
Curriculum Vitae – Zhichao Zhou (Chao), *Ph.D.*

NAME Zhou, Zhichao	CURRENT POSITION TITLE Scientist I
ADDRESS 4545 Microbial Sciences Building Department of Bacteriology University of Wisconsin-Madison Madison, WI 53706-1567	CONTACTS Email: zzhou388@wisc.edu zczhou2017@gmail.com Tel: +1-(608) 640-1102

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YY	FIELD OF STUDY
University of Wisconsin–Madison, United States	Postdoctoral Research Associate	12/22	Environmental microbiology and biogeochemistry
The Chinese University of Hong Kong, Hong Kong	Postdoctoral Research Assistant	11/18	Microbial Evolution and Ecology
The University of Hong Kong, Hong Kong	Ph.D.	11/17	Environmental Microbiology and biogeochemistry
Wuhan University, China	B.S.	06/10	General Biology (National Biology Base Class)

A. Positions and Honors

Positions

2023-	Scientist I, Department of Bacteriology, University of Wisconsin–Madison
2018-2022	Postdoctoral Research Associate, Department of Bacteriology, University of Wisconsin–Madison
2017-2018	Postdoctoral Research Assistant, Simon F.S. Li Marine Science Laboratory, School of Life Sciences, The Chinese University of Hong Kong
2012-2017	Student Research Assistant, School of Biological Sciences, The University of Hong Kong
2009-2010	Student Research Assistant, China Center for Type Culture Collection (CCTCC), Wuhan University

Honors

2023	<i>Diversity</i> 2023 Young Investigator Award
2022	First KBR Selected PostDoc Speaker, 2022 Kenneth B. Raper Symposium, University of Wisconsin–Madison
2016	Lorus J. & Margery J. Milne Scholarship, MBL Microbial Diversity Summer Course, Marine Biology Laboratory, Woods Hole, MA
2012	University Postgraduate Fellowship, The University of Hong Kong (one postgraduate student per school per year)
2012	Third prize of Polar Science Excellent Paper (2012, Polar Research Office, State Oceanic Administration)
2007-2010	Excellent Student Financial Aid, American Bodhi Education Foundation
2007-2010	Model Student of Academic Records, The Third Prize, Wuhan University
2009	Morningside Foundation's Scholarship, Kunming Institute of Zoology, Chinese Academy of Science
2009	University-level Outstanding Student, Wuhan University

B. Selected publications

Five representative publications

5. Zhichao Zhou, Patricia Q. Tran, Yang Liu, Kristopher Kieft, Karthik Anantharaman*. METABOLIC: high-throughput profiling of microbial genomes for functional traits, metabolism, biogeochemistry, and community-scale functional networks. *Microbiome* 10(1):33 (2022). DOI: 10.1186/s40168-021-01213-8 (IF=16.837) (Google citation: 79, in Jan 2023)

4. Kristopher Kieft[#], Zhichao Zhou[#], Rika E. Anderson, Alison Buchan, Barbara J. Campbell, Steven J. Hallam, Matthias Hess, Matthew B. Sullivan, David A. Walsh, Simon Roux, Karthik Anantharaman*. Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. *Nature Communications* 12(1):3503 (2021). DOI: 10.1038/s41467-021-23698-5 (IF=17.694) (Editors' Highlights in Earth Science)
 3. Zhichao Zhou, Yang Liu, Jie Pan, Brandi R. Cron, Brandy M. Toner, Karthik Anantharaman, John A. Breier, Gregory J. Dick, Meng Li*. Gammaproteobacteria mediating utilization of methyl-, sulfur- and petroleum organic compounds in deep ocean hydrothermal plumes. *The ISME Journal* 14(12):3136-3148 (2020). DOI: 10.1038/s41396-020-00745-5 (IF=11.217)
 2. Zhichao Zhou, Patricia Q. Tran, Kristopher Kieft, Karthik Anantharaman*. Genome diversification in globally distributed novel marine Proteobacteria is linked to environmental adaptation. *The ISME Journal* 14(8):2060-2077 (2020). DOI: 10.1038/s41396-020-0669-4 (IF=11.217)
 5. Zhichao Zhou, Patricia Q. Tran, Alyssa M. Adams, Kristopher Kieft, John A. Breier, Caroline S. Fortunato, Cody S. Sheik, Julie A. Huber, Meng Li, Gregory J. Dick, Karthik Anantharaman*. Sulfur cycling connects microbiomes and biogeochemistry in deep-sea hydrothermal plumes. *The ISME Journal* 17(8):1194-1207 (2023). DOI: 10.1038/s41396-023-01421-0
- Five other significant products**
5. Zhichao Zhou, Yang Liu, Karen G. Lloyd, Jie Pan, Yuchun Yang, Ji-Dong Gu*, Meng Li*. Genomic and transcriptomic insights into the ecology and metabolism of benthic archaeal cosmopolitan, Thermopfundales (MBG-D archaea). *The ISME Journal* 13(4):885-901 (2019). DOI: 10.1038/s41396-018-0321-8 (IF=11.217)
 4. Jun Feng, Yili Qian, Zhichao Zhou, Sarah Ertmer, Eugenio I. Vivas, Freeman Lan, Joshua J. Hamilton, Federico E. Rey, Karthik Anantharaman and Ophelia S. Venturelli*. Polysaccharide utilization loci in Bacteroides determine population fitness and community-level interactions. *Cell Host & Microbe* 30(2):200-215.e12 (2022). DOI: 10.1016/j.chom.2021.12.006 (IF=31.316)
 3. Kristopher Kieft, Adam M. Breister, Phil Huss, Alexandra M. Linz, Elizabeth Zanetakos, Zhichao Zhou, Janina Rahlff, Sarah P. Esser, Alexander J. Probst, Srivatsan Raman, Simon Roux, Karthik Anantharaman*. Virus-associated organosulfur metabolism in human and environmental systems. *Cell Reports* 36(5):109471 (2021). DOI: 10.1016/j.celrep.2021.109471 (IF=9.995)
 2. Kristopher Kieft, Zhichao Zhou, Karthik Anantharaman*. VIBRANT: automated recovery, annotation and curation of microbial viruses, and evaluation of viral community function from genomic sequences. *Microbiome* 8(1):90 (2020). DOI: 10.1186/s40168-020-00867-0 (Google citation: 261, in Jan 2023) (IF=16.837)
 1. Xiuran Yin[#], Mingwei Cai[#], Yang Liu, Guowei Zhou, Tim Richter-Heitmann, David A. Aromokeye, Ajinkya C. Kulkarni, Rolf Nimzyk, Henrik Cullhed, Zhichao Zhou, Jie Pan, Yuchun Yang, Ji-Dong Gu, Marcus Elvert, Meng Li*, Michael W. Friedrich*. Subgroup level differences of physiological activities in marine Lokiarchaeota. *The ISME Journal* 15(3):848-861 (2021). DOI: 10.1038/s41396-020-00818-5 (IF=11.217)

C. Full Publication list

Google Scholar [publication number: **50**; citations: **2,574**; H-index: **25** Oct 2023 updated]:
https://scholar.google.com/citations?hl=en&user=9e0nrQIAAAAJ&view_op=list_works&sortby=pubdate
 ORCID: <https://orcid.org/0000-0002-9120-6762>
 Personal website: <https://zczhou2017.wixsite.com/mysite>
 Research Gate: <https://www.researchgate.net/profile/Zhichao-Zhou-3>

bioRxiv and proposed publications:

Zhichao Zhou[#], Patricia Tran[#], Elise S. Cowley, Elizabeth Trembath-Reichert, Karthik Anantharaman. Diversity and ecology of microbial sulfur metabolism (invited review to *Nature Reviews Microbiology*) *equal contribution

Zhichao Zhou et al. Longterm time-series study unravels seasonally and yearly viral-host association and ecogenomics of lake virus (draft finished, initially aiming to *Nature Microbiology*)

Zhichao Zhou et al. High-throughput sequencing for applications in petroleum reservoirs for enhanced oil recovery: methods, advances and future directions (in submission to *Critical Reviews in Biotechnology*)

Yang Liu, Zhichao Zhou, Yuchun Yang, Ji-Dong Gu, Meng Li. Genome-scale co-occurrence and co-transcription networks reveal key microbial taxa in mangrove sediments (in preparation)

Freeman Lan*, Jason Saba, Tyler D Ross, [Zhichao Zhou](#), Katie Krauska, Karthik Anantharaman, Robert Landick, and Ophelia Venturelli*. Massively parallel single-cell sequencing in diverse microbial populations (in submission to **Nature Methods**)

First author publications:

22. [Zhichao Zhou](#), Patricia Q Tran, Alyssa M Adams, Kristopher Kieft, John A Breier, Caroline S Fortunato, Cody S Sheik, Julie A Huber, Meng Li, Gregory J Dick, Karthik Anantharaman*. Sulfur cycling connects microbiomes and biogeochemistry in deep-sea hydrothermal plumes. **The ISME Journal** 17(8):1194-1207 (2023). DOI: 10.1038/s41396-023-01421-0

21. [Zhichao Zhou](#), Cody Martin, James C Kosmopoulos, Karthik Anantharaman*. ViWrap: A modular pipeline to identify, bin, classify, and predict viral–host relationships for viruses from metagenomes. **iMeta** e118 (2023). DOI: 10.1002/imt2.118 (IF=N/A; new journal)

20. [Zhichao Zhou](#)[#], Yang Liu[#], Karthik Anantharaman, Meng Li*. The expanding Asgard archaea invoke novel insights into Tree of Life and eukaryogenesis. **mLife** 1:374-381 (2022). DOI: 10.1002/mlf2.12048 (IF=N/A; new journal)

19. [Zhichao Zhou](#)[#], Emily St. John[#], Karthik Anantharaman*, Anna-Louise Reysenbach*. Global patterns of diversity and metabolism of microbial communities in deep-sea hydrothermal vent deposits. **Microbiome** 10(1):241 (2022). DOI: 10.1186/s40168-022-01424-7 (IF=16.837)

18. [Zhichao Zhou](#), Han Meng, Wenjie Gu, Jing Li, Maocheng Deng, Ji-Dong Gu*. High-throughput sequencing reveals the main drivers of niche-differentiation of bacterial community in the surface sediments of the northern South China sea. **Marine Environmental Research** 178:105641 (2022). DOI: 10.1016/j.marenvres.2022.105641 (IF=3.737)

17. [Zhichao Zhou](#), Patricia Q. Tran, Yang Liu, Kristopher Kieft, Karthik Anantharaman*. METABOLIC: high-throughput profiling of microbial genomes for functional traits, metabolism, biogeochemistry, and community-scale functional networks. **Microbiome** 10(1):33 (2022). DOI: 10.1186/s40168-021-01213-8 (IF=16.837) (Google citation: 85, in Mar 2023)

16. Kristopher Kieft[#], [Zhichao Zhou](#)[#], Rika E. Anderson, Alison Buchan, Barbara J. Campbell, Steven J. Hallam, Matthias Hess, Matthew B. Sullivan, David A. Walsh, Simon Roux, Karthik Anantharaman*. Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. **Nature Communications** 12(1):3503 (2021). DOI: 10.1038/s41467-021-23698-5 (IF=17.694) (Editors' Highlights in Earth Science)

15. [Zhichao Zhou](#), Yang Liu, Jie Pan, Brandi R. Cron, Brandy M. Toner, Karthik Anantharaman, John A. Breier, Gregory J. Dick, Meng Li*. Gammaproteobacteria mediating utilization of methyl-, sulfur-and petroleum organic compounds in deep ocean hydrothermal plumes. **The ISME Journal** 14(12):3136-3148 (2020). DOI: 10.1038/s41396-020-00745-5 (IF=11.217)

14. [Zhichao Zhou](#), Patricia Q. Tran, Kristopher Kieft, Karthik Anantharaman*. Genome diversification in globally distributed novel marine Proteobacteria is linked to environmental adaptation. **The ISME Journal** 14(8):2060-2077 (2020). DOI: 10.1038/s41396-020-0669-4 (IF=11.217)

13. [Zhichao Zhou](#), Jing Chen, Wenjie Gu, Ji-Dong Gu*. Biogeographic pattern of the *nirS* gene-targeted anammox bacterial community and composition in the northern South China Sea and a coastal Mai Po mangrove wetland. **Applied Microbiology and Biotechnology** 104(7):3167-3181 (2020). DOI: 10.1007/s00253-020-10415-3 (IF=5.560)

12. [Zhichao Zhou](#), Yang Liu, Wei Xu, Jie Pan, Zhu-Hua Luo*, Meng Li*. Genome and community-level interaction insights on wide carbon utilizing and element cycling function of Hydrothermarchaeota from hydrothermal sediment. **mSystems** 5(1):e00795-19 (2020). DOI: 10.1128/mSystems.00795-19 (*mSystems*[®] Top Cited Collection; Editor-selected, highly cited articles; 5 papers in the last 2 years in Nov 2021) (IF=7.324)

11. [Zhichao Zhou](#), Bo Liang, Li-Ying Wang, Jin-Feng Liu, Bo-Zhong Mu*, Hojae Shim, Ji-Dong Gu*. Identifying the core bacterial microbiome of hydrocarbon degradation and a shift of dominant methanogenesis pathways in the oil and aqueous phases of petroleum reservoirs of different temperatures from China. **Biogeosciences** 16:4229-4241 (2019). DOI: 10.5194/bg-16-4229-2019 (IF=5.092)

10. [Zhichao Zhou](#), Yang Liu, Karen G. Lloyd, Jie Pan, Yuchun Yang, Ji-Dong Gu*, Meng Li*. Genomic and transcriptomic insights into the ecology and metabolism of benthic archaeal cosmopolitan, Thermoprofundales (MBG-D archaea). **The ISME Journal** 13(4):885-901 (2019). DOI: 10.1038/s41396-018-0321-8 (IF=11.217)

9. [Zhichao Zhou](#), Guo-Xia Zhang, Yan-Bin Xu, Ji-Dong Gu*. Successive transitory distribution of Thaumarchaeota and partitioned distribution of Bathyarchaeota from the Pearl River estuary to the northern South China Sea. **Applied Microbiology and Biotechnology** 102:8035-8048 (2018). DOI: 10.1007/s00253-018-9147-6 (IF=5.560)

8. Zhichao Zhou[#], Qiaoyan Wei[#], Yuchun Yang, Meng Li*, Ji-Dong Gu*. Practical applications of PCR primers in detection of anammox bacteria effectively from different types of samples. ***Applied Microbiology and Biotechnology*** 102:5859-5871 (2018). DOI: 10.1007/s00253-018-9078-2 (IF=5.560)
 7. Zhichao Zhou, Jie Pan, Fengping Wang, Ji-Dong Gu, Meng Li*. Bathyarchaeota: globally distributed metabolic generalists in anoxic environments. ***FEMS Microbiology Reviews*** 42(5):639-655 (2018). DOI: 10.1093/femsre/fuy023 (IF=15.177)
 6. Zhichao Zhou[#], Yang Liu[#], Meng Li*, Ji-Dong Gu. Two or three domains: a new view of tree of life in the genomics era. ***Applied Microbiology and Biotechnology*** 102(7):3049-3058 (2018). DOI: 10.1007/s00253-018-8831-x (IF=5.560)
 5. Zhichao Zhou, Han Meng, Yang Liu, Ji-Dong Gu*, Meng Li*. Stratified Bacterial and Archaeal Community in Mangrove and Intertidal Wetland Mudflats Revealed by High Throughput 16S rRNA Gene Sequencing. ***Frontiers in Microbiology*** 8:2148 (2017). DOI: 10.3389/fmicb.2017.02148 (IF=6.064)
 4. Zhichao Zhou, Jing Chen, Han Meng, Volodymyr Dvornyk, Ji-Dong Gu*. New PCR primers targeting hydrazine synthase and cytochrome c biogenesis proteins in anammox bacteria. ***Applied Microbiology and Biotechnology*** 101(3):1267-1287 (2017). DOI: 10.1007/s00253-016-8013-7 (IF=5.560)
 3. Zhichao Zhou, Jing Chen, Huiluo Cao, Ping Han, Ji-Dong Gu*. Analysis of methane-producing and metabolizing archaeal and bacterial communities in sediments of the northern South China Sea and coastal Mai Po Nature Reserve revealed by PCR amplification of *mcrA* and *pmoA* genes. ***Frontiers in Microbiology*** 5:789 (2015). DOI: 10.3389/fmicb.2014.00789 (IF=6.064)
 2. Zhichao Zhou, Ping Han, Ji-Dong Gu*. New PCR primers based on *mcrA* gene for retrieving more anaerobic methanotrophic archaea from coastal reedbed sediments. ***Applied Microbiology and Biotechnology*** 98(10):4663-70 (2014). DOI: 10.1007/s00253-014-5599-5 (IF=5.560)
 1. Zhichao Zhou, Fan Jiang, Shaohua Wang, Fang Peng*, Jun Dai, Wenxin Li, Chengxiang Fang. *Pedobacter arcticus* sp. nov., a facultative psychrophile isolated from Arctic soil, and emended descriptions of the genus *Pedobacter*, *Pedobacter heparinus*, *Pedobacter daechungensis*, *Pedobacter terricola*, *Pedobacter glucosidilyticus* and *Pedobacter lentus*. ***International Journal of Systematic and Evolutionary Microbiology*** 62:1963-1969 (2012). DOI: 10.1099/ijs.0.031104-0 (IF=2.689)
- 2nd and other author publications:**
28. Dinesh Kumar Kuppa Baskaran[#], Shreyansh Umale[#], Zhichao Zhou, Karthik Raman*, Karthik Anantharaman*. Metagenome-based metabolic modelling predicts unique microbial interactions in deep-sea hydrothermal plume microbiomes. ***ISME communications*** 3(1):42 (2023). DOI: 10.1038/s43705-023-00242-8
 27. Yu-Yu Cheng, Zhichao Zhou, James M. Papadopoulos, Jason D. Zuke, Tanya G. Falbel, Karthik Anantharaman, Briana M. Burton, and Ophelia S. Venturelli. Efficient plasmid transfer via natural competence in a microbial co-culture. ***Molecular Systems Biology*** e11406 (2023). DOI: 10.15252/msb.202211406 (IF=12.74)
 26. Jing Chen, Zhichao Zhou, Ji-Dong Gu*. Seasonal variations of n-damo bacterial community in the subtropical Mai Po mangrove wetland of Hong Kong. ***International Biodeterioration & Biodegradation*** 175:105503 (2022). DOI: 10.1016/j.ibiod.2022.105503 (IF=4.32)
 25. Jing Chen, Zhichao Zhou, Ji-Dong Gu*. Distribution pattern of N-damo bacteria along an anthropogenic nitrogen input gradient from the coastal mangrove wetland to the South China sea sediments. ***Marine Environmental Research*** 181:105739 (2022). DOI: 10.1016/j.marenvres.2022.105739 (IF=3.74)
 24. Jie Pan[#], Wei Xu[#], Zhichao Zhou, Zongze Shao, Chunming Dong, Lirui Liu, Zhunhua Luo*, Meng Li*. Genome-resolved evidence for functionally redundant communities and novel nitrogen fixers in the deyin-1 hydrothermal field, Mid-Atlantic Ridge. ***Microbiome*** 10(1):8 (2022). DOI: 10.1186/s40168-021-01202-x (IF=16.837)
 23. Jun Feng, Yili Qian, Zhichao Zhou, Sarah Ertmer, Eugenio I. Vivas, Freeman Lan, Joshua J. Hamilton, Federico E. Rey, Karthik Anantharaman and Ophelia S. Venturelli*. Polysaccharide utilization loci in *Bacteroides* determine population fitness and community-level interactions. ***Cell Host & Microbe*** 30(2):200-215.e12 (2022). DOI: 10.1016/j.chom.2021.12.006 (IF=31.316)
 22. Kristopher Kieft, Adam M. Breister, Phil Huss, Alexandra M. Linz, Elizabeth Zanetakos, Zhichao Zhou, Janina Rahlff, Sarah P. Esser, Alexander J. Probst, Srivatsan Raman, Simon Roux, Karthik Anantharaman*. Virus-associated organosulfur metabolism in human and environmental systems. ***Cell Reports*** 36(5):109471 (2021). DOI: 10.1016/j.celrep.2021.109471 (IF=9.995)

21. Lin Xu, Bingjian Zhu, Chaonan Li, [Zhichao Zhou](#), Minjie Yao, Xiaobing Zhou, Junming Wang, Bingchang Zhang*, Xiangzhen Li*. Increasing relative abundance of non-cyanobacterial photosynthetic organisms drives ecosystem multifunctionality during the succession of biological soil crusts. **Geoderma** 395:115052 (2021). DOI: 10.1016/j.geoderma.2021.115052 (IF=7.422)
20. Adam M. Breister[#], Muhammad A. Imam[#], [Zhichao Zhou](#), Md Ariful Ahsan, Juan C. Noveron, Karthik Anantharaman*, Pavana Prabhakar*. Soil microbiomes mediate degradation of vinyl ester-based polymer composites. **Communications Materials** 1:101 (2020). DOI: 10.1038/s43246-020-00102-1 (IF=N/A; new journal)
19. Xiuran Yin[#], Mingwei Cai[#], Yang Liu, Guowei Zhou, Tim Richter-Heitmann, David A. Aromokeye, Ajinkya C. Kulkarni, Rolf Nimzyk, Henrik Cullhed, [Zhichao Zhou](#), Jie Pan, Yuchun Yang, Ji-Dong Gu, Marcus Elvert, Meng Li*, Michael W. Friedrich*. Subgroup level differences of physiological activities in marine Lokiarchaeota. **The ISME Journal** 15(3):848-861 (2021). DOI: 10.1038/s41396-020-00818-5 (IF=11.217)
18. Meng Han*, Xiaowei Zhang, [Zhichao Zhou](#), Ling Luo, Wensheng Lan, Jih-Gaw Lin, Xiao-Yan Li, and Ji-Dong Gu*. Simultaneous occurrence and analysis of both anammox and n-damo bacteria in five full-scale wastewater treatment plants. **International Biodeterioration & Biodegradation** 156:105112 (2020). DOI: 10.1016/j.ibiod.2020.105112 (IF=4.907)
17. Kristopher Kieft, [Zhichao Zhou](#), Karthik Anantharaman*. VIBRANT: automated recovery, annotation and curation of microbial viruses, and evaluation of viral community function from genomic sequences. **Microbiome** 8(1):90 (2020). DOI: 10.1186/s40168-020-00867-0 (Google citation: 301, in Mar 2023) (IF=16.837)
16. Jie Pan, [Zhichao Zhou](#), Oded Béjà, Mingwei Cai, Yuchun Yang, Yang Liu, Ji-Dong Gu, Meng Li*. Genomic and transcriptomic evidence of light-sensing, porphyrin biosynthesis, Calvin-Benson-Bassham cycle, and urea production in Bathyarchaeota. **Microbiome** 8(1):43 (2020). DOI: 10.1186/s40168-020-00820-1 (IF=16.837)
15. Mingwei Cai[#], Yang Liu[#], Xiuran Yin, [Zhichao Zhou](#), Michael W. Friedrich, Tim Richter-Heitmann, Rolf Nimzyk, Ajinkya Kulkarni, Xiaowen Wang, Wenjin Li, Jie Pan, Yuchun Yang, Ji-Dong Gu, Meng Li*. Diverse Asgard archaea including the novel phylum Gerdarchaeota participate in organic matter degradation. **Science China Life Sciences** 63(6):886-897 (2020). DOI: 10.1007/s11427-020-1679-1 (IF=10.372)
14. Yongming Wang, Jie Pan, Jun Yang, [Zhichao Zhou](#), Yueping Pan, Meng Li*. Patterns and processes of free-living and particle-associated bacterioplankton and archaeaplankton communities in a subtropical river-bay system in South China. **Limnology and Oceanography** 65:S161-S179 (2020). DOI: 10.1002/lno.11314 (IF=5.019)
13. Yuchun Yang, Jie Pan, [Zhichao Zhou](#), Jiapeng Wu, Yang Liu, Jih-Gaw Lin, Yiguo Hong, Xiaoyan Li, Meng Li*, Ji-Dong Gu*. Complex microbial nitrogen-cycling networks in three distinct anammox-inoculated wastewater treatment systems. **Water Research** 168:115142 (2020). DOI: 10.1016/j.watres.2019.115142 (IF=13.400)
12. Lei Zhou, [Zhichao Zhou](#), Yu-Wei Lu, Lei Ma, Yang Bai, Xiao-Xiao Li, Serge Maurice Mbadinga, Yi-Fan Liu, Xin-Chen Yao, Yi-Jie Qiao, Zi-Rui Zhang, Jin-Feng Liu, Shi-Zhong Yang, Wei-Dong Wang, Ji-Dong Gu, Bo-Zhong Mu*. The newly proposed TACK and DPANN archaea detected in the production waters from a high-temperature petroleum reservoir. **International Biodeterioration & Biodegradation** 143:104729 (2019). DOI: 10.1016/j.ibiod.2019.104729 (IF=4.907)
11. Qian-Qian Hu, [Zhi-Chao Zhou](#), Yi-Fan Liu, Lei Zhou, Serge Maurice Mbadinga, Jin-Feng Liu, Shi-Zhong Yang, Ji-Dong Gu, Bo-Zhong Mu*. High microbial diversity of the nitric oxide dismutation reaction revealed by PCR amplification and analysis of the *nod* gene. **International Biodeterioration & Biodegradation** 143:104708 (2019). DOI: 10.1016/j.ibiod.2019.05.025 (IF=4.907)
10. Jin-Feng Liu, Kai Zhang, Bo Liang, [Zhi-Chao Zhou](#), Shi-Zhong Yang, Wei Li, Zhao-Wei Hou, Xiao-Lin Wu*, Ji-Dong Gu, Bo-Zhong Mu*. Key players in the methanogenic biodegradation of *n*-hexadecane identified by DNA-Stable isotope probing. **International Biodeterioration & Biodegradation** 143:104709 (2019). DOI: 10.1016/j.ibiod.2019.05.026 (IF=4.907)
9. Han Meng, [Zhichao Zhou](#), Ruonan Wu, Yongfeng Wang, Ji-Dong Gu*. Diazotrophic microbial community and abundance in acidic subtropical natural and re-vegetated forest soils revealed by high-throughput sequencing of *nifH* gene. **Applied Microbiology and Biotechnology** 103(2):995-1005 (2019). DOI: 10.1007/s00253-018-9466-7 (IF=5.560)
8. Jie Pan, Yulian Chen, Yongming Wang, [Zhichao Zhou](#), Meng Li*. Vertical Distribution of Bathyarchaeotal Communities in Mangrove Wetlands Suggests Distinct Lifestyle of Bathyarchaeota Subgroup-6. **Microbial Ecology** 77(2):417-428 (2019). DOI: 10.1007/s00248-018-1309-7 (IF=4.192)
7. Yang Liu, [Zhichao Zhou](#), Jie Pan, Brett J. Baker, Ji-Dong Gu, Meng Li*. Comparative genomic inference reveals mixotrophic lifestyle of Thorarchaeota. **The ISME Journal** 12(4):1021-1031 (2018). DOI: 10.1038/s41396-018-0060-x (IF=11.217)

6. Xiaobo Liu, Meng Li*, Cindy J. Castelle, Alexander J. Probst, Zhichao Zhou, Jie Pan, Yang Liu, Jillian F. Banfield, Ji-Dong Gu*. Insights into the ecology, evolution, and metabolism of the widespread Woese archaeal lineages. *Microbiome* 6(1):102 (2018). DOI: 10.1186/s40168-018-0488-2 (IF=16.837)
5. Bo Liang, Li-Ying Wang, Zhichao Zhou, Serge M. Mbadinga, Lei Zhou, Jin-Feng Liu, Shi-Zhong Yang, Ji-Dong Gu, Bo-Zhong Mu*. High frequency of *Thermodesulfovibrio* spp. and Anaerolineaceae in association with *Methanoculleus* spp. in a long-term incubation of *n*-alkanes-degrading methanogenic enrichment culture. *Frontiers in Microbiology* 7:1431 (2016). DOI: 10.3389/fmicb.2016.01431 (IF=6.064)
4. Ling Luo, Zhi-Chao Zhou, Ji-Dong Gu*. Distribution, diversity and abundance of bacterial laccase-like genes in different particle size fractions of sediments in a subtropical mangrove ecosystem. *Ecotoxicology* 24:1508-1516 (2015). DOI: 10.1007/s10646-015-1452-6 (IF=2.935)
3. Jing Chen, Zhichao Zhou, Ji-Dong Gu*. Complex community of nitrite-dependent anaerobic methane oxidation bacteria in coastal sediments of the Mai Po wetland by PCR amplification of both 16S rRNA and *pmoA* genes. *Applied Microbiology and Biotechnology* 99:1463-1473 (2015). DOI: 10.1007/s00253-014-6051-6 (IF=5.560)
2. Jing Chen, Zhi-Chao Zhou, Ji-Dong Gu*. Occurrence and diversity of nitrite-dependent anaerobic methane oxidation bacteria in the sediments of the South China Sea revealed by amplification of both 16S rRNA and *pmoA* genes. *Applied Microbiology and Biotechnology* 98:5685-5696 (2014). DOI: 10.1007/s00253-014-5733-4 (IF=5.560)
1. Wei Su, Zhichao Zhou, Fan Jiang, XuLu Chang, Ying Liu, Shaohua Wang, Wenjing Kan, Mengchen Xiao, Ming Shao, Fang Peng*, Chengxiang Fang. *Iodobacter limnosediminis* sp nov., isolated from Arctic lake sediment. *International Journal of Systematic and Evolutionary Microbiology* 63:1464-1470 (2013). DOI: 10.1099/ijs.0.039982-0 (IF=2.689)

D. Synergistic activities

Teaching and mentoring:

- 2016 SCNC1112 Fundamentals of Modern Science as demonstrator (UK university-style TA)
- 2016 BIOL2103 Biological Sciences Laboratory course as demonstrator
- 2015 BIOL2614/3110 Environmental Toxicology as demonstrator
- 2015 BIOL3317/4402 Microbial Biotechnology as demonstrator
- 2014 Course BIOL2606 Environmental Microbiology as demonstrator
- 2013, 2017, 2018 Local guide for professor and student visiting delegates from "Hong Yi" preeminent class, College of Life Sciences, Wuhan University to Hong Kong Universities
- 2013 Course BIOL2119 Genetics as demonstrator
- 2013, 2014 Course BIOL0135/BIOL1111 Introductory microbiology HKU+SPACE as demonstrator
- 2012, 2013 Course BIOL6001 Presentation Skills and Research Seminars in Biological Sciences, Ecology & Biodiversity Module as demonstrator
- 2012-2022 Mentor of 10+ undergraduate, graduate students, and visiting scholars in research labs

Teaching qualification:

- 2013 Certificate of teaching and learning in higher education (qualified as the excellent level), by Centre for the Enhancement of Teaching and Learning, HKU, Hong Kong, Dec 2013

Sample experience:

- 2012-2017 Mangrove sediment and water sampling trips, multiple times, in Mai Po coastal wetland (a Ramsar site under Ramsar Convention, managed by WWF Hong Kong Branch), Hong Kong, China
- 2017-2018 Mangrove root rhizospheric soil sampling trips, multiple times, at the eastern and western coasts of New Territory, Hong Kong, China
- 2017-2018 Root nodule sampling trips for culturing and studying Rhizobia bacterium, multiple times, in the CUHK campus and at the eastern and western coasts of New Territory, Hong Kong, China
- 2016-2017 Seawater and coastal mangrove sediment sampling trips, multiple times, in the Deep Bay and Futian Mangrove Nature Reserve, Shenzhen, China
- 2016-2017 Saline and freshwater sampling trips, two times, along the Dasha River (Dashahe), Shenzhen, China

Academic membership:

International Society for Microbial Ecology, American Society for Microbiology

Review activity:

Associate Editor: *Frontiers in Microbiology*
 Review Editor: *Frontiers in Microbiomes*

Journal reviews: Nature Communications, Microbiome, The ISME Journal, Water Research, Environmental Microbiology, Frontiers in Bioinformatics, Microbial Ecology, International Biodeterioration & Biodegradation, Ecotoxicology, Heliyon, Applied Environmental Biotechnology, BMC Bioinformatics

E. Social activities

2020-	Committee member of Wuhan University Alumni Association in Wisconsin
2019-2020	The Chairperson of Wuhan University Alumni Association in Wisconsin
2012-2018	The coordinator for Wuhan University Alumni in Hong Kong (Biology & Medicine)

F. Projects

2021	Maximizing Investigators' Research Award (MIRA) for Early Stage Investigators (R35, NIH) (US) (up to \$250,000 direct cost per year with the maximum period of five years) Computational frameworks for phage discovery, ecology, and dynamics from metagenomes Anantharaman, Karthik; My role: participant
2021	NSF CAREER award (US) Scalable approaches for systems virology Anantharaman, Karthik; My role: participant
2021	NSF Collaborative research project (US) Regulation and dynamics of microbial communities and biogeochemical cycling in hydrothermally-influenced habitats in the Gulf of California PI: Anantharaman, Karthik; My role: participant
2020	DOE-JGI Community Science Program Sequencing Grant Microbial and viral mediation of biogeochemical cycles from source to sink in hydrothermal vent systems PI: Anantharaman, Karthik; My role: participant
2019	DOE-JGI Community Science Program Sequencing Grant (US) Extended temporal dynamics of microbially-mediated freshwater carbon processing as revealed through time-series metagenomes Anantharaman, Karthik; My role: participant
2018	Wisconsin Alumni Research Foundation Grant Microbial controls on sulfur-methane dynamics PI: Anantharaman, Karthik; My role: participant
2018	Basic research project of Shenzhen Science and Technology Innovation Committee (China) Carbon metabolism diversity and molecular biological mechanism of Bathyarchaeota in mangrove wetland PI: Li, Meng; My role: participant
2017	NSFC Outstanding youth science project (China) Microbial ecology of Archaea PI: Li, Meng; My role: participant
2016	NSFC Youth Fund Project (China) Temporal and spatial variation of diversity and abundance of MCG Archaea in mangrove wetland ecosystem and its environmental effects PI: Li, Meng; My role: participant
2014	Basic research project of Shenzhen Science and Technology Innovation Committee (China) Population structure, function and ecological effect of MCG Archaea in coastal mangrove wetland PI: Li, Meng; My role: participant
2013	General Research Fund (Hong Kong) Phylogenetic Diversity and Contribution of Anaerobic Ammonium Oxidation (Anammox) Bacteria to Nitrogen Removal in Mangrove Wetland Ecosystem PI: Gu, Ji-Dong; My role: participant
2011	NSFC/RGC Joint Research Scheme (Mainland China and Hong Kong) Biological Methanogenesis of Alkanes: Thermodynamics and Microbial Ecology

PI: Gu, Ji-Dong & Mu Bo-Zhong; My role: participant

- 2011 Environment and Conservation Fund (Hong Kong)
Anaerobic ammonium oxidizing bacteria as bio-indicator for the anthropogenic pollution and its history
PI: Gu, Ji-Dong; My role: participant

G. Bioinformatics Tools

Main developer of:

- **METABOLIC**: A scalable high-throughput metabolic and biogeochemical functional trait profiler (written in Perl and R)
GitHub profile: <https://github.com/AnantharamanLab/METABOLIC>
- **ViWrap**: A wrapper to identify, bin, classify, and predict host-viral relationship for viruses from Metagenomes (written in Python)
GitHub profile: <https://github.com/AnantharamanLab/ViWrap>

Contributed to:

- **VIBRANT**: a tool for automated recovery, annotation and curation of microbial viruses, and evaluation of viral community function from genomic sequences (written in Python)
GitHub profile: <https://github.com/AnantharamanLab/VIBRANT>

H. Presentations

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| Oct 12, 2023 | (Invited talk) Zhichao Zhou and Jiarong Guo, Best practices on AMG curation, The 6th international viromics workshop at The Ohio State University. Columbus, OH |
| Sep 6, 2022 | (Oral presentation) New Tools for Studying Prokaryotes and Phages Based on Metagenomes (First KBR Selected PostDoc Speaker). 2022 Kenneth B. Raper Symposium, University of Wisconsin - Madison, Madison, WI |
| Jun 8-12, 2022 | (Poster) Zhichao Zhou, Kristopher Kieft, Patricia Q. Tran, Alyssa M. Adams, John A. Breier, Rupesh K. Sinha, Kottekkatu P. Krishnan, P. John Kurian, Julie A. Huber, Gregory J. Dick, Meng Li, Karthik Anantharaman. Sulfur cycle connects microbiomes, viruses, and biogeochemistry in deep-sea hydrothermal plumes. ASM Microbe 2022, Washington D.C. |
| May 1-6, 2022 | (Poster) Kristopher Kieft, Zhichao Zhou, Adam Breister, and Karthik Anantharaman. Widespread viral control of sulfur biogeochemistry and host metabolism. 2022 Gordon Research Conference - Ocean Biogeochemistry - Biogeochemical Processes Across Space and Time, Castelldefels, Spain. |
| May 3, 2022 | (Poster) Zhichao Zhou, Patricia Q. Tran, and Karthik Anantharaman. METABOLIC - A scalable high-throughput metabolic and biogeochemical functional trait profiler. 2022 Spring Center for Ecology and Environment Symposium, University of Wisconsin-Madison, Madison, WI |
| Apr 22, 2022 | (Invited talk) Karthik Anantharaman, Zhichao Zhou, and Patricia Tran. METABOLIC Bioinformatics Tool. Biotech bioinformatics tools and applications workshop invited presentation (virtual) by AA-BIOTECMAR (All-Atlantic Marine Biotechnology Initiative) |
| Feb 4, 2022 | (Invited talk) Karthik Anantharaman, Zhichao Zhou, and Patricia Tran. METABOLIC Bioinformatics Tool. 2022 C-DEBI Virtual Meeting Series invited presentation |
| Dec 1-17, 2020 | (Oral presentation) Karthik Anantharaman, Kristopher Kieft, Adam Breister, Zhichao Zhou, Philip Huss, Srivatsan Raman. Viral conversations with sulfur: Metabolic and biogeochemical implications of phage infections. 2020 AGU Fall Meeting (virtual) |

Sep 1, 2020	(Invited talk) Microbial diversity and metagenomics. The 221th Lubo Forum (virtual), College of Resources & Environment at Huazhong Agricultural University, Wuhan, China
Sep 1, 2020	(Poster and audio) METABOLIC: A scalable high-throughput metabolic and biogeochemical functional trait profiler based on microbial genomes. The 34th Annual Kenneth B. Raper Symposium (virtual), The University of Wisconsin-Madison, Madison, WI
Jan 24, 2020	(Oral presentation) Kristopher Kieft, Zhichao Zhou and Karthik Anantharaman. Using machine learning to automate the discovery of microbial viruses from sequencing data. (Poster) Zhichao Zhou, Patricia Q. Tran, Kristopher Kieft and Karthik Anantharaman. METABOLIC: A scalable high-throughput metabolic and biogeochemical functional trait profiler based on microbial genomes. 2020 UW-Madison Research Bazaar, The University of Wisconsin-Madison, Madison, WI
Jun 20-24, 2019	(Poster) Genomic and transcriptomic insights into the ecology and metabolism of benthic archaeal cosmopolitan, Thermopfundales (MBG-D archaea). ASM Microbe 2019, San Francisco
Jun 8-11, 2018	(Oral presentation) Two or three domains: a new view of tree of life in the genomics era (co-first contributor). The 7th National Geomicrobiology Conference, Shanghai Jiao Tong University, Shanghai, China
Nov 6-10, 2017	(Poster) Successive transition of thaumarchaeotal community and partitioned distribution of bathyarchaeotal community from Pearl River estuary to northern South China Sea. 2017 Conference of International Society for Subsurface Microbiology, Rotorua, New Zealand
Jul 23-28, 2017	(Poster) Stratified bacterial and archaeal community in mangrove and intertidal wetland mudflats revealed by high throughput 16S rRNA gene sequencing. 2017 Gordon Research Conference - Marine Molecular Ecology, The Hong Kong University of Science and Technology, Hong Kong
Jun 10-12, 2017	(Poster) Core Bacterial Microbiome of Hydrocarbon Degradation from Petroleum Reservoirs with Different Temperatures Across China. The 6th National Geomicrobiology Conference, Sun Yat-Sen University, Guangzhou, China
Aug 21-26, 2016	(Poster) Core Bacterial Microbiome of Hydrocarbon Degradation from Petroleum Reservoirs with Different Temperatures Across China. The 16th International Symposium on Microbial Ecology (ISME16), Montreal, Canada
Jun 28-Jul 1, 2015	(Poster) PCR amplification based community analysis of methane-producing and metabolizing archaea and bacteria in sediments of northern South China Sea and coastal Mai Po Nature Reserve. The 4th International Conference on Nitrification (and Related Processes), University of Alberta, Edmonton, Canada
Aug 24-29, 2014	(Poster) Comparison of Communities of both Methane-producing and Metabolizing Archaea and Bacteria in Sediments between the Northern South China Sea and Coastal Mai Po Nature Reserve Revealed by PCR Amplification of <i>mcrA</i> and <i>pmoA</i> Genes. The 15th International Symposium on Microbial Ecology (ISME15), Seoul, South Korea
Aug 11-16, 2013	(Poster) Codehop based primers retrieving more <i>mcrA</i> gene copies from ANME archaea. 2013 Gordon Research Conference - Marine Molecular Ecology, The Hong Kong University of Science and Technology, Hong Kong

I. Other academic activities

Jul 9, 2021	2021 Center for Dark Energy Biosphere Investigations (C-DEBI) C-DEBI Virtual Series - Isolating DNA from Tough Samples	Workshop & Meeting
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May 4 and 6, 2021	Machine Learning for Biology Workshop 2021 (virtual, organized by Anthony Gitter, MMI, UW-Madison), The University of Wisconsin-Madison, Madison, WI	Workshop & Meeting
Nov 25-26, 2017	The 2nd Shenzhen Forum on Ocean Sciences for Young Scholars, Southern University of Science and Technology, Shenzhen, China	Workshop & Meeting
Oct 14, 2017	2017 State Key Laboratory of Agrobiotechnology (SKL)-Institute of Plant Molecular Biology and Agricultural Biotechnology (IPMBAB) series meeting, The Chinese University of Hong Kong, Hong Kong	Workshop & Meeting
Jun 14, 2017	WUN Symposium cum Research Summit 2017: Impacts of Grain Legume Research and Development in Developing Countries, The Chinese University of Hong Kong, Hong Kong	Workshop & Meeting
Jun 13, 2017	The 2nd Interdisciplinary forum: Wisdom Gathered in Ocean: Exploring, Developing and Conserving", Shenzhen University, Shenzhen, China	Workshop & Meeting
Dec 07, 2016	"Big Data Workshop" hold by Faculty of Science, The University of Hong Kong, Hong Kong	Workshop & Meeting
May 27-31, 2015	2015 Next Generation Sequencing Data Analysis Workshop, School of Biological Sciences, The University of Hong Kong, Hong Kong	Workshop & Meeting
Sep 1-Nov 1, 2016	Conduct archaeal microbiome research in Meng Li's Lab, Institute for advanced study, Shenzhen University, Shenzhen, China	Extended research
Nov 25, 2014-Feb 11, 2015	Conduct petroleum and mangrove wetland microbiome research based on 16S high-throughput amplicon sequencing in Xiangzhen Li's Lab, Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, China	Extended research
Oct 18-28, 2013	Conduct petroleum microbiome research based on 16S high-throughput amplicon sequencing in Bo-Zhong Mu's Lab, Engineering Research Center for MEOR, MOE, East China University of Science and Technology, Shanghai, China	Extended research
Jul-Aug, 2016	Conduct the miniproject "Investigating on microbial community of Trunk River shore sediment core profile by CARD-FISH and qPCR" in MBL Microbial Diversity summer course 2016. Director: Jared Leadbetter and Dianne Newman	Summer course
Sep 20-29, 2009	The 7th Evolutionary Genomics summer course in Kunming Institute of Zoology, Chinese Academy of Science, Kunming, China supported by Morningside Foundation. Director: Wen Wang, Chip Aquadro, and Andrew Clark	Summer course
Jun 3, 2014	Accomplish online course: An Introduction to Interactive Programming in Python offered by Coursera	Skills
2013, 2014	Accomplish Course BIOL3325_2A Molecular phylogenetics and evolution [2013]	Skills