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New Jersey Institute for Food, Nutrition & Health

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EMPLOYMENT HISTORY

Rutgers University	New Jersey, United States
Assistant Research Professor, Co-director of Rutgers Center for Microbiome Analysis	March 2023 - Current
Research Associate	Oct 2021 – March 2023
Post-doctoral Associate	Aug 2018 – Sep 2021

EDUCATION

Shanghai Jiao Tong University	Shanghai, China
Ph.D., Microbiology	Sep 2012 - March 2018
Dissertation: Microbial genome-centric analysis for understanding the interactions among gut microbiome, diet and human health	
Supervisors: Professor Liping Zhao, Associate Professor Menghui Zhang	
Shanghai Jiao Tong University	Shanghai, China
Bachelor of Science, Bioinformatics	Sep 2008 - Jun 2012

FULL PUBLICATIONS (chronological order; * as co-first author)

H-index: 22, Citations: 4,702

Papers (refereed)

1. Millick, D.D., Ghosh, S., **Wu, G.**, Krzyzanowska, A.K., Osorio, L.J., Zhao, L., Strair, R. and Sant'Angelo, D.B. Dietary animal fat disrupts gut microbiota and aggravates Scl-cGVHD after allogeneic hematopoietic stem cell transfer. Blood Advances, pp.bloodadvances-2024014831. 2025. DOI: 10.1182/bloodadvances.2024014831

2. Ghosh, S., Li, Y., Yang, X., **Wu, G.**, Zhang, C. and Zhao, L. Bacterial guilds, not genus-level taxa, mediate the protective effects of time-restricted feeding against high-fat diet-induced obesity in mice. *ISME Communications*, 5(1), p.ycaf127. 2025.
3. Jung, J., Zhu, S., Lalani, A., Shakarchi, J., Matracz, B., **Wu, G.G.**, Zong, W.X., Zhao, L. and Xie, P. Commensal bacteria drive B-cell lymphomagenesis in the setting of innate immunodeficiency. *Blood Cancer Discovery*. 2025. DOI: 10.1158/2643-3230.BCD-24-0279.
4. Mezhibovsky, E., **Wu, G.**, Wu, Y., Ning, Z., Bacalia, K., Sadangi, S., Patel, R., Poulev, A., Duran, R.M., Macor, M., Coyle, S. Lam Y., Raskin I., Figeys D., Zhao, L. and Roopchand D. Grape polyphenols reduce fasting glucose and increase hyocholic acid in healthy humans: a meta-omics study. *npj Science of Food*, 9(1), pp.1-20. 2025. DOI: 10.1038/s41538-025-00443-6
5. **Wu, G.***, Xu, T.*, Zhao, N.*, Lam, Y.Y.*, Ding, X.*, Wei, D., Fan, J., Shi, Y., Li, X., Li, M., Ji, S., Wang, X., Fu, H., Zhang, F., Shi, Y., Zhang, C., Peng, Y. and Zhao, L. A core microbiome signature as an indicator of health. *Cell*, 187(23), pp.6550-6565. 2024. DOI: 10.1016/j.cell.2024.09.019
6. Tang, S.*, **Wu, G.***, Liu, Y.*, Xue, B., Zhang, S., Zhang, W., Jia, Y., Xie, Q., Liang, C., Wang, L., Heng, H. Wei, W., Shi, X., Hu, Y., Yang, J., Zhao, L., Wang, X., Zhao, L., and Yuan, H. Guild-level signature of gut microbiome for diabetic kidney disease. *mBio*, pp.e00735-24. 2024. DOI: 10.1128/mbio.00735-24
7. Derosa, L., Iebba, V., Silva, C.A.C., Piccinno, G., **Wu, G.**, Lordello, L., Routy, B., Zhao, N., Thelemaque, C., Birebent, R. and Marmorino, F. Custom scoring based on ecological topology of gut microbiota associated with cancer immunotherapy outcome. *Cell*, 187(13), pp.3373-3389. 2024. DOI: 10.1016/j.cell.2024.05.029
8. Yang, J.*, Yang, X.*, **Wu, G.***, Huang, F., Shi, X., Wei, W., Zhang, Y., Zhang, H., Cheng, L., Yu, L., Shang, J., Lv, Y., Wang, X., Zhai, R., Li, P., Cui, B., Fang, Y., Deng, X., Tang, S., Wang, L., Yuan, Q., Zhao, L., Zhang, F., Zhang, C., Yuan, H. Gut microbiota modulate distal symmetric polyneuropathy in patients with diabetes. *Cell Metabolism*, 35(9), pp.1548-1562. 2023. DOI: 10.1016/j.cmet.2023.06.010
9. Zhai, L., Xiao, H., Lin, C., Wong, H.L.X., Lam, Y.Y., Gong, M., **Wu, G.**, Ning, Z., Huang, C., Zhang, Y., Yang, C., Luo, J., Zhang, L., Zhao, L., Zhang, C., Lau, J.,

- Lu, A., Lau, L., Jia, W., Zhao, L. and Bian, X. Gut microbiota-derived tryptamine and phenethylamine impair insulin sensitivity in metabolic syndrome and irritable bowel syndrome. *Nature Communications*, 14(1), p.4986. 2023. DOI: 10.1038/s41467-023-40552-y
10. Yang, X., Wang, Z., Niu, J., Zhai, R., Xue, X., **Wu, G.**, Fang, Y., Meng, G., Yuan, H., Zhao, L. and Zhang, C. Pathobionts from chemically disrupted gut microbiota induce insulin-dependent diabetes in mice. *Microbiome*, 11(1), pp.1-20. 2023. DOI: 10.1186/s40168-023-01507-z
 11. Guo, M.*, **Wu, G.***, Tan, Y., Li, Y., Jin, X., Qi, W., Guo, X., Zhang, C., Zhu, Z. and Zhao, L. Guild-level microbiome signature associated with COVID-19 severity and prognosis. *Mbio*, pp.e03519-22. 2023. DOI: 10.1128/mbio.03519-22
 12. Vander Haar, E.L.*, **Wu, G.***, Gyamfi-Bannerman, C., Thomas, C., Wapner, R.J., Reddy, U.M., Zhao, L., Silver, R.M., Goldenberg, R.L. and Han, Y.W., 2022. Microbial Analysis of Umbilical Cord Blood Reveals Novel Pathogens Associated with Stillbirth and Early Preterm Birth. *Mbio*, 13(5), pp.e02036-22. 2022. DOI: 10.1128/mbio.02036-22
 13. Wang, Y., **Wu, G.**, Zhao, L. and Wang, W. Nutritional Modulation of Gut Microbiota Alleviates Severe Gastrointestinal Symptoms in a Patient with Post-Acute COVID-19 Syndrome. *Mbio*, pp.e03801-21. 2022. DOI: 10.1128/mbio.03801-21
 14. **Wu, G.***, Tawfeeq, H.R*, Lackey, A.I., Zhou, Y., Sifnakis, Z., Zacharisen, S.M., Xu, H., Doran, J.M., Sampath, H., Zhao, L., Lam, Y.Y., Storch J. Gut Microbiota and Phenotypic Changes Induced by Ablation of Liver-and Intestinal-Type Fatty Acid-Binding Proteins. *Nutrients*, 14(9), p.1762. 2022. DOI: 10.3390/nu14091762
 15. Yousaf, N.Y.*, **Wu, G.***, Melis, M., Mastinu, M., Contini, C., Cabras, T., Tomassini Barbarossa, I., Zhao, L., Lam, Y.Y. and Tepper, B.J. Daily Exposure to a Cranberry Polyphenol Oral Rinse Alters the Oral Microbiome but Not Taste Perception in PROP Taster Status Classified Individuals. *Nutrients*, 14(7), p.1492. 2022. DOI: 10.3390/nu14071492
 16. Jia, L*., **Wu, G.***, Alonso, S., Zhao, C., Lemenze, A., Lam, Y.Y., Zhao, L. and Edelblum, K.L. A transmissible $\gamma\delta$ intraepithelial lymphocyte hyperproliferative phenotype is associated with the intestinal microbiota and confers protection

- against acute infection. *Mucosal Immunology*, pp.1-11. 2022. DOI: 10.1038/s41385-022-00522-x
17. Wang, X., Xu, T., Liu, R., **Wu, G.**, Gu, L., Zhang, Y., Zhang, F., Fu, H., Ling, Y., Wei, X., Luo, Y., Shen, J., Zhao, L., Peng, Y., Zhang, C. and Ding, X. High-Fiber Diet or Combined With Acarbose Alleviates Heterogeneous Phenotypes of Polycystic Ovary Syndrome by Regulating Gut Microbiota. *Frontiers in endocrinology*, 12. 2021. DOI: 10.3389/fendo.2021.806331
 18. Li, H., **Wu, G.**, Zhao, L. and Zhang, M. Suppressed inflammation in obese children induced by a high-fiber diet is associated with the attenuation of gut microbial virulence factor genes. *Virulence*, 12(1), pp.1754-1770. 2021. DOI: 10.1080/21505594.2021.1948252
 19. Balaich, J., Estrella, M., **Wu, G.**, Jeffrey, P.D., Biswas, A., Zhao, L., Korennykh, A. and Donia, M.S. The human microbiome encodes resistance to the antidiabetic drug acarbose. *Nature*, 600(7887), pp.110-115. 2021. DOI: 10.1038/s41586-021-04091-0
 20. **Wu, G.***, Zhao, N.*, Zhang, C., Lam, Y.Y. and Zhao, L. Guild-based analysis for understanding gut microbiome in human health and diseases. *Genome medicine*, 13(1), pp.1-12. 2021. DOI: 10.1186/s13073-021-00840-y
 21. **Wu, G.***, Liu, A.B.*, Xu, Y., Wang, Y., Zhao, L., Hara, Y., Lam, Y.Y. and Yang, C.S. The Effects of Green Tea on Diabetes and Gut Microbiome in db/db Mice: Studies with Tea Extracts vs. Tea Powder. *Nutrients*, 13(9), p.3155. 2021. DOI: 10.3390/nu13093155
 22. Van Buiten, C.B., **Wu, G.**, Lam, Y.Y., Zhao, L. and Raskin, I. Elemental iron modifies the redox environment of the gastrointestinal tract: A novel therapeutic target and test for metabolic syndrome. *Free Radical Biology and Medicine*, 168, pp.203-213. 2021. DOI: 10.1016/j.freeradbiomed.2021.03.032
 23. Sharma, P.*, **Wu, G.***, Kumaraswamy, D., Burchat, N., Ye, H., Gong, Y., Zhao, L., Lam, Y.Y. and Sampath, H. Sex-Dependent Effects of 7, 8-Dihydroxyflavone on Metabolic Health Are Associated with Alterations in the Host Gut Microbiome. *Nutrients*, 13(2), p.637. 2021. DOI: 10.3390/nu13020637
 24. Ji, M., Tian, H., Wu, X., Li, J., Zhu, Y., **Wu, G.**, Xu, T., Wang, J. and Zhang, X. Enhanced N₂O emission rate in field soil undergoing conventional intensive fertilization is attributed to the shifts of denitrifying guilds. *Pedosphere*, 31(1),

- pp.145-156. 2021. DOI: 10.1016/S1002-0160(20)60050-9
25. Chung, M., Zhao, N., Meier, R., Koestler, D.C., **Wu, G.**, del Castillo, E., Paster, B.J., Charpentier, K., Izard, J., Kelsey, K.T. and Michaud, D.S. Comparisons of oral, intestinal, and pancreatic bacterial microbiomes in patients with pancreatic cancer and other gastrointestinal diseases. *Journal of oral microbiology*, 13(1), p.1887680. 2021. DOI: 10.1080/20002297.2021.1887680
 26. Chen, Y., Fang, H., Li, C., **Wu, G.**, Xu, T., Yang, X., Zhao, L., Ke, X. and Zhang, C. Gut Bacteria Shared by Children and Their Mothers Associate with Developmental Level and Social Deficits in Autism Spectrum Disorder. *Mosphere*, 5(6), pp.e01044-20. 2020. DOI: 10.1128/msphere.01044-20
 27. Sun, Y., Kong, L., **Wu, G.**, Cao, B., Pang, X., Deng, Z., Dedon, P.C., Zhang, C. and You, D. DNA phosphorothioate modifications are widely distributed in the human microbiome. *Biomolecules*, 10(8), p.1175. 2020. DOI: 10.3390/biom10081175
 28. Chen, Q., **Wu, G.**, Chen, H., Li, H., Li, S., Zhang, C., Pang, X., Wang, L., Zhao, L. and Shen, J. Quantification of human oral and fecal Streptococcus parasanguinis by use of quantitative real-time PCR targeting the groEL Gene. *Frontiers in microbiology*, 10, p.2910. 2019. DOI: 10.3389/fmicb.2019.02910
 29. Xia, H., Liu, C., Li, C.C., Fu, M., Takahashi, S., Hu, K.Q., Aizawa, K., Hiroyuki, S., **Wu, G.**, Zhao, L. and Wang, X.D., 2018. Dietary tomato powder inhibits high-fat diet–promoted hepatocellular carcinoma with alteration of gut microbiota in mice lacking carotenoid cleavage enzymes. *Cancer Prevention Research*, 11(12), pp.797-810. 2018. DOI: 10.1158/1940-6207.CAPR-18-0188
 30. Zhao, L.*, Zhang, F.*, Ding, X.*, **Wu, G.***, Lam, Y.Y.*, Wang, X., Fu, H., Xue, X., Lu, C., Ma, J., Yu, L. et al, 2018. Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes. *Science*, 359(6380), pp.1151-1156. 2018. DOI: 10.1126/science.aao5774
 31. Zhu, C., Miller, M., Marpaka, S., Vaysberg, P., Rühlemann, M.C., **Wu, G.**, Heinsen, F.A., Tempel, M., Zhao, L., Lieb, W., Franke, A. and Bromberg Y. Functional sequencing read annotation for high precision microbiome analysis. *Nucleic acids research*, 46(4), pp.e23-e23. 2018. DOI: 10.1093/nar/gkx1209
 32. Yao, X., Zhang, C., Xing, Y., Xue, G., Zhang, Q., Pan, F., **Wu, G.**, Hu, Y., Guo, Q., Lu, A., Zhang, X., Zhou, R., Tian, Z., Zeng, B., Wei, H., Strober, W., Zhao, L.,

- Meng, G. Remodelling of the gut microbiota by hyperactive NLRP3 induces regulatory T cells to maintain homeostasis. *Nature communications*, 8(1), pp.1-17. 2017. DOI: 10.1038/s41467-017-01917-2
33. **Wu, G.**, Zhang, C., Wu, H., Wang, R., Shen, J., Wang, L., Zhao, Y., Pang, X., Zhang, X., Zhao, L. and Zhang, M. Genomic microdiversity of *Bifidobacterium pseudocatenulatum* underlying differential strain-level responses to dietary carbohydrate intervention. *MBio*, 8(1), pp.e02348-16. 2017. DOI: 10.1128/mbio.02348-16
 34. Yan, H., Fei, N., **Wu, G.**, Zhang, C., Zhao, L. and Zhang, M. Regulated inflammation and lipid metabolism in colon mRNA expressions of obese germfree mice responding to *Enterobacter cloacae* B29 combined with the high fat diet. *Frontiers in microbiology*, 7, p.1786. 2016. DOI: 10.3389/fmicb.2016.01786
 35. Zhang, Q., Wu, Y., Wang, J., **Wu, G.**, Long, W., Xue, Z., Wang, L., Zhang, X., Pang, X., Zhao, Y., Zhao, L. et al. Accelerated dysbiosis of gut microbiota during aggravation of DSS-induced colitis by a butyrate-producing bacterium. *Scientific reports*, 6(1), pp.1-11. 2016. DOI: 10.1038/srep27572
 36. **Wu, G.**, Zhang, C., Wang, J., Zhang, F., Wang, R., Shen, J., Wang, L., Pang, X., Zhang, X., Zhao, L. and Zhang, M. Diminution of the gut resistome after a gut microbiota-targeted dietary intervention in obese children. *Scientific reports*, 6(1), pp.1-9. 2016. DOI: 10.1038/srep24030
 37. Zhang, C.*, Yin, A.*, Li, H.*, Wang, R.*, **Wu, G.***, Shen, J.*, Zhang, M., Wang, L., Hou, Y., Ouyang, H., Zhang, Y., Zhang, Y., Wang, J., Lv, X., Wang, Y., Zhang, F., Zeng, B., Li, W., Yan, F., Zhao, Y., Pang, X., Zhang, X., Fu, H., Cheng, F., Zhao, N., Hamaker, B., Bridgewater, L., Bork, P., Nicholson, J., Wei, H., Tang, H., Zhang, X. and Zhao, L. Dietary modulation of gut microbiota contributes to alleviation of both genetic and simple obesity in children. *EBioMedicine*, 2(8), pp.968-984. 2015. DOI: 10.1016/j.ebiom.2015.07.007
 38. **Wu, G.**, Zhang, M., Wei, C., Wang, Y., Yao, X., Zhao, L. and Zhang, X. Draft genome sequence of *Thauera* sp. DTG from a denitrifying quinoline degrading microbial consortium. *Applied Environmental Biotechnology*, 1(1), pp.38-43. 2015. DOI: 10.26789/AEB.2016.01.012
 39. Li, J., Qu, X., He, X., Duan, L., **Wu, G.**, Bi, D., Deng, Z., Liu, W. and Ou, H.Y., 2012. ThioFinder: a web-based tool for the identification of thiopeptide gene

clusters in DNA sequences. *PLoS One*, 7(9): e45878. 2012. DOI: 10.1371/journal.pone.0045878

Papers (non-refereed)

1. Zhao, L., **Wu, G.** and Zhao, N. Guild-based approach for mitigating information loss and distortion issues in microbiome analysis. *The Journal of Clinical Investigation*, 134(17). 2024. DOI: 10.1172/JCI185395
2. Zhao, N., **Wu, G.** and Zhao, L. H₂S as a metabolic saboteur. *Nature Metabolism*, 6(8), pp.1431-1432. 2024. DOI: 10.1038/s42255-024-01086-9
3. **Wu, G.**, Zhao, N. and Zhao, L. Microbial-host isozyme: A novel target in “drug the bug” strategies for diabetes. *Cell Metabolism*, 35(10), pp.1677-1679. 2023. DOI: 10.1016/j.cmet.2023.09.008
4. Wang, Y., Zhao, C., Lam, Y.Y., Zhao, L. and **Wu, G.** Saturated cell lysing is critical for high sensitivity microbiome analysis. *bioRxiv*, pp.2022-06. 2022. DOI: 10.1101/2022.06.04.494821
5. Wang, J., Zhang, Q., **Wu, G.**, Zhang, C., Zhang, M. and Zhao, L. *Minimizing spurious features in 16S rRNA gene amplicon sequencing* (No. e26872v1). PeerJ Preprints. 2018. DOI: 10.7287/peerj.preprints.26872v1

Book Chapters

1. Zhang, M., Wang, J., **Wu, G.**, Li, H. and Zhao, L. Gastrointestinal microbiology in the normal host. In *Encyclopedia of Microbiology* (pp. 362-369). Elsevier. 2019. DOI: 10.1016/B978-0-12-801238-3.99213-4

See also: <https://scholar.google.com/citations?user=SDTjBesAAAAJ&hl=en&oi=ao>

PATENTS

1. Methods for predicting responses to a therapy for a disorder through core microbiome guilds. Inventor: Liping Zhao, **Guojun Wu** and Chenhong Zhang.
2. Two competing guilds as core microbiome signature for human diseases. Inventor: Liping Zhao, **Guojun Wu** and Chenhong Zhang.
3. Fiber mix formulations and uses thereof. Liping Zhao, Yan Lam, Yongjia Gong,

Guojun Wu and Cuiping Zhao.

4. Probiotics Bifidobacteria strains. Inventor: Liping Zhao, **Guojun Wu**, Menghui Zhang, Chenhong Zhang and Huan Wu.

AWARDS

Outstanding doctoral thesis of 2018 (top 15 (1.2%) of the University) <u>Shanghai Jiao Tong University</u>	2019
Outstanding graduates of colleges and universities <u>Shanghai</u>	2018
AMD High Performance Computing Scholarship <u>Shanghai Jiao Tong University</u>	2016
National scholarship for graduate students <u>China</u>	2016
Postgraduate Academic Excellence Scholarship <u>Shanghai Jiao Tong University</u>	2015

GRANTS

California Table Grape Commission, 2025-26 Health Research Grant Program. PI: Guojun Wu. <i>Effects of grape powder on psychological distress and gut microbiota in college students</i>	Awarded
National Mango Board, Health & Nutrition Research – Fiscal Year 2206. PI: Guojun Wu <i>Effects of Fresh Mango Consumption on Blood Pressure and Gut Microbiota in Adults with hypertension: A Randomized Controlled Crossover Trial</i>	Pending decision
Rutgers-New York University Center for Asian Health Promotion and Excellence (CAHPE), Pilot study. PI: Guojun Wu <i>Psychosocial stress, gut microbiota and cardiometabolic outcomes of older Asian immigrants</i>	Pending decision

INTERNATIONAL CONFERENCE

ASM Microbe 2023, Jun 2023, Poster

Two Competing Guilds as a Core Microbiome Signature for Health Recovery

ASM Microbe 2023, Jun 2023, Poster

Guild-level microbiome signature associated with COVID-19 severity and prognosis

Keystone Symposia | Type 2 Diabetes: Understanding its Early Drivers and the Road to Therapeutics, May 2023, Poster

Two Competing Guilds as a Core Microbiome Signature for Health Recovery

Rutgers University Microbiome Program Annual Retreat 2023, Oral

Two Competing Guilds as a Core Microbiome Signature for Health Recovery

Rutgers University Microbiome Program Annual Retreat 2021, Oral

Guild-based analysis for understanding gut microbiome in human health and diseases,

Symposium of Standardization and Automation of High-throughput Analysis in big science Microbiome projects (SAHAM), Shenzhen, China, May 2019, Oral

Guild-based Analysis for Understanding Gut Microbiome in Human Health

16th International Society for Microbial Ecology Conference, Montreal, Canada. Aug. 2016, Poster

Diminution of the gut resistome after a gut microbiota-targeted dietary intervention in obese children.

International Conference on Metabolic Sciences 2015 (ICMS 2015), Shanghai, China, Dec. 2015, Poster

Comparative genomics of Bifidobacterium pseudocatenulatum taxon.

15th International Society for Microbial Ecology Conference, Seoul, South Korea. Aug. 2014, Poster

Metagenomic analysis of gut microbiota during dietary intervention of a severe obese child with Prader-Willi syndrome.

RESEARCH EXPERIENCE

Co-director of the Microbiome Core of IFNH (New Jersey Institute for Food, Nutrition and Health) and Rutgers Center for Microbiome Analysis (RCMA)

- Manage and analyze the raw microbiome sequencing datasets which are generated from RMCA. Use QIIME 2 platform for quality filtration and denoising to get amplicon sequence variants (ASVs). Conduct overall microbiota structure analysis, identify ASVs with significant contribution to outcome measures, perform co-abundance groups analysis to identify guilds and dissect their associations with host phenotypes.
- Have participated in more than 35 various microbiome projects, including human gut microbiome, human oral microbiome, and mice gut microbiome, in RCMA since Aug 2018.
- Have participated in the study design, data analysis, manuscript preparation, and grant application in various projects conducted in RCMA.

Study stable relationships to identify core microbiome guilds for modulating human health.

- Identification of “two competing guilds” (TCG) structure composed of stable genome pairs within co-abundance networks under varied environmental conditions, including different high fiber consumption phases and different healthy status.
- Conduct comparative genomics analysis on the genomes in TCGs and found the functional dichotomy of the guilds in TCGs and their association with human health.
- Build both specific and universal Random Forest models to perform disease diagnosis and treatment outcome prediction across various diseases, geographical locations, and ethnicities.

Explore the role of gut microbiota in modulating distal symmetric polyneuropathy (DSPN) in patients with diabetes.

- Find two competing guilds of gut microbiota that were associated with FMT-induced alleviation of DSPN.

- Compare genome-level enterotypes between transplants and donors in the FMT trial and found that matched enterotype between transplants and recipients linked to better FMT efficacy in DSPN patients.

Explore the role of gut microbiota in the alleviation of type 2 diabetes in adults undertaking high fiber dietary intervention

- Strain-level analysis of changes in the gut microbiome responding to high fiber diet via reconstructing high-quality draft genomes from metagenomic sequencing datasets.
- Discriminating strains with the same functional genes for short-chain fatty acid production but differentially responding to the same high fiber intervention via monitoring the abundances of draft genomes and genomic annotation for key functional genes.
- Identification of “ecosystem service providers” and development of a derived index for predicting efficacy of dietary intervention.
- Gene-centric analysis of the metagenomic datasets from high fiber intervention in patients with type 2 diabetes.

Explore the mechanisms underlying differential strain-level responses of *Bifidobacterium pseudocatenulatum* to dietary intervention via comparative genomics

- Monitoring the abundance changes of multiple strains from the same species in the same habitat via aligning metagenomic sequencing data against their genomes.
- Using the perspective of genomic microdiversity to explain the differential strain-level responses via applying comparative genomics analysis.

Study the changes of gut resistome in obese children after a gut microbiota-targeted dietary intervention

- Study the changes of gut resistome responding to the dietary intervention via identifying and monitoring the antibiotic resistance genes from metagenomic sequencing dataset.

- Explain the changes of gut resistome via identifying and monitoring their carriers based on the draft genomes reconstructed from metagenomes.

Explore the role of gut microbiota in the alleviation of genetic obesity in children

- Facilitate the analysis of gut microbiome at the strain level via establishing a metagenomic analytical pipeline, which can achieve various functions including constructing non-redundant gut microbial genes, reconstructing high-quality draft genomes, and characterizing the compositional and functional profile of gut microbial community.
- Facilitate the analysis, which considers functional groups of gut microbiota as “guilds” via creating a workflow to cluster individual gut microbial member into functional genome groups based on abundance profile and constructing genome interaction networks.
- Facilitate the identification of key functional gut bacteria via combining genomic annotation for functional genes with correlations between draft genomes and metabolites.

Establish a prediction tool for identifying thiopeptide gene clusters in DNA sequences

- Facilitate the study of thiopeptide biosynthetic gene clusters in bacteria via establishing the automatic module for prediction with a Hidden Markov Models (HMMs)-based approach.

MAJOR COURSES

Biology, Biochemistry, Molecular Biology, The Principle of Database systems, Genomics, Bioinformatics, Immunology, Development Biology, Microbiology

SKILLS/SPECIALTY

- ✧ Integrate and optimize pipelines for analyzing next generation sequencing datasets, especially metagenomes and whole bacterial genomes, to answer

biological questions.

- Skillful application in various bioinformatics tools involved in quality control, *do novo* assembly, binning, genomic annotation etc., including Qiime2, Flexbar, IDBA_UD, MetaGeneMark, CD-HIT, MetaBAT2, MetaWrap, Bowtie2, BLAST, CheckM, Diamond, HMMER, HUMAnN3, MetaPhlan4, PGAP, MUMmer and Prodigal etc.
 - Experience in using various databases including NCBI, KEGG, CAZys, dbCAN, IMG, ENA, VFDB and ARDB etc.
 - Apply ecological theories in bioinformatics analysis including a focus on strain/genome level analysis as bacterial functions are strain-specific, studying gut microbiota from the perspective of functional groups (guilds) as bacteria form complex ecological interactions in ecosystems and adopting ecosystem services concept to understand the mutualistic relationship between gut microbiome and human health
- ✧ Experience in high performance computing and large dataset
- Responsible for the management of four workstations and four storage servers in the Lab of Molecular Microbial Ecology and Ecogenomics, Shanghai Jiao Tong University
 - Experience in handling more than 450TB data and used more than 1.8 million CPU hours on Pi supercomputer (Center of High-Performance computing, Shanghai Jiao Tong University) and on Amaral (Office of Advanced Research computing, Rutgers University).
 - Write research proposal and get Rutgers Caliburn Allocation (since 2018 – 2021). Handling more than 25TB data and used more than 80,000 CPU hours on Caliburn supercomputer.
- ✧ Proficient in statistical analysis and software (R and MATLAB)
- ✧ Experience in handling multi-omics datasets
- ✧ Programming: Perl, shell scripting

MENTORING AND TEACHING EXPERIENCE

- | | |
|--|------------|
| 1. Teach 6 undergraduates, 4 graduates and 1 post-doctoral fellows | Aug 2018 - |
| microbiome research and data analysis in Dr. Liping Zhao's Lab | Current |

2. Mentor of the 2024 Aresty RA Program, “Impacts of duplicate reads on microbial differential abundance analysis”, Rui Zhang, Rutgers	Sep 2024 - Current
3. Guest lecturer of the course “Natural products and human health”, 2025FALL-16:765:540, Rutgers University	Oct 2025
4. Mentor of the 2025 Aresty Summer Science Program “In silico comparison of the identity between microbial 16S rRNA genes and genomes”, Maanya Jha, Rutgers	May 2025- Aug 2025
5. Guest lecturer of the course “Microbiomes & Health”, 2025SP – MICROBIOMES & HEALTH 11:680:475:01, Rutgers University	April 2024
6. Committee member, Division of Life Sciences: Biological Sciences Honors “Investigation of the Impact of Dietary Fiber on Antibiotic Induced Dysbiosis of the Gut Microbiome”, Gabriela Hizgiov, Rutgers University	April 2024
7. Guest lecturer of the course “Natural products and human health”, 2023FALL-16:765:540, Rutgers University	Oct 2023
8. Mentor of the 2023 Aresty Summer Science Program, “In silico comparison of the identity between microbial 16S rRNA genes and genomes”, Melanie Tan, Rutgers	May 2023- Aug 2023
9. Guest lecturer of the course “Microbiomes & Health”, 2023SP – MICROBIOMES & HEALTH 11:680:475:01, Rutgers University	April 2023
10. Guest lecturer of the course “Microbiomes”, 2023SP - MICROBIOMES 11:680:104:01, Rutgers University	Mar 2023
11. Speaker of “A reference-free and ecology-based approach for microbiome data mining”, Data Mining Technology Training 1st International Symposium on Microbiota Science, from Disease to Health-2021	Nov 2021
12. Guest lecturer of the course “Microbiome Data Analysis workshop”, 2021SP - SPEC TOPICS MIC BIOL 16:682:550:02, Rutgers University.	Jan 2021

ACADEMIC SERVICE

Editor:

Scientific Reports, Editorial Board Member	Sep 2025- Current
Guest associate editor of <i>Nutrients</i> Topic: Diet–Host–Gut Microbiota Interactions and Human Health	Aug 2024 – April 2025
Guest associate editor of <i>Frontiers in Endocrinology</i> Topic: The Mechanism in Gut Microbiota of Diabetes and Endocrine Complications: Preventive and Therapeutic Target	Jan 2024 - Aug 2025
Guest associate editor of <i>Frontiers in Immunology</i> Topic: Crosstalk Between the GI Redox Environment, Microbiome, and the Immune System	Feb 2023 – March 2024
Invited editor of <i>mBio</i> (invited by an editor, conduct reviewer assignment and decision recommendation)	2024
Handling editor of <i>Frontiers in Microbiology</i>	Mar 2021- May 2022

Grant/Funding Reviewer:

Israel Science Foundation	Apr 2024 – Apr 2024
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Journal Reviewer:

Antioxidants
Biology
Cell Metabolism
Frontiers in Cellular and Infection Microbiology
Frontiers in Immunology
Frontiers in Microbiology
Frontiers in Microbiomes
Gut Microbes
Medicine in Microecology
Microbiome
Molecules
Nutrients
The ISME Journal

Workshop:

Teacher of the microbiome analysis workshop 2024. (Rutgers University)	Feb 12, 2024
Speaker and moderator of the microbiome workshop, “Reference-free and Guild-based Analysis on High Quality-controlled Data in Human Microbiome Studies”. (Online)	Jul 6, 2022
Organizer and moderator of the workshop, “Reference-free and Ecology-based Data Analysis for Understanding Gut Microbiome in Human Health and Diseases”. (Online)	Dec 6, 2021