

DAVID WILKINS

Peer-reviewed publications

- D. Wilkins**, X. Tong, M. H. Y. Leung, C. E. Mason, and P. K. H. Lee. *Diurnal variation in the human skin microbiome affects accuracy of forensic microbiome matching*. Microbiome, 2021, 9(1).
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- D. Wilkins**, M. H. Y. Leung, and P. K. H. Lee. *Indoor air bacterial communities in Hong Kong households assemble independently of occupant skin microbiomes*. Environmental Microbiology, 2015, 18(6):1754-01763.
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- D. Wilkins**, S. Rao, X.-Y. Lu, and P. K. H. Lee. *Effects of sludge inoculum and organic feedstock on active microbial communities and methane yield during anaerobic digestion*. Frontiers in Microbiology, 2015, 6(1114).
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- D. Wilkins**, X.-Y. Lu, Z. Shen, J. Chen, and P. K. H. Lee. *Pyrosequencing of mcrA and archaeal 16S rRNA genes reveals diversity and substrate preference of anaerobic digester methanogen communities*. Applied and Environmental Microbiology, 2015, 81:604-613.
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- D. Wilkins**, E. van Seville, S. R. Rintoul, F. M. Lauro, and R. Cavicchioli. *Advection shapes Southern Ocean microbial assemblages independent of distance and environment effects*. Nature Communications, 2013.
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- D. Wilkins**, S. Yau, T. J. Williams, M. A. Allen, M. V. Brown, M. Z. DeMaere, F. M. Lauro, and R. Cavicchioli. *Key microbial drivers in Antarctic aquatic environments*. FEMS Microbiology Reviews, 2013, 37:303-335.
- Tong X, M. H. Y. Leung, **D. Wilkins**, H. H. L. Cheung, and P. K. H. Lee. *Neutral processes drive seasonal assembly of the skin mycobiome*. mSystems, 2019, 4(2), e00004-e00019.
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- Y. Jia, M. H. Y. Leung, X. Tong, **D. Wilkins**, and P. K. H. Lee. *Rare taxa exhibit disproportionate cell-level metabolic activity in enriched anaerobic digestion microbial communities*. mSystems, 2019, 4(1), e00208-e00218.
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- M. H. Y. Leung, X. Tong, **D. Wilkins**, H. H. L. Cheung, and P. K. H. Lee. *Individual and household attributes influence the dynamics of the personal skin microbiota and its association network*. Microbiome, 2018, 6(1), 26.
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- X. Tong, M. H. Y. Leung, **D. Wilkins**, and P. K. H. Lee. *City-scale distribution and dispersal routes of mycobiome in residences*. Microbiome, 2017, 5(1).
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- Y. Jia, **D. Wilkins**, H. Lu, M. Cai, and P. K. H. Lee. *Long-term enrichment on cellulose or xylan causes functional and taxonomic convergence of microbial communities from anaerobic digesters*. Applied and Environmental Microbiology, 2016, 82:1519-1529.
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T. J. Williams, **D. Wilkins**, E. Long, F. Evans, M. Z. DeMaere, M. J. Raftery, and R. Cavicchioli. *The role of planktonic Flavobacteria in processing algal organic matter in coastal East Antarctica revealed using metagenomics and metaproteomics*. Environmental Microbiology, 2013, 15:1302–1317.

M. V. Brown, F. M. Lauro, M. Z. DeMaere, L. Muir, **D. Wilkins**, T. Thomas, M. J. Riddle, J. A. Fuhrman, C. Andrews-Pfannkoch, J. M. Hoffman, J. B. McQuaid, A. Allen, S. R. Rintoul and R. Cavicchioli. *Global biogeography of SAR11 marine bacteria*. Molecular Systems Biology, 2012, 8:1–13.

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K. S. Siddiqui, T. J. Williams, **D. Wilkins**, S. Yau, M. A. Allen, M. V. Brown, F. M. Lauro, and R. Cavicchioli. *Psychrophiles*. Annual Review of Earth and Planetary Sciences, 2013, 41:87–115.

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*Conference
abstracts*

D. Wilkins, S. Orde, and A. S. Lane. *Adherence to a low tidal volume ventilation strategy in patients admitted to Nepean Hospital ICU with Acute Respiratory Distress Syndrome*. MD Research Symposium, Sydney School of Medicine, University of Sydney, Australia. September 25–26 2019.

D. Wilkins, M. H. Y. Leung, and P. K. H. Lee. *Household surface microbial assemblages are shaped by human-associated groups*. 15th International Symposium on Microbial Ecology, Seoul, Korea. August 24–29 2014.

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