

Sharon J Peacock

List of Publications by Year in descending order

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428
papers

42,502
citations

3919

88
h-index

3312

184
g-index

466
all docs

466
docs citations

466
times ranked

38801
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathophysiology, Transmission, Diagnosis, and Treatment of Coronavirus Disease 2019 (COVID-19). JAMA - Journal of the American Medical Association, 2020, 324, 782.	3.8	3,597
2	Multilocus Sequence Typing for Characterization of Methicillin-Resistant and Methicillin-Susceptible Clones of <i>Staphylococcus aureus</i> . Journal of Clinical Microbiology, 2000, 38, 1008-1015.	1.8	2,746
3	SARS-CoV-2 variants, spike mutations and immune escape. Nature Reviews Microbiology, 2021, 19, 409-424.	13.6	2,650
4	Evolution of MRSA During Hospital Transmission and Intercontinental Spread. Science, 2010, 327, 469-474.	6.0	1,054
5	Complete genomes of two clinical <i>Staphylococcus aureus</i> strains: Evidence for the rapid evolution of virulence and drug resistance. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9786-9791.	3.3	830
6	Methicillin-resistant <i>Staphylococcus aureus</i> with a novel <i>mecA</i> homologue in human and bovine populations in the UK and Denmark: a descriptive study. Lancet Infectious Diseases, The, 2011, 11, 595-603.	4.6	751
7	Predicted global distribution of <i>Burkholderia pseudomallei</i> and burden of melioidosis. Nature Microbiology, 2016, 1, .	5.9	704
8	Genomic plasticity of the causative agent of melioidosis, <i>Burkholderia pseudomallei</i> . Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14240-14245.	3.3	675
9	Emergence and global spread of epidemic healthcare-associated <i>Clostridium difficile</i> . Nature Genetics, 2013, 45, 109-113.	9.4	669
10	Melioidosis. New England Journal of Medicine, 2012, 367, 1035-1044.	13.9	648
11	Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak. New England Journal of Medicine, 2012, 366, 2267-2275.	13.9	609
12	Whole-genome sequencing to identify transmission of <i>Mycobacterium abscessus</i> between patients with cystic fibrosis: a retrospective cohort study. Lancet, The, 2013, 381, 1551-1560.	6.3	596
13	How Clonal Is <i>Staphylococcus aureus</i> ?. Journal of Bacteriology, 2003, 185, 3307-3316.	1.0	560
14	Virulent Combinations of Adhesin and Toxin Genes in Natural Populations of <i>Staphylococcus aureus</i> . Infection and Immunity, 2002, 70, 4987-4996.	1.0	539
15	Whole-genome sequencing for analysis of an outbreak of methicillin-resistant <i>Staphylococcus aureus</i> : a descriptive study. Lancet Infectious Diseases, The, 2013, 13, 130-136.	4.6	531
16	Melioidosis: insights into the pathogenicity of <i>Burkholderia pseudomallei</i> . Nature Reviews Microbiology, 2006, 4, 272-282.	13.6	526
17	Human placenta has no microbiome but can contain potential pathogens. Nature, 2019, 572, 329-334.	13.7	513
18	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. PLoS Pathogens, 2012, 8, e1002824.	2.1	450

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19	Melioidosis. <i>Nature Reviews Disease Primers</i> , 2018, 4, 17107.	18.1	430
20	Mechanisms of Methicillin Resistance in <i>Staphylococcus aureus</i> . <i>Annual Review of Biochemistry</i> , 2015, 84, 577-601.	5.0	429
21	Increasing Incidence of Human Melioidosis in Northeast Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 1113-1117.	0.6	353
22	Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1263-1271.	4.6	352
23	Microarrays Reveal that Each of the Ten Dominant Lineages of <i>Staphylococcus aureus</i> Has a Unique Combination of Surface-Associated and Regulatory Genes. <i>Journal of Bacteriology</i> , 2006, 188, 669-676.	1.0	303
24	What determines nasal carriage of <i>Staphylococcus aureus</i> ?. <i>Trends in Microbiology</i> , 2001, 9, 605-610.	3.5	290
25	Antibody response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2020, 15, e0244126.	1.1	269
26	The Cluster 1 Type VI Secretion System Is a Major Virulence Determinant in <i>Burkholderia pseudomallei</i> . <i>Infection and Immunity</i> , 2011, 79, 1512-1525.	1.0	258
27	Recognizing the reagent microbiome. <i>Nature Microbiology</i> , 2018, 3, 851-853.	5.9	255
28	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus <i>Leptospira</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004403.	1.3	253
29	Risk Factors For Hematogenous Complications of Intravascular Catheter-Associated <i>Staphylococcus aureus</i> Bacteremia. <i>Clinical Infectious Diseases</i> , 2005, 40, 695-703.	2.9	235
30	Whole-genome sequencing to control antimicrobial resistance. <i>Trends in Genetics</i> , 2014, 30, 401-407.	2.9	232
31	Systematic longitudinal survey of invasive <i>Escherichia coli</i> in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. <i>Genome Research</i> , 2017, 27, 1437-1449.	2.4	231
32	T cell response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2021, 16, e0245532.	1.1	228
33	Melioidosis: a clinical overview. <i>British Medical Bulletin</i> , 2011, 99, 125-139.	2.7	225
34	MntR modulates expression of the PerR regulon and superoxide resistance in <i>Staphylococcus aureus</i> through control of manganese uptake. <i>Molecular Microbiology</i> , 2002, 44, 1269-1286.	1.2	220
35	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	2.4	210
36	Improved Multilocus Sequence Typing Scheme for <i>Staphylococcus epidermidis</i> . <i>Journal of Clinical Microbiology</i> , 2007, 45, 616-619.	1.8	207

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37	Epidemiology and burden of multidrug-resistant bacterial infection in a developing country. <i>ELife</i> , 2016, 5, .	2.8	207
38	<i>Staphylococcus aureus</i> clumping factor B (ClfB) promotes adherence to human type I cytokeratin 10: implications for nasal colonization. <i>Cellular Microbiology</i> , 2002, 4, 759-770.	1.1	202
39	Bacterial fibronectin-binding proteins and endothelial cell surface fibronectin mediate adherence of <i>Staphylococcus aureus</i> to resting human endothelial cells. <i>Microbiology (United Kingdom)</i> , 1999, 145, 3477-3486.	0.7	196
40	Whole-Genome Sequencing for Rapid Susceptibility Testing of <i>M. tuberculosis</i> . <i>New England Journal of Medicine</i> , 2013, 369, 290-292.	13.9	195
41	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i> . <i>EMBO Molecular Medicine</i> , 2013, 5, 509-515.	3.3	192
42	Characterization of novel LPXTG-containing proteins of <i>Staphylococcus aureus</i> identified from genome sequences. <i>Microbiology (United Kingdom)</i> , 2003, 149, 643-654.	0.7	184
43	Identification of In Vivo Expressed Antigens of <i>Staphylococcus aureus</i> and Their Use in Vaccinations for Protection against Nasal Carriage. <i>Journal of Infectious Diseases</i> , 2006, 193, 1098-1108.	1.9	183
44	Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology. <i>JAMA Internal Medicine</i> , 2013, 173, 1397.	2.6	181
45	Molecular tracing of the emergence, diversification, and transmission of <i>S. aureus</i> sequence type 8 in a New York community. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6738-6743.	3.3	176
46	A <i>Burkholderia pseudomallei</i> protein microarray reveals serodiagnostic and cross-reactive antigens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13499-13504.	3.3	171
47	Fool's Gold: Why Imperfect Reference Tests Are Undermining the Evaluation of Novel Diagnostics: A Reevaluation of 5 Diagnostic Tests for Leptospirosis. <i>Clinical Infectious Diseases</i> , 2012, 55, 322-331.	2.9	171
48	Determinants of Acquisition and Carriage of <i>Staphylococcus aureus</i> in Infancy. <i>Journal of Clinical Microbiology</i> , 2003, 41, 5718-5725.	1.8	170
49	Workshop on Treatment of and Postexposure Prophylaxis for <i>Burkholderia pseudomallei</i> and <i>B. mallei</i> Infection, 2010. <i>Emerging Infectious Diseases</i> , 2012, 18, e2-e2.	2.0	170
50	A Dominant Clone of <i>Leptospira interrogans</i> Associated with an Outbreak of Human Leptospirosis in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2007, 1, e56.	1.3	167
51	Fibronectin-binding protein A of <i>Staphylococcus aureus</i> has multiple, substituting, binding regions that mediate adherence to fibronectin and invasion of endothelial cells. <i>Cellular Microbiology</i> , 2001, 3, 839-851.	1.1	162
52	The Lancet Infectious Diseases Commission on antimicrobial resistance: 6 years later. <i>Lancet Infectious Diseases</i> , The, 2020, 20, e51-e60.	4.6	161
53	Identification and preliminary characterization of cell-wall-anchored proteins of <i>Staphylococcus epidermidis</i> . <i>Microbiology (United Kingdom)</i> , 2005, 151, 1453-1464.	0.7	157
54	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	3.4	156

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55	Activities of Daily Living Associated with Acquisition of Melioidosis in Northeast Thailand: A Matched Case-Control Study. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2072.	1.3	155
56	A Single Multilocus Sequence Typing (MLST) Scheme for Seven Pathogenic <i>Leptospira</i> Species. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e1954.	1.3	153
57	IFN- γ at the Site of Infection Determines Rate of Clearance of Infection in Cryptococcal Meningitis. <i>Journal of Immunology</i> , 2005, 174, 1746-1750.	0.4	150
58	Management of Accidental Laboratory Exposure to <i>Burkholderia pseudomallei</i> and <i>B. mallei</i> . <i>Emerging Infectious Diseases</i> , 2008, 14, e2-e2.	2.0	140
59	Doxycycline versus Azithromycin for Treatment of Leptospirosis and Scrub Typhus. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 3259-3263.	1.4	139
60	Emergence of methicillin resistance predates the clinical use of antibiotics. <i>Nature</i> , 2022, 602, 135-141.	13.7	138
61	Defining the True Sensitivity of Culture for the Diagnosis of Melioidosis Using Bayesian Latent Class Models. <i>PLoS ONE</i> , 2010, 5, e12485.	1.1	136
62	One Health Genomic Surveillance of <i>Escherichia coli</i> Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. <i>MBio</i> , 2019, 10, .	1.8	130
63	Evolutionary dynamics of methicillin-resistant <i>Staphylococcus aureus</i> within a healthcare system. <i>Genome Biology</i> , 2015, 16, 81.	3.8	129
64	Toll-Like Receptor 2 Impairs Host Defense in Gram-Negative Sepsis Caused by <i>Burkholderia pseudomallei</i> (Melioidosis). <i>PLoS Medicine</i> , 2007, 4, e248.	3.9	128
65	Risk Factors for Recurrent Melioidosis in Northeast Thailand. <i>Clinical Infectious Diseases</i> , 2006, 43, 979-986.	2.9	124
66	Biological Relevance of Colony Morphology and Phenotypic Switching by <i>Burkholderia pseudomallei</i> . <i>Journal of Bacteriology</i> , 2007, 189, 807-817.	1.0	124
67	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	5.9	124
68	Phenotypic switching of antibiotic resistance circumvents permanent costs in <i>Staphylococcus aureus</i> . <i>Current Biology</i> , 2001, 11, 1810-1814.	1.8	120
69	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	2.6	120
70	Trimethoprim-sulfamethoxazole versus trimethoprim-sulfamethoxazole plus doxycycline as oral eradication treatment for melioidosis (MERTH): a multicentre, double-blind, non-inferiority, randomised controlled trial. <i>Lancet</i> , The, 2014, 383, 807-814.	6.3	118
71	Clonal differences in <i>Staphylococcus aureus</i> bacteraemia-associated mortality. <i>Nature Microbiology</i> , 2017, 2, 1381-1388.	5.9	118
72	AMR Surveillance in low and middle-income settings - A roadmap for participation in the Global Antimicrobial Surveillance System (GLASS). <i>Wellcome Open Research</i> , 2017, 2, 92.	0.9	114

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73	Systematic Review and Consensus Guidelines for Environmental Sampling of <i>Burkholderia pseudomallei</i> . PLoS Neglected Tropical Diseases, 2013, 7, e2105.	1.3	113
74	Genome sequencing defines phylogeny and spread of methicillin-resistant <i>Staphylococcus aureus</i> in a high transmission setting. Genome Research, 2015, 25, 111-118.	2.4	111
75	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eab19551.	6.0	111
76	Melioidosis in 6 Tsunami Survivors in Southern Thailand. Clinical Infectious Diseases, 2005, 41, 982-990.	2.9	108
77	Association of High <i>Orientia tsutsugamushi</i> DNA Loads with Disease of Greater Severity in Adults with Scrub Typhus. Journal of Clinical Microbiology, 2009, 47, 430-434.	1.8	106
78	A pilot study of rapid whole-genome sequencing for the investigation of a <i>Legionella</i> outbreak. BMJ Open, 2013, 3, e002175.	0.8	105
79	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. Nature Communications, 2015, 6, 6560.	5.8	105
80	A Randomized Controlled Trial of Granulocyte Colony-Stimulating Factor for the Treatment of Severe Sepsis Due to Melioidosis in Thailand. Clinical Infectious Diseases, 2007, 45, 308-314.	2.9	103
81	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. Science Translational Medicine, 2017, 9, .	5.8	103
82	A Link Between Virulence and Ecological Abundance in Natural Populations of <i>Staphylococcus aureus</i> . Science, 2001, 292, 114-116.	6.0	100
83	Management of melioidosis. Expert Review of Anti-Infective Therapy, 2006, 4, 445-455.	2.0	100
84	Antimicrobial resistance to ceftazidime involving loss of penicillin-binding protein 3 in <i>Burkholderia pseudomallei</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17165-17170.	3.3	98
85	Glyburide Is Anti-inflammatory and Associated with Reduced Mortality in Melioidosis. Clinical Infectious Diseases, 2011, 52, 717-725.	2.9	97
86	Evolution and Epidemiology of Multidrug-Resistant <i>Klebsiella pneumoniae</i> in the United Kingdom and Ireland. MBio, 2017, 8, .	1.8	97
87	A decade of genomic history for healthcare-associated <i>Enterococcus faecium</i> in the United Kingdom and Ireland. Genome Research, 2016, 26, 1388-1396.	2.4	96
88	Evolution of <i>Burkholderia pseudomallei</i> in Recurrent Melioidosis. PLoS ONE, 2012, 7, e36507.	1.1	96
89	A Shared Population of Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i> 15 Circulates in Humans and Companion Animals. MBio, 2014, 5, e00985-13.	1.8	95
90	Strategies to Reduce Mortality from Bacterial Sepsis in Adults in Developing Countries. PLoS Medicine, 2008, 5, e175.	3.9	94

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91	Melioidosis Vaccines: A Systematic Review and Appraisal of the Potential to Exploit Biodefense Vaccines for Public Health Purposes. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1488.	1.3	94
92	Diagnostic Accuracy of Real-Time PCR Assays Targeting 16S rRNA and <i>lipL32</i> Genes for Human Leptospirosis in Thailand: A Case-Control Study. <i>PLoS ONE</i> , 2011, 6, e16236.	1.1	94
93	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
94	Complex Routes of Nosocomial Vancomycin-Resistant <i>Enterococcus faecium</i> Transmission Revealed by Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2017, 64, 886-893.	2.9	93
95	DEVELOPMENT OF ANTIBODIES TO <i>BURKHOLDERIA PSEUDOMALLEI</i> DURING CHILDHOOD IN MELIOIDOSIS-ENDEMIC NORTHEAST THAILAND. <i>American Journal of Tropical Medicine and Hygiene</i> , 2006, 74, 1074-1075.	0.6	93
96	Genomic islands from five strains of <i>Burkholderia pseudomallei</i> . <i>BMC Genomics</i> , 2008, 9, 566.	1.2	90
97	Early insights into the potential of the Oxford Nanopore MinION for the detection of antimicrobial resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2775-2778.	1.3	90
98	CAUSES OF COMMUNITY-ACQUIRED BACTEREMIA AND PATTERNS OF ANTIMICROBIAL RESISTANCE IN VIENTIANE, LAOS. <i>American Journal of Tropical Medicine and Hygiene</i> , 2006, 75, 978-985.	0.6	89
99	The toxin/immunity network of <i>Burkholderia pseudomallei</i> contact-dependent growth inhibition (CDI) systems. <i>Molecular Microbiology</i> , 2012, 84, 516-529.	1.2	86
100	Melioidosis. <i>Current Opinion in Infectious Diseases</i> , 2006, 19, 421-428.	1.3	85
101	Open-Label Randomized Trial of Oral Trimethoprim-Sulfamethoxazole, Doxycycline, and Chloramphenicol Compared with Trimethoprim-Sulfamethoxazole and Doxycycline for Maintenance Therapy of Melioidosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 4020-4025.	1.4	84
102	The Microscopic Agglutination Test (MAT) Is an Unreliable Predictor of Infecting <i>Leptospira</i> Serovar in Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2009, 81, 695-697.	0.6	84
103	Leptospirosis Outbreak in Sri Lanka in 2008: Lessons for Assessing the Global Burden of Disease. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 85, 471-478.	0.6	83
104	What Is Resistance? Impact of Phenotypic versus Molecular Drug Resistance Testing on Therapy for Multi- and Extensively Drug-Resistant Tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	83
105	Recurrent Melioidosis in Patients in Northeast Thailand Is Frequently Due to Reinfection Rather than Relapse. <i>Journal of Clinical Microbiology</i> , 2005, 43, 6032-6034.	1.8	82
106	A Horizontal Gene Transfer Event Defines Two Distinct Groups within <i>Burkholderia pseudomallei</i> That Have Dissimilar Geographic Distributions. <i>Journal of Bacteriology</i> , 2007, 189, 9044-9049.	1.0	81
107	<i>Staphylococcus aureus</i> disease and drug resistance in resource-limited countries in south and east Asia. <i>Lancet Infectious Diseases</i> , The, 2009, 9, 130-135.	4.6	80
108	Rapid Whole-Genome Sequencing for Investigation of a Suspected Tuberculosis Outbreak. <i>Journal of Clinical Microbiology</i> , 2013, 51, 611-614.	1.8	80

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109	Novel mutations in penicillin-binding protein genes in clinical <i>Staphylococcus aureus</i> isolates that are methicillin resistant on susceptibility testing, but lack the <i>mec</i> gene. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 594-597.	1.3	80
110	Trimethoprim/sulfamethoxazole resistance in clinical isolates of <i>Burkholderia pseudomallei</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2005, 55, 1029-1031.	1.3	78
111	Survey of Antimicrobial Resistance in Clinical <i>Burkholderia pseudomallei</i> Isolates over Two Decades in Northeast Thailand. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 5388-5391.	1.4	76
112	Two Randomized Controlled Trials of Ceftazidime Alone versus Ceftazidime in Combination with Trimethoprim-Sulfamethoxazole for the Treatment of Severe Melioidosis. <i>Clinical Infectious Diseases</i> , 2005, 41, 1105-1113.	2.9	75
113	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
114	Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant <i>Staphylococcus aureus</i> : a genomic epidemiology analysis. <i>Lancet Microbe</i> , The, 2020, 1, e328-e335.	3.4	75
115	Recent independent emergence of multiple multidrug-resistant <i>Serratia marcescens</i> clones within the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1101-1109.	2.4	74
116	Nonrandom Distribution of <i>Burkholderia pseudomallei</i> Clones in Relation to Geographical Location and Virulence. <i>Journal of Clinical Microbiology</i> , 2006, 44, 2553-2557.	1.8	73
117	A novel hybrid SCCmec-mecC region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 911-918.	1.3	73
118	Whole genome sequencing of ESBL-producing <i>Escherichia coli</i> isolated from patients, farm waste and canals in Thailand. <i>Genome Medicine</i> , 2017, 9, 81.	3.6	73
119	Epidemiology, Microbiology and Mortality Associated with Community-Acquired Bacteremia in Northeast Thailand: A Multicenter Surveillance Study. <i>PLoS ONE</i> , 2013, 8, e54714.	1.1	72
120	The Core and Accessory Genomes of <i>Burkholderia pseudomallei</i> : Implications for Human Melioidosis. <i>PLoS Pathogens</i> , 2008, 4, e1000178.	2.1	71
121	Survival of <i>Burkholderia pseudomallei</i> in distilled water for 16 years. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2011, 105, 598-600.	0.7	71
122	Clinical and Molecular Epidemiology of <i>Staphylococcus argenteus</i> Infections in Thailand. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1005-1008.	1.8	71
123	Immunosuppression associated with interleukin-1R-associated-kinase-M upregulation predicts mortality in Gram-negative sepsis (melioidosis). <i>Critical Care Medicine</i> , 2009, 37, 569-576.	0.4	70
124	Genomic acquisition of a capsular polysaccharide virulence cluster by non-pathogenic <i>Burkholderia</i> isolates. <i>Genome Biology</i> , 2010, 11, R89.	13.9	70
125	The Genetic and Molecular Basis of O-Antigenic Diversity in <i>Burkholderia pseudomallei</i> Lipopolysaccharide. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1453.	1.3	69
126	A Spaetzle-like role for nerve growth factor $\hat{1}^2$ in vertebrate immunity to <i>Staphylococcus aureus</i> . <i>Science</i> , 2014, 346, 641-646.	6.0	68

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127	Improving the estimation of the global burden of antimicrobial resistant infections. <i>Lancet Infectious Diseases</i> , The, 2019, 19, e392-e398.	4.6	68
128	Rapid Detection of the Pandemic Methicillin-Resistant <i>Staphylococcus aureus</i> Clone ST 239, a Dominant Strain in Asian Hospitals. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1520-1522.	1.8	67
129	Activation of the Coagulation Cascade in Patients with Leptospirosis. <i>Clinical Infectious Diseases</i> , 2008, 46, 254-260.	2.9	67
130	A <i>Staphylococcus xylosus</i> Isolate with a New <i>mecC</i> Allotype. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1524-1528.	1.4	67
131	Accuracy of <i>Burkholderia pseudomallei</i> Identification Using the API 20NE System and a Latex Agglutination Test. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3774-3776.	1.8	66
132	<i>Burkholderia pseudomallei</i> genome plasticity associated with genomic island variation. <i>BMC Genomics</i> , 2008, 9, 190.	1.2	66
133	Genetic typing of the 56-kDa type-specific antigen gene of contemporary <i>Orientia tsutsugamushi</i> isolates causing human scrub typhus at two sites in north-eastern and western Thailand. <i>FEMS Immunology and Medical Microbiology</i> , 2008, 52, 335-342.	2.7	65
134	<i>Staphylococcus aureus</i> Bacteraemia in a Tropical Setting: Patient Outcome and Impact of Antibiotic Resistance. <i>PLoS ONE</i> , 2009, 4, e4308.	1.1	65
135	Genome-based characterization of hospital-adapted <i>Enterococcus faecalis</i> lineages. <i>Nature Microbiology</i> , 2016, 1, .	5.9	65
136	Optimization of Culture of <i>Leptospira</i> from Humans with Leptospirosis. <i>Journal of Clinical Microbiology</i> , 2007, 45, 1363-1365.	1.8	64
137	Melioidosis Caused by <i>Burkholderia pseudomallei</i> in Drinking Water, Thailand, 2012. <i>Emerging Infectious Diseases</i> , 2014, 20, 265-268.	2.0	63
138	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. <i>Genome Research</i> , 2016, 26, 263-270.	2.4	63
139	Genomic Surveillance of <i>Enterococcus faecium</i> Reveals Limited Sharing of Strains and Resistance Genes between Livestock and Humans in the United Kingdom. <i>MBio</i> , 2018, 9, .	1.8	63
140	From genotype to phenotype: can systems biology be used to predict <i>Staphylococcus aureus</i> virulence?. <i>Nature Reviews Microbiology</i> , 2012, 10, 791-797.	13.6	62
141	Loop-Mediated Isothermal Amplification Method Targeting the TTS1 Gene Cluster for Detection of <i>Burkholderia pseudomallei</i> and Diagnosis of Melioidosis. <i>Journal of Clinical Microbiology</i> , 2008, 46, 568-573.	1.8	61
142	Arthropod Borne Disease: The Leading Cause of Fever in Pregnancy on the Thai-Burmese Border. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e888.	1.3	61
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415	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption” authors as a response. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2823-2823.	1.3	2
416	The prevalence and implications of single nucleotide polymorphisms in genes encoding the RNA polymerase of clinical isolates of <i>Staphylococcus aureus</i> . <i>MicrobiologyOpen</i> , 2020, 9, e1058.	1.2	2
417	Surveillance and Epidemiology of Drug Resistant Infections Consortium (SEDRIC): Supporting the transition from strategy to action. <i>Wellcome Open Research</i> , 0, 3, 59.	0.9	2
418	Invasive <i>Erysipelothrix rhusiopathiae</i> infection in northeast Thailand. <i>Southeast Asian Journal of Tropical Medicine and Public Health</i> , 2007, 38, 478-81.	1.0	2
419	<i>Melioidosis</i> . , 2011, , 219-222.		1
420	Reply to Dookie et al., “Whole-Genome Sequencing To Guide the Selection of Treatment for Drug-Resistant Tuberculosis”, <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	1
421	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption” authors as a response. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 785-786.	1.3	1
422	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		1
423	In Response. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014, 90, 386-386.	0.6	0
424	The Dynamics of <i>Staphylococcus aureus</i> carriage and Comparisons by Age in Two Studies of an Investigational <i>S aureus</i> 4-Antigen Vaccine (SA4Ag). <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.4	0
425	<i>Melioidosis</i> . , 2010, , 1213-1217.		0
426	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0
427	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0
428	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0