Derek S Sarovich

List of Publications by Year in descending order

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DEDER S SADOVICH

| # | Article | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Within-Host Evolution of Burkholderia pseudomallei over a Twelve-Year Chronic Carriage Infection. MBio, 2013, 4, . | 4.1 | 121 |
| 2 | Variable Virulence Factors in Burkholderia pseudomallei (Melioidosis) Associated with Human Disease. PLoS ONE, 2014, 9, e91682. | 2.5 | 99 |
| 3 | SPANDx: a genomics pipeline for comparative analysis of large haploid whole genome re-sequencing datasets. BMC Research Notes, 2014, 7, 618. | 1.4 | 94 |
| 4 | Development of a Prototype Lateral Flow Immunoassay (LFI) for the Rapid Diagnosis of Melioidosis. PLoS Neglected Tropical Diseases, 2014, 8, e2727. | 3.0 | 93 |
| 5 | Molecular Epidemiologic Investigation of an Anthrax Outbreak among Heroin Users, Europe. Emerging Infectious Diseases, 2012, 18, 1307-1313. | 4.3 | 77 |
| 6 | Characterization of Ceftazidime Resistance Mechanisms in Clinical Isolates of Burkholderia pseudomallei from Australia. PLoS ONE, 2012, 7, e30789. | 2.5 | 75 |
| 7 | Burkholderia pseudomallei Isolates from Sarawak, Malaysian Borneo, Are Predominantly Susceptible to Aminoglycosides and Macrolides. Antimicrobial Agents and Chemotherapy, 2014, 58, 162-166. | 3.2 | 72 |
| 8 | Within-Host Evolution of <i>Burkholderia pseudomallei</i> during Chronic Infection of Seven Australasian Cystic Fibrosis Patients. MBio, 2017, 8, . | 4.1 | 70 |
| 9 | Development of ceftazidime resistance in an acute Burkholderia pseudomallei infection. Infection and Drug Resistance, 2012, 5, 129. | 2.7 | 60 |
| 10 | Phylogenomic Analysis Reveals an Asian Origin for African Burkholderia pseudomallei and Further Supports Melioidosis Endemicity in Africa. MSphere, 2016, 1, . | 2.9 | 57 |
| 11 | Haemophilus influenzae: using comparative genomics to accurately identify a highly recombinogenic human pathogen. BMC Genomics, 2015, 16, 641. | 2.8 | 53 |
| 12 | Within-Host Evolution of Burkholderia pseudomallei in Four Cases of Acute Melioidosis. PLoS Pathogens, 2010, 6, e1000725. | 4.7 | 50 |
| 13 | Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant Staphylococcus aureus Lineage from the Indian Subcontinent. MBio, 2019, 10, . | 4.1 | 50 |
| 14 | Development and Validation of Burkholderia pseudomallei-Specific Real-Time PCR Assays for Clinical, Environmental or Forensic Detection Applications. PLoS ONE, 2012, 7, e37723. | 2.5 | 50 |
| 15 | The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. MBio, 2016, 7, . | 4.1 | 49 |
| 16 | Mechanisms of Resistance to Folate Pathway Inhibitors in <i>Burkholderia pseudomallei</i> : Deviation from the Norm. MBio, 2017, 8, . | 4.1 | 47 |
| 17 | Unprecedented Melioidosis Cases in Northern Australia Caused by an Asian Burkholderia pseudomallei Strain Identified by Using Large-Scale Comparative Genomics. Applied and Environmental Microbiology, 2016, 82, 954-963. | 3.1 | 46 |
| 18 | Distribution of Burkholderia pseudomallei in Northern Australia, a Land of Diversity. Applied and Environmental Microbiology, 2014, 80, 3463-3468. | 3.1 | 45 |

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|----|---|------|-----------|
| 19 | Comparison of TaqMan PCR Assays for Detection of the Melioidosis Agent Burkholderia pseudomallei in Clinical Specimens. Journal of Clinical Microbiology, 2012, 50, 2059-2062. | 3.9 | 44 |
| 20 | Whole-Genome Sequencing Confirms that Burkholderia pseudomallei Multilocus Sequence Types Common to Both Cambodia and Australia Are Due to Homoplasy. Journal of Clinical Microbiology, 2015, 53, 323-326. | 3.9 | 44 |
| 21 | Recurrent Melioidosis in the Darwin Prospective Melioidosis Study: Improving Therapies Mean that Relapse Cases Are Now Rare. Journal of Clinical Microbiology, 2014, 52, 650-653. | 3.9 | 43 |
| 22 | Chlamydia trachomatis from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. Nature Communications, 2016, 7, 10688. | 12.8 | 42 |
| 23 | Use of Whole-Genome Sequencing to Link <i>Burkholderia pseudomallei</i> from Air Sampling to Mediastinal Melioidosis, Australia. Emerging Infectious Diseases, 2015, 21, 2052-2054. | 4.3 | 41 |
| 24 | Genomic epidemiology of severe community-onset Acinetobacter baumannii infection. Microbial Genomics, 2019, 5, . | 2.0 | 40 |
| 25 | Whole-Genome Sequences of 80 Environmental and Clinical Isolates of Burkholderia pseudomallei. Genome Announcements, 2015, 3, . | 0.8 | 38 |
| 26 | Comparative Genomics of Burkholderia singularis sp. nov., a Low G+C Content, Free-Living Bacterium That Defies Taxonomic Dissection of the Genus Burkholderia. Frontiers in Microbiology, 2017, 8, 1679. | 3.5 | 36 |
| 27 | Tracing Melioidosis Back to the Source: Using Whole-Genome Sequencing To Investigate an Outbreak Originating from a Contaminated Domestic Water Supply. Journal of Clinical Microbiology, 2015, 53, 1144-1148. | 3.9 | 35 |
| 28 | Simultaneous identification of <i>Haemophilus influenzae</i> and <i>Haemophilus haemolyticus</i> using real-time PCR. Future Microbiology, 2017, 12, 585-593. | 2.0 | 35 |
| 29 | Raising the Stakes: Loss of Efflux Pump Regulation Decreases Meropenem Susceptibility in Burkholderia pseudomallei. Clinical Infectious Diseases, 2018, 67, 243-250. | 5.8 | 34 |
| 30 | Absence of an Important Vaccine and Diagnostic Target in Carriage- and Disease-Related Nontypeable Haemophilus influenzae. Vaccine Journal, 2014, 21, 250-252. | 3.1 | 33 |
| 31 | Whole-Genome Sequencing of Burkholderia pseudomallei Isolates from an Unusual Melioidosis Case Identifies a Polyclonal Infection with the Same Multilocus Sequence Type. Journal of Clinical Microbiology, 2015, 53, 282-286. | 3.9 | 32 |
| 32 | Dominance of multidrug resistant CC271 clones in macrolide-resistant streptococcus pneumoniae in Arizona. BMC Microbiology, 2012, 12, 12. | 3.3 | 31 |
| 33 | Endemic Melioidosis in Residents of Desert Region after Atypically Intense Rainfall in Central Australia, 2011. Emerging Infectious Diseases, 2015, 21, 1038-1040. | 4.3 | 30 |
| 34 | Suspected cases of intracontinental Burkholderia pseudomallei sequence type homoplasy resolved using whole-genome sequencing. Microbial Genomics, 2017, 3, . | 2.0 | 30 |
| 35 | Transcriptomic analysis of longitudinal Burkholderia pseudomallei infecting the cystic fibrosis lung. Microbial Genomics, 2018, 4, . | 2.0 | 30 |
| 36 | Comparative Genomics and Antimicrobial Resistance Profiling of <i>Elizabethkingia</i> Isolates Reveal Nosocomial Transmission and <i>In Vitro</i> Susceptibility to Fluoroquinolones, Tetracyclines, and Trimethoprim-Sulfamethoxazole. Journal of Clinical Microbiology, 2020, 58, . | 3.9 | 27 |

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|----|---|-----|-----------|
| 37 | Single-molecule sequencing reveals the molecular basis of multidrug-resistance in ST772 methicillin-resistant Staphylococcus aureus. BMC Genomics, 2015, 16, 388. | 2.8 | 24 |
| 38 | Plasmacytoid dendritic cells appear inactive during sub-microscopic Plasmodium falciparum blood-stage infection, yet retain their ability to respond to TLR stimulation. Scientific Reports, 2017, 7, 2596. | 3.3 | 24 |
| 39 | Loss of Methyltransferase Function and Increased Efflux Activity Leads to Doxycycline Resistance in Burkholderia pseudomallei. Antimicrobial Agents and Chemotherapy, 2017, 61, . | 3.2 | 23 |
| 40 | Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. Microbial Genomics, 2016, 2, e000067. | 2.0 | 23 |
| 41 | Accurate and Rapid Identification of the Burkholderia pseudomallei Near-Neighbour, Burkholderia ubonensis, Using Real-Time PCR. PLoS ONE, 2013, 8, e71647. | 2.5 | 21 |
| 42 | Melioidosis from Contaminated Bore Water and Successful UV Sterilization. American Journal of Tropical Medicine and Hygiene, 2013, 89, 367-368. | 1.4 | 19 |
| 43 | Autochthonous Melioidosis in Humans, Madagascar, 2012 and 2013. Emerging Infectious Diseases, 2014, 20, 1735-1737. | 4.3 | 19 |
| 44 | Comparative genomics confirms a rare melioidosis human-to-human transmission event and reveals incorrect phylogenomic reconstruction due to polyclonality. Microbial Genomics, 2020, 6, . | 2.0 | 19 |
| 45 | Taking the next-gen step: Comprehensive antimicrobial resistance detection from Burkholderia pseudomallei. EBioMedicine, 2021, 63, 103152. | 6.1 | 18 |
| 46 | Improved multilocus sequence typing of Burkholderia pseudomallei and closely related species. Journal of Medical Microbiology, 2016, 65, 992-997. | 1.8 | 18 |
| 47 | pPSX: A novel vector for the cloning and heterologous expression of antitumor antibiotic gene clusters. Plasmid, 2007, 57, 306-313. | 1.4 | 17 |
| 48 | Burkholderia pseudomallei Genotype Distribution in the Northern Territory, Australia. American Journal of Tropical Medicine and Hygiene, 2016, 94, 68-72. | 1.4 | 17 |
| 49 | Genomic Insights Into the Melioidosis Pathogen, Burkholderia pseudomallei. Current Tropical Medicine Reports, 2017, 4, 95-102. | 3.7 | 17 |
| 50 | Increased Neurotropic Threat from <i>Burkholderia pseudomallei</i> Strains with a <i>B. mallei</i> –like Variation in the <i>bimA</i> Motility Gene, Australia. Emerging Infectious Diseases, 2017, 23, . | 4.3 | 17 |
| 51 | <i>Burkholderia pseudomallei</i> Lipopolysaccharide Genotype Does Not Correlate With Severity or Outcome in Melioidosis: Host Risk Factors Remain the Critical Determinant. Open Forum Infectious Diseases, 2019, 6, ofz091. | 0.9 | 16 |
| 52 | Phylogeographic, genomic, and meropenem susceptibility analysis of Burkholderia ubonensis. PLoS Neglected Tropical Diseases, 2017, 11, e0005928. | 3.0 | 16 |
| 53 | Whole-Genome Sequences of Burkholderia pseudomallei Isolates Exhibiting Decreased Meropenem Susceptibility. Genome Announcements, 2017, 5, . | 0.8 | 15 |
| 54 | Investigation of trimethoprim/sulfamethoxazole resistance in an emerging sequence type 5 methicillin-resistant Staphylococcus aureus clone reveals discrepant resistance reporting. Clinical Microbiology and Infection, 2018, 24, 1027-1029. | 6.0 | 15 |

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| 55 | Tracing the environmental footprint of the Burkholderia pseudomallei lipopolysaccharide genotypes in the tropical "Top End―of the Northern Territory, Australia. PLoS Neglected Tropical Diseases, 2019, 13, e0007369. | 3.0 | 14 |
| 56 | Virulence of the Melioidosis Pathogen Burkholderia pseudomallei Requires the Oxidoreductase Membrane Protein DsbB. Infection and Immunity, 2018, 86, . | 2.2 | 13 |
| 57 | Molecular Signatures of Non-typeable Haemophilus influenzae Lung Adaptation in Pediatric Chronic Lung Disease. Frontiers in Microbiology, 2019, 10, 1622. | 3.5 | 13 |
| 58 | Peptidyl-Prolyl Isomerase <i>ppiB</i> Is Essential for Proteome Homeostasis and Virulence in Burkholderia pseudomallei. Infection and Immunity, 2019, 87, . | 2.2 | 12 |
| 59 | Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year Burkholderia pseudomallei infection. PLoS Pathogens, 2020, 16, e1008298. | 4.7 | 12 |
| 60 | Burkholderia pseudomallei distribution in Australasia is linked to paleogeographic and anthropogenic history. PLoS ONE, 2018, 13, e0206845. | 2.5 | 11 |
| 61 | Whole-Genome Sequences of Five Burkholderia pseudomallei Isolates from Australian Cystic Fibrosis Patients. Genome Announcements, 2015, 3, . | 0.8 | 10 |
| 62 | Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. Microbial Genomics, 2017, 3, e000117. | 2.0 | 10 |
| 63 | Selective isolation of Yersinia pestis from plague-infected fleas. Journal of Microbiological Methods, 2010, 82, 95-97. | 1.6 | 9 |
| 64 | A Persisting Nontropical Focus of Burkholderia pseudomallei with Limited Genome Evolution over Five Decades. MSystems, 2020, 5, . | 3.8 | 9 |
| 65 | Molecular Epidemiology of Third-Generation-Cephalosporin-Resistant <i>Enterobacteriaceae</i> in Southeast Queensland, Australia. Antimicrobial Agents and Chemotherapy, 2021, 65, . | 3.2 | 9 |
| 66 | Identification and typing of <i>Francisella tularensis</i> with a highly automated genotyping assay. Letters in Applied Microbiology, 2013, 56, 128-134. | 2.2 | 8 |
| 67 | Staphylococcus aureus from patients with chronic rhinosinusitis show minimal genetic association between polyp and non-polyp phenotypes. BMC Ear, Nose and Throat Disorders, 2018, 18, 16. | 2.6 | 8 |
| 68 | Quantitative real-time PCR assay for the rapid identification of the intrinsically multidrug-resistant bacterial pathogen Stenotrophomonas maltophilia. Microbial Genomics, 2019, 5, . | 2.0 | 8 |
| 69 | pPSY: A vector for the stable cloning and expression of streptomycete single gene phenotypes in Escherichia coli. Plasmid, 2008, 60, 53-58. | 1.4 | 7 |
| 70 | Development and validation of a triplex quantitative real-time PCR assay to detect efflux pump-mediated antibiotic resistance in <i>Burkholderia pseudomallei</i> . Future Microbiology, 2018, 13, 1403-1418. | 2.0 | 7 |
| 71 | Pharmacodynamic Evaluation of Plasma and Epithelial Lining Fluid Exposures of Amikacin against Pseudomonas aeruginosa in a Dynamic <i>In Vitro</i> Hollow-Fiber Infection Model. Antimicrobial Agents and Chemotherapy, 2020, 64, . | 3.2 | 7 |
| 72 | Human Infection with Burkholderia thailandensis, China, 2013. Emerging Infectious Diseases, 2018, 24, 953-954. | 4.3 | 6 |

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| 73 | Comparative genomic analysis identifies X-factor (haemin)-independent Haemophilus haemolyticus: a formal re-classification of 'Haemophilus intermedius'. Microbial Genomics, 2020, 6, . | 2.0 | 6 |
| 74 | Genomic diversity and antimicrobial resistance of Prevotella species isolated from chronic lung disease airways. Microbial Genomics, 2022, 8, . | 2.0 | 6 |
| 75 | Plasmid encoded antibiotics inhibit protozoan predation of Escherichia coli K12. Plasmid, 2011, 66, 152-158. | 1.4 | 5 |
| 76 | Complete sequence and analysis of the stability functions of pPSX, a vector that allows stable cloning and expression of Streptomycete genes in Escherichia coli K12. Plasmid, 2009, 62, 39-43. | 1.4 | 4 |
| 77 | Molecular genotyping of Acinetobacter spp. isolated in Arizona, USA, using multilocus PCR and mass spectrometry. Journal of Medical Microbiology, 2013, 62, 1295-1300. | 1.8 | 4 |
| 78 | Melioidosis in New Caledonia: a dominant strain in a transmission hotspot. Epidemiology and Infection, 2016, 144, 1330-1337. | 2.1 | 4 |
| 79 | Express Yourself: Quantitative Real-Time PCR Assays for Rapid Chromosomal Antimicrobial Resistance Detection in Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 2022, 66, e0020422. | 3.2 | 4 |
| 80 | Whole-Genome Sequencing to Differentiate Relapse From Reinfection in Community-Onset Bacteremic Acinetobacter baumannii Pneumonia. Open Forum Infectious Diseases, 2019, 6, ofz263. | 0.9 | 3 |
| 81 | Duplex real-time PCR assay for the simultaneous detection of Achromobacter xylosoxidans and Achromobacter spp Microbial Genomics, 2020, 6, . | 2.0 | 3 |
| 82 | Complete Genome Sequence of the Environmental Burkholderia pseudomallei Sequence Type 131 Isolate MSHR1435, Associated with a Chronic Melioidosis Infection. Genome Announcements, 2018, 6, . | 0.8 | 2 |
| 83 | The Scourge of Antibiotic-resistant Infections in Cystic Fibrosis. Trends in Microbiology, 2019, 27, 289-291. | 7.7 | 1 |
| 84 | Comparative genomics of Nocardia seriolae reveals recent importation and subsequent widespread dissemination in mariculture farms in the South Central Coast region, Vietnam. Microbial Genomics, 2022, 8, . | 2.0 | 1 |