

Erin P Price

List of Publications by Year in descending order

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90
papers

2,859
citations

147566

31
h-index

214527

47
g-index

107
all docs

107
docs citations

107
times ranked

2357
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. BMC Biology, 2009, 7, 78.	1.7	155
2	Within-Host Evolution of Burkholderia pseudomallei over a Twelve-Year Chronic Carriage Infection. MBio, 2013, 4, .	1.8	121
3	High-Resolution DNA Melt Curve Analysis of the Clustered, Regularly Interspaced Short-Palindromic-Repeat Locus of Campylobacter jejuni. Applied and Environmental Microbiology, 2007, 73, 3431-3436.	1.4	105
4	Variable Virulence Factors in Burkholderia pseudomallei (Meloidosis) Associated with Human Disease. PLoS ONE, 2014, 9, e91682.	1.1	99
5	SPANDx: a genomics pipeline for comparative analysis of large haploid whole genome re-sequencing datasets. BMC Research Notes, 2014, 7, 618.	0.6	94
6	Molecular Epidemiologic Investigation of an Anthrax Outbreak among Heroin Users, Europe. Emerging Infectious Diseases, 2012, 18, 1307-1313.	2.0	77
7	Characterization of Ceftazidime Resistance Mechanisms in Clinical Isolates of Burkholderia pseudomallei from Australia. PLoS ONE, 2012, 7, e30789.	1.1	75
8	Melt Analysis of Mismatch Amplification Mutation Assays (Melt-MAMA): A Functional Study of a Cost-Effective SNP Genotyping Assay in Bacterial Models. PLoS ONE, 2012, 7, e32866.	1.1	73
9	Burkholderia pseudomallei Isolates from Sarawak, Malaysian Borneo, Are Predominantly Susceptible to Aminoglycosides and Macrolides. Antimicrobial Agents and Chemotherapy, 2014, 58, 162-166.	1.4	72
10	Within-Host Evolution of <i>Burkholderia pseudomallei</i> during Chronic Infection of Seven Australasian Cystic Fibrosis Patients. MBio, 2017, 8, .	1.8	70
11	Identification and interrogation of highly informative single nucleotide polymorphism sets defined by bacterial multilocus sequence typing databases. Journal of Medical Microbiology, 2004, 53, 35-45.	0.7	67
12	Methicillin-resistant Staphylococcus aureus genotyping using a small set of polymorphisms. Journal of Medical Microbiology, 2006, 55, 43-51.	0.7	63
13	Development of ceftazidime resistance in an acute Burkholderia pseudomallei infection. Infection and Drug Resistance, 2012, 5, 129.	1.1	60
14	Phylogenomic Analysis Reveals an Asian Origin for African Burkholderia pseudomallei and Further Supports Melioidosis Endemicity in Africa. MSphere, 2016, 1, .	1.3	57
15	Haemophilus influenzae: using comparative genomics to accurately identify a highly recombinogenic human pathogen. BMC Genomics, 2015, 16, 641.	1.2	53
16	Within-Host Evolution of Burkholderia pseudomallei in Four Cases of Acute Melioidosis. PLoS Pathogens, 2010, 6, e1000725.	2.1	50
17	Development and Validation of Burkholderia pseudomallei-Specific Real-Time PCR Assays for Clinical, Environmental or Forensic Detection Applications. PLoS ONE, 2012, 7, e37723.	1.1	50
18	High prevalence and two dominant host-specific genotypes of Coxiella burnetii in U.S. milk. BMC Microbiology, 2014, 14, 41.	1.3	49

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19	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	1.8	49
20	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
21	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
22	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
23	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
24	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
25	Molecular Epidemiology of Glanders, Pakistan. <i>Emerging Infectious Diseases</i> , 2009, 15, 2036-2039.	2.0	42
26	Molecular Epidemiology of Anthrax Cases Associated with Recreational Use of Animal Hides and Yarn in the United States. <i>PLoS ONE</i> , 2011, 6, e28274.	1.1	42
27	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
28	Whole-Genome Sequences of 80 Environmental and Clinical Isolates of <i>Burkholderia pseudomallei</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	38
29	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
30	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
31	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
32	<i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> Genotyping by High-Resolution Melting Analysis of a <i>flaA</i> Fragment. <i>Applied and Environmental Microbiology</i> , 2010, 76, 493-499.	1.4	34
33	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
34	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
35	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
36	Genotyping of <i>Campylobacter jejuni</i> using seven single-nucleotide polymorphisms in combination with <i>flaA</i> short variable region sequencing. <i>Journal of Medical Microbiology</i> , 2006, 55, 1061-1070.	0.7	31

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37	Fingerprinting of <i>Campylobacter jejuni</i> by Using Resolution-Optimized Binary Gene Targets Derived from Comparative Genome Hybridization Studies. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7793-7803.	1.4	30
38	Microevolution of <i>Burkholderia pseudomallei</i> during an Acute Infection. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3418-3421.	1.8	30
39	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
40	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
41	Transcriptomic analysis of longitudinal <i>Burkholderia pseudomallei</i> infecting the cystic fibrosis lung. <i>Microbial Genomics</i> , 2018, 4, .	1.0	30
42	Epidemiological Tracking and Population Assignment of the Non-Clonal Bacterium, <i>Burkholderia pseudomallei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1381.	1.3	27
43	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
44	An attenuated strain of <i>Bacillus anthracis</i> (CDC 684) has a large chromosomal inversion and altered growth kinetics. <i>BMC Genomics</i> , 2011, 12, 477.	1.2	24
45	Computer-aided identification of polymorphism sets diagnostic for groups of bacterial and viral genetic variants. <i>BMC Bioinformatics</i> , 2007, 8, 278.	1.2	23
46	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
47	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
48	Molecular Phylogeny of <i>Burkholderia pseudomallei</i> from a Remote Region of Papua New Guinea. <i>PLoS ONE</i> , 2011, 6, e18343.	1.1	21
49	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
50	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
51	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
52	Taking the next-gen step: Comprehensive antimicrobial resistance detection from <i>Burkholderia pseudomallei</i> . <i>EBioMedicine</i> , 2021, 63, 103152.	2.7	18
53	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
54	Cost-effective interrogation of single nucleotide polymorphisms using the mismatch amplification mutation assay and capillary electrophoresis. <i>Electrophoresis</i> , 2010, 31, 3881-3888.	1.3	17

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55	Burkholderia pseudomallei Genotype Distribution in the Northern Territory, Australia. American Journal of Tropical Medicine and Hygiene, 2016, 94, 68-72.	0.6	17
56	Genomic Insights Into the Melioidosis Pathogen, Burkholderia pseudomallei. Current Tropical Medicine Reports, 2017, 4, 95-102.	1.6	17
57	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, .	2.0	17
58	<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.	0.4	16
59	Phylogeographic, genomic, and meropenem susceptibility analysis of Burkholderia ubonensis. PLoS Neglected Tropical Diseases, 2017, 11, e0005928.	1.3	16
60	Whole-Genome Sequences of Burkholderia pseudomallei Isolates Exhibiting Decreased Meropenem Susceptibility. Genome Announcements, 2017, 5, .	0.8	15
61	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.	1.3	14
62	Characterisation of chicken Campylobacter jejuni isolates using resolution optimised single nucleotide polymorphisms and binary gene markers. International Journal of Food Microbiology, 2008, 128, 304-308.	2.1	13
63	Melioidosis as a Consequence of Sporting Activity. American Journal of Tropical Medicine and Hygiene, 2013, 89, 365-366.	0.6	13
64	The melioidosis agent <i>Burkholderia pseudomallei</i> and related opportunistic pathogens detected in faecal matter of wildlife and livestock in northern Australia. Epidemiology and Infection, 2016, 144, 1924-1932.	1.0	13
65	Molecular Signatures of Non-typeable Haemophilus influenzae Lung Adaptation in Pediatric Chronic Lung Disease. Frontiers in Microbiology, 2019, 10, 1622.	1.5	13
66	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year Burkholderia pseudomallei infection. PLoS Pathogens, 2020, 16, e1008298.	2.1	12
67	Burkholderia pseudomallei distribution in Australasia is linked to paleogeographic and anthropogenic history. PLoS ONE, 2018, 13, e0206845.	1.1	11
68	Whole-Genome Sequences of Five Burkholderia pseudomallei Isolates from Australian Cystic Fibrosis Patients. Genome Announcements, 2015, 3, .	0.8	10
69	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. Microbial Genomics, 2017, 3, e000117.	1.0	10
70	Selective isolation of Yersinia pestis from plague-infected fleas. Journal of Microbiological Methods, 2010, 82, 95-97.	0.7	9
71	A Persisting Nontropical Focus of Burkholderia pseudomallei with Limited Genome Evolution over Five Decades. MSystems, 2020, 5, .	1.7	9
72	Molecular Epidemiology of Third-Generation-Cephalosporin-Resistant <i>Enterobacteriaceae</i> in Southeast Queensland, Australia. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	9

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73	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
74	Emergence of <i>Burkholderia pseudomallei</i> Sequence Type 562, Northern Australia. Emerging Infectious Diseases, 2021, 27, 1057-1067.	2.0	8
75	Quantitative real-time PCR assay for the rapid identification of the intrinsically multidrug-resistant bacterial pathogen <i>Stenotrophomonas maltophilia</i> . Microbial Genomics, 2019, 5, .	1.0	8
76	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.	1.0	7
77	Melioidosis in the Western Indian Ocean and the Importance of Improving Diagnosis, Surveillance, and Molecular Typing. Tropical Medicine and Infectious Disease, 2018, 3, 30.	0.9	7
78	Human Infection with <i>Burkholderia thailandensis</i> , China, 2013. Emerging Infectious Diseases, 2018, 24, 953-954.	2.0	6
79	Comparative genomic analysis identifies X-factor (haemin)-independent <i>Haemophilus haemolyticus</i> : a formal re-classification of ' <i>Haemophilus intermedius</i> '. Microbial Genomics, 2020, 6, .	1.0	6
80	Genomic diversity and antimicrobial resistance of <i>Prevotella</i> species isolated from chronic lung disease airways. Microbial Genomics, 2022, 8, .	1.0	6
81	Molecular genotyping of <i>Acinetobacter</i> spp. isolated in Arizona, USA, using multilocus PCR and mass spectrometry. Journal of Medical Microbiology, 2013, 62, 1295-1300.	0.7	4
82	The Mountain Meadows Massacre and "poisoned springs" scientific testing of the more recent, anthrax theory. International Journal of Legal Medicine, 2013, 127, 77-83.	1.2	4
83	Melioidosis in New Caledonia: a dominant strain in a transmission hotspot. Epidemiology and Infection, 2016, 144, 1330-1337.	1.0	4
84	Express Yourself: Quantitative Real-Time PCR Assays for Rapid Chromosomal Antimicrobial Resistance Detection in <i>Pseudomonas aeruginosa</i> . Antimicrobial Agents and Chemotherapy, 2022, 66, e0020422.	1.4	4
85	Duplex real-time PCR assay for the simultaneous detection of <i>Achromobacter xylosoxidans</i> and <i>Achromobacter</i> spp.. Microbial Genomics, 2020, 6, .	1.0	3
86	Complete Genome Sequence of the Environmental <i>Burkholderia pseudomallei</i> Sequence Type 131 Isolate MSHR1435, Associated with a Chronic Melioidosis Infection. Genome Announcements, 2018, 6, .	0.8	2
87	Geographic consistency in dominant, non-typeable <i>Haemophilus influenzae</i> genotypes colonising four distinct Australian paediatric groups: a cohort study. Pneumonia (Nathan Qld), 2016, 8, 13.	2.5	1
88	The Scourge of Antibiotic-resistant Infections in Cystic Fibrosis. Trends in Microbiology, 2019, 27, 289-291.	3.5	1
89	Comparative genomics of <i>Nocardia seriolae</i> reveals recent importation and subsequent widespread dissemination in mariculture farms in the South Central Coast region, Vietnam. Microbial Genomics, 2022, 8, .	1.0	1
90	Pan-drug-resistant and biofilm-producing strain of <i>Burkholderia pseudomallei</i> : first report of melioidosis from a diabetic patient in Yogyakarta, Indonesia [Letter]. International Medical Case Reports Journal, 2019, Volume 12, 117-118.	0.3	0