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EDUCATION and TRANING

Rothamsted Research, Harpenden, Hertfordshire, UK, Functions and Diversity of Soil Microbiology, Underwood Fellow, Biotechnology and Biological Sciences Research Council, September, 2009-February, 2010
Oak Ridge National Laboratory, TN, USA, Genomics and Environmental Microbiology, Postdoctoral Training, 2001-2002
Hunan Agricultural University & Michigan State University, Molecular and Environmental Microbiology, Joint program, PhD, 2001
Hunan Agricultural University, Plant Pathology, M.S., 1987
Hunan Agricultural University, Plant Pathology, B.S., 1982

PROFESSIONAL POSITIONS

Adjunct professor/Research Scientist (highest level), the School of Biological Sciences & the Institute for Environmental Genomics, University of Oklahoma, 2011-present
Adjunct Associate professor/Research Scientist (highest level), the Department of Botany/Microbiology & the Institute for Environmental Genomics, University of Oklahoma, 2007-2011
Research Assistant Professor, University of Oklahoma, 2006-2007
Staff Scientist, Oak Ridge National Laboratory, 2002-2006
Postdoctoral Research Associate, Oak Ridge National Laboratory, 2001-2002
Visiting Scientist, Michigan State University & Oak Ridge National Laboratory, 1997-2001
Professor, Hunan Agricultural University, 1998-present
Associate Professor, Hunan Agricultural University, 1993-1997
Lecturer, Hunan Agricultural University, 1988-1993
Teaching Assistant, Hunan Agricultural University, 1987-1988
Graduate Research and Teaching Assistant, Hunan Agricultural University, 1984-1987
Research Assistant, Taojiang Agricultural Institute, 1982-1984

RESEARCH PROJECTS

1. Dimensions US-China: Collaborative Research: Quantifying the Impact of Eutrophication on the World's Grassland Soil Microbial Biodiversity and Functioning, : $ 1,000,000, for the period of 10/01/2020 – 9/30/2025 (Co-PI), NSF.
2. ENIGMA: From Genomes to Ecosystems: Systems-Level Mechanistic Understanding of Microbial Stress Responses at Chromium Contaminated Sites, $3,500,000, for the period of 10/1/2019-9/30/2024 (Senior researcher), DOE.
3. Establishment to Senescence: Plant-Microbe and Microbe-Microbe Interactions Mediate Switchgrass Sustainability, $2,492,783, for the period of 8/15/2015 - 8/14/2020, (Co-PI), DOE
4. Development of a Sequence Capture Approach for Monitoring in situ Nitrogen Cycling Potential in Microbial Communities, $225,000 for the period of 2/21/2017~11/20/2017, (PI), DOE SBIR.
5. Establishment to senescence: plant-microbe and microbe-microbe interactions mediate switchgrass sustainability. $15,000,000 for the period of 7/1/2015 – 6/30/2020 (Co-PI with the PI Mary Finston at UC Berkeley), DOE (Genomic Science Program: Sustainable Bioenergy Crop Development).
6. From Structure to Functions: Metagenomics-Enabled Predictive Understanding of Soil Microbial Feedbacks to Climate Change. $2,099,980 for the period of 10/1/2013-9/30/2016. (Co-PI with the PI Jizhong Zhou et al. at OU), DOE Gemincs: GTL Program
7. Metagenomic-Enabled Predictive Understanding of Temperature Sensitivity jof Soil Carbon Decompossition to Climate Warming. $1,000,000 for the period of 10/1/2010-9/30/2013. (Co-PI with the PI Jizhong Zhou et al. at OU), DOE Gemincs: GTL Program
8. From Community Structure to Functions: Metagenomic-Enabled predictive Understanding of Temperature Sensitivity jof Soil Carbon Decompossition to Climate Warming. $1,000,000 for the period of 10/1/2010-9/30/2013, co-PI, Department of Energy
9. Systems-Level Understanding of Factors Controlling Feedstock. $480,000 for the period of 09/1/2009-08/31/2011, **Principal Investigator**, Oklahoma Bioenergy Center.
10. Linking community structure to functions: Metagenomic analysis of Feedstock-Related Microbial Communities using GeoChip and Pyrosequencing. $761,982 for the period of 1/1/2008-12/31/2009, **Principal Investigator**, Oklahoma Bioenergy Center.
11. Whole genomic DNA Array for Bacteria Detection and Identification. $300,000 for the period of 2/1/2008-1/302011, **Principal Investigator**, Oklahoma Applied Research Support (OARS) Program of Oklahoma Center for the Advancement of Science & Technology (OCAST).
12. Microbial Diversity Observation in Grassland under different Agricultural Practices. £48,200, March 5, 2009-April 4, 2010, **Principal Investigator,** Biotechnology and Biological Science Research Council, UK, Underwood Fellowship
13. Isolation and Characterization of novel microbial catalysts for direct fermentation of lignocellulose to ethanol. $294 K for the period of 1/1/2008 - 12/31/2009, **Co- Principal Investigator**, Oklahoma Bioenergy Center.
14. Improvement of the Performance of Novel Microbial Catalysts for Direct Fermentation of Lignocellulose to Ethanol. $300K for the period of 09/01/2009-8/31/2011, **Co- Principal Investigator**, Oklahoma Bioenergy Center.
15. Integrated genome-based studies of Shewanella ecophysiology. $1,000K for the period of 10/1/2006-9/30/2009 **Co- Principal Investigator**, Genomics: GTL program, the Department of Energy.
16. METASOIL3 - An NSF/USDA contribution to the worldwide TERRAGENOME project. Pending, about $600K for the period of 09/1/2009-08/31/2012 was requested, **Co- Principal Investigator,** USDA & NSF, Agriculture and Food Research Initiative - Microbial Genomics: Genome Sequencing.
17. From Community Structure to Functions: Metagenomics-Enabled Predictive Understanding of Temperature Sensitivity of Soil Carbon Decomposition to Climate Warming. Pending, $2,998,407 was requested for the period of 1/1/2010-12/31/2012, **Co-Principal Investigator**, Genomics: GTL program, the Department of Energy.

SYNERGISTIC ACTIVITIES

1. **Deputy Section Editor, BMC Microbiology, 2009-present**
2. Editorial Board of the journal, Sequencing
3. Facility manager, the Institute for Environmental Genomics, the University of Oklahoma

4. Occasional reviewer: Journal of Microbiological Methods, Applied Microbiology and Biotechnology, Current Microbiology, Journal of Phytopathology, Journal of Biotechnology, the Minnesota Sea Grant, and the Innovational Research Incentives Scheme Vidi 2011 of NWO Earth and Life Sciences.

AWARDS AND HONORS

1. US patent: Method for analyzing microbial communities. patent # 7759057
2. **R&D 100 award, OU Geochip, R&D Magazine, 2009**
3. Second Prize from Hunan Education Committee for the Project of Reforming Teaching Model of Phytopathology, 1997.
4. Second Prize from Huadong Area Society of Publication Committee for the book, Breeding Technique of Virus-free Fruit Trees, 1996.
5. First Prize from Hunan Science and Technology Committee for the Project of Establishment of Virus-free Citrus Propagation System in Hunan Province, 1994.

EXPERTISE AND RELEVANT EXPERIENCE

Molecular and environmental microbiology, microbial ecology, microbial community analysis using microarray technology and other genomic technology

PUBLICATIONS

1. Lei, J., Y. Su, S. Jian, X. Guo, M. Yuan, C. T. Bates, Z. J. Shi, J. Li, Y. Su, D. Ning, L. Wu, J. Zhou and Y. Yang (2024). "Warming effects on grassland soil microbial communities are amplified in cool months." Isme Journal 18(1).
2. Ning, D., Y. Wang, Y. Fan, J. Wang, J.D. Van Nostrand, **L. Wu**, P. Zhang, D.J. Curtis, R. Tian, L. Lui, T.C. Hazen, E.J. Alm, M.W. Fields, F. Poole, M.W.W. Adams, R. Chakraborty, D.A. Stahl, P.D. Adams, A.P. Arkin, Z. He and J. Zhou (2024). "Environmental stress mediates groundwater microbial community assembly". Nature Microbiology 9.
3. Qin, Y., **L. Wu* (co-first and corresponding author)**, Q. Zhang, C. Wen, J.D. Van Nostrand, D. Ning, L. Raskin, A. Pinto and J. Zhou (2023). "Effects of error, chimera, bias, and GC content on the accuracy of amplicon sequencing". Msystems 8.
4. Zhang, Y., D. Ning, L. Wu, M.M. Yuan, X. Zhou, X. Guo, Y. Hu, S. Jian, Z. Yang, S. Han, J. Feng, J. Kuang, C.R. Cornell, C.T. Bates, Y. Fan, J.P. Michael, Y. Ouyang, J. Guo, Z. Gao, Z. Shi, N. Xiao, Y. Fu, A. Zhou, L. Wu, X. Liu, Y. Yang, J.M. Tiedje and J. Zhou (2023). "Experimental warming leads to convergent succession of grassland archaeal community". Nature Climate Change 13:561-+.
5. Guo, X., M. Yuan, J. Lei, Z. Shi, X. Zhou, J. Li, Y. Deng, Y. Yang, **L. Wu**, Y. Luo, J.M. Tiedje and J. Zhou (2022). "Climate warming restructures seasonal dynamics of grassland soil microbial communities". Mlife 1:245-256.
6. Cornell, C.R., Y. Zhang, D. Ning, L. Wu, P. Wagle, J.L. Steiner, X. Xiao and J. Zhou (2022). "Temporal Dynamics of Bacterial Communities along a Gradient of Disturbance in a US Southern Plains Agroecosystem". Mbio 13.
7. Bates, C.T., A. Escalas, J. Kuang, L. Hale, Y. Wang, D. Herman, E.E. Nuccio, X. Wan, A. Bhattacharyya, Y. Fu, R. Tian, G. Wang, D. Ning, Y. Yang, **L. Wu**, J. Pett-Ridge, M. Saha, K. Craven, E.L. Brodie, M. Firestone and J. Zhou (2022). "Conversion of marginal land into switchgrass conditionally accrues soil carbon but reduces methane consumption". Isme Journal 16:10-25.
8. Wu, L., Y. Zhang, X. Guo, D. Ning, X. Zhou, J. Feng, M.M. Yuan, S. Liu, J. Guo, Z. Gao, J. Ma, J. Kuang, S. Jian, S. Han, Z. Yang, Y. Ouyang, Y. Fu, N. Xiao, X. Liu, L. Wu, A. Zhou, Y. Yang, J.M. Tiedje and J. Zhou (2022). "Reduction of microbial diversity in grassland soil is driven by long-term climate warming". Nature Microbiology 7:1054-+.
9. Yuan, M. M., X. Guo, L. Wu, Y. Zhang, N. Xiao, D. Ning, Z. Shi, X. Zhou, **L. Wu**, Y. Yang, J. M. Tiedje and J. Zhou (2021). "Climate warming enhances microbial network complexity and stability." Nature Climate Change.
10. Yu, H., Y. Deng, Z. He, E. Pendall, Y. Carrillo, S. Wang, D. Jin, **L. Wu**, A. Wang, Y. Xu, B. Liu, X. Tai and J. Zhou (2021). "Stimulation of soil microbial functioning by elevated CO2 may surpass effects mediated by irrigation in a semiarid grassland." Geoderma 401.
11. Turkarslan, S., N. Stopnisek, A. W. Thompson, C. E. Arens, J. J. Valenzuela, J. Wilson, K. A. Hunt, J. Hardwicke, A. L. G. de Lomana, S. Lim, Y. M. Seah, Y. Fu, **L. Wu**, J. Zhou, K. L. Hillesland, D. A. Stahl

and N. S. Baliga (2021). "Synergistic epistasis enhances the co-operativity of mutualistic interspecies interactions." Isme Journal 15(8): 2233-2247.

12. Cheng, J., Y. Yang, M. M. Yuan, Q. Gao, **L. Wu**, Z. Qin, Z. J. Shi, E. A. G. Schuur, J. R. Cole, J. M. Tiedje and J. Zhou (2021). "Winter warming rapidly increases carbon degradation capacities of fungal communities in tundra soil: Potential consequences on carbon stability." Molecular Ecology 30(4): 926-937.
13. Bates, C. T., A. Escalas, J. Kuang, L. Hale, Y. Wang, D. Herman, E. E. Nuccio, X. Wan, A. Bhattacharyya, Y. Fu, R. Tian, G. Wang, D. Ning, Y. Yang, **L. Wu**, J. Pett-Ridge, M. Saha, K. Craven, E. L. Brodie, M. Firestone and J. Zhou (2021). "Conversion of marginal land into switchgrass conditionally accrues soil carbon but reduces methane consumption." Isme Journal.
14. Tu, Q., Q. Yan, Y. Deng, S. T. Michaletz, V. Buzzard, M. D. Weiser, R. Waide, D. Ning, **L. Wu**, Z. He and J. Zhou (2020). "Biogeographic patterns of microbial co-occurrence ecological networks in six American forests." Soil Biology & Biochemistry 148.
15. Liang, Y., D. Ning, Z. Lu, N. Zhang, L. Hale, **L. Wu**, I. M. Clark, S. P. McGrath, J. Storkey, P. R. Hirsch, B. Sun and J. Zhou (2020). "Century long fertilization reduces stochasticity controlling grassland microbial community succession." Soil Biology & Biochemistry 151.
16. He, Z., Y. Deng, M. Xu, J. Li, J. Liang, J. Xiong, H. Yu, B. Wu, **L. Wu**, K. Xue, S. Shi, Y. Carrillo, J. D. Van Nostrand, S. E. Hobbie, P. B. Reich, C. W. Schadt, A. D. Kent, E. Pendall, M. Wallenstein, Y. Luo, Q. Yan and J. Zhou (2020). "Microbial functional genes commonly respond to elevated carbon dioxide." Environment International 144.
17. Guo, X., Q. Gao, M. Yuan, G. Wang, X. Zhou, J. Feng, Z. Shi, L. Hale, L. Wu, A. Zhou, R. Tian, F. Liu, B. Wu, L. Chen, C. G. Jung, S. Niu, D. Li, X. Xu, L. Jiang, A. Escalas, **L. Wu**, Z. He, J. D. Van Nostrand, D. Ning, X. Liu, Y. Yang, E. A. G. Schuur, K. T. Konstantinidis, J. R. Cole, C. R. Penton, Y. Luo, J. M. Tiedje and J. Zhou (2020). "Gene-informed decomposition model predicts lower soil carbon loss due to persistent microbial adaptation to warming." Nature Communications 11(1).
18. Feng, J., C. Wang, J. Lei, Y. Yang, Q. Yan, X. Zhou, X. Tao, D. Ning, M. M. Yuan, Y. Qin, Z. J. Shi, X. Guo, Z. He, J. D. Van Nostrand, **L. Wu**, R. G. Bracho-Garillo, C. R. Penton, J. R. Cole, K. T. Konstantinidis, Y. Luo, E. A. G. Schuur, J. M. Tiedje and J. Zhou (2020). "Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community." Microbiome 8(1).
19. Cheng, J., Y. Yang, M. M. Yuan, Q. Gao, **L. Wu**, Z. Qin, Z. J. Shi, E. A. G. Schuur, J. R. Cole, J. M. Tiedje and J. Zhou (2020). "Winter warming rapidly increases carbon degradation capacities of fungal communities in tundra soil: Potential consequences on carbon stability." Molecular Ecology.
20. Wu, L., D. Ning, B. Zhang, Y. Li, P. Zhang, X. Shan, Q. Zhang, M. R. Brown, Z. Li, J. D. Van Nostrand, F. Ling, N. Xiao, Y. Zhang, J. Vierheilig, G. F. Wells, Y. Yang, Y. Deng, Q. Tu, A. Wang, D. Acevedo, M. Agullo-Barcelo, G. L. Andersen, J. C. de Araujo, K. F. Boehnke, P. Bond, C. B. Bott, P. Bovio, R. K. Brewster, F. Bux, A. Cabezas, L. Cabrol, S. Chen, C. Etchebehere, A. Ford, D. Frigon, J. S. Gómez, J. S. Griffin, A. Z. Gu, M. Habagil, L. Hale, S. D. Hardeman, M. Harmon, H. Horn, Z. Hu, S. Jauffur, D. R. Johnson, A. Keucken, S. Kumari, C. D. Leal, L. A. Lebrun, J. Lee, M. Lee, Z. M. P. Lee, M. Li, X. Li, Y. Liu, R. G. Luthy, L. C. Mendonça-Hagler, F. G. R. de Menezes, A. J. Meyers, A. Mohebbi, A. Noyola, A. Oehmen, A. Palmer, P. Parameswaran, J. Park, D. Patsch, V. Reginatto, F. L. de los Reyes, S. Rossetti, J. Sidhu, W. T. Sloan, K. Smith, O. V. de Sousa, K. Stephens, R. Tian, N. B. Tooker, D. De los Cobos Vasconcelos, S. Wakelin, B. Wang, J. E. Weaver, S. West, P. Wilmes, S.-G. Woo, J.-H. Wu, **L. Wu**, C. Xi, M. Xu, T. Yan, M. Yang, M. Young, H. Yue, Q. Zhang, W. Zhang, Y. Zhang, H. Zhou, T. Zhang, Z. He, J. Keller, P. H. Nielsen, P. J. J. Alvarez, C. S. Criddle, M. Wagner, J. M. Tiedje, Q. He, T. P. Curtis, D. A. Stahl, L. Alvarez-Cohen, B. E. Rittmann, X. Wen and J. Zhou (2019). "Global diversity and biogeography of bacterial communities in wastewater treatment plants." Nature Microbiology 4: 1183–1195.
21. Shi, Z., H. Yin, J. D. Van Nostrand, J. W. Voordeckers, Q. Tu, Y. Deng, M. Yuan, A. Zhou, P. Zhang, N. Xiao, D. Ning, Z. He, **L. Wu** and J. Zhou (2019). "Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities." Msystems 4(4).
22. Johnston, E. R., J. K. Hatt, Z. He, **L. Wu**, X. Guo, Y. Luo, E. A. G. Schuur, J. M. Tiedje, J. Zhou and K. T. Konstantinidis (2019). "Responses of tundra soil microbial communities to half a decade of experimental warming at two critical depths." Proceedings of the National Academy of Sciences of the United States of America 116(30): 15096-15105.
23. Huang, R., S. P. McGrath, P. R. Hirsch, I. M. Clark, J. Storkey, **L. Wu**, J. Zhou and Y. Liang (2019). "Plant-microbe networks in soil are weakened by century-long use of inorganic fertilizers." Microbial Biotechnology 12(6): 1464-1475.

24. Hale, L. R., W. T. Feng, H. Q. Yin, X. Guo, X. S. Zhou, R. Bracho, E. Pegoraro, C. R. Penton, **L. Y. Wu**, J. Cole, K. T. Konstantinidis, Y. Q. Luo, J. M. Tiedje, E. A. G. Schuur and J. Z. Zhou (2019). "Tundra microbial community taxa and traits predict decomposition parameters of stable, old soil organic carbon." Isme Journal 13(12): 2901-2915.
25. Guo, X., X. Zhou, L. Hale, M. Yuan, D. Ning, J. Feng, Z. Shi, Z. Li, B. Feng, Q. Gao, **L. Wu**, W. Shi, A. Zhou, Y. Fu, L. Wu, Z. He, J. D. Van Nostrand, G. Qiu, X. Liu, Y. Luo, J. M. Tiedje, Y. Yang and J. Zhou (2019). "Climate warming accelerates temporal scaling of grassland soil microbial biodiversity." Nature Ecology & Evolution 3(4): 612-619.
26. Gao, Q., Y. Yang, J. Feng, R. Tian, X. Guo, D. Ning, L. Hale, M. Wang, J. Cheng, **L. Wu**, M. Zhao, J. Zhao, L. Wu, Y. Qin, Q. Qi, Y. Liang, B. Sun, H. Chu and J. Zhou (2019). "The spatial scale dependence of diazotrophic and bacterial community assembly in paddy soil." Global Ecology and Biogeography 28(8): 1093-1105.
27. Feng, J., C. R. Penton, Z. He, J. D. Van Nostrand, M. M. Yuan, **L. Wu**, C. Wang, Y. Qin, Z. J. Shi, X. Guo, E. A. G. Schuur, Y. Luo, R. Bracho, K. T. Konstantinidis, J. R. Cole, J. M. Tiedje, Y. Yang and J. Zhou (2019). "Long-Term Warming in Alaska Enlarges the Diazotrophic Community in Deep Soils." Mbio 10(1).
28. Yuan, M. M., J. Zhang, K. Xue, **L. Wu**, Y. Deng, J. Deng, L. Hale, X. Zhou, Z. He, Y. Yang, J. D. Van Nostrand, E. A. G. Schuur, K. T. Konstantinidis, C. R. Penton, J. R. Cole, J. M. Tiedje, Y. Luo and J. Zhou (2018). "Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil." Global Change Biology 24(1): 297-307.
29. Yu, H., Z. He, A. Wang, J. Xie, **L. Wu**, J. D. Van Nostrand, D. Jin, Z. Shao, C. W. Schadt, J. Zhou and Y. Deng (2018). "Divergent Responses of Forest Soil Microbial Communities under Elevated CO2 in Different Depths of Upper Soil Layers." Applied and Environmental Microbiology 84(1).
30. Yu, H., Y. Deng, Z. He, J. D. Van Nostrand, S. Wang, D. Jin, A. Wang, **L. Wu**, D. Wang, X. Tai and J. Zhou (2018). "Elevated CO2 and Warming Altered Grassland Microbial Communities in Soil Top-Layers." Frontiers in Microbiology 9.
31. Yu H, He ZL, Wang AJ, Xie JP, **Wu LY**, Van Nostrand JD, Jin DC, Shao ZM, Schadt CW, Zhou JZ, Deng Y. 2018. Divergent Responses of Forest Soil Microbial Communities under Elevated CO2 in Different Depths of Upper Soil Layers. Applied and Environmental Microbiology 84.
32. Xue, M., **L. Wu**, Y. He, H. Liang and C. Wen (2018). "Biases during DNA extraction affect characterization of the microbiota associated with larvae of the Pacific white shrimp, Litopenaeus vannamei." Peerj 6.
33. Wu, X., **L. Wu**, Y. Liu, P. Zhang, Q. Li, J. Zhou, N. J. Hess, T. C. Hazen, W. Yang and R. Chakraborty (2018). "Microbial Interactions With Dissolved Organic Matter Drive Carbon Dynamics and Community Succession." Frontiers in Microbiology 9.
34. Wu, B., F. Liu, M. D. Weiser, D. Ning, J. G. Okie, L. Shen, J. Li, B. Chai, Y. Deng, K. Feng, **L. Wu**, S. Chen, J. Zhou and Z. He (2018). "Temperature determines the diversity and structure of N2O-reducing microbial assemblages." Functional Ecology 32(7): 1867-1878.
35. Wang, Z. G., Y. M. You, W. H. Xu, W. J. Chen, J. Zeng, X. S. Zhao, Y. P. Su and **L. Y. Wu** (2018). "Dimethyl phthalate altered the microbial metabolic pathways in a Mollisol." European Journal of Soil Science 69(3): 439-449.
36. Shi, Z., Y. Lin, K. R. Wilcox, L. Souza, L. Jiang, J. Jiang, C. G. Jung, X. Xu, M. Yuan, X. Guo, **L. Wu**, J. Zhou and Y. Luo (2018). "Successional change in species composition alters climate sensitivity of grassland productivity." Global Change Biology 24(10): 4993-5003.
37. Shi, S., D. J. Herman, Z. He, J. Pett-Ridge, **L. Wu**, J. Zhou and M. K. Firestone (2018). "Plant roots alter microbial functional genes supporting root litter decomposition." Soil Biology & Biochemistry 127: 90-99.
38. Liang, J., Z. Zhou, C. Huo, Z. Shi, J. R. Cole, L. Huang, K. T. Konstantinidis, X. Li, B. Liu, Z. Luo, C. R. Penton, E. A. G. Schuur, J. M. Tiedje, Y.-P. Wang, **L. Wu**, J. Xia, J. Zhou and Y. Luo (2018). "More replenishment than priming loss of soil organic carbon with additional carbon input." Nature Communications 9.
39. He, Z., P. Zhang, L. Wu, A. M. Rocha, Q. Tu, Z. Shi, B. Wu, Y. Qin, J. Wang, Q. Yan, D. Curtis, D. Ning, J. D. Van Nostrand, **L. Wu**, Y. Yang, D. A. Elias, D. B. Watson, M. W. W. Adams, M. W. Fields, E. J. Alm, T. C. Hazen, P. D. Adams, A. P. Arkin and J. Zhou (2018). "Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning." Mbio 9(1).
40. Guo, X., X. Zhou, L. Hale, M. Yuan, J. Feng, D. Ning, Z. Shi, Y. Qin, F. Liu, **L. Wu**, Z. He, J. D. Van Nostrand, X. Liu, Y. Luo, J. M. Tiedje and J. Zhou (2018). "Taxonomic and Functional Responses of Soil Microbial Communities to Annual Removal of Aboveground Plant Biomass." Frontiers in Microbiology 9.

41. Guo, X., J. Feng, Z. Shi, X. Zhou, M. Yuan, X. Tao, L. Hale, T. Yuan, J. Wang, Y. Qin, A. Zhou, Y. Fu, **L. Wu**, Z. He, J. D. Van Nostrand, D. Ning, X. Liu, Y. Luo, J. M. Tiedje, Y. Yang and J. Zhou (2018). "Climate warming leads to divergent succession of grassland microbial communities." Nature Climate Change 8(9): 813-+.
42. Deng, Y., D. Ning, Y. Qin, K. Xue, **L. Wu**, Z. He, H. Yin, Y. Liang, V. Buzzard, S. T. Michaletz and J. Zhou (2018). "Spatial scaling of forest soil microbial communities across a temperature gradient." Environmental Microbiology 20(10): 3504-3513.
43. Chen, C., C. Hemme, J. Beleno, Z. J. Shi, D. Ning, Y. Qin, Q. Tu, M. Jorgensen, Z. He, **L. Wu** and J. Zhou (2018). "Oral microbiota of periodontal health and disease and their changes after nonsurgical periodontal therapy." Isme Journal 12(5): 1210-1224.
44. Mengting M. Yuan, Jin Zhang, Kai Xue, **Liyou Wu**, Ye Deng, Jie Deng, Lauren Hale, Xishu Zhou, Zhili He , Yunfeng Yang, Joy D. Van Nostrand, Edward A. G. Schuur, Konstantinos T. Konstantinidis, Christopher R. Penton, James R. Cole, James M. Tiedje, Yiqi Luo, Jizhong Zhou. 2017. Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil. Global Change Biology. 24: 297-307
45. Casey Chen, Chris Hemme, Joan Beleno, Zhou Jason Shi, Daliang Ning, Yujia Qin, Qichao Tu, Michael Jorgensen, Zhili He, **Liyou Wu**, Jizhong Zhou. 2017. Oral microbiota of periodontal health and disease and their changes after nonsurgical periodontal therapy. ISME Journal. doi.org/10.1038/s41396-017-0037-1
46. Zhou AF, Lau R, Baran R, Ma JC, von Netzer F, Shi WL, Gorman-Lewis D, Kempher ML, He ZL, Qin YJ, Shi Z, Zane GM, **Wu LY**, Bowen BP, Northen TR, Hillesland KL, Stahl DA, Wall JD, Arkin AP, Zhou JZ. 2017. Key Metabolites and Mechanistic Changes for Salt Tolerance in an Experimentally Evolved Sulfate-Reducing Bacterium, Desulfovibrio vulgaris. Mbio 8.
47. Zhang P, He ZL, Van Nostrand JD, Qin YJ, Deng Y, **Wu LY**, Tu QC, Wang JJ, Schadt CW, Fields MW, Hazen TC, Arkin AP, Stahl DA, Zhou JZ. 2017. Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. Environmental Science & Technology 51:3609-3620.
48. Yu DZ, Xia M, Zhang LP, Song YL, Duan Y, Yuan T, Yao MJ, **Wu LY**, Tian CY, Wu ZB, Li XZ, Zhou JH, Qiu DR. 2017. RpoN (sigma(54)) Is Required for Floc Formation but Not for Extracellular Polysaccharide Biosynthesis in a Floc-Forming Aquincola tertiaricarbonis Strain. Applied and Environmental Microbiology 83.
49. Yan QY, Stegen JC, Yu YH, Deng Y, Li XH, Wu S, Dai LL, Zhang X, Li JJ, Wang C, Ni JJ, Li XM, Hu HJ, Xiao FS, Feng WS, Ning DL, He ZL, Van Nostrand JD, **Wu LY**, Zhou JZ. 2017. Nearly a decade-long repeatable seasonal diversity patterns of bacterioplankton communities in the eutrophic Lake Donghu (Wuhan, China). Molecular Ecology 26:3839-3850.
50. Wen CQ, **Wu LY** (**Co-first, and corresponding author**), Qin YJ, Van Nostrand JD, Ning DL, Sun B, Xue K, Liu FF, Deng Y, Liang YT, Zhou JZ. 2017. Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. Plos One 12.
51. Tu QC, He ZL, **Wu LY**, Xue K, Xie G, Chain P, Reich PB, Hobbie SE, Zhou JZ. 2017. Metagenomic reconstruction of nitrogen cycling pathways in a CO2- enriched grassland ecosystem. Soil Biology & Biochemistry 106:99-108.
52. Gu YF, Van Nostrand JD, **Wu LY**, He ZL, Qin YJ, Zhao FJ, Zhou JZ. 2017. Bacterial community and arsenic functional genes diversity in arsenic contaminated soils from different geographic locations. Plos One 12.
53. Feng WT, Liang JY, Hale LE, Jung CG, Chen J, Zhou JZ, Xu MG, Yuan MT, **Wu LY**, Bracho R, Pegoraro E, Schuur EAG, Luo YQ. 2017. Enhanced decomposition of stable soil organic carbon and microbial catabolic potentials by long-term field warming. Global Change Biology 23:4765-4776.
54. Cheng L, Zhang NF, Yuan MT, Xiao J, Qin YJ, Deng Y, Tu QC, Xue K, Van Nostrand JD, **Wu LY**, He ZL, Zhou XH, Leigh MB, Konstantinidis KT, Schuur EAG, Luo YQ, Tiedje JM, Zhou JZ. 2017. Warming enhances old organic carbon decomposition through altering functional microbial communities. Isme Journal 11:1825-1835.
55. Wu, B., F. Liu, M. Weiser, D. Ning, L. Shen, J. Li, Y. Deng, **L. Wu**, S. Chen, J.-Z. Zhou, and Z. He. 2017. The diversity and biogeography of N2O-reducing microbial communities in forest soils along a temperature gradient. Functional Ecol., in press
56. Z. G. Wang, Y. M. You, W. H. Xu, W. J. Chen, J. Zeng, X. S. Zhao, Y. P. Su, **L. Y. Wu***. 2018. Dimethyl phthalate altered the microbial metabolic pathways in a Mollisol. European Journal of Soil Science, doi: 10.1111/ejss.12545

57. Zhou JZ, Deng Y, Shen LN, Wen CQ, Yan QY, Ning DL, Qin YJ, Xue K, **Wu LY**, He ZL, Voordeckers JW, Van Nostrand JD, Buzzard V, Michaletz ST, Enquist BJ, Weiser MD, Kaspari M, Waide R, Yang YF, Brown JH. 2016. Temperature mediates continental-scale diversity of microbes in forest soils. Nature Communications 7.
58. Yang CY, Li Y, Zhou YY, Lei XQ, Zheng W, Tian Y, Van Nostrand JD, He ZL, **Wu LY**, Zhou JZ, Zheng TL. 2016. A comprehensive insight into functional profiles of free-living microbial community responses to a toxic Akashiwo sanguinea bloom. Scientific Reports 6.
59. Yan QY, Li JJ, Yu YH, Wang JJ, He ZL, Van Nostrand JD, Kempher ML, **Wu LY**, Wang YP, Liao LJ, Li XH, Wu S, Ni JJ, Wang C, Zhou JZ. 2016. Environmental filtering decreases with fish development for the assembly of gut microbiota. Environmental Microbiology 18:4739-4754.
60. Xue K, Yuan MTM, Xie JP, Li DJ, Qin YJ, Hale LE, **Wu LY**, Deng Y, He ZL, Van Nostrand JD, Luo YQ, Tiedje JM, Zhou JZ. 2016. Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. Mbio 7.
61. Xue K, Yuan MM, Shi ZJ, Qin YJ, Deng Y, Cheng L, **Wu LY**, He ZL, Van Nostrand JD, Bracho R, Natali S, Schuur EAG, Luo CW, Konstantinidis KT, Wang Q, Cole JR, Tiedje JM, Luo YQ, Zhou JZ. 2016. Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. Nature Climate Change 6:595-+.
62. Xue K, Xie JP, Zhou AF, Liu FF, Li DJ, **Wu LY**, Deng Y, He ZL, Van Nostrand JD, Luo YQ, Zhou JZ. 2016. Warming Alters Expressions of Microbial Functional Genes Important to Ecosystem Functioning. Frontiers in Microbiology 7.
63. Tu QC, Zhou XS, He ZL, Xue K, **Wu LY**, Reich P, Hobbie S, Zhou JZ. 2016. The Diversity and Co-occurrence Patterns of N-2-Fixing Communities in a CO2-Enriched Grassland Ecosystem. Microbial Ecology 71:604-615.
64. Tu QC, Deng Y, Yan QY, Shen LN, Lin L, He ZL, **Wu LY**, Van Nostrand JD, Buzzard V, Michaletz ST, Enquist BJ, Weiser MD, Kaspari M, Waide RB, Brown JH, Zhou JZ. 2016. Biogeographic patterns of soil diazotrophic communities across six forests in the North America. Molecular Ecology 25:2937-2948.
65. Penton CR, Yang CY, **Wu LY**, Wang Q, Zhang J, Liu FF, Qin YJ, Deng Y, Hemme CL, Zheng TL, Schuur EAG, Tiedje J, Zhou JZ. 2016. NifH-Harboring Bacterial Community Composition across an Alaskan Permafrost Thaw Gradient. Frontiers in Microbiology 7.
66. Johnston ER, Rodriguez-R LM, Luo CW, Yuan MM, **Wu LY**, He ZL, Schuur EAG, Luo YQ, Tiedje JM, Zhou JZ, Konstantinidis KT. 2016. Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. Frontiers in Microbiology 7.
67. Hemme CL, Green SJ, Rishishwar L, Prakash O, Pettenato A, Chakraborty R, Deutschbauer AM, Van Nostrand JD, **Wu LY**, He ZL, Jordan IK, Hazen TC, Arkin AP, Kostka JE, Zhou JZ. 2016. Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. Mbio 7.
68. Bracho R, Natali S, Pegoraro E, Crummer KG, Schadel C, Celis G, Hale L, **Wu LY**, Yin HQ, Tiedje JM, Konstantinidis KT, Luo YQ, Zhou JZ, Schuur EAG. 2016. Temperature sensitivity of organic matter decomposition of permafrost-region soils during laboratory incubations. Soil Biology & Biochemistry 97:1-14.
69. Yang C, Li Y, Zhou B, Zhou Y, Zheng W, Tian Y, Van Nostrand JD, **Wu L**, He Z, Zhou J, Zheng T. 2015. Illumina sequencing-based analysis of free-living bacterial community dynamics during an Akashiwo sanguine bloom in Xiamen sea, China. Scientific Reports 5.
70. Yan Q, Bi Y, Deng Y, He Z, **Wu L**, Van Nostrand JD, Shi Z, Li J, Wang X, Hu Z, Yu Y, Zhou J. 2015. Impacts of the Three Gorges Dam on microbial structure and potential function. Scientific Reports 5.
71. Xue K, Yuan M, Shi Z, **Wu L**, He Z, Bracho R, Natali S, Schuur ET, Luo C, Konstantinidis K, Wang Q, Cole J, Tiedje J, Luo Y, Zhou J. 2015. Rapid Microbial Feedbacks Reveals Vulnerability of Permafrost Ecosystem Carbon to Climate Warming. Nature Climate Change In press.
72. Xiong J, He Z, Shi S, Kent A, Deng Y, **Wu L**, Van Nostrand JD, Zhou J. 2015. Elevated CO2 shifts the functional structure and metabolic potentials of soil microbial communities in a C-4 agroecosystem. Scientific Reports 5.
73. **Wu L**, Wen C, Qin Y, Yin H, Tu Q, Van Nostrand JD, Yuan T, Yuan M, Deng Y, Zhou J. 2015. Phasing amplicon sequencing on Illumina Miseq for robust environmental microbial community analysis. Bmc Microbiology 15.
74. Tu Q, Zhou X, He Z, Xue K, **Wu LY**, Reich P, Hobbie S, Zhou J-Z. 2015. The diversity and co-occurrence patterns of N2-fixing communities in a CO2 enriched grassland ecosystem,. Microbial Ecol in press.

75. Tu Q, Yuan M, He Z, Deng Y, Xue K, **Wu L**, Hobbie SE, Reich PB, Zhou J. 2015. Fungal Communities Respond to Long-Term CO2 Elevation by Community Reassembly. Applied and Environmental Microbiology 81:2445-2454.
76. Smith MB, Rocha AM, Smillie CS, Olesen SW, Paradis C, **Wu L**, Campbell JH, Fortney JL, Mehlhorn TL, Lowe KA, Earles JE, Phillips J, Techtmann SM, Joyner DC, Elias DA, Bailey KL, Hurt RA, Jr., Preheim SP, Sanders MC, Yang J, Mueller MA, Brooks S, Watson DB, Zhang P, He Z, Dubinsky EA, Adams PD, Arkin AP, Fields MW, Zhou J, Alm EJ, Hazen TC. 2015. Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. Mbio 6.
77. Qu Y, Zhang X, Ma Q, Deng J, Deng Y, Van Nostrand JD, **Wu L**, He Z, Qin Y, Zhou J, Zhou J. 2015. Microbial Community Dynamics and Activity Link to Indigo Production from Indole in Bioaugmented Activated Sludge Systems. Plos One 10.
78. Penton CR, Louis DS, Pham A, Cole JR, **Wu L**, Luo Y, Schuur EAG, Zhou J, Tiedje JM. 2015. Denitrifying and diazotrophic community responses to artificial warming in permafrost and tallgrass prairie soils. Frontiers in Microbiology 6.
79. Liang Y, **Wu L**, Clark IM, Xue K, Yang Y, Van Nostrand JD, Deng Y, He Z, McGrath S, Storkey J, Hirsch PR, Sun B, Zhou J. 2015. Over 150 Years of Long-Term Fertilization Alters Spatial Scaling of Microbial Biodiversity. Mbio 6.
80. Liang Y, Jiang Y, Wang F, Wen C, Deng Y, Xue K, Qin Y, Yang Y, **Wu L**, Zhou J, Sun B. 2015. Long-term soil transplant simulating climate change with latitude significantly alters microbial temporal turnover. Isme Journal 9:2561-2572.
81. Hemme CL, Tu Q, Shi Z, Qin Y, Gao W, Deng Y, Van Nostrand JD, **Wu L**, He Z, Chain PSG, Tringe SG, Fields MW, Rubin EM, Tiedje JM, Hazen TC, Arkin AP, Zhou J. 2015. Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. Frontiers in Microbiology 6.
82. Deng J, Gu Y, Zhang J, Xue K, Qin Y, Yuan M, Yin H, He Z, **Wu L**, Schuur EAG, Tiedje JM, Zhou J. 2015. Shifts of tundra bacterial and archaeal communities along a permafrost thaw gradient in Alaska. Molecular Ecology 24:222-234.
83. Zhou J, Deng Y, Zhang P, Xue K, Liang Y, Van Nostrand JD, Yang Y, He Z, **Wu L**, Stahl DA, Hazen TC, Tiedje JM, Arkin AP. 2014. Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. Proceedings of the National Academy of Sciences of the United States of America 111:E836-E845.
84. Yan Q, Bi Y, Deng Y, He Z, **Wu L**, Shi Z, Li J, Wang X, Hu Z, Yu Y, Zhou J. 2014. Impacts of the world's largest dam (Three-Gorges Dam) on microbial functions as revealed by comparative metagenomics. Scientific Reports.
85. Varrone C, Van Nostrand JD, Liu W, Zhou B, Wang Z, Liu F, He Z, **Wu L**, Zhou J, Wang A. 2014. Metagenomic-based analysis of biofilm communities for electrohydrogenesis: From wastewater to hydrogen. International Journal of Hydrogen Energy 39:4222-4233.
86. Tu Q, Yu H, He Z, Deng Y, **Wu L**, Van Nostrand JD, Zhou A, Voordeckers J, Lee Y-J, Qin Y, Hemme CL, Shi Z, Xue K, Yuan T, Wang A, Zhou J. 2014. GeoChip 4: a functional gene-array-based high-throughput environmental technology for microbial community analysis. Molecular Ecology Resources 14:914-928.
87. Tu Q, He Z, Li Y, Chen Y, Deng Y, Lin L, Hemme CL, Yuan T, Van Nostrand JD, **Wu L**, Zhou X, Shi W, Li L, Xu J, Zhou J. 2014. Development of HuMiChip for Functional Profiling of Human Microbiomes. Plos One 9.
88. Paula FS, Rodrigues JLM, Zhou J, **Wu L**, Mueller RC, Mirza BS, Bohannan BJM, Nuesslein K, Deng Y, Tiedje JM, Pellizari VH. 2014. Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. Molecular Ecology 23:2988-2999.
89. Luo C, Rodriguez-R LM, Johnston ER, **Wu L**, Cheng L, Xue K, Tu Q, Deng Y, He Z, Shi JZ, Yuan MM, Sherry RA, Li D, Luo Y, Schuur EAG, Chain P, Tiedje JM, Zhou J, Konstantinidis KT. 2014. Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. Applied and Environmental Microbiology 80:1777-1786.
90. Liang B, Cheng H, Van Nostrand JD, Ma J, Yu H, Kong D, Liu W, Ren N, **Wu L**, Wang A, Lee D-J, Zhou J. 2014. Microbial community structure and function of Nitrobenzene reduction biocathode in response to carbon source switchover. Water Research 54:137-148.
91. Li Y, He J, He Z, Zhou Y, Yuan M, Xu X, Sun F, Liu C, Li J, Xie W, Deng Y, Qin Y, VanNostrand JD, Xiao L, **Wu L**, Zhou J, Shi W, Zhou X. 2014. Phylogenetic and functional gene structure shifts of the oral microbiomes in periodontitis patients. Isme Journal 8:1879-1891.

92. Jia X, Zhou X, Luo Y, Xue K, Xue X, Xu X, Yang Y, **Wu L**, Zhou J. 2014. Effects of Substrate Addition on Soil Respiratory Carbon Release Under Long-Term Warming and Clipping in a Tallgrass Prairie. Plos One 9.
93. Hillesland KL, Lim S, Flowers JJ, Turkarslan S, Pinel N, Zane GM, Elliott N, Qin Y, **Wu L**, Baliga NS, Zhou J, Wall JD, Stahl DA. 2014. Erosion of functional independence early in the evolution of a microbial mutualism. Proceedings of the National Academy of Sciences of the United States of America 111:14822-14827.
94. He Z, Xiong J, Kent AD, Deng Y, Xue K, Wang G, **Wu L**, Van Nostrand JD, Zhou J. 2014. Distinct responses of soil microbial communities to elevated CO2 and O-3 in a soybean agro-ecosystem. Isme Journal 8:714-726.
95. Deng J, Gu Y, Zhang J, Xue K, Qin Y, Yuan M, Yin H, He Z, **Wu L**, Schuur E, Tiedje J, Zhou J. 2014. Shifts of tundra bacterial and archaeal communities along a permafrost thaw gradient in Alaska. Mol Ecol doi:10.1111/mec.13015.
96. Chen YP, Pettis JS, Corona M, Chen WP, Li CJ, Spivak M, Visscher PK, DeGrandi-Hoffman G, Boncristiani H, Zhao Y, Vanengelsdorp D, Delaplane K, Solter L, Drummond F, Kramer M, Lipkin WI, Palacios G, Hamilton MC, Smith B, Huang SK, Zheng HQ, Li JL, Zhang X, Zhou AF, **Wu LY**, Zhou JZ, Lee M-L, Teixeira EW, Li ZG, Evans JD. 2014. Israeli Acute Paralysis Virus: Epidemiology, Pathogenesis and Implications for Honey Bee Health. Plos Pathogens 10.
97. Jiang, H.-L., Q. He, Z. He, C. L. Hemme, **L. Wu**, and J. Zhou. 2013. Continuous Cellulosic Bioethanol Fermentation by Cyclic Fed-Batch Cocultivation. Appl. Environ. Microbiol. 79:1580-1589.
98. Lee, Y.-J., J. D. van Nostrand, Q. Tu, Z. Lu, L. Cheng, T. Yuan, Y. Deng, M. Q. Carter, Z. He, **L. Wu**, F. Yang, J. Xu, and J. Zhou. 2013. The PathoChip, a functional gene array for assessing pathogenic properties of diverse microbial communities. Isme Journal 7:1974-1984.
99. Li, D., X. Zhou, **L. Wu**, J. Zhou, and Y. Luo. 2013. Contrasting responses of heterotrophic and autotrophic respiration to experimental warming in a winter annual-dominated prairie. Global Change Biology 19:3553-3564.
100. Li, Y., J. He, Z. He, Y. Zhou, M. Yuan, X. Xu, F. Sun, C. Liu, J. Li, W. Xie, Y. Deng, Y. Qin, J. D. VanNostrand, L. Xiao, **L. Wu**, J. Zhou, W. Shi, and X. Zhou. 2014. Phylogenetic and functional gene structure shifts of the oral microbiomes in periodontitis patients. Isme Journal 8:1879-1891.
101. 1Liang, B., H. Cheng, J. D. Van Nostrand, J. Ma, H. Yu, D. Kong, W. Liu, N. Ren, **L. Wu**, A. Wang, D.-J. Lee, and J. Zhou. 2014. Microbial community structure and function of Nitrobenzene reduction biocathode in response to carbon source switchover. Water Research 54:137-148.
102. Liang, Y., Y. Jiang, F. Wang, C. Wen, Y. Deng, K. Xue, Y. Qin, Y. Yang, **L. Wu**, J. Zhou, and B. Sun. 2015. Long-term soil transplant simulating climate change with latitude significantly alters microbial temporal turnover. Isme Journal 9:2561-2572.
103. Liang, Y., **L. Wu**, I. M. Clark, K. Xue, Y. Yang, J. D. Van Nostrand, Y. Deng, Z. He, S. McGrath, J. Storkey, P. R. Hirsch, B. Sun, and J. Zhou. 2015. Over 150 Years of Long-Term Fertilization Alters Spatial Scaling of Microbial Biodiversity. Mbio 6.
104. Luo, C., L. M. Rodriguez-R, E. R. Johnston, **L. Wu**, L. Cheng, K. Xue, Q. Tu, Y. Deng, Z. He, J. Z. Shi, M. M. Yuan, R. A. Sherry, D. Li, Y. Luo, E. A. G. Schuur, P. Chain, J. M. Tiedje, J. Zhou, and K. T. Konstantinidis. 2014. Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. Appl. Environ. Microbiol. 80:1777-1786.
105. Paula, F. S., J. L. M. Rodrigues, J. Zhou, **L. Wu**, R. C. Mueller, B. S. Mirza, B. J. M. Bohannan, K. Nuesslein, Y. Deng, J. M. Tiedje, and V. H. Pellizari. 2014. Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. Mol. Ecol. 23:2988-2999.
106. Penton, C. R., D. S. Louis, A. Pham, J. R. Cole, **L. Wu**, Y. Luo, E. A. G. Schuur, J. Zhou, and J. M. Tiedje. 2015. Denitrifying and diazotrophic community responses to artificial warming in permafrost and tallgrass prairie soils. Frontiers in Microbiology 6.
107. Penton, C. R., D. St Louis, J. R. Cole, Y. Luo, **L. Wu**, E. A. G. Schuur, J. Zhou, and J. M. Tiedje. 2013. Fungal Diversity in Permafrost and Tallgrass Prairie Soils under Experimental Warming Conditions. Appl. Environ. Microbiol. 79:7063-7072.
108. Qu, Y., X. Zhang, Q. Ma, J. Deng, Y. Deng, J. D. Van Nostrand, **L. Wu**, Z. He, Y. Qin, J. Zhou, and J. Zhou. 2015. Microbial Community Dynamics and Activity Link to Indigo Production from Indole in Bioaugmented Activated Sludge Systems. Plos One 10.
109. Smith, M. B., A. M. Rocha, C. S. Smillie, S. W. Olesen, C. Paradis, **L. Wu**, J. H. Campbell, J. L. Fortney, T. L. Mehlhorn, K. A. Lowe, J. E. Earles, J. Phillips, S. M. Techtmann, D. C. Joyner, D. A. Elias, K. L. Bailey,

R. A. Hurt, Jr., S. P. Preheim, M. C. Sanders, J. Yang, M. A. Mueller, S. Brooks, D. B. Watson, P. Zhang, Z. He, E. A. Dubinsky, P. D. Adams, A. P. Arkin, M. W. Fields, J. Zhou, E. J. Alm, and T. C. Hazen. 2015. Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. Mbio 6.

110. Tu, Q., Z. He, Y. Li, Y. Chen, Y. Deng, L. Lin, C. L. Hemme, T. Yuan, J. D. Van Nostrand, **L. Wu**, X. Zhou, W. Shi, L. Li, J. Xu, and J. Zhou. 2014. Development of HuMiChip for Functional Profiling of Human Microbiomes. Plos One 9.
111. Tu, Q., H. Yu, Z. He, Y. Deng, **L. Wu**, J. D. Van Nostrand, A. Zhou, J. Voordeckers, Y.-J. Lee, Y. Qin, C. L. Hemme, Z. Shi, K. Xue, T. Yuan, A. Wang, and J. Zhou. 2014. GeoChip 4: a functional gene-array-based high-throughput environmental technology for microbial community analysis. Molecular Ecology Resources 14:914-928.
112. Tu, Q., M. Yuan, Z. He, Y. Deng, K. Xue, **L. Wu**, S. E. Hobbie, P. B. Reich, and J. Zhou. 2015. Fungal Communities Respond to Long-Term CO2 Elevation by Community Reassembly. Appl. Environ. Microbiol. 81:2445-2454.
113. Tu, Q., X. Zhou, Z. He, K. Xue, **L. Y. Wu**, P. Reich, S. Hobbie, and J.-Z. Zhou. 2015. The diversity and co-occurrence patterns of N2-fixing communities in a CO2 enriched grassland ecosystem,. Microbial Ecol in press.
114. Varrone, C., J. D. Van Nostrand, W. Liu, B. Zhou, Z. Wang, F. Liu, Z. He, **L. Wu**, J. Zhou, and A. Wang. 2014. Metagenomic-based analysis of biofilm communities for electrohydrogenesis: From wastewater to hydrogen. International Journal of Hydrogen Energy 39:4222-4233.
115. **Wu, L**., C. Wen, Y. Qin, H. Yin, Q. Tu, J. D. Van Nostrand, T. Yuan, M. Yuan, Y. Deng, and J. Zhou. 2015. Phasing amplicon sequencing on Illumina Miseq for robust environmental microbial community analysis. Bmc Microbiology 15.
116. Xiong, J., Z. He, S. Shi, A. Kent, Y. Deng, **L. Wu**, J. D. Van Nostrand, and J. Zhou. 2015. Elevated CO2 shifts the functional structure and metabolic potentials of soil microbial communities in a C-4 agroecosystem. Scientific Reports 5.
117. Xu, M., Z. He, Y. Deng, **L. Wu**, J. D. van Nostrand, S. E. Hobbie, P. B. Reich, and J. Zhou. 2013. Elevated CO2 influences microbial carbon and nitrogen cycling. Bmc Microbiology 13.
118. Xue, K., **L. Wu**, Y. Deng, Z. He, J. Van Nostrand, P. G. Robertson, T. M. Schmidt, and J. Zhou. 2013. Functional Gene Differences in Soil Microbial Communities from Conventional, Low-Input, and Organic Farmlands. Appl. Environ. Microbiol. 79:1284-1292.
119. Xue, K., M. Yuan, Z. Shi, **L. Wu**, Z. He, R. Bracho, S. Natali, E. T. Schuur, C. Luo, K. Konstantinidis, Q. Wang, J. Cole, J. Tiedje, Y. Luo, and J. Zhou. 2015. Rapid Microbial Feedbacks Reveals Vulnerability of Permafrost Ecosystem Carbon to Climate Warming. Nature Climate Change In press.
120. Yan, Q., Y. Bi, Y. Deng, Z. He, **L. Wu**, Z. Shi, J. Li, X. Wang, Z. Hu, Y. Yu, and J. Zhou. 2014. Impacts of the world's largest dam (Three-Gorges Dam) on microbial functions as revealed by comparative metagenomics. Scientific Reports.
121. Yan, Q., Y. Bi, Y. Deng, Z. He, **L. Wu**, J. D. Van Nostrand, Z. Shi, J. Li, X. Wang, Z. Hu, Y. Yu, and J. Zhou. 2015. Impacts of the Three Gorges Dam on microbial structure and potential function. Scientific Reports 5.
122. Yang, C., Y. Li, B. Zhou, Y. Zhou, W. Zheng, Y. Tian, J. D. Van Nostrand, **L. Wu**, Z. He, J. Zhou, and T. Zheng. 2015. Illumina sequencing-based analysis of free-living bacterial community dynamics during an Akashiwo sanguine bloom in Xiamen sea, China. Scientific Reports 5.
123. Zhao, F.-J., E. Harris, J. Yan, J. Ma, **L. Wu**, W. Liu, S. P. McGrath, J. Zhou, and Y.-G. Zhu. 2013. Arsenic Methylation in Soils and Its Relationship with Microbial arsM Abundance and Diversity, and As Speciation in Rice. Environmental Science & Technology 47:7147-7154.
124. Zhou, J., Y. Deng, P. Zhang, K. Xue, Y. Liang, J. D. Van Nostrand, Y. Yang, Z. He, **L. Wu**, D. A. Stahl, T. C. Hazen, J. M. Tiedje, and A. P. Arkin. 2014. Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. Proc. Natl. Acad. Sci. U. S. A. 111:E836-E845.
125. Zhou, J., Y.-H. Jiang, Y. Deng, Z. Shi, B. Y. Zhou, K. Xue, **L. Wu**, Z. He, and Y. Yang. 2013. Random Sampling Process Leads to Overestimation of beta-Diversity of Microbial Communities. Mbio 4.
126. Zhou, J., W. Liu, Y. Deng, Y.-H. Jiang, K. Xue, Z. He, J. D. Van Nostrand, L. Wu, Y. Yang, and A. Wang. 2013. Stochastic Assembly Leads to Alternative Communities with Distinct Functions in a Bioreactor Microbial Community. Mbio 4.
127. Carter, M. Q., K. Xue, M. T. Brandl, F. Liu, **L. Wu**, J. W. Louie, R. E. Mandrell and J. Zhou (2012). "Functional Metagenomics of Escherichia coli O157:H7 Interactions with Spinach Indigenous Microorganisms during Biofilm Formation." Plos One 7(9).

128. Deng, Y., Z. L. He, M. Y. Xu, Y. J. Qin, J. D. Van Nostrand, **L. Y. Wu**, B. A. Roe, G. Wiley, S. E. Hobbie, P. B. Reich and J. Z. Zhou (2012). "Elevated Carbon Dioxide Alters the Structure of Soil Microbial Communities." Applied and Environmental Microbiology 78(8): 2991-2995.
129. Liang, Y. T., J. D. Van Nostrand, L. A. N'Guessan, A. D. Peacock, Y. Deng, P. E. Long, C. T. Resch, **L. Y. Wu**, Z. L. He, G. H. Li, T. C. Hazen, D. R. Lovley and J. Z. Zhou (2012). "Microbial Functional Gene Diversity with a Shift of Subsurface Redox Conditions during In Situ Uranium Reduction." Applied and Environmental Microbiology 78(8): 2966-2972.
130. Lomax, C., W.-J. Liu, **L. Wu**, K. Xue, J. Xiong, J. Zhou, S. P. McGrath, A. A. Meharg, A. J. Miller and F.-J. Zhao (2012). "Methylated arsenic species in plants originate from soil microorganisms." New Phytologist 193(3): 665-672.
131. Xie, J.-p., **L.-y. Wu**, J. D. van Nostrand, Z.-l. He, Z.-m. Lu, H. Yu, J.-b. Xiong, X.-x. Liu and J.-z. Zhou (2012). "Improvements on environmental DNA extraction and purification procedures for matagenomic analysis." Journal of Central South University 19(11): 3055-3063.
132. Zhou, J. Z., K. Xue, J. P. Xie, Y. Deng, **L. Y. Wu**, X. H. Cheng, S. F. Fei, S. P. Deng, Z. L. He, J. D. Van Nostrand and Y. Q. Luo (2012). "Microbial mediation of carbon-cycle feedbacks to climate warming." Nature Climate Change 2(2): 106-110.
133. Zhou, J.Z., Liu, W.Z., Deng, Y., Jiang, Y.H., Xue, K., He, Z.L., van Nostrand, J., **Wu, L.Y**., Yang, Y.F. and Wang, A.J. Stochastic assembly leads to alternative communities with distinct functions. Accepted by mBio.
134. Xue, K., **Wu, L.Y**., Deng, Y., He, Z.L., van Nostrand, J., Robertson, P., Schmidt, T. and Zhou, J.Z. Functional gene differences in soil microbial communities from conventional, low-input and organic farmlands. Applied and Environmental Microbiology doi: 10.1128/AEM.03393-12.
135. Hemme, C. L., M. W. Fields, Q. He, Y. Deng, L. Lin, Q. C. Tu, H. Mouttaki, A. F. Zhou, X. Y. Feng, Z. Zuo, B. D. Ramsay, Z. L. He, **L. Wu**, J. Van Nostrand, J. Xu, Y. J. Tang, J. Wiegel, T. J. Phelps, and J. Zhou. 2011. Correlation of Genomic and Physiological Traits of Thermoanaerobacter Species with Biofuel Yields. Appl. Environ. Microbiol. 77:7998-8008.
136. Liang, Y. T., J. D. Van Nostrand, Y. Deng, Z. L. He, **L. Y. Wu**, X. Zhang, G. H. Li, and J. Z. Zhou. 2011. Functional gene diversity of soil microbial communities from five oil-contaminated fields in China. Isme Journal 5:403-413.
137. Liu, A. H., **L. Y. Wu** (**co-corresponding author**), Z. L. He, and J. Z. Zhou. 2011. Development of highly fluorescent silica nanoparticles chemically doped with organic dye for sensitive DNA microarray detection. Analytical and Bioanalytical Chemistry 401:2003-2011.
138. Van Nostrand, J. D., **L. Y. Wu** (**co-first and co-corresponding author**), W. M. Wu, Z. J. Huang, T. J. Gentry, Y. Deng, J. Carley, S. Carroll, Z. L. He, B. H. Gu, J. Luo, C. S. Criddle, D. B. Watson, P. M. Jardine, T. L. Marsh, J. M. Tiedje, T. C. Hazen, and J. Z. Zhou. 2011. Dynamics of Microbial Community Composition and Function during In Situ Bioremediation of a Uranium-Contaminated Aquifer. Appl. Environ. Microbiol. 77:3860-3869.
139. Wang, J., J. D. Van Nostrand, **L. Y. Wu**, Z. L. He, G. H. Li, and J. Z. Zhou. 2011. Microarray-Based Evaluation of Whole-Community Genome DNA Amplification Methods. Appl. Environ. Microbiol. 77:4241-4245.
140. Wu, W. M. J. Carley, D. Watson, B. H. Gu, S. Brooks, S. D. Kelly, K. Kemner, J. D. van Nostrand , **L. Y. Wu**, M. Xu, J.Z. Zhou, J. Luo, E. Cardenas, C. C. Hwang, M. W. Fields, T. L. Marsh, J. M. Tiedje, S. J. Green, J. E. Kostka, P. K. Kitanidis, P. M. Jardine, C. S. Criddle (2011). Bioreduction and immobilization of uranium in situ: a case study at a USA Department of Energy radioactive waste site, Oak Ridge, Tennessee. Acta Scientiae Circumstantiae (in Chinese). 31 (3), 449-459.
141. Xie, J. P., Z. L. He, X. X. Liu, X. D. Liu, J. D. Van Nostrand, Y. Deng, **L. Y. Wu**, J. Z. Zhou, and G. Z. Qiu. 2011. GeoChip-Based Analysis of the Functional Gene Diversity and Metabolic Potential of Microbial Communities in Acid Mine Drainage. Appl. Environ. Microbiol. 77:991-999.
142. Zhou, J. Z., **L. Y. Wu** (**co-first author**), Y. Deng, X. Y. Zhi, Y. H. Jiang, Q. C. Tu, J. P. Xie, J. D. Van Nostrand, Z. L. He, and Y. F. Yang. 2011. Reproducibility and quantitation of amplicon sequencing-based detection. Isme Journal 5:1303-1313.
143. Zhou,J.-Z., K. Xue, J.-P. Xie, Y. Deng, **L.Y. Wu**, X.L. Cheng, S.F .Fei, S.P. Deng, Z.-H. He, J.D. van Nostrand, and Y.Q. Luo . 2011. Microbial Mediation of Carbon Cycle Feedbacks to Climate Warming. Nature Climate Change. doi:10.1038/nclimate1331.
144. He, Z. L., Y. Deng, J. D. Van Nostrand, Q. C. Tu, M. Y. Xu, C. L. Hemme, X. Y. Li, **L. Y. Wu**, T. J. Gentry, Y. F. Yin, J. Liebich, T. C. Hazen and J. Z. Zhou (2010). "GeoChip 3.0 as a high-throughput tool for

analyzing microbial community composition, structure and functional activity." Isme Journal 4(9): 1167-1179.
145. He ZL, Xu MY, Deng Y, Kang SH, Kellogg **L, Wu LY** et al (2010). Metagenomic analysis reveals a marked divergence in the structure of belowground microbial communities at elevated CO2. Ecology Letters 13: 564-575.
146. Hemme, C. L., Y. Deng, T. J. Gentry, M. W. Fields, **L. Y. Wu**, S. Barua, K. Barry, S. G. Tringe, D. B. Watson, Z. L. He, T. C. Hazen, J. M. Tiedje, E. M. Rubin and J. Z. Zhou (2010). "Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community." Isme Journal 4(5): 660-672.
147. Hemme, C. L., H. Mouttaki, Y. J. Lee, G. X. Zhang, L. Goodwin, S. Lucas, A. Copeland, A. Lapidus, T. G. del Rio, H. Tice, E. Saunders, T. Brettin, J. C. Detter, C. S. Han, S. Pitluck, M. L. Land, L. J. Hauser, N. Kyrpides, N. Mikhailova, Z. L. He, **L. Y. Wu**, J. D. Van Nostrand, B. Henrissat, Q. He, P. A. Lawson, R. S. Tanner, L. R. Lynd, J. Wiegel, M. W. Fields, A. P. Arkin, C. W. Schadt, B. S. Stevenson, M. J. McInerney, Y. F. Yang, H. L. Dong, D. F. Xing, N. Q. Ren, A. J. Wang, R. L. Huhnke, J. R. Mielenz, S. Y. Ding, M. E. Himmel, S. Taghavi, D. van der Lelie, E. M. Rubin and J. Z. Zhou (2010). "Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production." Journal of Bacteriology 192(24): 6494-6496.
148. Liang YT, He ZL, **Wu LY**, Deng Y, Li GH, Zhou JZ (2010). Development of a Common Oligonucleotide Reference Standard for Microarray Data Normalization and Comparison across Different Microbial Communities. Applied and Environmental Microbiology 76: 1088-1094.
149. Liu, W. Z., A. J. Wang, S. A. Cheng, B. E. Logan, H. Yu, Y. Deng, J. D. Van Nostrand, **L. Y. Wu**, Z. L. He and J. Z. Zhou (2010). "Geochip-Based Functional Gene Analysis of Anodophilic Communities in Microbial Electrolysis Cells under Different Operational Modes." Environmental Science & Technology 44(19): 7729-7735.
150. Xiong JB, **Wu LY**, Tu SX, Van Nostrand JD, He ZL, Zhou JZ et al (2010). Microbial Communities and Functional Genes Associated with Soil Arsenic Contamination and the Rhizosphere of the Arsenic-Hyperaccumulating Plant Pteris vittata L. Applied and Environmental Microbiology 76: 7277-7284.
151. Xu MY, Wu WM, **Wu LY**, He ZL, Van Nostrand JD, Deng Y et al (2010). Responses of microbial community functional structures to pilot-scale uranium in situ bioremediation. Isme Journal 4: 1060-1070.
152. Jianping Xie, Zhili He, Xinxing Liu, Xueduan Liu, Joy D. Van Nostrand, Ye, Deng, **Liyou Wu**, Jizhong Zhou, and Guanzhou Qiu (2010). GeoChip-based analysis of the functional gene diversity and metabolic potential of microbial communities in acid mine drainage. Applied and Environmental Microbiology. doi:10.1128/AEM.01798-10
153. Liang YL, Gao HC, Chen JR, Dong YY, **Wu L**, He ZL et al (2010). Pellicle formation in Shewanella oneidensis. Bmc Microbiology 10.
154. **Wu, L.**, L. Kellogg, A. H. Devol, J. M. Tiedje, and J. Zhou. 2008. Microarray-based characterization of microbial community functional structure and heterogeneity in marine sediments from the gulf of Mexico. Applied and Environmental Microbiology 74:4516-4529.
155. **Wu, L. Y.**, X. D. Liu, M. W. Fields, D. K. Thompson, C. E. Bagwell, J. M. Tiedje, T. C. Hazen, and J. Z. Zhou. 2008. Microarray-based whole-genome hybridization as a tool for determining procaryotic species relatedness. Isme Journal 2:642-655.
156. **Wu, L. Y**., X. Liu, C. W. Schadt, and J. Z. Zhou. 2006. Microarray-based analysis of subnanogram quantities of microbial community DNAs by using whole-community genome amplification. Applied and Environmental Microbiology 72:4931-4941.
157. He, Z. L., **L. Y. Wu**, X. Y. Li, M. W. Fields, and J. Z. Zhou. 2005. Empirical establishment of oligonucleotide probe design criteria. Applied and Environmental Microbiology 71:3753-3760.
158. He, Z. L., **L. Y. Wu**, M. W. Fields, and J. Z. Zhou. 2005. Use of microarrays with different probe sizes for monitoring gene expression. Applied and Environmental Microbiology 71:5154-5162.
159. **Wu, L. Y.**, D. K. Thompson, X. D. Liu, M. W. Fields, C. E. Bagwell, J. M. Tiedje, and J. Z. Zhou. 2004. Development and evaluation of microarray-based whole-genome hybridization for detection of microorganisms within the context of environmental applications. Environmental Science & Technology 38:6775-6782.
160. Tiquia, S. M., **L. Y. Wu (co-first author)**, S. C. Chong, S. Passovets, D. Xu, Y. Xu, and J. Z. Zhou. 2004. Evaluation of 50-mer oligonucleotide arrays for detecting microbial populations in environmental samples. Biotechniques 36:664-+.

161. **Wu, L. Y.**, D. K. Thompson, G. S. Li, R. A. Hurt, J. M. Tiedje, and J. Z. Zhou. 2001. Development and evaluation of functional gene arrays for detection of selected genes in the environment. Applied and Environmental Microbiology 67:5780-5790.
162. Yang, Y. F., D. P. Harris, F. Luo, W. L. Xiong, M. Joachimiak, **L. Y. Wu**, P. Dehal, J. Jacobsen, Z. M. Yang, A. V. Palumbo, A. P. Arkin, and J. Z. Zhou. 2009. Snapshot of iron response in Shewanella oneidensis by gene network reconstruction. Bmc Genomics 10.
163. Wang, F. P., H. Y. Zhou, J. Meng, X. T. Peng, L. J. Jiang, P. Sun, C. L. Zhang, J. D. Van Nostrand, Y. Deng, Z. L. He, **L. Y. Wu**, J. H. Zhou, and X. Xiao. 2009. GeoChip-based analysis of metabolic diversity of microbial communities at the Juan de Fuca Ridge hydrothermal vent. Proceedings of the National Academy of Sciences of the United States of America 106:4840-4845.
164. Waldron, P. J., **L. Y. Wu**, J. D. Van Nostrand, C. W. Schadt, Z. L. He, D. B. Watson, P. M. Jardine, A. V. Palumbo, T. C. Hazen, and J. Z. Zhou. 2009. Functional Gene Array-Based Analysis of Microbial Community Structure in Groundwaters with a Gradient of Contaminant Levels. Environmental Science & Technology 43:3529-3534.
165. Van Nostrand, J. D., W. M. Wu, **L. Y. Wu**, Y. Deng, J. Carley, S. Carroll, Z. L. He, B. H. Gu, J. Luo, C. S. Criddle, D. B. Watson, P. M. Jardine, T. L. Marsh, J. M. Tiedje, T. C. Hazen, and J. Z. Zhou. 2009. GeoChip-based analysis of functional microbial communities during the reoxidation of a bioreduced uranium-contaminated aquifer. Environmental Microbiology 11:2611-2626.
166. Liang, Y. T., G. H. Li, J. D. Van Nostrand, Z. L. He, **L. Y. Wu**, Y. Den, X. Zhang, and J. Z. Zhou. 2009. Microarray-based analysis of microbial functional diversity along an oil contamination gradient in oil field. Fems Microbiology Ecology 70:324-333.
167. Yin, H. Q., L. H. Cao, M. Xie, Q. J. Chen, G. Z. Qiu, J. Z. Zhou, **L. Y. Wu**, D. Z. Wang, and X. D. Liu. 2008. Bacterial diversity based on 16S rRNA and gyrB genes at Yinshan mine, China. Systematic and Applied Microbiology 31:302-311.
168. Yin, H. Q., G. Z. Qiu, **L. Y. Wu**, M. Xie, J. H. Zhou, Z. M. Dai, D. Z. Wang, L. Kellogg, L. H. Cao, and X. D. Liu. 2008. Microbial community diversity and changes associated with a mine drainage gradient at the Dexing copper mine, China. Aquatic Microbial Ecology 51:67-76.
169. He, Z. L., J. D. Van Nostrand, **L. Y. Wu**, and J. Z. Zhou. 2008.
170. Zhang, Y. G., X. Q. Zhang, X. D. Liu, Y. Xiao, L. J. Qu, **L. Y. Wu**, and J. Z. Zhou. 2007. Microarray-based analysis of changes in diversity of microbial genes involved in organic carbon decomposition following land use/cover changes. Fems Microbiology Letters 266:144-151.
171. Yang, Y. F., M. X. Zhu, **L. Y. Wu**, and J. Z. Zhou. 2007. Assessment of data processing to improve reliability of microarray experiments using genomic DNA reference. Bmc Genomics 9.
172. Yang, Y. F., D. P. Harris, F. Luo, **L. Y. Wu**, A. B. Parsons, A. V. Palumbo, and J. Z. Zhou. 2007. Characterization of the Shewanella oneidensis Fur gene: roles in iron and acid tolerance response. Bmc Genomics 9.
173. Wu, W. M., J. Carley, J. Luo, M. A. Ginder-Vogel, E. Cardenas, M. B. Leigh, C. C. Hwang, S. D. Kelly, C. M. Ruan, **L. Y. Wu**, J. Van Nostrand, T. Gentry, K. Lowe, T. Mehlhorn, S. Carroll, W. S. Luo, M. W. Fields, B. H. Gu, D. Watson, K. M. Kemner, T. Marsh, J. Tiedje, J. Z. Zhou, S. Fendorf, P. K. Kitanidis, P. M. Jardine, and C. S. Criddle. 2007. In situ bioreduction of uranium (VI) to submicromolar levels and reoxidation by dissolved oxygen. Environmental Science & Technology 41:5716-5723.
174. He, Z. L., T. J. Gentry, C. W. Schadt, **L. Y. Wu**, J. Liebich, S. C. Chong, Z. J. Huang, W. M. Wu, B. H. Gu, P. Jardine, C. Criddle, and J. Zhou. 2007. GeoChip: a comprehensive microarray for investigating biogeochemical, ecological and environmental processes. Isme Journal 1:67-77.
175. Gao, H. C., Z. M. K. Yang, T. J. Gentry, **L. Y. Wu**, C. W. Schadt, and J. Z. Zhou. 2007. Microarray-based analysis of microbial community RNAs by whole-community RNA amplification. Applied and Environmental Microbiology 73:563-571.
176. Wei, X. M., T. F. Yan, N. G. Hommes, X. D. Liu, **L. Y. Wu**, C. McAlvin, M. G. Klotz, L. A. Sayavedra-Soto, J. Z. Zhou, and D. J. Arp. 2006. Transcript profiles of Nitrosomonas europaea during growth and upon deprivation of ammonia and carbonate. Fems Microbiology Letters 257:76-83.
177. Qiu, X. Y., M. J. Daly, A. Vasilenko, M. V. Omelchenko, E. K. Gaidamakova, **L. Y. Wu**, J. Z. Zhou, G. W. Sundin, and J. M. Tiedje. 2006. Transcriptome analysis applied to survival of Shewanella oneidensis MR-1 exposed to ionizing radiation. Journal of Bacteriology 188:1199-1204.
178. Leaphart, A. B., D. K. Thompson, K. Huang, E. Alm, X. F. Wan, A. Arkin, S. D. Brown, **L. Y. Wu**, T. F. Yan, X. D. Liu, G. S. Wickham, and J. Z. Zhou. 2006. Transcriptome profiling of Shewanella oneidensis gene expression following exposure to acidic and alkaline pH. Journal of Bacteriology 188:1633-1642.

179. Gao, W. M., Y. Q. Liu, C. S. Giometti, S. L. Tollaksen, T. Khare, **L. Y. Wu**, D. M. Klingeman, M. W. Fields, and J. Zhou. 2006. Knock-out of SO1377 gene, which encodes the member of a conserved hypothetical bacterial protein family COG2268, results in alteration of iron metabolism, increased spontaneous mutation and hydrogen peroxide sensitivity in Shewanella oneidensis MR-1. Bmc Genomics 7.
180. Gao, H. C., Z. M. K. Yang, **L. Y. Wu**, D. K. Thompson, and J. Z. Zhou. 2006. Global transcriptome analysis of the cold shock response of Shewanella oneidensis MR-1 and mutational analysis of its classical cold shock proteins. Journal of Bacteriology 188:4560-4569.
181. Cho, C. M. H., T. F. Yan, X. D. Liu, **L. Y. Wu**, J. Z. Zhou, and L. Y. Stein. 2006. Transcriptome of a Nitrosomonas europaea mutant with a disrupted nitrite reductase gene (nirK). Applied and Environmental Microbiology 72:4450-4454.
182. Brown, S. D., M. Martin, S. Deshpande, S. Seal, K. Huang, E. Alm, Y. F. Yang, **L. Y. Wu**, T. F. Yan, X. D. Liu, A. Arkin, K. Chourey, J. Z. Zhou, and D. K. Thompson. 2006. Cellular response of Shewanella oneidensis to strontium stress. Applied and Environmental Microbiology 72:890-900.
183. Bagwell, C. E., X. Liu, L. Wu, and J. Zhou. 2006. Effects of legacy nuclear waste on the compositional diversity and distributions of sulfate-reducing bacteria in a terrestrial subsurface aquifer. Fems Microbiology Ecology 55:424-431.
184. Qiu, X. Y., G. W. Sundin, **L. Y. Wu**, J. Z. Zhou, and J. M. Tiedje. 2005. Comparative analysis of differentially expressed genes in Shewanella oneidensis MR-1 following exposure to UVC, UVB, and UVA radiation. Journal of Bacteriology 187:3556-3564.
185. Oda, Y., S. K. Samanta, F. E. Rey, **L. Y. Wu**, X. D. Liu, T. F. Yan, J. Z. Zhou, and C. S. Harwood. 2005. Functional genomic analysis of three nitrogenase isozymes in the photosynthetic bacterium Rhodopseudomonas palustris. Journal of Bacteriology 187:7784-7794.
186. Liu, Y. Q., W. M. Gao, Y. Wang, **L. Y. Wu**, X. D. Liu, T. F. Yan, E. Alm, A. Arkin, D. K. Thompson, M. W. Fields, and J. Z. Zhou. 2005. Transcriptome analysis of Shewanella oneidensis MR-1 in response to elevated salt conditions. Journal of Bacteriology 187:2501-2507.
187. Bencheikh-Latmani, R., S. M. Williams, L. Haucke, C. S. Criddle, **L. Y. Wu**, J. Z. Zhou, and B. M. Tebo. 2005. Global transcriptional profiling of Shewanella oneidensis MR-1 during Cr(VI) and U(VI) reduction. Applied and Environmental Microbiology 71:7453-7460.
188. Beliaev, A. S., D. M. Klingeman, J. A. Klappenbach, L. Wu, M. F. Romine, J. A. Tiedje, K. H. Nealson, J. K. Fredrickson, and J. Zhou. 2005. Global transcriptome analysis of Shewanella oneidensis MR-1 exposed to different terminal electron acceptors. Journal of Bacteriology 187:7138-7145.
189. Zhou, X. C., **L. Y. Wu**, and J. Z. Zhou. 2004. Fabrication of DNA microarrays on nanoengineered polymeric ultrathin film prepared by self-assembly of polyelectrolyte multilayers. Langmuir 20:8877-88
190. Wan, X. F., N. C. VerBerkmoes, L. A. McCue, D. Stanek, H. Connelly, L. J. Hauser, **L. Y. Wu**, X. D. Liu, T. F. Yan, A. Leaphart, R. L. Hettich, J. Z. Zhou, and D. K. Thompson. 2004. Transcriptomic and proteomic characterization of the fur modulon in the metal-reducing bacterium Shewanella oneidensis. Journal of Bacteriology 186:8385-8400.
191. Rhee, S. K., X. D. Liu, **L. Y. Wu**, S. C. Chong, X. F. Wan, and J. Z. Zhou. 2004. Detection of genes involved in biodegradation and biotransformation in microbial communities by using 50-mer oligonucleotide microarrays. Applied and Environmental Microbiology 70:4303-4317.
192. Qiu, X. Y., R. A. Hurt, **L. Y. Wu**, C. H. Chen, J. M. Tiedje, and Z. Zhou. 2004. Detection and quantification of copper-denitrifying bacteria by quantitative competitive PCR. Journal of Microbiological Methods 59:199-210.
193. Gao, H. C., Y. Wang, X. D. Liu, T. F. Yan, **L. Y. Wu**, E. Alm, A. Arkin, D. K. Thompson, and J. Z. Zhou. 2004.
194. Gao, H. C., Y. Wang, X. D. Liu, T. F. Yan, **L. Y. Wu**, E. Alm, A. Arkin, D. K. Thompson, and J. Z. Zhou. 2004. Global transcriptome analysis of the heat shock response of Shewanella oneidensis. Journal of Bacteriology 186:7796-7803.
195. Yan, T. F., M. W. Fields, **L. Y. Wu**, Y. G. Zu, J. M. Tiedje, and J. Z. Zhou. 2003. Molecular diversity and characterization of nitrite reductase gene fragments (nirK and nirS) from nitrate- and uranium-contaminated groundwater. Environmental Microbiology 5:13-24.
196. Liu, Y. Q., J. Z. Zhou, M. V. Omelchenko, A. S. Beliaev, A. Venkateswaran, J. Stair, **L. Y. Wu**, D. K. Thompson, D. Xu, I. B. Rogozin, E. K. Gaidamakova, M. Zhai, K. S. Makarova, E. V. Koonin, and M. J. Daly. 2003. Transcriptome dynamics of Deinococcus radiodurans recovering from ionizing radiation. Proceedings of the National Academy of Sciences of the United States of America 100:4191-4196.

197. Liu, X. D., S. M. Tiquia, G. Holguin, **L. Y. Wu**, S. C. Nold, A. H. Devol, K. Luo, A. V. Palumbo, J. M. Tiedje, and J. Z. Zhou. 2003. Molecular diversity of denitrifying genes in continental margin sediments within the oxygen-deficient zone off the Pacific coast of Mexico. Applied and Environmental Microbiology 69:3549-3560.
198. Liu, X. D., C. E. Bagwell, **L. Y. Wu**, A. H. Devol, and J. H. Zhou. 2003. Molecular diversity of sulfate-reducing bacteria from two different continental margin habitats. Applied and Environmental Microbiology 69:6073-6081.
199. Zhou, J. Z., B. C. Xia, D. S. Treves, **L. Y. Wu**, T. L. Marsh, R. V. O'Neill, A. V. Palumbo, and J. M. Tiedje. 2002. Spatial and resource factors influencing high microbial diversity in soil. Applied and Environmental Microbiology 68:326-334.
200. Xu, D., G. S. Li, **L. Y. Wu**, J. Z. Zhou, and Y. Xu. 2002. PRIMEGENS: robust and efficient design of gene-specific probes for microarray analysis. Bioinformatics 18:1432-1437.
201. Gu, B. H., D. B. Watson, **L. Y. Wu**, D. H. Phillips, D. C. White, and J. Z. Zhou. 2002. Microbiological characteristics in a zero-valent iron reactive barrier. Environmental Monitoring and Assessment 77:293-309.
202. Beliaev, A. S., D. K. Thompson, M. W. Fields, **L. Y. Wu**, D. P. Lies, K. H. Nealson, and J. Z. Zhou. 2002. Microarray transcription profiling of a Shewanella oneidensis etrA mutant. Journal of Bacteriology 184:4612-4616.
203. Qiu, X. Y., **L. Y. Wu**, H. S. Huang, P. E. McDonel, A. V. Palumbo, J. M. Tiedje, and J. Z. Zhou. 2001. Evaluation of PCR-generated chimeras: Mutations, and heteroduplexes with 16S rRNA gene-based cloning. Applied and Environmental Microbiology 67:880-887.
204. Hurt, R. A., X. Y. Qiu, **L. Y. Wu**, Y. Roh, A. V. Palumbo, J. M. Tiedje, and J. H. Zhou. 2001. Simultaneous recovery of RNA and DNA from soils and sediments. Applied and Environmental Microbiology 67:4495-4503.
205. Braker, G., J. Z. Zhou, **L. Y. Wu**, A. H. Devol, and J. M. Tiedje. 2000. Nitrite reductase genes (nirK and nirS) as functional markers to investigate diversity of denitrifying bacteria in Pacific northwest marine sediment communities. Applied and Environmental Microbiology 66:2096-2104.