Nuria Montserrat and Katalin Susztak<sup>#</sup>. The Nuclear Receptor ESRRA Protects from Kidney Disease by Coupling Metabolism and Differentiation, *Cell Metabolism*, 33, 379-394.e378. (2021)
32. Yuting Guan\*, **Hongbo Liu**\*, Ziyuan Ma, Szu-Yuan Li, Jihwan Park, Xin Sheng and Katalin Susztak<sup>#</sup>. Dnmt3a and Dnmt3b-Decommissioned Fetal Enhancers are Linked to Kidney Disease, *Journal of the American Society of Nephrology*, 31, 765-782. (2020)
33. Xin Sheng, Chengxiang Qiu, **Hongbo Liu**, Caroline Gluck, Jesse Y. Hsu, Jiang He, Chi-Yuan Hsu, Daohang Sha, Matthew R. Weir, Tamara Isakova, Dominic Raj, Hernan Rincon-Choles, Harold I. Feldman, Raymond Townsend, Hongzhe Li and Katalin Susztak<sup>#</sup>. Systematic integrated analysis of genetic and epigenetic variation in diabetic kidney disease, *Proceedings of the National Academy of Sciences*, 117, 29013-29024. (2020)

## Hongbo Liu, Ph.D.

34. Shouping Xu\*, **Hongbo Liu\***, Lin Wan\*, Weijia Zhang, Qin Wang, Shumei Zhang, Shipeng Shang, Yan Zhang# and Da Pang#. 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. (2019)
35. Yuanzheng He\*, Jingjing Shi\*, Quang Tam Nguyen\*, Erli You, **Hongbo Liu**, Xin Ren, Zhongshan Wu, Jianshuang Li, Wenli Qiu, Sok Kean Khoo, Tao Yang, Wei Yi#, Feng Sun, Zhijian Xi, Xiaozhu Huang, Karsten Melcher, Booki Min and H. Eric Xu#. Development of highly potent glucocorticoids for steroid-resistant severe asthma, *Proceedings of the National Academy of Sciences*, 116, 6932-6937. (2019)
36. Yuting Guan, **Hongbo Liu** and Katalin Susztak#. Long-Range Chromatin Interactions in the Kidney, *Journal of the American Society of Nephrology*, 30, 367-369. (2019)
37. Shumei Zhang, Yihan Wang, Yue Gu, Jiang Zhu, Ce Ci, Zhongfu Guo, Chuangeng Chen, Yanjun Wei, Wenhua Lv, **Hongbo Liu**, Dongwei Zhang and Yan Zhang#. Specific breast cancer prognosis-subtype distinctions based on DNA methylation patterns, *Molecular Oncology*, 12, 1047-1060. (2018)
38. Huihan Wang\*, Weili Yan\*, Shumei Zhang\*, Yue Gu, Yihan Wang, Yanjun Wei, **Hongbo Liu**, Fang Wang, Qiong Wu and Yan Zhang#. Survival differences of CIMP subtypes integrated with CNA information in human breast cancer, *Oncotarget*, 8, 48807-48819. (2017)
39. Yichun Xiong\*, Yanjun Wei\*, Yue Gu\*, Shumei Zhang, Jie Lyu, Bin Zhang, Chuangeng Chen, Jiang Zhu, Yihan Wang, **Hongbo Liu#** and Yan Zhang#. DiseaseMeth version 2.0: a major expansion and update of the human disease methylation database, *Nucleic Acids Research*, 45, D888-d895. (2017)
40. Yanhua Wen\*, Yanjun Wei\*, Shumei Zhang, Song Li, **Hongbo Liu**, Fang Wang, Yue Zhao, Dongwei Zhang# and Yan Zhang#. Cell subpopulation deconvolution reveals breast cancer heterogeneity based on DNA methylation signature, *Briefings in Bioinformatics*, 18, 426-440. (2017)
41. Jingyu Li, Zhengling Gao, Xingyu Wang, **Hongbo Liu**, Yan Zhang# and Zhonghua Liu#. Identification and functional analysis of long intergenic noncoding RNA genes in porcine pre-implantation embryonic development, *Scientific Reports*, 6, 38333. (2016)
42. Hui Liu\*, Jie Lyu\*, **Hongbo Liu\***, Yang Gao, Jing Guo, Hongjuan He, Zhengbin Han, Yan Zhang and Qiong Wu#. Computational identification of putative lincRNAs in mouse embryonic stem cell, *Scientific Reports*, 6, 34892. (2016)
43. **Hongbo Liu#**, Song Li, Xinyu Wang, Jiang Zhu, Yanjun Wei, Yihan Wang, Yanhua Wen, Libo Wang, Yan Huang, Bin Zhang, Shipeng Shang and Yan Zhang#. DNA methylation dynamics: identification and functional annotation, *Briefings in Functional Genomics*, 15, 470-484. (2016)
44. Yihan Wang\*, Jingyu Zhang\*, Xingjun Xiao\*, **Hongbo Liu**, Fang Wang, Song Li, Yanhua Wen, Yanjun Wei, Jianzhong Su, Yunming Zhang# and Yan Zhang#. The identification of age-associated cancer markers by an integrative analysis of dynamic DNA methylation changes, *Scientific Reports*, 6, 22722. (2016)
45. **Hongbo Liu#**, Xiaojuan Liu\*, Shumei Zhang\*, Jie Lv, Song Li, Shipeng Shang, Shanshan Jia, Yanjun Wei, Fang Wang, Jianzhong Su, Qiong Wu and Yan Zhang#. 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. (2016)
46. Wen Li, Huan Liu, Min Yu, Xumei Zhang, Yan Zhang, **Hongbo Liu**, John X. Wilson and Guowei Huang#. Folic Acid Alters Methylation Profile of JAK-STAT and Long-Term Depression Signaling Pathways in Alzheimer's Disease Models, *Molecular Neurobiology*, 53, 6548-6556. (2016)
47. Yanjun Wei\*, Shumei Zhang\*, Shipeng Shang\*, Bin Zhang, Song Li, Xinyu Wang, Fang Wang, Jianzhong Su, Qiong Wu, **Hongbo Liu#** and Yan Zhang#. SEA: a super-enhancer archive, *Nucleic Acids Research*, 44, D172-179. (2016)
48. Fang Wang\*, Shaojun Zhang\*, **Hongbo Liu**, Yanjun Wei, Yihan Wang, Xiaole Han, Jianzhong Su, Dongwei Zhang, Baodong Xie# and Yan Zhang#. CellMethy: Identification of a focal concordantly methylated pattern of CpGs revealed wide differences between normal and cancer tissues, *Scientific Reports*, 5, 18037. (2015)
49. Min Zhang, Shaojun Zhang, Yanhua Wen, Yihan Wang, Yanjun Wei, **Hongbo Liu**, Dongwei Zhang, Jianzhong Su, Fang Wang# and Yan Zhang#. DNA Methylation Patterns Can Estimate Nonequivalent Outcomes of Breast Cancer with the Same Receptor Subtypes, *PLoS One*, 10, e0142279. (2015)
50. Chunlong Zhang\*, Hongyan Zhao\*, Jie Li, **Hongbo Liu**, Fang Wang, Yanjun Wei, Jianzhong Su, Dongwei Zhang, Tiefu Liu# and Yan Zhang#. The identification of specific methylation patterns across different cancers, *PLoS One*, 10, e0120361. (2015)

## Hongbo Liu, Ph.D.

---

51. Haidan Yan\*, Dongwei Zhang\*, **Hongbo Liu**, Yanjun Wei, Jie Lv, Fang Wang, Chunlong Zhang, Qiong Wu, Jianzhong Su<sup>#</sup> and Yan Zhang<sup>#</sup>. Chromatin modifications and genomic contexts linked to dynamic DNA methylation patterns across human cell types, *Scientific Reports*, 5, 8410. (2015)
52. Jie Lv\*, Hui Liu\*, Shihuan Yu\*, **Hongbo Liu**\*, Wei Cui, Yang Gao, Tao Zheng, Geng Qin, Jing Guo, Tiebo Zeng, Zhengbin Han, Yan Zhang and Qiong Wu<sup>#</sup>. Identification of 4438 novel lincRNAs involved in mouse pre-implantation embryonic development, *Molecular Genetics and Genomics*, 290, 685-697. (2015)
53. Jie Lv\*, Zhijun Huang\*, Hui Liu\*, **Hongbo Liu**\*, Wei Cui, Bao Li, Hongjuan He, Jing Guo, Qi Liu, Yan Zhang and Qiong Wu<sup>#</sup>. Identification and characterization of long intergenic non-coding RNAs related to mouse liver development, *Molecular Genetics and Genomics*, 289, 1225-1235. (2014)
54. Yanjun Wei, Jianzhong Su, **Hongbo Liu**, Jie Lv, Fang Wang, Haidan Yan, Yanhua Wen, Hui Liu, Qiong Wu<sup>#</sup> and Yan Zhang<sup>#</sup>. MetalImprint: an information repository of mammalian imprinted genes, *Development*, 141, 2516-2523. (2014)
55. Hui Liu\*, Tongtong Wang\*, **Hongbo Liu**, Yanjun Wei, Guofeng Zhao, Jianzhong Su, Qiong Wu, Hong Qiao<sup>#</sup> and Yan Zhang<sup>#</sup>. Detection of type 2 diabetes related modules and genes based on epigenetic networks, *BMC Systems Biology*, 8 Suppl 1, S5. (2014)
56. **Hongbo Liu**\*, Rangfei Zhu\*, Jie Lv, Hongjuan He, Lin Yang, Zhijun Huang, Jianzhong Su, Yan Zhang, Shihuan Yu and Qiong Wu<sup>#</sup>. DevMouse, the mouse developmental methylome database and analysis tools, *Database*, 2014, bat084. (2014)
57. Fang Wang\*, Shaojun Zhang\*, Yanhua Wen, Yanjun Wei, Haidan Yan, **Hongbo Liu**, Jianzhong Su, Yan Zhang<sup>#</sup> and Jianhua Che<sup>#</sup>. Revealing the architecture of genetic and epigenetic regulation: a maximum likelihood model, *Briefings in Bioinformatics*, 15, 1028-1043. (2014)
58. Jie Lv\*, **Hongbo Liu**\*, Zhijun Huang\*, Jianzhong Su, Hongjuan He, Youcheng Xiu, Yan Zhang and Qiong Wu<sup>#</sup>. Long non-coding RNA identification over mouse brain development by integrative modeling of chromatin and genomic features, *Nucleic Acids Research*, 41, 10044-10061. (2013)
59. **Hongbo Liu**\*, Yanjun Chen\*, Jie Lv, Hui Liu, Rangfei Zhu, Jianzhong Su, Xiaojuan Liu, Yan Zhang and Qiong Wu<sup>#</sup>. Quantitative epigenetic co-variation in CpG islands and co-regulation of developmental genes, *Scientific Reports*, 3, 2576. (2013)
60. Jie Lv\*, Wei Cui\*, **Hongbo Liu**\*, Hongjuan He, Youcheng Xiu, Jing Guo, Hui Liu, Qi Liu, Tiebo Zeng, Yan Chen, Yan Zhang and Qiong Wu<sup>#</sup>. Identification and characterization of long non-coding RNAs related to mouse embryonic brain development from available transcriptomic data, *PLoS One*, 8, e71152. (2013)
61. Xueting Wu, Hui Liu, **Hongbo Liu**, Jianzhong Su, Jie Lv, Ying Cui, Fang Wang and Yan Zhang<sup>#</sup>. Z curve theory-based analysis of the dynamic nature of nucleosome positioning in *Saccharomyces cerevisiae*, *Gene*, 530, 8-18. (2013)
62. Xue Xiao, Zhe Li, **Hongbo Liu**, Jianzhong Su, Fang Wang, Xueting Wu, Hui Liu, Qiong Wu and Yan Zhang<sup>#</sup>. Genome-wide identification of Polycomb target genes in human embryonic stem cells, *Gene*, 518, 425-430. (2013)
63. Jianzhong Su\*, Haidan Yan\*, Yanjun Wei, **Hongbo Liu**, Hui Liu, Fang Wang, Jie Lv, Qiong Wu and Yan Zhang<sup>#</sup>. CpG\_MPs: identification of CpG methylation patterns of genomic regions from high-throughput bisulfite sequencing data, *Nucleic Acids Research*, 41, e4. (2013)
64. Jie Lv\*, **Hongbo Liu**\*, Jianzhong Su\*, Xueting Wu, Hui Liu, Boyan Li, Xue Xiao, Fang Wang, Qiong Wu<sup>#</sup> and Yan Zhang<sup>#</sup>. DiseaseMeth: a human disease methylation database, *Nucleic Acids Research*, 40, D1030-1035. (2012)
65. Jianzhong Su<sup>#</sup>, Xiujuan Shao, **Hongbo Liu**, Shengqiang Liu, Qiong Wu and Yan Zhang<sup>#</sup>. Genome-wide dynamic changes of DNA methylation of repetitive elements in human embryonic stem cells and fetal fibroblasts, *Genomics*, 99, 10-17. (2012)
66. Jianzhong Su<sup>#</sup>, Yunfeng Qi, Shengqiang Liu, Xueting Wu, Jie Lv, **Hongbo Liu**, Ruijie Zhang and Yan Zhang<sup>#</sup>. Revealing epigenetic patterns in gene regulation through integrative analysis of epigenetic interaction network, *Molecular Biology Reports*, 39, 1701-1712. (2012)
67. Lin Yang<sup>#</sup>, Jiahou Chen, Tong Xu, Wei Qiu, Yan Zhang, Lanwei Zhang, Fuping Xu and **Hongbo Liu**. Rice protein extracted by different methods affects cholesterol metabolism in rats due to its lower digestibility, *International Journal of Molecular Sciences*, 12, 7594-7608. (2011)
68. Hui Liu\*, Jianzhong Su\*, Junhua Li, **Hongbo Liu**, Jie Lv, Boyan Li, Hong Qiao<sup>#</sup> and Yan Zhang<sup>#</sup>. Prioritizing cancer-related genes with aberrant methylation based on a weighted protein-protein interaction network, *BMC Systems Biology*, 5, 158. (2011)

## Hongbo Liu, Ph.D.

69. Yan Zhang<sup>\*\*</sup>, **Hongbo Liu**<sup>\*</sup>, Jie Lv<sup>\*</sup>, Xue Xiao, Jiang Zhu, Xiaojuan Liu, Jianzhong Su, Xia Li, Qiong Wu, Fang Wang and Ying Cui. QDMR: a quantitative method for identification of differentially methylated regions by entropy, *Nucleic Acids Research*, 39, e58. (2011)
70. Jie Lv<sup>\*</sup>, Hong Qiao<sup>\*</sup>, **Hongbo Liu**, Xueting Wu, Jiang Zhu, Jianzhong Su, Fang Wang, Ying Cui and Yan Zhang<sup>#</sup>. Discovering cooperative relationships of chromatin modifications in human T cells based on a proposed closeness measure, *PLoS One*, 5, e14219. (2010)
71. Jie Lv, Jianzhong Su, Fang Wang, Yunfeng Qi, **Hongbo Liu** and Yan Zhang<sup>#</sup>. Detecting novel hypermethylated genes in breast cancer benefiting from feature selection, *Computers in Biology and Medicine*, 40, 159-167. (2010)
72. Jianzhong Su<sup>\*</sup>, Yan Zhang<sup>\*\*</sup>, Jie Lv<sup>\*</sup>, **Hongbo Liu**, Xiaoyan Tang, Fang Wang, Yunfeng Qi, Yujia Feng and Xia Li<sup>#</sup>. CpG\_MI: a novel approach for identifying functional CpG islands in mammalian genomes, *Nucleic Acids Research*, 38, e6. (2010)
73. Yan Zhang<sup>\*\*</sup>, Jie Lv<sup>\*</sup>, **Hongbo Liu**<sup>\*</sup>, Jiang Zhu, Jianzhong Su, Qiong Wu, Yunfeng Qi, Fang Wang and Xia Li<sup>#</sup>. HHMD: the human histone modification database, *Nucleic Acids Research*, 38, D149-154. (2010)

### Software and Resources

- Open4Gene A R package for Peak-to-Gene linkage analysis in single cell multiome sequencing data  
<https://github.com/hbliu/Open4Gene>
- 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>
- ScoreCard eGFRcrea GWAS and genetic scorecard based on 2.2 million individuals  
<https://susztaklab.com/GWAS2M>
- Kidney\_Epi\_Pri A pipeline for prioritization of disease-causal genes by integrating GWAS with the epigenome  
[https://github.com/hbliu/Kidney\\_Epi\\_Pri](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](https://susztaklab.com/Kidney_meQTL)
- Kidney\_eQTL Human kidney expression QTL atlas based on 686 human kidneys  
[https://susztaklab.com/Kidney\\_eQTL](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](https://susztaklab.com/Human_snATAC)

### Grants

- 2024 – 2029 National Institute on Aging, #2P01AG047200-11 (PI: Vera Gorbunova)
- 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)

### Scientific Society Member

- 2025 – present Affiliate Membership of the Impact of Genomic Variation on Function Consortium (IGVF)
- 2022 – present Membership of the American Society of Human Genetics (ASHG)

## Hongbo Liu, Ph.D.

---

- 2019 – present Membership of the American Society of Nephrology (ASN)
- 2018 – 2020 Membership of the American Association for Cancer Research (AACR)

### 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

### Invited Talks

- 01/03/2025 *Invited speaker*, Nephrology Academic Seminar, Peking Union Medical College Hospital (virtual)
- 12/26/2024 *Invited speaker*, The Third Nutsheller Symposium (virtual)
- 12/18/2024 *Invited speaker*, Chromatin Collective, University of Rochester (Rochester, NY)
- 11/27/2024 *Invited speaker*, Renal Clinical Research Seminar, University of Rochester (Rochester, NY)
- 06/26/2024 *Invited speaker*, Summer Applied Genomics Seminar, University of Rochester (Rochester, NY)
- 10/07/2022 *Lightning round presenter*, 7<sup>th</sup> 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 (virtual)
- 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

- 09/18/2024 *Poster presenter*, Epigenetics & Chromatin (Cold Spring Harbor, NY)
- 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)

### Professional Service

#### Teaching

- 2025 – PTH 51: Cell Biology of Disease, Co-instructor (University of Rochester)
- 2025 – IND 419: Introduction to Quantitative Biology, Co-instructor (University of Rochester)
- 2024 – Current Topics in Bioinformatics, Co-instructor (University of Rochester)
- 2015 – 2016 Computational Epigenetics, Co-instructor (Harbin Medical University)
- 2015 – 2016 Biomolecular Network Analysis, Instructor (Harbin Medical University)



## Hongbo Liu, Ph.D.

---

- 2015 – 2016 Combinatorics and Graph Theory, Instructor (Harbin Medical University)
- 2011 – 2012 Database Principles and Applications, Instructor (Harbin Medical University)
- 2010 – 2011 System Biology, Co-Instructor (Harbin Medical University)

### Postdoctoral Fellows Trained

- 2024 – present Mengying Zhang, Ph.D.

### Graduate Students Trained

- 2025 – present Nidhi Shah (Pathology and Laboratory Medicine, University of Rochester)

### Graduate Student Committees

- 2025 – present Elijah Sterling Neuroscience & Behavioral Biology Advisor: Kaixiong Ye, Ph.D.

### Undergraduate Students Trained

- 2024 – present Naidhruva Deb (Microbiology and Anthropology, University of Rochester)
- 2024 – present Jessica Chen (Cell & Developmental Biology, University of Rochester)
- 2024 – present Sreejato Chatterjee (Computational Biology, University of Rochester)
- 2024 – present Xuke Wang (Cell & Developmental Biology, University of Rochester)
- 2024 – present Zihang Yu (Biomedical Engineering, University of Rochester)
- 2015 – 2016 Shanshan Zhang (current position: Postdoctoral Associate in Kellis Lab at MIT)
- 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)

### Grant Review

- 2024 Reviewer, UK Research and Innovation of the United Kingdom

### Conference Organization Committee

- 2025 Workshop/Tutorial Committee, International Conference on Intelligent Biology and Medicine (ICIBM 2025)
- 2024 Trainee Committee, International Conference on Intelligent Biology and Medicine (ICIBM 2024)

### Journal Editorial Board

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

### Ad-hoc Journal Reviewer

Aging	Journal for ImmunoTherapy of Cancer
Biochemical Society Transactions	Journal of Cancer
Bioinformatics	Journal of the American Society of Nephrology
Biology Methods & Protocols	Journal of Translational Medicine
Briefings in Bioinformatics	Kidney International
Briefings in Functional Genomics	Kidney International Reports
Cell & Bioscience	MedComm
Cell Proliferation	Methods
Circulation: Genomic and Precision Medicine	Molecular Oncology

## Hongbo Liu, Ph.D.

---

Computational and Structural Biotechnology Journal	Molecular Psychiatry
Computers in Biology and Medicine	Molecular Therapy - Nucleic Acids
Current Bioinformatics	Nature Communications
Epigenetics & Chromatin	Nucleic Acids Research
Epigenomics	Oncotarget
Frontiers in Aging Neuroscience	Phenomics
Frontiers in Cell and Developmental Biology	PLOS Computational Biology
Frontiers in Genetics	PLOS Genetics
Frontiers in Oncology	PLOS ONE
Genes	Quantitative Biology
Genome Medicine	Science Translational Medicine
Healthcare	Scientific Data
Human Molecular Genetics	The International Journal of Molecular Sciences