

Derek S Sarovich

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88
papers

1,627
citations

24
h-index

35
g-index

102
ext. papers

2,174
ext. citations

5.7
avg, IF

4.4
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 88 | Within-host evolution of <i>Burkholderia pseudomallei</i> over a twelve-year chronic carriage infection. <i>MBio</i> , 2013 , 4, | 7.8 | 80 |
| 87 | Variable virulence factors in <i>Burkholderia pseudomallei</i> (melioidosis) associated with human disease. <i>PLoS ONE</i> , 2014 , 9, e91682 | 3.7 | 69 |
| 86 | SPANDx: a genomics pipeline for comparative analysis of large haploid whole genome re-sequencing datasets. <i>BMC Research Notes</i> , 2014 , 7, 618 | 2.3 | 69 |
| 85 | Development of a prototype lateral flow immunoassay (LFI) for the rapid diagnosis of melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2727 | 4.8 | 61 |
| 84 | Molecular epidemiologic investigation of an anthrax outbreak among heroin users, Europe. <i>Emerging Infectious Diseases</i> , 2012 , 18, 1307-13 | 10.2 | 58 |
| 83 | Characterization of ceftazidime resistance mechanisms in clinical isolates of <i>Burkholderia pseudomallei</i> from Australia. <i>PLoS ONE</i> , 2012 , 7, e30789 | 3.7 | 53 |
| 82 | Within-host evolution of <i>Burkholderia pseudomallei</i> in four cases of acute melioidosis. <i>PLoS Pathogens</i> , 2010 , 6, e1000725 | 7.6 | 45 |
| 81 | Development of ceftazidime resistance in an acute <i>Burkholderia pseudomallei</i> infection. <i>Infection and Drug Resistance</i> , 2012 , 5, 129-32 | 4.2 | 43 |
| 80 | <i>Burkholderia pseudomallei</i> isolates from Sarawak, Malaysian Borneo, are predominantly susceptible to aminoglycosides and macrolides. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 162-6 | 5.9 | 42 |
| 79 | Phylogenomic Analysis Reveals an Asian Origin for African <i>Burkholderia pseudomallei</i> and Further Supports Melioidosis Endemicity in Africa. <i>MSphere</i> , 2016 , 1, | 5 | 40 |
| 78 | <i>Haemophilus influenzae</i> : using comparative genomics to accurately identify a highly recombinogenic human pathogen. <i>BMC Genomics</i> , 2015 , 16, 641 | 4.5 | 39 |
| 77 | The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016 , 7, | 7.8 | 37 |
| 76 | Whole-genome sequencing confirms that <i>Burkholderia pseudomallei</i> multilocus sequence types common to both Cambodia and Australia are due to homoplasmy. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 323-6 | 9.7 | 37 |
| 75 | Unprecedented Melioidosis Cases in Northern Australia Caused by an Asian <i>Burkholderia pseudomallei</i> Strain Identified by Using Large-Scale Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 954-63 | 4.8 | 34 |
| 74 | Recurrent melioidosis in the Darwin Prospective Melioidosis Study: improving therapies mean that relapse cases are now rare. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 650-3 | 9.7 | 34 |
| 73 | Within-Host Evolution of during Chronic Infection of Seven Australasian Cystic Fibrosis Patients. <i>MBio</i> , 2017 , 8, | 7.8 | 33 |
| 72 | Comparison of TaqMan PCR assays for detection of the melioidosis agent <i>Burkholderia pseudomallei</i> in clinical specimens. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 2059-62 | 9.7 | 33 |

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|----|--|------|----|
| 71 | Development and validation of Burkholderia pseudomallei-specific real-time PCR assays for clinical, environmental or forensic detection applications. <i>PLoS ONE</i> , 2012 , 7, e37723 | 3.7 | 33 |
| 70 | Distribution of Burkholderia pseudomallei in northern Australia, a land of diversity. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 3463-8 | 4.8 | 32 |
| 69 | Mechanisms of Resistance to Folate Pathway Inhibitors in : Deviation from the Norm. <i>MBio</i> , 2017 , 8, | 7.8 | 31 |
| 68 | Use of Whole-Genome Sequencing to Link Burkholderia pseudomallei from Air Sampling to Mediastinal Melioidosis, Australia. <i>Emerging Infectious Diseases</i> , 2015 , 21, 2052-4 | 10.2 | 31 |
| 67 | Absence of an important vaccine and diagnostic target in carriage- and disease-related nontypeable Haemophilus influenzae. <i>Vaccine Journal</i> , 2014 , 21, 250-2 | | 30 |
| 66 | Chlamydia trachomatis from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. <i>Nature Communications</i> , 2016 , 7, 10688 | 17.4 | 30 |
| 65 | Tracing melioidosis back to the source: using whole-genome sequencing to investigate an outbreak originating from a contaminated domestic water supply. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 1144-8 | 8.7 | 24 |
| 64 | Whole-genome sequencing of Burkholderia pseudomallei isolates from an unusual melioidosis case identifies a polyclonal infection with the same multilocus sequence type. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 282-6 | 9.7 | 23 |
| 63 | Comparative Genomics of sp. nov., a Low G+C Content, Free-Living Bacterium That Defies Taxonomic Dissection of the Genus. <i>Frontiers in Microbiology</i> , 2017 , 8, 1679 | 5.7 | 22 |
| 62 | Dominance of multidrug resistant CC271 clones in macrolide-resistant streptococcus pneumoniae in Arizona. <i>BMC Microbiology</i> , 2012 , 12, 12 | 4.5 | 22 |
| 61 | Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant Staphylococcus aureus Lineage from the Indian Subcontinent. <i>MBio</i> , 2019 , 10, | 7.8 | 22 |
| 60 | Endemic melioidosis in residents of desert region after atypically intense rainfall in central Australia, 2011. <i>Emerging Infectious Diseases</i> , 2015 , 21, 1038-40 | 10.2 | 21 |
| 59 | Whole-Genome Sequences of 80 Environmental and Clinical Isolates of Burkholderia pseudomallei. <i>Genome Announcements</i> , 2015 , 3, | | 21 |
| 58 | Suspected cases of intracontinental Burkholderia pseudomallei sequence type homoplasmy resolved using whole-genome sequencing. <i>Microbial Genomics</i> , 2017 , 3, | 4.4 | 21 |
| 57 | Simultaneous identification of Haemophilus influenzae and Haemophilus haemolyticus using real-time PCR. <i>Future Microbiology</i> , 2017 , 12, 585-593 | 2.9 | 20 |
| 56 | Raising the Stakes: Loss of Efflux Pump Regulation Decreases Meropenem Susceptibility in Burkholderia pseudomallei. <i>Clinical Infectious Diseases</i> , 2018 , 67, 243-250 | 11.6 | 20 |
| 55 | Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. <i>Microbial Genomics</i> , 2016 , 2, e000067 | 4.4 | 20 |
| 54 | Transcriptomic analysis of longitudinal Burkholderia pseudomallei infecting the cystic fibrosis lung. <i>Microbial Genomics</i> , 2018 , 4, | 4.4 | 20 |

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| 53 | Plasmacytoid dendritic cells appear inactive during sub-microscopic Plasmodium falciparum blood-stage infection, yet retain their ability to respond to TLR stimulation. <i>Scientific Reports</i> , 2017 , 7, 2596 | 4.9 | 18 |
| 52 | Autochthonous melioidosis in humans, Madagascar, 2012 and 2013. <i>Emerging Infectious Diseases</i> , 2014 , 20, 1739-41 | 10.2 | 18 |
| 51 | Accurate and rapid identification of the Burkholderia pseudomallei near-neighbour, Burkholderia ubonensis, using real-time PCR. <i>PLoS ONE</i> , 2013 , 8, e71647 | 3.7 | 17 |
| 50 | pPSX: a novel vector for the cloning and heterologous expression of antitumor antibiotic gene clusters. <i>Plasmid</i> , 2007 , 57, 306-13 | 3.3 | 16 |
| 49 | Improved multilocus sequence typing of Burkholderia pseudomallei and closely related species. <i>Journal of Medical Microbiology</i> , 2016 , 65, 992-997 | 3.2 | 16 |
| 48 | Single-molecule sequencing reveals the molecular basis of multidrug-resistance in ST772 methicillin-resistant Staphylococcus aureus. <i>BMC Genomics</i> , 2015 , 16, 388 | 4.5 | 15 |
| 47 | Burkholderia pseudomallei Genotype Distribution in the Northern Territory, Australia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016 , 94, 68-72 | 3.2 | 15 |
| 46 | Genomic epidemiology of severe community-onset Acinetobacter baumannii infection. <i>Microbial Genomics</i> , 2019 , 5, | 4.4 | 15 |
| 45 | Loss of Methyltransferase Function and Increased Efflux Activity Leads to Doxycycline Resistance in Burkholderia pseudomallei. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61, | 5.9 | 14 |
| 44 | Whole-Genome Sequences of Isolates Exhibiting Decreased Meropenem Susceptibility. <i>Genome Announcements</i> , 2017 , 5, | | 12 |
| 43 | Lipopolysaccharide Genotype Does Not Correlate With Severity or Outcome in Melioidosis: Host Risk Factors Remain the Critical Determinant. <i>Open Forum Infectious Diseases</i> , 2019 , 6, ofz091 | 1 | 12 |
| 42 | Comparative Genomics and Antimicrobial Resistance Profiling of Isolates Reveal Nosocomial Transmission and Susceptibility to Fluoroquinolones, Tetracyclines, and Trimethoprim-Sulfamethoxazole. <i>Journal of Clinical Microbiology</i> , 2020 , 58, | 9.7 | 12 |
| 41 | Melioidosis from contaminated bore water and successful UV sterilization. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013 , 89, 367-8 | 3.2 | 12 |
| 40 | Genomic Insights Into the Melioidosis Pathogen, Burkholderia pseudomallei. <i>Current Tropical Medicine Reports</i> , 2017 , 4, 95-102 | 5 | 11 |
| 39 | Increased Neurotropic Threat from Burkholderia pseudomallei Strains with a B. mallei-like Variation in the bimA Motility Gene, Australia. <i>Emerging Infectious Diseases</i> , 2017 , 23, | 10.2 | 10 |
| 38 | Virulence of the Melioidosis Pathogen Burkholderia pseudomallei Requires the Oxidoreductase Membrane Protein DsbB. <i>Infection and Immunity</i> , 2018 , 86, | 3.7 | 10 |
| 37 | Investigation of trimethoprim/sulfamethoxazole resistance in an emerging sequence type 5 methicillin-resistant Staphylococcus aureus clone reveals discrepant resistance reporting. <i>Clinical Microbiology and Infection</i> , 2018 , 24, 1027-1029 | 9.5 | 10 |
| 36 | Phylogeographic, genomic, and meropenem susceptibility analysis of Burkholderia ubonensis. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005928 | 4.8 | 9 |

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|----|---|------|---|
| 35 | Tracing the environmental footprint of the <i>Burkholderia pseudomallei</i> lipopolysaccharide genotypes in the tropical "Top End" of the Northern Territory, Australia. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007369 | 4.8 | 8 |
| 34 | Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. <i>Microbial Genomics</i> , 2017 , 3, e000117 | 4.4 | 8 |
| 33 | Comparative genomics confirms a rare melioidosis human-to-human transmission event and reveals incorrect phylogenomic reconstruction due to polyclonality. <i>Microbial Genomics</i> , 2020 , 6, | 4.4 | 8 |
| 32 | Molecular Signatures of Non-typeable Lung Adaptation in Pediatric Chronic Lung Disease. <i>Frontiers in Microbiology</i> , 2019 , 10, 1622 | 5.7 | 7 |
| 31 | Whole-Genome Sequences of Five <i>Burkholderia pseudomallei</i> Isolates from Australian Cystic Fibrosis Patients. <i>Genome Announcements</i> , 2015 , 3, | | 7 |
| 30 | Identification and typing of <i>Francisella tularensis</i> with a highly automated genotyping assay. <i>Letters in Applied Microbiology</i> , 2013 , 56, 128-34 | 2.9 | 7 |
| 29 | Selective isolation of <i>Yersinia pestis</i> from plague-infected fleas. <i>Journal of Microbiological Methods</i> , 2010 , 82, 95-7 | 2.8 | 7 |
| 28 | pPSY: a vector for the stable cloning and expression of streptomycete single gene phenotypes in <i>Escherichia coli</i> . <i>Plasmid</i> , 2008 , 60, 53-8 | 3.3 | 7 |
| 27 | Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year <i>Burkholderia pseudomallei</i> infection. <i>PLoS Pathogens</i> , 2020 , 16, e1008298 | 7.6 | 6 |
| 26 | Peptidyl-Prolyl Isomerase Is Essential for Proteome Homeostasis and Virulence in <i>Burkholderia pseudomallei</i> . <i>Infection and Immunity</i> , 2019 , 87, | 3.7 | 6 |
| 25 | Quantitative real-time PCR assay for the rapid identification of the intrinsically multidrug-resistant bacterial pathogen. <i>Microbial Genomics</i> , 2019 , 5, | 4.4 | 6 |
| 24 | Human Infection with <i>Burkholderia thailandensis</i> , China, 2013. <i>Emerging Infectious Diseases</i> , 2018 , 24, 953-954 | 10.2 | 5 |
| 23 | A Persisting Nontropical Focus of <i>Burkholderia pseudomallei</i> with Limited Genome Evolution over Five Decades. <i>MSystems</i> , 2020 , 5, | 7.6 | 5 |
| 22 | Taking the next-gen step: Comprehensive antimicrobial resistance detection from <i>Burkholderia pseudomallei</i> . <i>EBioMedicine</i> , 2021 , 63, 103152 | 8.8 | 5 |
| 21 | from patients with chronic rhinosinusitis show minimal genetic association between polyp and non-polyp phenotypes. <i>BMC Ear, Nose and Throat Disorders</i> , 2018 , 18, 16 | 8 | 5 |
| 20 | Plasmid encoded antibiotics inhibit protozoan predation of <i>Escherichia coli</i> K12. <i>Plasmid</i> , 2011 , 66, 152-83,3 | 3.3 | 4 |
| 19 | <i>Burkholderia pseudomallei</i> distribution in Australasia is linked to paleogeographic and anthropogenic history. <i>PLoS ONE</i> , 2018 , 13, e0206845 | 3.7 | 4 |
| 18 | Molecular genotyping of <i>Acinetobacter</i> spp. isolated in Arizona, USA, using multilocus PCR and mass spectrometry. <i>Journal of Medical Microbiology</i> , 2013 , 62, 1295-1300 | 3.2 | 3 |

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| 17 | Complete sequence and analysis of the stability functions of pPSX, a vector that allows stable cloning and expression of Streptomyces genes in Escherichia coli K12. <i>Plasmid</i> , 2009 , 62, 39-43 | 3-3 | 3 |
| 16 | Comparative genomic analysis identifies X-factor (haemin)-independent : a formal re-classification of ". <i>Microbial Genomics</i> , 2020 , 6, | 4-4 | 3 |
| 15 | Molecular Epidemiology of Third-Generation-Cephalosporin-Resistant in Southeast Queensland, Australia. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, | 5-9 | 3 |
| 14 | Development and validation of a triplex quantitative real-time PCR assay to detect efflux pump-mediated antibiotic resistance in Burkholderia pseudomallei. <i>Future Microbiology</i> , 2018 , 13, 1403-1418 | 2-9 | 3 |
| 13 | Genomic diversity and antimicrobial resistance of species isolated from chronic lung disease airways.. <i>Microbial Genomics</i> , 2022 , 8, | 4-4 | 2 |
| 12 | Tracing the environmental footprint of the Burkholderia pseudomallei lipopolysaccharide genotypes in the tropical Top End of the Northern Territory, Australia | | 2 |
| 11 | Pharmacodynamic Evaluation of Plasma and Epithelial Lining Fluid Exposures of Amikacin against Pseudomonas aeruginosa in a Dynamic Hollow-Fiber Infection Model. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64, | 5-9 | 2 |
| 10 | Complete Genome Sequence of the Environmental Burkholderia pseudomallei Sequence Type 131 Isolate MSHR1435, Associated with a Chronic Melioidosis Infection. <i>Genome Announcements</i> , 2018 , 6, | | 1 |
| 9 | Whole-Genome Sequencing to Differentiate Relapse From Reinfection in Community-Onset Bacteremic Pneumonia. <i>Open Forum Infectious Diseases</i> , 2019 , 6, ofz263 | 1 | 1 |
| 8 | Rapid fluoroquinolone resistance detection in Pseudomonas aeruginosa using mismatch amplification mutation assay-based real-time PCR | | 1 |
| 7 | Duplex real-time PCR assay for the simultaneous detection of and spp. <i>Microbial Genomics</i> , 2020 , 6, | 4-4 | 1 |
| 6 | Evolution and global transmission of a multidrug-resistant, community-associated MRSA lineage from the Indian subcontinent | | 1 |
| 5 | Molecular signatures of non-typeable Haemophilus influenzae lung adaptation in paediatric chronic lung disease | | 1 |
| 4 | Melioidosis in New Caledonia: a dominant strain in a transmission hotspot. <i>Epidemiology and Infection</i> , 2016 , 144, 1330-7 | 4-3 | 1 |
| 3 | Genomic diversity and antimicrobial resistance of Prevotella spp. isolated from chronic lung disease airways | | 1 |
| 2 | Express Yourself: Quantitative Real-Time PCR Assays for Rapid Chromosomal Antimicrobial Resistance Detection in Pseudomonas aeruginosa.. <i>Antimicrobial Agents and Chemotherapy</i> , 2022 , e0020422 | 5-9 | 1 |
| 1 | The Scourge of Antibiotic-resistant Infections in Cystic Fibrosis. <i>Trends in Microbiology</i> , 2019 , 27, 289-291 | 12-4 | |