

# DAVID WILKINS

david@wilcox.org

CURRENT POSITION	<b>City University of Hong Kong</b> , Hong Kong SAR <i>Postdoctoral Fellow, microbial ecology</i> December 2013–present
EDUCATION	<b>University of New South Wales</b> , Sydney, Australia <i>Ph.D, molecular genetics</i> July 2009–November 2013 <ul style="list-style-type: none"><li>• Thesis title: <i>Microbial Ecology and Biogeography of the Southern Ocean.</i></li><li>• Supervisor: Prof. Ricardo Cavicchioli.</li><li>• Cosupervisor: Dr. Federico M. Lauro.</li></ul> <i>B.Sc. (Honours, 1<sup>st</sup> class)</i> March 2005–April 2009 <ul style="list-style-type: none"><li>• Major: Microbiology.</li><li>• Minor: Development studies.</li></ul>
PEER-REVIEWED PUBLICATIONS	<b>D. Wilkins</b> , E. van Seville, S. R. Rintoul, F. M. Lauro, and R. Cavicchioli. <i>Advection shapes Southern Ocean microbial assemblages independent of distance and environment effects.</i> Nature Communications, 2013. DOI: 10.1038/ncomms3457  <b>D. Wilkins</b> , 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. <i>Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics.</i> Environmental Microbiology, 2013, 15:1318–1333.  <b>D. Wilkins</b> , S. Yau, T. J. Williams, M. A. Allen, M. V. Brown, M. Z. DeMaere, F. M. Lauro, and R. Cavicchioli. <i>Key microbial drivers in Antarctic aquatic environments.</i> FEMS Microbiology Reviews, 2013, 37:303–335.  T. J. Williams, <b>D. Wilkins</b> , E. Long, F. Evans, M. Z. DeMaere, M. J. Raftery, and R. Cavicchioli. <i>The role of planktonic Flavobacteria in processing algal organic matter in coastal East Antarctica revealed using metagenomics and metaproteomics.</i> Environmental Microbiology, 2013, 15:1302–1317.  M. V. Brown, F. M. Lauro, M. Z. DeMaere, L. Muir, <b>D. Wilkins</b> , 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. <i>Global biogeography of SAR11 marine bacteria.</i> Molecular Systems Biology, 2012, 8:1–13.  F. M. Lauro, M. Z. DeMaere, S. Yau, M. V. Brown, C. Ng, <b>D. Wilkins</b> , M. J. Raftery, J. A. E. Gibson, C. Andrews-Pfannkoch, M. Lewis, J. M. Hoffman, T. Thomas, and R. Cavicchioli. <i>An integrative study of a meromictic lake ecosystem in Antarctica.</i> The ISME Journal, 2010, 5:879–895.
OTHER PUBLICATIONS	K. S. Siddiqui, T. J. Williams, <b>D. Wilkins</b> , S. Yau, M. A. Allen, M. V. Brown, F. M. Lauro, and R. Cavicchioli. <i>Psychrophiles.</i> Annual Review of Earth and Planetary Sciences, 2013, 41:87–115.  T. J. Williams, <b>D. Wilkins</b> , M. Z. DeMaere, F. Lauro, and R. Cavicchioli. <i>Microbes under the microscope.</i> Australian Antarctic Magazine, June 2011  F. M. Lauro, M. Allen, <b>D. Wilkins</b> , T. J. Williams and R. Cavicchioli. <i>Genetics, genomics and evolution of psychrophiles</i> , in Extremophiles Handbook. Springer Verlag GmbH, Heidelberg, Germany, 2010.
CONFERENCE ABSTRACTS	<b>D. Wilkins</b> , F. M. Lauro, T. J. Williams, R. Cavicchioli. <i>Biogeographic partitioning of Southern Ocean picoplankton.</i> 14 <sup>th</sup> 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**. *Microbial ecology of Antarctic aquatic ecosystems determined using metagenomics and metaproteomics*. 14<sup>th</sup> 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*. 9<sup>th</sup> International Congress on Extremophiles, Sevilla, Spain. September 10–13 2012.

#### TECHNICAL SKILLS

##### *Bioinformatic*

- Programming in a range of languages, but with particular expertise in Perl and R for biological and bioinformatic applications.
- Microbial community analysis using high-throughput sequencing, including both 16S rRNA tag pyrosequencing and shotgun metagenomics.
- Statistical and machine learning techniques to examine microbial community structure and biogeographic distribution.
- Statistical visualisation and graphics, both exploratory and publication quality.
- High-throughput management of large volumes of genetic data and experimental results in Unix-like environments.

##### *Laboratory*

- Standard microbiological laboratory techniques including culturing, media preparation, biochemical testing, staining and microscopy and microbial identification, for both research and clinical microbiology.
- Standard laboratory molecular biology techniques including cloning, nucleic acid extraction and purification, PCR and RT-PCR, gel electrophoresis, spectrophotometry and fluorescence microscopy.
- Experienced in recovery of DNA and RNA from low-yield and recalcitrant samples.

#### TEACHING

**University of New South Wales, Sydney, Australia**

**March 2009–October 2012**

Postgraduate tutor, demonstrator and marker for courses *Genetics*, *Genetics (advanced)*, *Microbiology 1*, *Molecules Cells and Genes*, *Microbial Genetics* and undergraduate medicine classes including medical microbiology, biochemistry, molecular biology and genetics.

#### SCHOLARSHIPS

**Australian Postgraduate Award**

**August 2009–February 2013**