

# Erin P Price

## List of Publications by Year in Descending Order

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**Version:** 2024-04-25

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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.

93  
papers

2,086  
citations

29  
h-index

41  
g-index

107  
ext. papers

2,598  
ext. citations

5.4  
avg, IF

4.49  
L-index

#	Paper	IF	Citations
93	Genomic diversity and antimicrobial resistance of species isolated from chronic lung disease airways.. <i>Microbial Genomics</i> , <b>2022</b> , 8,	4.4	2
92	Express Yourself: Quantitative Real-Time PCR Assays for Rapid Chromosomal Antimicrobial Resistance Detection in <i>Pseudomonas aeruginosa</i> .. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2022</b> , e0020422	5.9	1
91	Molecular Epidemiology of Third-Generation-Cephalosporin-Resistant in Southeast Queensland, Australia. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , 65,	5.9	3
90	Taking the next-gen step: Comprehensive antimicrobial resistance detection from <i>Burkholderia pseudomallei</i> . <i>EBioMedicine</i> , <b>2021</b> , 63, 103152	8.8	5
89	Emergence of <i>Burkholderia pseudomallei</i> Sequence Type 562, Northern Australia. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 1057-1067	10.2	3
88	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> , <b>2020</b> , 16, e1008298	7.6	6
87	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> , <b>2020</b> , 58,	9.7	12
86	Comparative genomic analysis identifies X-factor (haemin)-independent : a formal re-classification of ". <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	3
85	Comparative genomics confirms a rare melioidosis human-to-human transmission event and reveals incorrect phylogenomic reconstruction due to polyclonality. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	8
84	Duplex real-time PCR assay for the simultaneous detection of and spp. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	1
83	A Persisting Nontropical Focus of <i>Burkholderia pseudomallei</i> with Limited Genome Evolution over Five Decades. <i>MSystems</i> , <b>2020</b> , 5,	7.6	5
82	Molecular Signatures of Non-typeable Lung Adaptation in Pediatric Chronic Lung Disease. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1622	5.7	7
81	The Scourge of Antibiotic-resistant Infections in Cystic Fibrosis. <i>Trends in Microbiology</i> , <b>2019</b> , 27, 289-291	12.4	
80	Lipopolysaccharide Genotype Does Not Correlate With Severity or Outcome in Melioidosis: Host Risk Factors Remain the Critical Determinant. <i>Open Forum Infectious Diseases</i> , <b>2019</b> , 6, ofz091	1	12
79	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> , <b>2019</b> , 13, e0007369	4.8	8
78	Pan-drug-resistant and biofilm-producing strain of : first report of melioidosis from a diabetic patient in Yogyakarta, Indonesia [Letter]. <i>International Medical Case Reports Journal</i> , <b>2019</b> , 12, 117-118	1	
77	Quantitative real-time PCR assay for the rapid identification of the intrinsically multidrug-resistant bacterial pathogen. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	6

76	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> , <b>2018</b> , 6,		1
75	Raising the Stakes: Loss of Efflux Pump Regulation Decreases Meropenem Susceptibility in <i>Burkholderia pseudomallei</i> . <i>Clinical Infectious Diseases</i> , <b>2018</b> , 67, 243-250	11.6	20
74	Human Infection with <i>Burkholderia thailandensis</i> , China, 2013. <i>Emerging Infectious Diseases</i> , <b>2018</b> , 24, 953-954	10.2	5
73	Melioidosis in the Western Indian Ocean and the Importance of Improving Diagnosis, Surveillance, and Molecular Typing. <i>Tropical Medicine and Infectious Disease</i> , <b>2018</b> , 3,	3.5	4
72	Transcriptomic analysis of longitudinal <i>Burkholderia pseudomallei</i> infecting the cystic fibrosis lung. <i>Microbial Genomics</i> , <b>2018</b> , 4,	4.4	20
71	<i>Burkholderia pseudomallei</i> distribution in Australasia is linked to paleogeographic and anthropogenic history. <i>PLoS ONE</i> , <b>2018</b> , 13, e0206845	3.7	4
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> , <b>2018</b> , 13, 1403-1418	2.9	3
69	from patients with chronic rhinosinusitis show minimal genetic association between polyp and non-polyp phenotypes. <i>BMC Ear, Nose and Throat Disorders</i> , <b>2018</b> , 18, 16	8	5
68	Within-Host Evolution of during Chronic Infection of Seven Australasian Cystic Fibrosis Patients. <i>MBio</i> , <b>2017</b> , 8,	7.8	33
67	Simultaneous identification of <i>Haemophilus influenzae</i> and <i>Haemophilus haemolyticus</i> using real-time PCR. <i>Future Microbiology</i> , <b>2017</b> , 12, 585-593	2.9	20
66	Whole-Genome Sequences of Isolates Exhibiting Decreased Meropenem Susceptibility. <i>Genome Announcements</i> , <b>2017</b> , 5,		12
65	Loss of Methyltransferase Function and Increased Efflux Activity Leads to Doxycycline Resistance in <i>Burkholderia pseudomallei</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2017</b> , 61,	5.9	14
64	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. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23,	10.2	10
63	Genomic Insights Into the Melioidosis Pathogen, <i>Burkholderia pseudomallei</i> . <i>Current Tropical Medicine Reports</i> , <b>2017</b> , 4, 95-102	5	11
62	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> , <b>2017</b> , 8, 1679	5.7	22
61	Phylogeographic, genomic, and meropenem susceptibility analysis of <i>Burkholderia ubonensis</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2017</b> , 11, e0005928	4.8	9
60	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. <i>Microbial Genomics</i> , <b>2017</b> , 3, e000117	4.4	8
59	Suspected cases of intracontinental <i>Burkholderia pseudomallei</i> sequence type homoplasmy resolved using whole-genome sequencing. <i>Microbial Genomics</i> , <b>2017</b> , 3,	4.4	21

58	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , <b>2016</b> , 7,	7.8	37
57	Geographic consistency in dominant, non-typeable genotypes colonising four distinct Australian paediatric groups: a cohort study. <i>Pneumonia (Nathan Qld)</i> , <b>2016</b> , 8, 13	2.8	1
56	Unprecedented Melioidosis Cases in Northern Australia Caused by an Asian Burkholderia pseudomallei Strain Identified by Using Large-Scale Comparative Genomics. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 954-63	4.8	34
55	Burkholderia pseudomallei Genotype Distribution in the Northern Territory, Australia. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2016</b> , 94, 68-72	3.2	15
54	Improved multilocus sequence typing of Burkholderia pseudomallei and closely related species. <i>Journal of Medical Microbiology</i> , <b>2016</b> , 65, 992-997	3.2	16
53	Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000067	4.4	20
52	Phylogenomic Analysis Reveals an Asian Origin for African Burkholderia pseudomallei and Further Supports Melioidosis Endemicity in Africa. <i>MSphere</i> , <b>2016</b> , 1,	5	40
51	Melioidosis in New Caledonia: a dominant strain in a transmission hotspot. <i>Epidemiology and Infection</i> , <b>2016</b> , 144, 1330-7	4.3	1
50	The melioidosis agent Burkholderia pseudomallei and related opportunistic pathogens detected in faecal matter of wildlife and livestock in northern Australia. <i>Epidemiology and Infection</i> , <b>2016</b> , 144, 1924-32	4.3	9
49	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> , <b>2015</b> , 53, 282-6	9.7	23
48	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> , <b>2015</b> , 53, 1144-8	8.7	24
47	Endemic melioidosis in residents of desert region after atypically intense rainfall in central Australia, 2011. <i>Emerging Infectious Diseases</i> , <b>2015</b> , 21, 1038-40	10.2	21
46	Whole-Genome Sequences of Five Burkholderia pseudomallei Isolates from Australian Cystic Fibrosis Patients. <i>Genome Announcements</i> , <b>2015</b> , 3,		7
45	Haemophilus influenzae: using comparative genomics to accurately identify a highly recombinogenic human pathogen. <i>BMC Genomics</i> , <b>2015</b> , 16, 641	4.5	39
44	Use of Whole-Genome Sequencing to Link Burkholderia pseudomallei from Air Sampling to Mediastinal Melioidosis, Australia. <i>Emerging Infectious Diseases</i> , <b>2015</b> , 21, 2052-4	10.2	31
43	Whole-Genome Sequences of 80 Environmental and Clinical Isolates of Burkholderia pseudomallei. <i>Genome Announcements</i> , <b>2015</b> , 3,		21
42	Whole-genome sequencing confirms that Burkholderia pseudomallei multilocus sequence types common to both Cambodia and Australia are due to homoplasy. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 323-6	9.7	37
41	High prevalence and two dominant host-specific genotypes of Coxiella burnetii in U.S. milk. <i>BMC Microbiology</i> , <b>2014</b> , 14, 41	4.5	44

40	Microevolution of <i>Burkholderia pseudomallei</i> during an acute infection. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 3418-21	9.7	19
39	Variable virulence factors in <i>Burkholderia pseudomallei</i> (melioidosis) associated with human disease. <i>PLoS ONE</i> , <b>2014</b> , 9, e91682	3.7	69
38	<i>Burkholderia pseudomallei</i> isolates from Sarawak, Malaysian Borneo, are predominantly susceptible to aminoglycosides and macrolides. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2014</b> , 58, 162-6	5.9	42
37	Recurrent melioidosis in the Darwin Prospective Melioidosis Study: improving therapies mean that relapse cases are now rare. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 650-3	9.7	34
36	SPANDx: a genomics pipeline for comparative analysis of large haploid whole genome re-sequencing datasets. <i>BMC Research Notes</i> , <b>2014</b> , 7, 618	2.3	69
35	Distribution of <i>Burkholderia pseudomallei</i> in northern Australia, a land of diversity. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 3463-8	4.8	32
34	Absence of an important vaccine and diagnostic target in carriage- and disease-related nontypeable <i>Haemophilus influenzae</i> . <i>Vaccine Journal</i> , <b>2014</b> , 21, 250-2		30
33	Molecular genotyping of <i>Acinetobacter</i> spp. isolated in Arizona, USA, using multilocus PCR and mass spectrometry. <i>Journal of Medical Microbiology</i> , <b>2013</b> , 62, 1295-1300	3.2	3
32	The Mountain Meadows Massacre and "poisoned springs": scientific testing of the more recent, anthrax theory. <i>International Journal of Legal Medicine</i> , <b>2013</b> , 127, 77-83	3.1	3
31	Within-host evolution of <i>Burkholderia pseudomallei</i> over a twelve-year chronic carriage infection. <i>MBio</i> , <b>2013</b> , 4,	7.8	80
30	Melioidosis from contaminated bore water and successful UV sterilization. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2013</b> , 89, 367-8	3.2	12
29	Melioidosis as a consequence of sporting activity. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2013</b> , 89, 365-6	3.2	12
28	Accurate and rapid identification of the <i>Burkholderia pseudomallei</i> near-neighbour, <i>Burkholderia ubonensis</i> , using real-time PCR. <i>PLoS ONE</i> , <b>2013</b> , 8, e71647	3.7	17
27	Melt analysis of mismatch amplification mutation assays (Melt-MAMA): a functional study of a cost-effective SNP genotyping assay in bacterial models. <i>PLoS ONE</i> , <b>2012</b> , 7, e32866	3.7	63
26	Molecular epidemiologic investigation of an anthrax outbreak among heroin users, Europe. <i>Emerging Infectious Diseases</i> , <b>2012</b> , 18, 1307-13	10.2	58
25	Development of ceftazidime resistance in an acute <i>Burkholderia pseudomallei</i> infection. <i>Infection and Drug Resistance</i> , <b>2012</b> , 5, 129-32	4.2	43
24	Comparison of TaqMan PCR assays for detection of the melioidosis agent <i>Burkholderia pseudomallei</i> in clinical specimens. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 2059-62	9.7	33
23	Characterization of ceftazidime resistance mechanisms in clinical isolates of <i>Burkholderia pseudomallei</i> from Australia. <i>PLoS ONE</i> , <b>2012</b> , 7, e30789	3.7	53

22	Development and validation of Burkholderia pseudomallei-specific real-time PCR assays for clinical, environmental or forensic detection applications. <i>PLoS ONE</i> , <b>2012</b> , 7, e37723	3.7	33
21	Molecular phylogeny of Burkholderia pseudomallei from a remote region of Papua New Guinea. <i>PLoS ONE</i> , <b>2011</b> , 6, e18343	3.7	14
20	Molecular epidemiology of anthrax cases associated with recreational use of animal hides and yarn in the United States. <i>PLoS ONE</i> , <b>2011</b> , 6, e28274	3.7	32
19	An attenuated strain of Bacillus anthracis (CDC 684) has a large chromosomal inversion and altered growth kinetics. <i>BMC Genomics</i> , <b>2011</b> , 12, 477	4.5	22
18	Epidemiological tracking and population assignment of the non-clonal bacterium, Burkholderia pseudomallei. <i>PLoS Neglected Tropical Diseases</i> , <b>2011</b> , 5, e1381	4.8	22
17	Campylobacter jejuni and Campylobacter coli genotyping by high-resolution melting analysis of a flaA fragment. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 493-9	4.8	31
16	Within-host evolution of Burkholderia pseudomallei in four cases of acute melioidosis. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1000725	7.6	45
15	Selective isolation of Yersinia pestis from plague-infected fleas. <i>Journal of Microbiological Methods</i> , <b>2010</b> , 82, 95-7	2.8	7
14	Cost-effective interrogation of single nucleotide polymorphisms using the mismatch amplification mutation assay and capillary electrophoresis. <i>Electrophoresis</i> , <b>2010</b> , 31, 3881-8	3.6	14
13	Molecular epidemiology of glanders, Pakistan. <i>Emerging Infectious Diseases</i> , <b>2009</b> , 15, 2036-9	10.2	34
12	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. <i>BMC Biology</i> , <b>2009</b> , 7, 78	7.3	129
11	Characterisation of chicken Campylobacter jejuni isolates using resolution optimised single nucleotide polymorphisms and binary gene markers. <i>International Journal of Food Microbiology</i> , <b>2008</b> , 128, 304-8	5.8	12
10	Computer-aided identification of polymorphism sets diagnostic for groups of bacterial and viral genetic variants. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 278	3.6	21
9	High-resolution DNA melt curve analysis of the clustered, regularly interspaced short-palindromic-repeat locus of Campylobacter jejuni. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 3431-6	4.8	92
8	Genotyping of Campylobacter jejuni using seven single-nucleotide polymorphisms in combination with flaA short variable region sequencing. <i>Journal of Medical Microbiology</i> , <b>2006</b> , 55, 1061-1070	3.2	29
7	Fingerprinting of Campylobacter jejuni by using resolution-optimized binary gene targets derived from comparative genome hybridization studies. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 7793-803	4.8	29
6	Methicillin-resistant Staphylococcus aureus genotyping using a small set of polymorphisms. <i>Journal of Medical Microbiology</i> , <b>2006</b> , 55, 43-51	3.2	60
5	Identification and interrogation of highly informative single nucleotide polymorphism sets defined by bacterial multilocus sequence typing databases. <i>Journal of Medical Microbiology</i> , <b>2004</b> , 53, 35-45	3.2	59

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| 4 | Rapid fluoroquinolone resistance detection in <i>Pseudomonas aeruginosa</i> using mismatch amplification mutation assay-based real-time PCR                           | 1 |
| 3 | Tracing the environmental footprint of the <i>Burkholderia pseudomallei</i> lipopolysaccharide genotypes in the tropical Top End of the Northern Territory, Australia | 2 |
| 2 | Molecular signatures of non-typeable <i>Haemophilus influenzae</i> lung adaptation in paediatric chronic lung disease   | 1 |
| 1 | Genomic diversity and antimicrobial resistance of <i>Prevotella</i> spp. isolated from chronic lung disease airways   | 1 |