

DAVID WILKINS

Peer-reviewed
publications

D. Wilkins, M. H. Y. Leung, and P. K. H. Lee. *Microbiota fingerprints lose individually identifying features over time*. *Microbiome*, 2017, 5:6477.
doi:10.1186/s40168-016-0209-7

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.
doi:10.1111/1462-2920.12889

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.
doi:10.3389/fmicb.2015.01114

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.
doi:10.1128/AEM.02566-14

D. Wilkins, E. van Sebille, S. R. Rintoul, F. M. Lauro, and R. Cavicchioli. *Advection shapes Southern Ocean microbial assemblages independent of distance and environment effects*. *Nature Communications*, 2013.
doi:10.1038/ncomms3457

D. Wilkins, F. M. Lauro, T. J. Williams, M. Z. DeMere, M. V. Brown, J. M. Hoffman, C. Andrews-Pfannkoch, J. B. McQuaid, M. J. Riddle, S. R. Rintoul, and R. Cavicchioli. *Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics*. *Environmental Microbiology*, 2013, 15:1318–1333.

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.

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.
doi:10.1128/AEM.03360-15.

M. Cai, **D. Wilkins**, J. Chen, S. K. Ng, H. Lu, Y. Jia, P. K. H. Lee. *Metagenomic reconstruction of key anaerobic digestion pathways in municipal sludge and industrial wastewater biogas-producing systems*. *Frontiers in Microbiology*, 2016, 7(e99221):70.
doi:10.3389/fmicb.2016.00778

M. H. Y. Leung, **D. Wilkins**, and P. K. H. Lee. *Insights into the pan-microbiome: skin microbial communities of Chinese individuals differ from other racial groups*. *Scientific Reports*, 2015.
doi:10.1038/srep11845

M. H. Y. Leung, **D. Wilkins**, E. K. T. Li, F. K. F. Kong, and P. K. H. Lee. *Diversity and dynamics of the indoor air microbiome in an urban subway network*. *Applied and Environmental Microbiology*, 2014.
doi:10.1128/AEM.02244-14

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.

F. M. Lauro, M. Z. DeMaere, S. Yau, M. V. Brown, C. Ng, **D. Wilkins**, M. J. Raftery, J. A. E. Gibson, C. Andrews-Pfannkoch, M. Lewis, J. M. Hoffman, T. Thomas, and R. Cavicchioli. *An integrative study of a meromictic lake ecosystem in Antarctica*. *The ISME Journal*, 2010, 5:879–895.

Other
publications

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.

T. J. Williams, **D. Wilkins**, M. Z. DeMaere, F. M. Lauro, and R. Cavicchioli. *Microbes under the microscope*. Australian Antarctic Magazine, June 2011

F. M. Lauro, M. A. Allen, **D. Wilkins**, T. J. Williams and R. Cavicchioli. *Genetics, genomics and evolution of psychrophiles*, in Extremophiles Handbook. Springer Verlag GmbH, Heidelberg, Germany, 2010.

*Conference
abstracts*

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.

D. Wilkins, F. M. Lauro, T. J. Williams, and R. Cavicchioli. *Biogeographic partitioning of Southern Ocean picoplankton*. 14th International Symposium on Microbial Ecology, Copenhagen, Denmark. August 19–24 2012.

M. H. Y. Leung, **D. Wilkins**, and P. K. H. Lee. *Comparison of bacterial microbiomes in Hong Kong urban household aerosols*. 15th International Symposium on Microbial Ecology, Seoul, Korea. August 24–29 2014.

R. Cavicchioli, F. M. Lauro, M. Z. DeMaere, T. J. Williams, M. V. Brown, S. Yau and **D. Wilkins**. *Microbial ecology of Antarctic aquatic ecosystems determined using metagenomics and metaproteomics*. 14th International Symposium on Microbial Ecology, Copenhagen, Denmark. August 19–24 2012.

R. Cavicchioli, F. M. Lauro, M. Z. DeMaere, T. J. Williams, M. V. Brown, S. Yau and **D. Wilkins**. *Extremophiles in Antarctica: insight into adaptation, evolution and ecosystem function of cold aquatic systems using metagenomics and metaproteomics*. 9th International Congress on Extremophiles, Sevilla, Spain. September 10–13 2012.