Derek S Sarovich

List of Publications by Year in Descending Order

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88	1,627	24	35
papers	citations	h-index	g-index
102	**2,174**	**5.7**	**4.4**
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
88	Genomic diversity and antimicrobial resistance of species isolated from chronic lung disease airways.. *Microbial Genomics*, **2022**, 8,	4.4	2
87	Express Yourself: Quantitative Real-Time PCR Assays for Rapid Chromosomal Antimicrobial Resistance Detection in Pseudomonas aeruginosa.. *Antimicrobial Agents and Chemotherapy*, **2022**, e0020422	5.9	1
86	Molecular Epidemiology of Third-Generation-Cephalosporin-Resistant in Southeast Queensland, Australia. *Antimicrobial Agents and Chemotherapy*, **2021**, 65,	5.9	3
85	Taking the next-gen step: Comprehensive antimicrobial resistance detection from Burkholderia pseudomallei. *EBioMedicine*, **2021**, 63, 103152	8.8	5
84	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year Burkholderia pseudomallei infection. *PLoS Pathogens*, **2020**, 16, e1008298	7.6	6
83	Comparative Genomics and Antimicrobial Resistance Profiling of Isolates Reveal Nosocomial Transmission and Susceptibility to Fluoroquinolones, Tetracyclines, and Trimethoprim-Sulfamethoxazole. *Journal of Clinical Microbiology*, **2020**, 58,	9.7	12
82	Comparative genomic analysis identifies X-factor (haemin)-independent : a formal re-classification of ''. *Microbial Genomics*, **2020**, 6,	4.4	3
81	Comparative genomics confirms a rare melioidosis human-to-human transmission event and reveals incorrect phylogenomic reconstruction due to polyclonality. *Microbial Genomics*, **2020**, 6,	4.4	8
80	Duplex real-time PCR assay for the simultaneous detection of and spp. *Microbial Genomics*, **2020**, 6,	4.4	1
79	Pharmacodynamic Evaluation of Plasma and Epithelial Lining Fluid Exposures of Amikacin against Pseudomonas aeruginosa in a Dynamic Hollow-Fiber Infection Model. *Antimicrobial Agents and Chemotherapy*, **2020**, 64,	5.9	2
78	A Persisting Nontropical Focus of Burkholderia pseudomallei with Limited Genome Evolution over Five Decades. *MSystems*, **2020**, 5,	7.6	5
77	Molecular Signatures of Non-typeable Lung Adaptation in Pediatric Chronic Lung Disease. *Frontiers in Microbiology*, **2019**, 10, 1622	5.7	7
76	The Scourge of Antibiotic-resistant Infections in Cystic Fibrosis. *Trends in Microbiology*, **2019**, 27, 289-291	12.4	
75	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	1	12
74	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	4.8	8
73	Whole-Genome Sequencing to Differentiate Relapse From Reinfection in Community-Onset Bacteremic Pneumonia. *Open Forum Infectious Diseases*, **2019**, 6, ofz263	1	1
72	Peptidyl-Prolyl Isomerase Is Essential for Proteome Homeostasis and Virulence in Burkholderia pseudomallei. *Infection and Immunity*, **2019**, 87,	3.7	6

71	Genomic epidemiology of severe community-onset Acinetobacter baumannii infection. *Microbial Genomics*, **2019**, 5,	4.4	15
70	Quantitative real-time PCR assay for the rapid identification of the intrinsically multidrug-resistant bacterial pathogen. *Microbial Genomics*, **2019**, 5,	4.4	6
69	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant Staphylococcus aureus Lineage from the Indian Subcontinent. *MBio*, **2019**, 10,	7.8	22
68	Virulence of the Melioidosis Pathogen Burkholderia pseudomallei Requires the Oxidoreductase Membrane Protein DsbB. *Infection and Immunity*, **2018**, 86,	3.7	10
67	Complete Genome Sequence of the Environmental Burkholderia pseudomallei Sequence Type 131 Isolate MSHR1435, Associated with a Chronic Melioidosis Infection. *Genome Announcements*, **2018**, 6,		1
66	Raising the Stakes: Loss of Efflux Pump Regulation Decreases Meropenem Susceptibility in Burkholderia pseudomallei. *Clinical Infectious Diseases*, **2018**, 67, 243-250	11.6	20
65	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	9.5	10
64	Human Infection with Burkholderia thailandensis, China, 2013. *Emerging Infectious Diseases*, **2018**, 24, 953-954	10.2	5
63	Transcriptomic analysis of longitudinal Burkholderia pseudomallei infecting the cystic fibrosis lung. *Microbial Genomics*, **2018**, 4,	4.4	20
62	Burkholderia pseudomallei distribution in Australasia is linked to paleogeographic and anthropogenic history. *PLoS ONE*, **2018**, 13, e0206845	3.7	4
61	Development and validation of a triplex quantitative real-time PCR assay to detect efflux pump-mediated antibiotic resistance in Burkholderia pseudomallei. *Future Microbiology*, **2018**, 13, 1403-1418	2.9	3
60	from patients with chronic rhinosinusitis show minimal genetic association between polyp and non-polyp phenotypes. *BMC Ear, Nose and Throat Disorders*, **2018**, 18, 16	8	5
59	Within-Host Evolution of during Chronic Infection of Seven Australasian Cystic Fibrosis Patients. *MBio*, **2017**, 8,	7.8	33
58	Simultaneous identification of Haemophilus influenzae and Haemophilus haemolyticus using real-time PCR. *Future Microbiology*, **2017**, 12, 585-593	2.9	20
57	Whole-Genome Sequences of Isolates Exhibiting Decreased Meropenem Susceptibility. *Genome Announcements*, **2017**, 5,		12
56	Loss of Methyltransferase Function and Increased Efflux Activity Leads to Doxycycline Resistance in Burkholderia pseudomallei. *Antimicrobial Agents and Chemotherapy*, **2017**, 61,	5.9	14
55	Mechanisms of Resistance to Folate Pathway Inhibitors in : Deviation from the Norm. *MBio*, **2017**, 8,	7.8	31
54	Increased Neurotropic Threat from Burkholderia pseudomallei Strains with a B. mallei-like Variation in the bimA Motility Gene, Australia. *Emerging Infectious Diseases*, **2017**, 23,	10.2	10

53	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	4.9	18
52	Genomic Insights Into the Melioidosis Pathogen, Burkholderia pseudomallei. *Current Tropical Medicine Reports*, **2017**, 4, 95-102	5	11
51	Comparative Genomics of sp. nov., a Low G+C Content, Free-Living Bacterium That Defies Taxonomic Dissection of the Genus. *Frontiers in Microbiology*, **2017**, 8, 1679	5.7	22
50	Phylogeographic, genomic, and meropenem susceptibility analysis of Burkholderia ubonensis. *PLoS Neglected Tropical Diseases*, **2017**, 11, e0005928	4.8	9
49	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. *Microbial Genomics*, **2017**, 3, e000117	4.4	8
48	Suspected cases of intracontinental Burkholderia pseudomallei sequence type homoplasy resolved using whole-genome sequencing. *Microbial Genomics*, **2017**, 3,	4.4	21
47	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. *MBio*, **2016**, 7,	7.8	37
46	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, 954-63	4.8	34
45	Burkholderia pseudomallei Genotype Distribution in the Northern Territory, Australia. *American Journal of Tropical Medicine and Hygiene*, **2016**, 94, 68-72	3.2	15
44	Improved multilocus sequence typing of Burkholderia pseudomallei and closely related species. *Journal of Medical Microbiology*, **2016**, 65, 992-997	3.2	16
43	Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. *Microbial Genomics*, **2016**, 2, e000067	4.4	20
42	Phylogenomic Analysis Reveals an Asian Origin for African Burkholderia pseudomallei and Further Supports Melioidosis Endemicity in Africa. *MSphere*, **2016**, 1,	5	40
41	Chlamydia trachomatis from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. *Nature Communications*, **2016**, 7, 10688	17.4	30
40	Melioidosis in New Caledonia: a dominant strain in a transmission hotspot. *Epidemiology and Infection*, **2016**, 144, 1330-7	4.3	1
39	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, 282-6	9.7	23
38	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, 1144-8	9.7	24
37	Single-molecule sequencing reveals the molecular basis of multidrug-resistance in ST772 methicillin-resistant Staphylococcus aureus. *BMC Genomics*, **2015**, 16, 388	4.5	15
36	Endemic melioidosis in residents of desert region after atypically intense rainfall in central Australia, 2011. *Emerging Infectious Diseases*, **2015**, 21, 1038-40	10.2	21

35	Whole-Genome Sequences of Five Burkholderia pseudomallei Isolates from Australian Cystic Fibrosis Patients. *Genome Announcements*, **2015**, 3,		7
34	Haemophilus influenzae: using comparative genomics to accurately identify a highly recombinogenic human pathogen. *BMC Genomics*, **2015**, 16, 641	4.5	39
33	Use of Whole-Genome Sequencing to Link Burkholderia pseudomallei from Air Sampling to Mediastinal Melioidosis, Australia. *Emerging Infectious Diseases*, **2015**, 21, 2052-4	10.2	31
32	Whole-Genome Sequences of 80 Environmental and Clinical Isolates of Burkholderia pseudomallei. *Genome Announcements*, **2015**, 3,		21
31	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, 323-6	9.7	37
30	Variable virulence factors in Burkholderia pseudomallei (melioidosis) associated with human disease. *PLoS ONE*, **2014**, 9, e91682	3.7	69
29	Autochthonous melioidosis in humans, Madagascar, 2012 and 2013. *Emerging Infectious Diseases*, **2014**, 20, 1739-41	10.2	18
28	Development of a prototype lateral flow immunoassay (LFI) for the rapid diagnosis of melioidosis. *PLoS Neglected Tropical Diseases*, **2014**, 8, e2727	4.8	61
27	Burkholderia pseudomallei isolates from Sarawak, Malaysian Borneo, are predominantly susceptible to aminoglycosides and macrolides. *Antimicrobial Agents and Chemotherapy*, **2014**, 58, 162-6	5.9	42
26	Recurrent melioidosis in the Darwin Prospective Melioidosis Study: improving therapies mean that relapse cases are now rare. *Journal of Clinical Microbiology*, **2014**, 52, 650-3	9.7	34
25	SPANDx: a genomics pipeline for comparative analysis of large haploid whole genome re-sequencing datasets. *BMC Research Notes*, **2014**, 7, 618	2.3	69
24	Distribution of Burkholderia pseudomallei in northern Australia, a land of diversity. *Applied and Environmental Microbiology*, **2014**, 80, 3463-8	4.8	32
23	Absence of an important vaccine and diagnostic target in carriage- and disease-related nontypeable Haemophilus influenzae. *Vaccine Journal*, **2014**, 21, 250-2		30
22	Molecular genotyping of Acinetobacter spp. isolated in Arizona, USA, using multilocus PCR and mass spectrometry. *Journal of Medical Microbiology*, **2013**, 62, 1295-1300	3.2	3
21	Identification and typing of Francisella tularensis with a highly automated genotyping assay. *Letters in Applied Microbiology*, **2013**, 56, 128-34	2.9	7
20	Within-host evolution of Burkholderia pseudomallei over a twelve-year chronic carriage infection. *MBio*, **2013**, 4,	7.8	80
19	Melioidosis from contaminated bore water and successful UV sterilization. *American Journal of Tropical Medicine and Hygiene*, **2013**, 89, 367-8	3.2	12
18	Accurate and rapid identification of the Burkholderia pseudomallei near-neighbour, Burkholderia ubonensis, using real-time PCR. *PLoS ONE*, **2013**, 8, e71647	3.7	17

17	Dominance of multidrug resistant CC271 clones in macrolide-resistant streptococcus pneumoniae in Arizona. *BMC Microbiology*, **2012**, 12, 12	4.5	22
16	Molecular epidemiologic investigation of an anthrax outbreak among heroin users, Europe. *Emerging Infectious Diseases*, **2012**, 18, 1307-13	10.2	58
15	Development of ceftazidime resistance in an acute Burkholderia pseudomallei infection. *Infection and Drug Resistance*, **2012**, 5, 129-32	4.2	43
14	Comparison of TaqMan PCR assays for detection of the melioidosis agent Burkholderia pseudomallei in clinical specimens. *Journal of Clinical Microbiology*, **2012**, 50, 2059-62	9.7	33
13	Characterization of ceftazidime resistance mechanisms in clinical isolates of Burkholderia pseudomallei from Australia. *PLoS ONE*, **2012**, 7, e30789	3.7	53
12	Development and validation of Burkholderia pseudomallei-specific real-time PCR assays for clinical, environmental or forensic detection applications. *PLoS ONE*, **2012**, 7, e37723	3.7	33
11	Plasmid encoded antibiotics inhibit protozoan predation of Escherichia coli K12. *Plasmid*, **2011**, 66, 152-8	3.3	4
10	Within-host evolution of Burkholderia pseudomallei in four cases of acute melioidosis. *PLoS Pathogens*, **2010**, 6, e1000725	7.6	45
9	Selective isolation of Yersinia pestis from plague-infected fleas. *Journal of Microbiological Methods*, **2010**, 82, 95-7	2.8	7
8	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	3.3	3
7	pPSY: a vector for the stable cloning and expression of streptomycete single gene phenotypes in Escherichia coli. *Plasmid*, **2008**, 60, 53-8	3.3	7
6	pPSX: a novel vector for the cloning and heterologous expression of antitumor antibiotic gene clusters. *Plasmid*, **2007**, 57, 306-13	3.3	16
5	Rapid fluoroquinolone resistance detection in Pseudomonas aeruginosa using mismatch amplification mutation assay-based real-time PCR		1
4	Evolution and global transmission of a multidrug-resistant, community-associated MRSA lineage from the Indian subcontinent		1
3	Tracing the environmental footprint of theBurkholderia pseudomalleilipopolysaccharide genotypes in the tropical ▯Top End▯of the Northern Territory, Australia		2
2	Molecular signatures of non-typeable Haemophilus influenzae lung adaptation in paediatric chronic lung disease		1
1	Genomic diversity and antimicrobial resistance of Prevotella spp. isolated from chronic lung disease airways		1