

Derek S Sarovich

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5719203/publications.pdf>

Version: 2024-02-01

84
papers

2,429
citations

196777

29
h-index

299063

42
g-index

102
all docs

102
docs citations

102
times ranked

2243
citing authors

#	ARTICLE	IF	CITATIONS
1	Within-Host Evolution of <i>Burkholderia pseudomallei</i> over a Twelve-Year Chronic Carriage Infection. <i>MBio</i> , 2013, 4, .	1.8	121
2	Variable Virulence Factors in <i>Burkholderia pseudomallei</i> (Meloidosis) Associated with Human Disease. <i>PLoS ONE</i> , 2014, 9, e91682.	1.1	99
3	SPANDx: a genomics pipeline for comparative analysis of large haploid whole genome re-sequencing datasets. <i>BMC Research Notes</i> , 2014, 7, 618.	0.6	94
4	Development of a Prototype Lateral Flow Immunoassay (LFI) for the Rapid Diagnosis of Melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2727.	1.3	93
5	Molecular Epidemiologic Investigation of an Anthrax Outbreak among Heroin Users, Europe. <i>Emerging Infectious Diseases</i> , 2012, 18, 1307-1313.	2.0	77
6	Characterization of Ceftazidime Resistance Mechanisms in Clinical Isolates of <i>Burkholderia pseudomallei</i> from Australia. <i>PLoS ONE</i> , 2012, 7, e30789.	1.1	75
7	<i>Burkholderia pseudomallei</i> Isolates from Sarawak, Malaysian Borneo, Are Predominantly Susceptible to Aminoglycosides and Macrolides. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 162-166.	1.4	72
8	Within-Host Evolution of <i>Burkholderia pseudomallei</i> during Chronic Infection of Seven Australasian Cystic Fibrosis Patients. <i>MBio</i> , 2017, 8, .	1.8	70
9	Development of ceftazidime resistance in an acute <i>Burkholderia pseudomallei</i> infection. <i>Infection and Drug Resistance</i> , 2012, 5, 129.	1.1	60
10	Phylogenomic Analysis Reveals an Asian Origin for African <i>Burkholderia pseudomallei</i> and Further Supports Melioidosis Endemicity in Africa. <i>MSphere</i> , 2016, 1, .	1.3	57
11	<i>Haemophilus influenzae</i> : using comparative genomics to accurately identify a highly recombinogenic human pathogen. <i>BMC Genomics</i> , 2015, 16, 641.	1.2	53
12	Within-Host Evolution of <i>Burkholderia pseudomallei</i> in Four Cases of Acute Melioidosis. <i>PLoS Pathogens</i> , 2010, 6, e1000725.	2.1	50
13	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage from the Indian Subcontinent. <i>MBio</i> , 2019, 10, .	1.8	50
14	Development and Validation of <i>Burkholderia pseudomallei</i> -Specific Real-Time PCR Assays for Clinical, Environmental or Forensic Detection Applications. <i>PLoS ONE</i> , 2012, 7, e37723.	1.1	50
15	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	1.8	49
16	Mechanisms of Resistance to Folate Pathway Inhibitors in <i>Burkholderia pseudomallei</i> : Deviation from the Norm. <i>MBio</i> , 2017, 8, .	1.8	47
17	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, 954-963.	1.4	46
18	Distribution of <i>Burkholderia pseudomallei</i> in Northern Australia, a Land of Diversity. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3463-3468.	1.4	45

#	ARTICLE	IF	CITATIONS
19	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, 2059-2062.	1.8	44
20	Whole-Genome Sequencing Confirms that <i>Burkholderia pseudomallei</i> Multilocus Sequence Types Common to Both Cambodia and Australia Are Due to Homoplasy. <i>Journal of Clinical Microbiology</i> , 2015, 53, 323-326.	1.8	44
21	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, 650-653.	1.8	43
22	<i>Chlamydia trachomatis</i> from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. <i>Nature Communications</i> , 2016, 7, 10688.	5.8	42
23	Use of Whole-Genome Sequencing to Link <i>Burkholderia pseudomallei</i> from Air Sampling to Mediastinal Melioidosis, Australia. <i>Emerging Infectious Diseases</i> , 2015, 21, 2052-2054.	2.0	41
24	Genomic epidemiology of severe community-onset <i>Acinetobacter baumannii</i> infection. <i>Microbial Genomics</i> , 2019, 5, .	1.0	40
25	Whole-Genome Sequences of 80 Environmental and Clinical Isolates of <i>Burkholderia pseudomallei</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	38
26	Comparative Genomics of <i>Burkholderia singularis</i> sp. nov., a Low G+C Content, Free-Living Bacterium That Defies Taxonomic Dissection of the Genus <i>Burkholderia</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1679.	1.5	36
27	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, 1144-1148.	1.8	35
28	Simultaneous identification of <i>Haemophilus influenzae</i> and <i>Haemophilus haemolyticus</i> using real-time PCR. <i>Future Microbiology</i> , 2017, 12, 585-593.	1.0	35
29	Raising the Stakes: Loss of Efflux Pump Regulation Decreases Meropenem Susceptibility in <i>Burkholderia pseudomallei</i> . <i>Clinical Infectious Diseases</i> , 2018, 67, 243-250.	2.9	34
30	Absence of an Important Vaccine and Diagnostic Target in Carriage- and Disease-Related Nontypeable <i>Haemophilus influenzae</i> . <i>Vaccine Journal</i> , 2014, 21, 250-252.	3.2	33
31	Whole-Genome Sequencing of <i>Burkholderia pseudomallei</i> Isolates from an Unusual Melioidosis Case Identifies a Polyclonal Infection with the Same Multilocus Sequence Type. <i>Journal of Clinical Microbiology</i> , 2015, 53, 282-286.	1.8	32
32	Dominance of multidrug resistant CC271 clones in macrolide-resistant streptococcus pneumoniae in Arizona. <i>BMC Microbiology</i> , 2012, 12, 12.	1.3	31
33	Endemic Melioidosis in Residents of Desert Region after Atypically Intense Rainfall in Central Australia, 2011. <i>Emerging Infectious Diseases</i> , 2015, 21, 1038-1040.	2.0	30
34	Suspected cases of intracontinental <i>Burkholderia pseudomallei</i> sequence type homoplasy resolved using whole-genome sequencing. <i>Microbial Genomics</i> , 2017, 3, .	1.0	30
35	Transcriptomic analysis of longitudinal <i>Burkholderia pseudomallei</i> infecting the cystic fibrosis lung. <i>Microbial Genomics</i> , 2018, 4, .	1.0	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. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	27

#	ARTICLE	IF	CITATIONS
37	Single-molecule sequencing reveals the molecular basis of multidrug-resistance in ST772 methicillin-resistant <i>Staphylococcus aureus</i> . <i>BMC Genomics</i> , 2015, 16, 388.	1.2	24
38	Plasmacytoid dendritic cells appear inactive during sub-microscopic <i>Plasmodium falciparum</i> blood-stage infection, yet retain their ability to respond to TLR stimulation. <i>Scientific Reports</i> , 2017, 7, 2596.	1.6	24
39	Loss of Methyltransferase Function and Increased Efflux Activity Leads to Doxycycline Resistance in <i>Burkholderia pseudomallei</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	23
40	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.	1.0	23
41	Accurate and Rapid Identification of the <i>Burkholderia pseudomallei</i> Near-Neighbour, <i>Burkholderia ubonensis</i> , Using Real-Time PCR. <i>PLoS ONE</i> , 2013, 8, e71647.	1.1	21
42	Melioidosis from Contaminated Bore Water and Successful UV Sterilization. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 367-368.	0.6	19
43	Autochthonous Melioidosis in Humans, Madagascar, 2012 and 2013. <i>Emerging Infectious Diseases</i> , 2014, 20, 1735-1737.	2.0	19
44	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, .	1.0	19
45	Taking the next-gen step: Comprehensive antimicrobial resistance detection from <i>Burkholderia pseudomallei</i> . <i>EBioMedicine</i> , 2021, 63, 103152.	2.7	18
46	Improved multilocus sequence typing of <i>Burkholderia pseudomallei</i> and closely related species. <i>Journal of Medical Microbiology</i> , 2016, 65, 992-997.	0.7	18
47	pPSX: A novel vector for the cloning and heterologous expression of antitumor antibiotic gene clusters. <i>Plasmid</i> , 2007, 57, 306-313.	0.4	17
48	<i>Burkholderia pseudomallei</i> Genotype Distribution in the Northern Territory, Australia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 94, 68-72.	0.6	17
49	Genomic Insights Into the Melioidosis Pathogen, <i>Burkholderia pseudomallei</i> . <i>Current Tropical Medicine Reports</i> , 2017, 4, 95-102.	1.6	17
50	Increased Neurotropic Threat from <i>Burkholderia pseudomallei</i> Strains with a B. mallei-like Variation in the <i>bimA</i> Motility Gene, Australia. <i>Emerging Infectious Diseases</i> , 2017, 23, .	2.0	17
51	<i>Burkholderia pseudomallei</i> 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.	0.4	16
52	Phylogeographic, genomic, and meropenem susceptibility analysis of <i>Burkholderia ubonensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005928.	1.3	16
53	Whole-Genome Sequences of <i>Burkholderia pseudomallei</i> Isolates Exhibiting Decreased Meropenem Susceptibility. <i>Genome Announcements</i> , 2017, 5, .	0.8	15
54	Investigation of trimethoprim/sulfamethoxazole resistance in an emerging sequence type 5 methicillin-resistant <i>Staphylococcus aureus</i> clone reveals discrepant resistance reporting. <i>Clinical Microbiology and Infection</i> , 2018, 24, 1027-1029.	2.8	15

#	ARTICLE	IF	CITATIONS
55	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.	1.3	14
56	Virulence of the Melioidosis Pathogen <i>Burkholderia pseudomallei</i> Requires the Oxidoreductase Membrane Protein DsbB. <i>Infection and Immunity</i> , 2018, 86, .	1.0	13
57	Molecular Signatures of Non-typeable <i>Haemophilus influenzae</i> Lung Adaptation in Pediatric Chronic Lung Disease. <i>Frontiers in Microbiology</i> , 2019, 10, 1622.	1.5	13
58	Peptidyl-Prolyl Isomerase <i>ppiB</i> Is Essential for Proteome Homeostasis and Virulence in <i>Burkholderia pseudomallei</i> . <i>Infection and Immunity</i> , 2019, 87, .	1.0	12
59	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.	2.1	12
60	<i>Burkholderia pseudomallei</i> distribution in Australasia is linked to paleogeographic and anthropogenic history. <i>PLoS ONE</i> , 2018, 13, e0206845.	1.1	11
61	Whole-Genome Sequences of Five <i>Burkholderia pseudomallei</i> Isolates from Australian Cystic Fibrosis Patients. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
62	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. <i>Microbial Genomics</i> , 2017, 3, e000117.	1.0	10
63	Selective isolation of <i>Yersinia pestis</i> from plague-infected fleas. <i>Journal of Microbiological Methods</i> , 2010, 82, 95-97.	0.7	9
64	A Persisting Nontropical Focus of <i>Burkholderia pseudomallei</i> with Limited Genome Evolution over Five Decades. <i>MSystems</i> , 2020, 5, .	1.7	9
65	Molecular Epidemiology of Third-Generation-Cephalosporin-Resistant <i>Enterobacteriaceae</i> in Southeast Queensland, Australia. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	9
66	Identification and typing of <i>Francisella tularensis</i> with a highly automated genotyping assay. <i>Letters in Applied Microbiology</i> , 2013, 56, 128-134.	1.0	8
67	<i>Staphylococcus aureus</i> 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.	2.6	8
68	Quantitative real-time PCR assay for the rapid identification of the intrinsically multidrug-resistant bacterial pathogen <i>Stenotrophomonas maltophilia</i> . <i>Microbial Genomics</i> , 2019, 5, .	1.0	8
69	pPSY: A vector for the stable cloning and expression of streptomycete single gene phenotypes in <i>Escherichia coli</i> . <i>Plasmid</i> , 2008, 60, 53-58.	0.4	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> . <i>Future Microbiology</i> , 2018, 13, 1403-1418.	1.0	7
71	Pharmacodynamic Evaluation of Plasma and Epithelial Lining Fluid Exposures of Amikacin against <i>Pseudomonas aeruginosa</i> in a Dynamic <i>In Vitro</i> Hollow-Fiber Infection Model. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	7
72	Human Infection with <i>Burkholderia thailandensis</i> , China, 2013. <i>Emerging Infectious Diseases</i> , 2018, 24, 953-954.	2.0	6

#	ARTICLE	IF	CITATIONS
73	Comparative genomic analysis identifies X-factor (haemin)-independent <i>Haemophilus haemolyticus</i> : a formal re-classification of ' <i>Haemophilus intermedius</i> '. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
74	Genomic diversity and antimicrobial resistance of <i>Prevotella</i> species isolated from chronic lung disease airways. <i>Microbial Genomics</i> , 2022, 8, .	1.0	6
75	Plasmid encoded antibiotics inhibit protozoan predation of <i>Escherichia coli</i> K12. <i>Plasmid</i> , 2011, 66, 152-158.	0.4	5
76	Complete sequence and analysis of the stability functions of pPSX, a vector that allows stable cloning and expression of <i>Streptomyces</i> genes in <i>Escherichia coli</i> K12. <i>Plasmid</i> , 2009, 62, 39-43.	0.4	4
77	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.	0.7	4
78	Melioidosis in New Caledonia: a dominant strain in a transmission hotspot. <i>Epidemiology and Infection</i> , 2016, 144, 1330-1337.	1.0	4
79	Express Yourself: Quantitative Real-Time PCR Assays for Rapid Chromosomal Antimicrobial Resistance Detection in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0020422.	1.4	4
80	Whole-Genome Sequencing to Differentiate Relapse From Reinfection in Community-Onset Bacteremic <i>Acinetobacter baumannii</i> Pneumonia. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz263.	0.4	3
81	Duplex real-time PCR assay for the simultaneous detection of <i>Achromobacter xylosoxidans</i> and <i>Achromobacter</i> spp.. <i>Microbial Genomics</i> , 2020, 6, .	1.0	3
82	Complete Genome Sequence of the Environmental <i>Burkholderia pseudomallei</i> Sequence Type 131 Isolate MSHR1435, Associated with a Chronic Melioidosis Infection. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
83	The Scourge of Antibiotic-resistant Infections in Cystic Fibrosis. <i>Trends in Microbiology</i> , 2019, 27, 289-291.	3.5	1
84	Comparative genomics of <i>Nocardia seriolae</i> reveals recent importation and subsequent widespread dissemination in mariculture farms in the South Central Coast region, Vietnam. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1