



JAMS

Joint Academic Microbiology Seminars

presents

The 8th Annual JAMS Symposium

Student poster competition and dinner

Wednesday 20 March 2019

Australian Museum, Sydney, Australia



WESTERN SYDNEY
UNIVERSITY



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Who are we?

First established in 2010 in Sydney, and now in Brisbane, Adelaide, and Singapore, JAMS is a group of microbiologists that meet once a month in each city to chat about all things microbiology over a beer or two. We're always looking for new speakers, so if you'd like to practice a talk in a low pressure environment, please contact one of our committee members for more information.



Here at JAMS, our motto is *Minima maxima sunt*. This roughly translates as, “the small things are the greatest”.

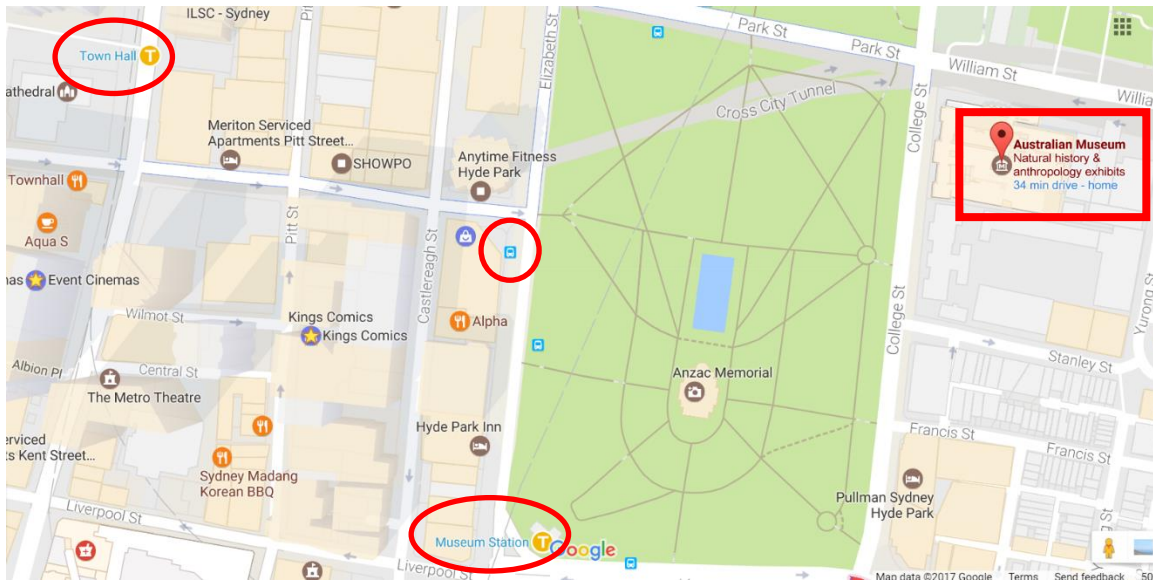
Directions

To the Australian Museum 1 William St, Sydney, New South Wales 2010

The Australian Museum is most easily accessed by public transport

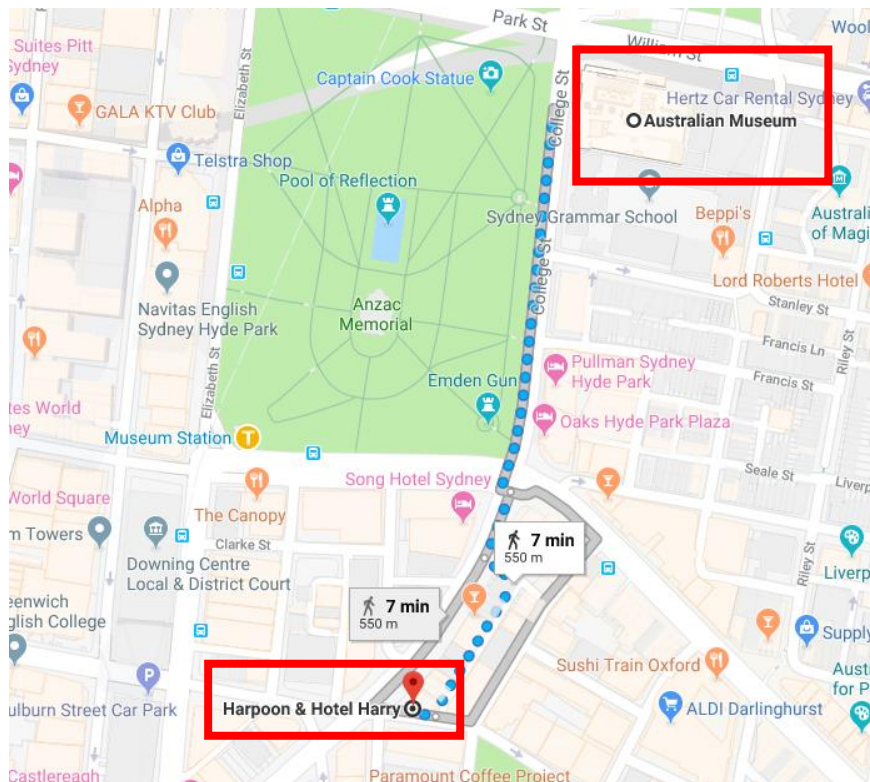
- Train: the closest stations are Town Hall or Museum (highlighted on map)
- Bus: many bus routes travel down Elizabeth St, stopping at Museum Station, Elizabeth St, Stand D (highlighted on map)

From either train station or bus stop, the museum is just a short walk through Hyde Park.



To Harpoon Harry: 40-44 Wentworth Ave, Surry Hills NSW 2010

Walking instructions from The Australian Museum to Harpoon Harry:

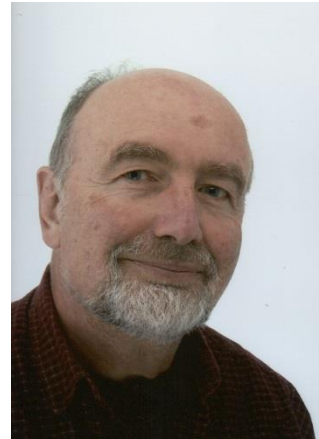


Symposium schedule

11:00am – 12:00pm	Registration and student poster setup Register at the Hallstrom Theatre, Australian Museum, 1 William Street Sydney Posters to be set up in Harbour View Room, Level 4 of the Australian Museum
12:00pm – 12:15pm	Welcome and acknowledgement of Country
12:15pm – 12:45pm	Daniel Vaultot, CNRS & Nanyang Technological University, Singapore <i>"A short history of oceanic picoplankton. . ."</i>
12:45pm – 1:15pm	Erica Donner, Future Industries Institute, University of South Australia <i>"Antimicrobial resistance in the water cycle"</i>
1:15pm – 1:45pm	Andrew Holmes, University of Sydney <i>"New microbial ecology – the future beyond developing techniques for data generation"</i>
1:45pm – 2:00pm	Presentations by Platinum and Gold sponsors
2:00pm – 2:05pm	Justin Seymour – Australian Microbiome
2:05pm – 2:10pm	Federico Lauro – Sustainability & the microbiome
2:10pm – 3:10pm	Student poster session with refreshments Harbour View Room, Level 4 of the Australian Museum
3:15pm – 3:45pm	Emma Gagen, University of Queensland <i>"Harnessing microbial processes for accelerated iron duricrust re-formation"</i>
3:45pm – 4:15pm	Liz Watkin, Curtin University, Western Australia <i>"Acidihalobacter: Novel, halotolerant, iron-and Sulfur oxidizing acidophiles with potential for saline water bioleaching"</i>
4:15pm – 5:00pm	James Tiedje, Michigan State University, United States <i>"Drilling deeper into microbiome's status and future"</i>
5:00pm	Symposium conclusion Short walk to Harpoon Harry's for dinner and drinks
6:00 – 10.30pm	Dinner at Harpoon Harry's
6.15pm	Concluding remarks and announcement of the winner of the Jeff Powell Forever-Student Award

Daniel Vaultot

CNRS & Nanyang Technological University,
Singapore



Abstract

A short history of oceanic picoplankton. . .

Station Biologique de Roscoff UMR7144, CNRS and Sorbonne Université,
France & Asian School of the Environment, Nanyang Technological
University, Singapore

Forty years ago, J. Waterbury discovered that marine *Synechococcus*, small unicellular cyanobacteria of about 1 μm , were very abundant in the oceans. This was the start of an incredible string of discoveries that changed the way we view oceanic ecosystems and food webs, placing picoplankton (cells smaller than 2 μm) at the base of marine life. I will briefly retrace some of the major advances of these four decades focusing on the eukaryotic photosynthetic plankton. Techniques such as flow cytometry, epifluorescence microscopy and cloning were instrumental to increase our understanding of these tiny organisms. During these decades, a number of new organisms such as *Prochlorococcus* or *Ostreococcus* were discovered and found to be very important for the functioning of marine ecosystems, providing new biological models for genetics. Our view of eukaryotic phytoplankton taxonomy has also been deeply modified with the establishment of many novel classes such as Mamiellophyceae or Bolidophyceae. I will wrap up by discussing the latest research developments linked in particular to advances in molecular phylogeny, metabarcoding and genomics with thoughts about what will be the next frontier.

Biography

Directeur de Recherche de Classe Exceptionnelle

Centre National de la Recherche Scientifique, France

After attending the Ecole Polytechnique in Paris, the Ecole Nationale du Génie Rural and working for a few years as an engineer, Daniel Vaultot did a PhD on the cell cycle regulation of phytoplankton with Penny Chisholm at MIT. Since 1983, he is a researcher at CNRS (now a Senior Scientist), working at the Station Biologique of Roscoff (France). He initially developed applications of flow cytometry to measure picoplankton and bacteria abundance in the ocean. These methods have become *de facto* standards in oceanography. About 25 years ago, he focused on the diversity and ecology of eukaryotic pico-phytoplankton which had received very little attention, pioneering molecular approaches such as gene cloning, metabarcoding and metagenomics. Currently his interests revolve around green algae, a group that had been long neglected. He had always a keen interest in data processing and software development, focusing recently on the open source R language. The group he initiated in Roscoff is now a global leader in plankton research with 35 researchers, post-docs and students. He also created in 1998 the Roscoff Culture Collection, by now the biggest collection in the world for marine phytoplankton. Daniel Vaultot co-authored more than 150 papers, including some in top journals such as Nature, Science or PNAS. He received the CNRS silver medal and is a member of the EMBO (European Molecular Biology Organization). He is currently spending one year at the Asian School of the Environment at NTU (Singapore) as a visiting Professor.

More information: <http://daniel-vaultot.fr> @daniel_vaultot

Erica Donner

Future Industries Institute, University of South Australia



Abstract

Antimicrobial resistance in the water cycle

Antimicrobial resistance is a designated global health emergency, and nations worldwide are currently responding to the World Health Organisation's call to take a One Health approach in addressing this challenge. This broad, integrated health perspective has drawn increasing attention to the environmental dimensions of AMR. Largely overlooked in earlier research efforts focussed predominantly on clinical- and veterinary-samples, environmental systems are now recognised to play an important role as both sources and sinks of resistant microbes and genes. The role of (waste) water in the propagation and transmission of antibiotic resistance has become a key aspect of the AMR discussion, particularly in relation to concerns about wastewater treatment and reuse in agricultural and urban environments. Municipal wastewater treatment plants continually receive influents containing pathogenic bacteria from a multitude of sources and are in the spotlight as potential 'evolutionary hotspots' of antibiotic resistance development and transfer. This presentation will provide insight into the environmental dimensions of AMR, with a particular focus on the relevance of water environments. Examples will be drawn from our recent research on wastewater, recycled water, coastal effluents, recreational waters, and wildlife habitats.

Biography

Erica Donner is an Associate Professor and Research Leader in the Future Industries Institute at the University of South Australia. She works across a range of topics in environmental science, with a major emphasis on contaminant fate and effects in (waste) water, biosolids, and soil. Her current research focuses on understanding the links between selective pressure, microbial ecology and resistance, particularly in relation to the risks associated with wastewater treatment and reuse, and the role of physico-chemical stressors in promoting the development and spread of antibiotic resistance.

<http://people.unisa.edu.au/erica.donner>

Andrew Holmes

University of Sydney, Australia



Abstract

New microbial ecology – the future beyond developing techniques for data generation

The great challenge for microbial ecology is that small things matter to big questions - by virtue of large numbers coupled with diverse and distinctive biochemistry. Consequently, for most of its history microbial ecology has been a technique-orientated field. The focus has been development of the means to describe the composition of microbial communities and determine the activity of their members. Despite the technical hurdles the true catalyst for the modern microbiome era was a conceptual advance - the idea that analysis of a single orthologous molecule could simultaneously serve as a universal framework for classification and a tool for community description. This was not well-received at first and there was a slow genesis from 1970 to 1990, followed by three decades of explosive technical advances. We now have the following amazing capabilities: To 'completely' describe the Bacterial and Archaeal composition of an environmental sample in terms of a marker gene. To infer (and in some cases measure) biochemical processes within a single *in situ* cell. To infer the genome and predict the physiological capabilities of cells that have never been brought into pure culture. All three of these capabilities are incredibly reliant on specialist expertise that is far outside the traditional training of the biologist. A consequence of this is a disjunction between the expertise in collecting and handling these data and their relation to key concepts in biology, let alone ecology. This is a huge barrier to advances. I believe that the next revolution in microbial ecology will be catalyzed by a return to the emphasis of the 1970's - conceptual advances to enable us to more successfully derive biological meaning from these datasets - and discuss ways we might approach this.

Biography

A/Prof Andrew Holmes,
School of Life and Environmental Sciences and Charles Perkins Centre
The University of Sydney, NSW, 2006

Andrew has general interests in microbial diversity, its evolutionary origins and ecological applications. After an attempted career as an Agricultural labourer in outback Queensland he took the soft option of PhD studies at the University of Queensland (1989-1992). Finding that the lack of hard physical labour agreed with him, he spent time at the University of Warwick, UK and Macquarie University, before settling down far from all forms of farming at the University of Sydney. Andrew's current research has a particular focus on understanding the mechanisms of host-microbe interaction in the gut and management of the gut microbial ecosystem for health. He is located in the School of Environmental and Life Sciences and leads the Microbiome Project node in the Charles Perkins Centre where his title of Ass. Professor is a source of ironical amusement to colleagues. He is a Senior Editor with *The ISME Journal*.

<https://sydney.edu.au/science/people/andrew.holmes.php>

Emma Gagen

University of Queensland, Australia

Abstract

Harnessing microbial processes for accelerated iron duricrust re-formation

Gagen, Emma J.¹, Tyson, Gene W.², Oliveira, Guilherme³, Vasconcelos, Paulo M.¹, Southam, Gordon¹.

¹ School of Earth and Environmental Sciences, The University of Queensland, St Lucia, Qld, 4072, Australia

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High grade iron ore deposits in tropical areas are capped by a hard, erosion-resistant iron duricrust that protects the friable ore below [1]. Geochemical evidence suggests that biogeochemical cycling of iron has played a critical role in formation and ongoing evolution of these duricrusts even until the present day [2]. Combining microbiology and geochemistry approaches has shed light on past and present day microbial iron cycling in these environments and indicates a critical role for biologically mediated iron reduction/dissolution.

In the present study, a novel iron reducing microbial consortia that was effective at goethite dissolution (up to 20% goethite reduction) was enriched. Laboratory observations with this culture were then tested at pilot scale (~14 tonnes of iron mine waste material) in attempts to promote microbial iron cycling for accelerated iron duricrust re-formation, during a 15 month pilot-scale experiment in Brazil. Effective microbial iron reduction was observed in all treatments during the pilot scale experiment. At end-harvest, the strongest aggregation of the iron duricrust fragments was observed in treatments that involved *in situ* microbial iron reduction (compared to *ex situ*). Harnessing microbial processes has potential for accelerated remediation of iron ore deposits post-mining.

1. Dorr, JVN (1964) 'Supergene iron ores of Minas Gerais, Brazil' Economic Geology, vol 59, pp 1203-1240.

2. Monteiro HS, Vasconcelos, PM, Farley, KA, Spier, CA, Mello CL (2014) (U-Th)/He geochronology of goethite and the origin and evolution of cangas. Geochimica et Cosmochimica Acta, vol 131, pp 267-289.

Biography

Emma Gagen is a Research Fellow in geomicrobiology in the School of Earth and Environmental Sciences at the University of Queensland. Her research focuses on harnessing microbial processes for accelerated mine site rehabilitation (iron ore mines in Brazil, coal mines in central Queensland). Other projects she contributes to relate to microbial colonisation of meteorites, bacterial degradation of anhydrite, microbiology of sulphur rich environments and formation of seafloor iron-manganese crusts. Emma's research interests extend to all areas of environmental microbiology and she is fascinated by the role microorganisms play in geochemical processes. <https://researchers.uq.edu.au/researcher/1244> @EmmaJGagen



Liz Watkin

Curtin University, Western Australia

Abstract

Acidihalobacter: Novel, halotolerant, iron-and Sulfur oxidizing acidophiles with potential for saline water bioleaching

Himel N. Khaleque^{1,2} Melissa K. Corbett¹, Anna H. Kaksonen², Naomi J. Boxall² and Elizabeth L.J. Watkin¹,



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Members of the *Acidihalobacter* (*Ac.*) genus are a unique group of iron-and sulfur-oxidising acidophiles that are able to withstand high chloride concentrations and low pH simultaneously. As such, they hold great potential for use in saline water bioleaching of mineral ores. The ability of four strains of *Acidihalobacter* to bioleach sulfide ores under saline conditions was investigated; namely *Ac. prosperus* V6, F5 and DSM 5130^T and, “*Ac. ferrooxidans*” V8. All isolates were able to oxidise iron/sulfur efficiently at up to 30 g L⁻¹ Cl⁻. Isolates V6, V8 and DSM 5130^T had a minimum requirement of 2 g L⁻¹ Cl⁻, whereas F5 was able to oxidise iron in the absence of Cl⁻. Strains V6, V8 and F5 were able to oxidise 1 % pyrite at Cl⁻ concentrations of 30 g L⁻¹, which is higher than the Cl⁻ concentration found in seawater (19 g.L⁻¹). This was superior to DSM 5130^T that was only able to oxidise pyrite at up to 18 g L⁻¹ Cl⁻.

Whole proteome analysis of differentially abundant proteins in *Ac. prosperus* V6 at high (30 g L⁻¹) and low (5 g L⁻¹) Cl⁻ concentrations was studied using Sequential Window Acquisition of all Theoretical Mass Spectra (SWATH-MS). The most marked response included the production of osmotic stress regulators that potentially induced the production of compatible solutes, most significantly, the synthesis of ectoine. Other responses to the increased Cl⁻ levels included the increased synthesis of glutathione, changes in carbon flux, the increased production of amino acids, the efflux of metals and protons, and the increase in proteins involved in DNA repair and membrane biosynthesis. Energy generation through iron oxidation and sulfur oxidation were decreased. This differed from the proteome response of DSM 5130^T, showing differences in mechanisms of salt tolerance between the members of the same genus.

The results of this work indicated novel mechanisms of salt tolerance under acidic conditions. The understanding of salt tolerance mechanisms by these acidophiles will help to extend the applicability of these microorganisms in bioleaching applications in regions of high salinity.

Biography

Elizabeth Watkin is Professor of Microbiology and Deputy Head of School in the School of Pharmacy and Biomedical Sciences, Curtin University. She obtained her undergraduate degree in physiology from UWA and after a long break from science completed a PhD as a

mature age student from Murdoch University in 1999. She completed Postdoctoral Research Fellowships with CSIRO-Plant Industry and the Centre for *Rhizobium* Studies, Murdoch University. She commenced her current academic appointment at Curtin University in June 2002.

The overarching theme of her research is the microbial ecology of environmental systems and covers the fields of mining biotechnology and mineral resource recovery, microbial induced corrosion, microbial fouling of water (particularly within mining systems) . Her research team investigates biotechnological processes for environmental and industrial applications and approaches to mitigate microbially caused problems such as biocorrosion, biofouling and bioclogging.

She has industry contacts with a number of mining companies and has conducted contract research for Bioheap Ltd, Fortescue Metals Group, Metalobus Pty Ltd, and has undertaken research on the microbial fouling of water bores with the Water Corporation. She has a long-term collaboration with CSIRO-Land and Water and CSIRO-Mineral Resources and has published widely with all groups in the areas of mining biotechnology and mineral resource recovery.

<https://staffportal.curtin.edu.au/staff/profile/view/E.Watkin>

James Tiedje

Michigan State University, United States

Abstract

Drilling deeper into microbiome's status and future

James M. Tiedje, Center for Microbial Ecology and Departments of Plant, Soil and Microbial Sciences and of Microbiology and Molecular Genetics, Michigan State University



Metagenomics and its derivative, the microbiome, has become a core of new age microbial ecology. Metagenomics has advanced rapidly and taken many directions - those determined by the various methods employed, the complexity of the different communities, the resources available and of course the compelling questions. My lab has focused recently on ecofunctional genes, i.e. those genes that directly control important ecological function. I will illustrate with two examples: one of soil and its rhizosphere microbiome of biofuel crops, and the other of understanding the ecology of antibiotic resistance genes in the environment. I will show how new computational tools, especially gene-targeted assembly using Xander, helps quantify and categorize N cycle and other genes, and how we can assimilate metagenomic, metatranscriptomic and metaproteomic data from field soil to gain some insight into rhizosphere activities. For antibiotic resistance we used highly parallel qPCR, with over 300 primer pairs for antibiotic resistances and mobile genetic elements, and long read sequencing, to assess quantity, type, potential mobility and fate of natural and human selected resistomes. Metagenomics and microbiome science is a field with big opportunities since there are many habitats, directions and needs, especially for creative ways to interrogate data to uncover new knowledge. I will also speculate a bit into the future of what microbiome science may look like and contribute too. It is a great opportunity area for students.

Biography

Dr. Tiedje is University Distinguished Professor of Microbiology and Molecular Genetics and of Plant, Soil and Microbial Sciences at Michigan State University, and is also Director of the Center for Microbial Ecology. His contributions have been on microbial ecology, physiology and diversity, especially regarding the nitrogen cycle, biodegradation of pollutants and on the use of genomics and metagenomics to understand speciation, community structure and functions. He served as Editor-in-Chief of *Applied and Environmental Microbiology* and Editor of *Microbial and Molecular Biology Reviews* and *mBio*. He served on the Board on Life Sciences of the National Research Council, EPA's Science Advisory Panel and on DOE's Biological and Environmental Research Advisory Committee. He was President of the American Society for Microbiology (ASM) and the International Society of Microbial Ecology (ISME). He is Fellow of the AAAS, the American Academy of Microbiology, the Ecological Society of America, the Soil Science Society of America, and a member of the U.S. National Academy of Sciences.

Publications: <http://scholar.google.com/citations?user=5ekyvtAAAAAJ>

<http://www.cme.msu.edu/tiedjelab/jtiedje.shtml>

https://www.canr.msu.edu/people/james_m_tiedje

Student posters

Catherine Allen	Necromicrobiome persistence in soils as a PMI indicator	
Nathan Danckert	Microbiomes of Australian aquacultured abalone through production	The University of Sydney
Gemma Deakin	Bacterial-Fungal Interactions in Model Polymicrobial Biofilms	Western Sydney University
Belinda Fabian		Macquarie University
Benjamin Ford	Solving the annotation puzzle: Using substrate-binding proteins to redefine nutrient acquisition in Cyanobacteria	Macquarie University
Daniela Gaio	Insight into the porcine gut microbiome from 5 Tbp of metagenomic time series data across 850 samples and Hi-C	The itthree institutie, UTS
Christaline George	Early detection and characterization of eukaryotic algal blooms with third generation sequencing in the coastal waters of Singapore	Nanyang Technological University
Carolina Gutierrez-Chavez	Microbial Bioactivities and Their Role in Antarctica	UNSW Sydney
Jieyu (Jayne) Liu	Evaluation of soil washing for a urea-amended biopile soil from Antarctica	UNSW Sydney
Fraser MacLeod	Biofilm Architecture in Microbial Mat Haloarchaea	UNSW Sydney
Varsha Naidu		Macquarie University
Yolanda Plowman	AMF community assembly on wheat plants driven by crop rotation and P fertiliser	The University of Sydney
Carl Ramirez	Investigating the factors determining Aspergillus fumigatus virulence and the variations of virulence between clinical isolates	Western Sydney University
Jessica Taylor	Phylogeny resolved, metabolism revealed: The tale of uncultured sponge-associated relatives of the Betaproteobacteriales	CMB, UNSW Sydney
Silas Vick		Macquarie University
Le Zhang	recA deficiency promotes bacterial evolution to β -lactams antibiotics resistance	University of Technology Sydney

JAMS organising committee



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