

Sharon J Peacock

List of Publications by Year in descending order

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Version: 2024-02-01

428
papers

42,502
citations

3933

88
h-index

3323

184
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466
all docs

466
docs citations

466
times ranked

38801
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. <i>Clinical Microbiology and Infection</i> , 2022, 28, 93-100.	6.0	21
2	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. <i>Lancet Microbe</i> , The, 2022, 3, e151-e158.	7.3	25
3	Co-evolutionary Signals Identify <i>Burkholderia pseudomallei</i> Survival Strategies in a Hostile Environment. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
4	Emergence of methicillin resistance predates the clinical use of antibiotics. <i>Nature</i> , 2022, 602, 135-141.	27.8	138
5	A2B-COVID: A Tool for Rapidly Evaluating Potential SARS-CoV-2 Transmission Events. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	12
6	Multiple phylogenetically-diverse, differentially-virulent <i>Burkholderia pseudomallei</i> isolated from a single soil sample collected in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010172.	3.0	3
7	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	12.8	27
8	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
9	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. <i>Communications Biology</i> , 2022, 5, 266.	4.4	4
10	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. <i>Virus Evolution</i> , 2022, 8, veac023.	4.9	19
11	<i>Mycobacterium tuberculosis</i> Lineages Associated with Mutations and Drug Resistance in Isolates from India. <i>Microbiology Spectrum</i> , 2022, 10, e0159421.	3.0	10
12	Miniaturised broth microdilution for simplified antibiotic susceptibility testing of Gram negative clinical isolates using microcapillary devices. <i>Analyst</i> , The, 2022, 147, 3558-3569.	3.5	5
13	Horses for courses? Assessing the potential value of a surrogate, point-of-care test for SARS-CoV-2 epidemic control. <i>Influenza and Other Respiratory Viruses</i> , 2021, 15, 3-6.	3.4	8
14	Impact of low blood culture usage on rates of antimicrobial resistance. <i>Journal of Infection</i> , 2021, 82, 355-362.	3.3	12
15	Quantifying acquisition and transmission of <i>Enterococcus faecium</i> using genomic surveillance. <i>Nature Microbiology</i> , 2021, 6, 103-111.	13.3	53
16	A common protocol for the simultaneous processing of multiple clinically relevant bacterial species for whole genome sequencing. <i>Scientific Reports</i> , 2021, 11, 193.	3.3	3
17	Genomic epidemiology of COVID-19 in care homes in the east of England. <i>ELife</i> , 2021, 10, .	6.0	20
18	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021, 19, 409-424.	28.6	2,650

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19	Laboratory informatics capacity for effective antimicrobial resistance surveillance in resource-limited settings. <i>Lancet Infectious Diseases</i> , The, 2021, 21, e170-e174.	9.1	13
20	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	8.8	53
21	Applying prospective genomic surveillance to support investigation of hospital-onset COVID-19. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 916-917.	9.1	14
22	Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections. <i>ELife</i> , 2021, 10, .	6.0	34
23	Defining nosocomial transmission of <i>Escherichia coli</i> and antimicrobial resistance genes: a genomic surveillance study. <i>Lancet Microbe</i> , The, 2021, 2, e472-e480.	7.3	39
24	T cell response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2021, 16, e0245532.	2.5	228
25	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	12.6	111
26	Significant variability exists in the cytotoxicity of global methicillin-resistant <i>Staphylococcus aureus</i> lineages. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	10
27	Genomic Surveillance of Methicillin-resistant <i>Staphylococcus aureus</i> : A Mathematical Early Modeling Study of Cost-effectiveness. <i>Clinical Infectious Diseases</i> , 2020, 70, 1613-1619.	5.8	27
28	A One Health Study of the Genetic Relatedness of <i>Klebsiella pneumoniae</i> and Their Mobile Elements in the East of England. <i>Clinical Infectious Diseases</i> , 2020, 70, 219-226.	5.8	46
29	A review of published spoligotype data indicates the diversity of <i>Mycobacterium tuberculosis</i> from India is under-represented in global databases. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104072.	2.3	6
30	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption” authors’ response. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 785-786.	3.0	1
31	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.	9.1	352
32	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.	3.0	2
33	Fetal inheritance of chromosomally integrated human herpesvirus 6 predisposes the mother to pre-eclampsia. <i>Nature Microbiology</i> , 2020, 5, 901-908.	13.3	29
34	Setting priorities for patient-centered surveillance of drug-resistant infections. <i>International Journal of Infectious Diseases</i> , 2020, 97, 60-65.	3.3	4
35	Association between bacterial homoplastic variants and radiological pathology in tuberculosis. <i>Thorax</i> , 2020, 75, 584-591.	5.6	8
36	Phylogenetically informative mutations in genes implicated in antibiotic resistance in <i>Mycobacterium tuberculosis</i> complex. <i>Genome Medicine</i> , 2020, 12, 27.	8.2	58

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37	Pathophysiology, Transmission, Diagnosis, and Treatment of Coronavirus Disease 2019 (COVID-19). JAMA - Journal of the American Medical Association, 2020, 324, 782.	7.4	3,597
38	The Lancet Infectious Diseases Commission on antimicrobial resistance: 6 years later. Lancet Infectious Diseases, The, 2020, 20, e51-e60.	9.1	161
39	Evaluation of a fully automated bioinformatics tool to predict antibiotic resistance from MRSA genomes. Journal of Antimicrobial Chemotherapy, 2020, 75, 1117-1122.	3.0	10
40	Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant Staphylococcus aureus: a genomic epidemiology analysis. Lancet Microbe, The, 2020, 1, e328-e335.	7.3	75
41	Genomic surveillance of Escherichia coli ST131 identifies local expansion and serial replacement of subclones. Microbial Genomics, 2020, 6, .	2.0	33
42	Defining metrics for whole-genome sequence analysis of MRSA in clinical practice. Microbial Genomics, 2020, 6, .	2.0	4
43	Leapfrogging laboratories: the promise and pitfalls of high-tech solutions for antimicrobial resistance surveillance in low-income settings. BMJ Global Health, 2020, 5, e003622.	4.7	30
44	Antibody response to SARS-CoV-2 infection in humans: A systematic review. PLoS ONE, 2020, 15, e0244126.	2.5	269
45	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		1
46	Automating the Generation of Antimicrobial Resistance Surveillance Reports: Proof-of-Concept Study Involving Seven Hospitals in Seven Countries. Journal of Medical Internet Research, 2020, 22, e19762.	4.3	14
47	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0
48	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0
49	Antibody response to SARS-CoV-2 infection in humans: A systematic review. , 2020, 15, e0244126.		0
50	Improving the estimation of the global burden of antimicrobial resistant infections. Lancet Infectious Diseases, The, 2019, 19, e392-e398.	9.1	68
51	Identification and Characterization of Genetic Determinants of Isoniazid and Rifampicin Resistance in Mycobacterium tuberculosis in Southern India. Scientific Reports, 2019, 9, 10283.	3.3	32
52	Human placenta has no microbiome but can contain potential pathogens. Nature, 2019, 572, 329-334.	27.8	513
53	The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. Microbiome, 2019, 7, 137.	11.1	22
54	Pilot Evaluation of a Fully Automated Bioinformatics System for Analysis of Methicillin-Resistant Staphylococcus aureus Genomes and Detection of Outbreaks. Journal of Clinical Microbiology, 2019, 57, .	3.9	9

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55	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7 years in a single center. <i>Genome Biology</i> , 2019, 20, 184.	8.8	22
56	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption” authors’ response. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2823-2823.	3.0	2
57	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption” authors’ response. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3406-3408.	3.0	3
58	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, .	4.1	130
59	Harnessing alternative sources of antimicrobial resistance data to support surveillance in low-resource settings. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 541-546.	3.0	18
60	Genomic identification of cryptic susceptibility to penicillins and β -lactamase inhibitors in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Nature Microbiology</i> , 2019, 4, 1680-1691.	13.3	47
61	“Antibiotic footprint” as a communication tool to aid reduction of antibiotic consumption. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2122-2127.	3.0	35
62	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate <i>Mycobacterium canettii</i> and Members of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	20
63	Rapid sequencing of MRSA direct from clinical plates in a routine microbiology laboratory. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2153-2156.	3.0	8
64	Methodology for Whole-Genome Sequencing of Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates in a Routine Hospital Microbiology Laboratory. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	22
65	Detection of vancomycin-resistant <i>Enterococcus faecium</i> hospital-adapted lineages in municipal wastewater treatment plants indicates widespread distribution and release into the environment. <i>Genome Research</i> , 2019, 29, 626-634.	5.5	40
66	Genome Sequencing of Polydrug-, Multidrug-, and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Strains from South India. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	5
67	Clinical Epidemiology of 7,126 Melioidosis Patients in Thailand and the Implications for a National Notifiable Diseases Surveillance System. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz498.	0.9	38
68	The Emergence of Successful <i>Streptococcus pyogenes</i> Lineages through Convergent Pathways of Capsule Loss and Recombination Directing High Toxin Expression. <i>MBio</i> , 2019, 10, .	4.1	22
69	Predictive Validity of the qSOFA Score for Sepsis in Adults with Community-Onset Staphylococcal Infection in Thailand. <i>Journal of Clinical Medicine</i> , 2019, 8, 1908.	2.4	3
70	Isolation and comparative genomics of <i>Mycobacterium tuberculosis</i> isolates from cattle and their attendants in South India. <i>Scientific Reports</i> , 2019, 9, 17892.	3.3	14
71	Genetic variation associated with infection and the environment in the accidental pathogen <i>Burkholderia pseudomallei</i> . <i>Communications Biology</i> , 2019, 2, 428.	4.4	19
72	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, .	4.1	50

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73	Nasal carriage of <i>Staphylococcus pseudintermedius</i> in patients with granulomatosis with polyangiitis. <i>Rheumatology</i> , 2019, 58, 548-550.	1.9	8
74	Molecular epidemiology and expression of capsular polysaccharides in <i>Staphylococcus aureus</i> clinical isolates in the United States. <i>PLoS ONE</i> , 2019, 14, e0208356.	2.5	33
75	Genomic surveillance of <i>Escherichia coli</i> in municipal wastewater treatment plants as an indicator of clinically relevant pathogens and their resistance genes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	29
76	Whole-Genome Sequencing of a <i>Mycobacterium orygis</i> Strain Isolated from Cattle in Chennai, India. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	12
77	Prospective genomic surveillance of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. <i>Eurosurveillance</i> , 2019, 24, .	7.0	19
78	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019, 8, .	6.0	39
79	Melioidosis. <i>Nature Reviews Disease Primers</i> , 2018, 4, 17107.	30.5	430
80	Genome-Based Analysis of <i>Enterococcus faecium</i> Bacteremia Associated with Recurrent and Mixed-Strain Infection. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	14
81	Duration of exposure to multiple antibiotics is associated with increased risk of VRE bacteraemia: a nested case-control study. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1692-1699.	3.0	40
82	Analysis of mutations in <i>pncA</i> reveals non-overlapping patterns among various lineages of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2018, 8, 4628.	3.3	5
83	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, .	3.2	83
84	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, .	4.1	63
85	Detecting eukaryotic microbiota with single-cell sensitivity in human tissue. <i>Microbiome</i> , 2018, 6, 151.	11.1	21
86	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	7.8	156
87	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, .	3.2	1
88	Recognizing the reagent microbiome. <i>Nature Microbiology</i> , 2018, 3, 851-853.	13.3	255
89	Effect of temperature on <i>Burkholderia pseudomallei</i> growth, proteomic changes, motility and resistance to stress environments. <i>Scientific Reports</i> , 2018, 8, 9167.	3.3	18
90	Genomic survey of <i>Clostridium difficile</i> reservoirs in the East of England implicates environmental contamination of wastewater treatment plants by clinical lineages. <i>Microbial Genomics</i> , 2018, 4, .	2.0	19

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91	<i>Streptococcus bovimastitidis</i> sp. nov., isolated from a dairy cow with mastitis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 21-27.	1.7	12
92	Are commercial providers a viable option for clinical bacterial sequencing?. <i>Microbial Genomics</i> , 2018, 4, .	2.0	5
93	Naturally occurring polymorphisms in the virulence regulator Rsp modulate <i>Staphylococcus aureus</i> survival in blood and antibiotic susceptibility. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1189-1195.	1.8	6
94	Changing the paradigm for hospital outbreak detection by leading with genomic surveillance of nosocomial pathogens. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1213-1219.	1.8	61
95	Surveillance and Epidemiology of Drug Resistant Infections Consortium (SEDRIC): Supporting the transition from strategy to action. <i>Wellcome Open Research</i> , 2018, 3, 59.	1.8	5
96	Presence of <i>B. thailandensis</i> and <i>B. thailandensis</i> expressing <i>B. pseudomallei</i> -like capsular polysaccharide in Thailand, and their associations with serological response to <i>B. pseudomallei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006193.	3.0	22
97	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	13.3	124
98	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in <i>Mycobacterium tuberculosis</i> Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	29
99	Whole genome sequencing reveals high-resolution epidemiological links between clinical and environmental <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2017, 9, 6.	8.2	61
100	Evolution and Epidemiology of Multidrug-Resistant <i>Klebsiella pneumoniae</i> in the United Kingdom and Ireland. <i>MBio</i> , 2017, 8, .	4.1	97
101	Patient Characteristics, Management, and Predictors of Outcome from Severe Community-Onset Staphylococcal Sepsis in Northeast Thailand: A Prospective Multicenter Study. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 96, 16-0606.	1.4	7
102	Multitarget Quantitative PCR Improves Detection and Predicts Cultivability of the Pathogen <i>Burkholderia pseudomallei</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	20
103	Complex Routes of Nosocomial Vancomycin-Resistant <i>Enterococcus faecium</i> Transmission Revealed by Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2017, 64, 886-893.	5.8	93
104	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	103
105	Investigation of a Cluster of Sequence Type 22 Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission in a Community Setting. <i>Clinical Infectious Diseases</i> , 2017, 65, 2069-2077.	5.8	11
106	Role of Alanine Racemase Mutations in <i>Mycobacterium tuberculosis</i> <i>scpD</i> -Cycloserine Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	24
107	Community outbreaks of group A <i>Streptococcus</i> revealed by genome sequencing. <i>Scientific Reports</i> , 2017, 7, 8554.	3.3	26
108	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.	5.5	231

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109	Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in the East of England. <i>Scientific Reports</i> , 2017, 7, 7406.	3.3	25
110	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.	8.2	73
111	Clonal differences in <i>Staphylococcus aureus</i> bacteraemia-associated mortality. <i>Nature Microbiology</i> , 2017, 2, 1381-1388.	13.3	118
112	Evolution of the <i>Staphylococcus argenteus</i> ST2250 Clone in Northeastern Thailand Is Linked with the Acquisition of Livestock-Associated Staphylococcal Genes. <i>MBio</i> , 2017, 8, .	4.1	44
113	Melioidosis. , 2017, , 1073-1077.e1.		2
114	Population Structure of Multidrug-Resistant <i>Klebsiella oxytoca</i> within Hospitals across the United Kingdom and Ireland Identifies Sharing of Virulence and Resistance Genes with <i>K. pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 574-584.	2.5	35
115	Gastrointestinal tract involvement in melioidosis. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2017, 111, 185-187.	1.8	10
116	Evolution of mobile genetic element composition in an epidemic methicillin-resistant <i>Staphylococcus aureus</i> : temporal changes correlated with frequent loss and gain events. <i>BMC Genomics</i> , 2017, 18, 684.	2.8	43
117	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.	1.8	114
118	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for the identification of <i>Burkholderia pseudomallei</i> from Asia and Australia and differentiation between <i>Burkholderia</i> species. <i>PLoS ONE</i> , 2017, 12, e0175294.	2.5	36
119	Longitudinal genomic surveillance of multidrug-resistant <i>Escherichia coli</i> carriage in a long-term care facility in the United Kingdom. <i>Genome Medicine</i> , 2017, 9, 70.	8.2	44
120	Within-host evolution of <i>Enterococcus faecium</i> during longitudinal carriage and transition to bloodstream infection in immunocompromised patients. <i>Genome Medicine</i> , 2017, 9, 119.	8.2	26
121	Prospective Surveillance and Rapid Whole-Genome Sequencing Detects Two Unsuspected Outbreaks of Carbapenemase-Producing <i>Klebsiella pneumoniae</i> in a UK Teaching Hospital. <i>Open Forum Infectious Diseases</i> , 2017, 4, S43-S44.	0.9	3
122	Sharing of carbapenemase-encoding plasmids between <i>Enterobacteriaceae</i> in UK sewage uncovered by MinION sequencing. <i>Microbial Genomics</i> , 2017, 3, e000114.	2.0	33
123	Population genetic structuring of methicillin-resistant <i>Staphylococcus aureus</i> clone EMRSA-15 within UK reflects patient referral patterns. <i>Microbial Genomics</i> , 2017, 3, e000113.	2.0	19
124	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. <i>Microbial Genomics</i> , 2017, 3, e000117.	2.0	10
125	Increased Von Willebrand factor, decreased ADAMTS13 and thrombocytopenia in melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005468.	3.0	7
126	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. <i>PLoS ONE</i> , 2017, 12, e0189838.	2.5	19

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127	Presence of <i>Burkholderia pseudomallei</i> in Soil and Paddy Rice Water in a Rice Field in Northeast Thailand, but Not in Air and Rainwater. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 1702-1705.	1.4	14
128	Local Persistence of Novel MRSA Lineage after Hospital Ward Outbreak, Cambridge, UK, 2011–2013. <i>Emerging Infectious Diseases</i> , 2016, 22, 1658-1659.	4.3	4
129	Epidemiology and burden of multidrug-resistant bacterial infection in a developing country. <i>ELife</i> , 2016, 5, .	6.0	207
130	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus <i>Leptospira</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004403.	3.0	253
131	Barriers and Recommended Interventions to Prevent Melioidosis in Northeast Thailand: A Focus Group Study Using the Behaviour Change Wheel. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004823.	3.0	34
132	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, .	0.9	0
133	Reconstructing transmission trees for communicable diseases using densely sampled genetic data. <i>Annals of Applied Statistics</i> , 2016, 10, 395-417.	1.1	52
134	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.	5.5	63
135	<i>dhfrA thyA</i> Double Deletion in <i>para</i> -Aminosalicylic Acid-Resistant <i>Mycobacterium tuberculosis</i> Beijing Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3864-3867.	3.2	20
136	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.	5.5	74
137	Transmission of methicillin-resistant <i>Staphylococcus aureus</i> in long-term care facilities and their related healthcare networks. <i>Genome Medicine</i> , 2016, 8, 102.	8.2	30
138	Soil Nutrient Depletion Is Associated with the Presence of <i>Burkholderia pseudomallei</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 7086-7092.	3.1	37
139	Whole-genome sequencing of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates from Myanmar. <i>Journal of Global Antimicrobial Resistance</i> , 2016, 6, 113-117.	2.2	28
140	The dissemination of multidrug-resistant <i>Enterobacter cloacae</i> throughout the UK and Ireland. <i>Nature Microbiology</i> , 2016, 1, 16173.	13.3	24
141	Genome-based characterization of hospital-adapted <i>Enterococcus faecalis</i> lineages. <i>Nature Microbiology</i> , 2016, 1, .	13.3	65
142	A decade of genomic history for healthcare-associated <i>Enterococcus faecium</i> in the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1388-1396.	5.5	96
143	Predicted global distribution of <i>Burkholderia pseudomallei</i> and burden of melioidosis. <i>Nature Microbiology</i> , 2016, 1, .	13.3	704
144	Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 in the East of England. <i>Journal of Infectious Diseases</i> , 2016, 214, 447-453.	4.0	45

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145	Wild-Type and Non-Wild-Type Mycobacterium tuberculosis MIC Distributions for the Novel Fluoroquinolone Antofloxacin Compared with Those for Ofloxacin, Levofloxacin, and Moxifloxacin. Antimicrobial Agents and Chemotherapy, 2016, 60, 5232-5237.	3.2	15
146	Comparison of two chromogenic media for the detection of vancomycin-resistant enterococcal carriage by nursing home residents. Diagnostic Microbiology and Infectious Disease, 2016, 85, 409-412.	1.8	7
147	PBP2a substitutions linked to ceftaroline resistance in MRSA isolates from the UK: Table 1.. Journal of Antimicrobial Chemotherapy, 2016, 71, 268-269.	3.0	16
148	Comparison of 2 chromogenic media for the detection of extended-spectrum β -lactamase producing Enterobacteriaceae stool carriage in nursing home residents. Diagnostic Microbiology and Infectious Disease, 2016, 84, 181-183.	1.8	16
149	Whole-genome sequencing reveals transmission of vancomycin-resistant Enterococcus faecium in a healthcare network. Genome Medicine, 2016, 8, 4.	8.2	58
150	Validation of self-administered nasal swabs and postage for the isolation of Staphylococcus aureus. Journal of Medical Microbiology, 2016, 65, 1434-1437.	1.8	3
151	Pan-genomic perspective on the evolution of the Staphylococcus aureus USA300 epidemic. Microbial Genomics, 2016, 2, e000058.	2.0	34
152	Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. Microbial Genomics, 2016, 2, e000067.	2.0	23
153	Comparison of bacterial genome assembly software for MinION data and their applicability to medical microbiology. Microbial Genomics, 2016, 2, e000085.	2.0	33
154	Moving pathogen genomics out of the lab and into the clinic: what will it take?. Genome Medicine, 2015, 7, 132.	8.2	5
155	Consensus on the Development of Vaccines against Naturally Acquired Melioidosis. Emerging Infectious Diseases, 2015, 21, .	4.3	57
156	Public Awareness of Melioidosis in Thailand and Potential Use of Video Clips as Educational Tools. PLoS ONE, 2015, 10, e0121311.	2.5	18
157	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of Staphylococcus aureus. PLoS Biology, 2015, 13, e1002229.	5.6	120
158	Emergent and evolving antimicrobial resistance cassettes in community-associated fusidic acid and methicillin-resistant Staphylococcus aureus. International Journal of Antimicrobial Agents, 2015, 45, 477-484.	2.5	39
159	Evolutionary dynamics of methicillin-resistant Staphylococcus aureus within a healthcare system. Genome Biology, 2015, 16, 81.	8.8	129
160	Mechanisms of Methicillin Resistance in <i>Staphylococcus aureus</i> . Annual Review of Biochemistry, 2015, 84, 577-601.	11.1	429
161	Cost-effectiveness analysis of parenteral antimicrobials for acute melioidosis in Thailand: Figure A1.. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2015, 109, 416-418.	1.8	6
162	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, 323-326.	3.9	44

#	ARTICLE	IF	CITATIONS
163	Drug-resistance mechanisms and tuberculosis drugs. <i>Lancet</i> , The, 2015, 385, 305-307.	13.7	22
164	Public perceptions of bacterial whole-genome sequencing for tuberculosis. <i>Trends in Genetics</i> , 2015, 31, 58-60.	6.7	5
165	Clinical and Molecular Epidemiology of <i>Staphylococcus argenteus</i> Infections in Thailand. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1005-1008.	3.9	71
166	Genome sequencing defines phylogeny and spread of methicillin-resistant <i>Staphylococcus aureus</i> in a high transmission setting. <i>Genome Research</i> , 2015, 25, 111-118.	5.5	111
167	Trimethoprim/sulfamethoxazole resistance in clinical isolates of <i>Burkholderia pseudomallei</i> from Thailand. <i>International Journal of Antimicrobial Agents</i> , 2015, 45, 557-559.	2.5	24
168	Colony Morphology Variation of <i>Burkholderia pseudomallei</i> Is Associated with Antigenic Variation and O-Polysaccharide Modification. <i>Infection and Immunity</i> , 2015, 83, 2127-2138.	2.2	28
169	Competition between <i>Burkholderia pseudomallei</i> and <i>B. thailandensis</i> . <i>BMC Microbiology</i> , 2015, 15, 56.	3.3	32
170	Old Drugs To Treat Resistant Bugs: Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates with <i>mecC</i> Are Susceptible to a Combination of Penicillin and Clavulanic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7396-7404.	3.2	32
171	Clinical, Environmental, and Serologic Surveillance Studies of Melioidosis in Gabon, 2012–2013. <i>Emerging Infectious Diseases</i> , 2015, 21, 40-47.	4.3	36
172	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. <i>Nature Communications</i> , 2015, 6, 6560.	12.8	105
173	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.	3.0	90
174	Antimicrobial Disk Susceptibility Testing of <i>Leptospira</i> spp. Using <i>Leptospira</i> Vanaporn Wuthiekanun (LVW) Agar. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 241-243.	1.4	24
175	Characterization of Plasmids in Extensively Drug-Resistant <i>Acinetobacter</i> Strains Isolated in India and Pakistan. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 923-929.	3.2	54
176	Increasing Incidence of Hospital-Acquired and Healthcare-Associated Bacteremia in Northeast Thailand: A Multicenter Surveillance Study. <i>PLoS ONE</i> , 2014, 9, e109324.	2.5	37
177	Melioidosis Caused by <i>Burkholderia pseudomallei</i> in Drinking Water, Thailand, 2012. <i>Emerging Infectious Diseases</i> , 2014, 20, 265-268.	4.3	63
178	Microbial sequencing to improve individual and population health. <i>Genome Medicine</i> , 2014, 6, 103.	8.2	3
179	NLRC4 and TLR5 Each Contribute to Host Defense in Respiratory Melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3178.	3.0	27
180	Development of a Prototype Lateral Flow Immunoassay (LFI) for the Rapid Diagnosis of Melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2727.	3.0	93

#	ARTICLE	IF	CITATIONS
181	Molecular tracing of the emergence, diversification, and transmission of <i>S. aureus</i> sequence type 8 in a New York community. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6738-6743.	7.1	176
182	<i>Burkholderia pseudomallei</i> in Water Supplies, Southern Thailand. Emerging Infectious Diseases, 2014, 20, 1947-1949.	4.3	13
183	Impact of infectious diseases consultation on the management of Staphylococcus aureus bacteraemia in children. BMJ Open, 2014, 4, e004659-e004659.	1.9	18
184	A Shared Population of Epidemic Methicillin-Resistant Staphylococcus aureus 15 Circulates in Humans and Companion Animals. MBio, 2014, 5, e00985-13.	4.1	95
185	Whole Genome Sequencing of a Methicillin-Resistant Staphylococcus aureus Pseudo-Outbreak in a Professional Football Team. Open Forum Infectious Diseases, 2014, 1, ofu096.	0.9	6
186	Next-generation pathogen genomics. Genome Biology, 2014, 15, 528.	8.8	2
187	Zero tolerance for healthcare-associated MRSA bacteraemia: is it realistic?. Journal of Antimicrobial Chemotherapy, 2014, 69, 2238-2245.	3.0	27
188	Comment on: Characterization of the embB gene in Mycobacterium tuberculosis isolates from Barcelona and rapid detection of main mutations related to ethambutol resistance using a low-density DNA array. Journal of Antimicrobial Chemotherapy, 2014, 69, 2298-2299.	3.0	8
189	Trimethoprim-sulfamethoxazole versus trimethoprim-sulfamethoxazole plus doxycycline as oral eradication treatment for melioidosis (MERTH): a multicentre, double-blind, non-inferiority, randomised controlled trial. Lancet, The, 2014, 383, 807-814.	13.7	118
190	Rapid single-colony whole-genome sequencing of bacterial pathogens. Journal of Antimicrobial Chemotherapy, 2014, 69, 1275-1281.	3.0	49
191	A Spaetzle-like role for nerve growth factor β in vertebrate immunity to <i>Staphylococcus aureus</i> . Science, 2014, 346, 641-646.	12.6	68
192	Fatal Melioidosis in Goats in Bangkok, Thailand. American Journal of Tropical Medicine and Hygiene, 2014, 91, 287-290.	1.4	7
193	Microevolution of Burkholderia pseudomallei during an Acute Infection. Journal of Clinical Microbiology, 2014, 52, 3418-3421.	3.9	30
194	Whole-genome sequencing to control antimicrobial resistance. Trends in Genetics, 2014, 30, 401-407.	6.7	232
195	Novel mutations in penicillin-binding protein genes in clinical Staphylococcus aureus isolates that are methicillin resistant on susceptibility testing, but lack the mec gene. Journal of Antimicrobial Chemotherapy, 2014, 69, 594-597.	3.0	80
196	A novel hybrid SCCmec-mecC region in Staphylococcus sciuri. Journal of Antimicrobial Chemotherapy, 2014, 69, 911-918.	3.0	73
197	Neutrophil extracellular traps in the host defense against sepsis induced by Burkholderia pseudomallei (melioidosis). Intensive Care Medicine Experimental, 2014, 2, 21.	1.9	26
198	The Role of NOD2 in Murine and Human Melioidosis. Journal of Immunology, 2014, 192, 300-307.	0.8	13

#	ARTICLE	IF	CITATIONS
199	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	5.5	210
200	Genetic diversity within <i>Mycobacterium tuberculosis</i> complex impacts on the accuracy of genotypic pyrazinamide drug-susceptibility assay. <i>Tuberculosis</i> , 2014, 94, 451-453.	1.9	11
201	Health care: Bring microbial sequencing to hospitals. <i>Nature</i> , 2014, 509, 557-559.	27.8	36
202	In Response. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014, 90, 386-386.	1.4	0
203	Common TLR1 Genetic Variation Is Not Associated with Death from Melioidosis, a Common Cause of Sepsis in Rural Thailand. <i>PLoS ONE</i> , 2014, 9, e83285.	2.5	4
204	New Insights from the 7th World Melioidosis Congress 2013. <i>Emerging Infectious Diseases</i> , 2014, 20, .	4.3	9
205	Read and assembly metrics inconsequential for clinical utility of whole-genome sequencing in mapping outbreaks. <i>Nature Biotechnology</i> , 2013, 31, 592-594.	17.5	26
206	Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology. <i>JAMA Internal Medicine</i> , 2013, 173, 1397.	5.1	181
207	Whole-genome sequencing to identify transmission of <i>Mycobacterium abscessus</i> between patients with cystic fibrosis: a retrospective cohort study. <i>Lancet</i> , The, 2013, 381, 1551-1560.	13.7	596
208	Whole-Genome Sequencing for Rapid Susceptibility Testing of <i>M. tuberculosis</i> . <i>New England Journal of Medicine</i> , 2013, 369, 290-292.	27.0	195
209	The BpeEF-OprC Efflux Pump Is Responsible for Widespread Trimethoprim Resistance in Clinical and Environmental <i>Burkholderia pseudomallei</i> Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 4381-4386.	3.2	50
210	Emergence and global spread of epidemic healthcare-associated <i>Clostridium difficile</i> . <i>Nature Genetics</i> , 2013, 45, 109-113.	21.4	669
211	Whole-genome sequencing for analysis of an outbreak of methicillin-resistant <i>Staphylococcus aureus</i> : a descriptive study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 130-136.	9.1	531
212	Rapid Whole-Genome Sequencing for Investigation of a Suspected Tuberculosis Outbreak. <i>Journal of Clinical Microbiology</i> , 2013, 51, 611-614.	3.9	80
213	Rapid Isolation and Susceptibility Testing of <i>Leptospira</i> spp. Using a New Solid Medium, LVW Agar. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 297-302.	3.2	33
214	Impaired TLR5 Functionality Is Associated with Survival in Melioidosis. <i>Journal of Immunology</i> , 2013, 190, 3373-3379.	0.8	41
215	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.	6.9	192
216	A pilot study of rapid whole-genome sequencing for the investigation of a <i>Legionella</i> outbreak. <i>BMJ Open</i> , 2013, 3, e002175.	1.9	105

#	ARTICLE	IF	CITATIONS
217	Use of Vitek 2 Antimicrobial Susceptibility Profile To Identify <i>mecC</i> in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2013, 51, 2732-2734.	3.9	53
218	Molecular Confirmation of Co-Infection by Pathogenic <i>Leptospira</i> spp. and <i>Orientia tsutsugamushi</i> in Patients with Acute Febrile Illness in Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 797-799.	1.4	15
219	Clinical Definitions of Melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 88, 411-413.	1.4	48
220	Monoclonal Antibody-Based Immunofluorescence Microscopy for the Rapid Identification of <i>Burkholderia pseudomallei</i> in Clinical Specimens. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 165-168.	1.4	29
221	<i>Leptospira</i> Species in Floodwater during the 2011 Floods in the Bangkok Metropolitan Region, Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 794-796.	1.4	25
222	Rapid Detection of <i>Burkholderia pseudomallei</i> in Blood Cultures Using a Monoclonal Antibody-Based Immunofluorescent Assay. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 971-972.	1.4	21
223	Prevalence of Melioidosis in Patients with Suspected Pulmonary Tuberculosis and Sputum Smear Negative for Acid-Fast Bacilli in Northeast Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 983-985.	1.4	17
224	Glyburide Reduces Bacterial Dissemination in a Mouse Model of Melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2500.	3.0	34
225	A Single Multilocus Sequence Typing (MLST) Scheme for Seven Pathogenic <i>Leptospira</i> Species. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e1954.	3.0	153
226	Systematic Review and Consensus Guidelines for Environmental Sampling of <i>Burkholderia pseudomallei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2105.	3.0	113
227	A <i>Staphylococcus xylosus</i> Isolate with a New <i>mecC</i> Allotype. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1524-1528.	3.2	67
228	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.	3.0	155
229	Consequences of <i>whiB7</i> (<i>Rv3197A</i>) Mutations in Beijing Genotype Isolates of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3461-3461.	3.2	17
230	Host Responses to Melioidosis and Tuberculosis Are Both Dominated by Interferon-Mediated Signaling. <i>PLoS ONE</i> , 2013, 8, e54961.	2.5	55
231	Subpopulations of <i>Staphylococcus aureus</i> Clonal Complex 121 Are Associated with Distinct Clinical Entities. <i>PLoS ONE</i> , 2013, 8, e58155.	2.5	43
232	Epidemiology, Microbiology and Mortality Associated with Community-Acquired Bacteremia in Northeast Thailand: A Multicenter Surveillance Study. <i>PLoS ONE</i> , 2013, 8, e54714.	2.5	72
233	Incidence and Characterisation of Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) from Nasal Colonisation in Participants Attending a Cattle Veterinary Conference in the UK. <i>PLoS ONE</i> , 2013, 8, e68463.	2.5	28
234	Using a Web-Based Application to Define the Accuracy of Diagnostic Tests When the Gold Standard Is Imperfect. <i>PLoS ONE</i> , 2013, 8, e79489.	2.5	45

#	ARTICLE	IF	CITATIONS
235	Survey of Innate Immune Responses to <i>Burkholderia pseudomallei</i> in Human Blood Identifies a Central Role for Lipopolysaccharide. <i>PLoS ONE</i> , 2013, 8, e81617.	2.5	30
236	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. <i>PLoS Pathogens</i> , 2012, 8, e1002824.	4.7	450
237	The Genetic and Molecular Basis of O-Antigenic Diversity in <i>Burkholderia pseudomallei</i> Lipopolysaccharide. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1453.	3.0	69
238	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.	3.0	94
239	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.	5.8	171
240	Accuracy of a Commercial IgM ELISA for the Diagnosis of Human Leptospirosis in Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2012, 86, 524-527.	1.4	52
241	Characterization of Ceftazidime Resistance Mechanisms in Clinical Isolates of <i>Burkholderia pseudomallei</i> from Australia. <i>PLoS ONE</i> , 2012, 7, e30789.	2.5	75
242	Expression and Function of Transforming Growth Factor $\beta 2$ in Melioidosis. <i>Infection and Immunity</i> , 2012, 80, 1853-1857.	2.2	13
243	Typhoid Fever among Hospitalized Febrile Children in Siem Reap, Cambodia. <i>Journal of Tropical Pediatrics</i> , 2012, 58, 68-70.	1.5	13
244	In the critically ill patient, diabetes predicts mortality independent of statin therapy but is not associated with acute lung injury. <i>Critical Care Medicine</i> , 2012, 40, 1835-1843.	0.9	27
245	Prospective observational study of the frequency and features of intra-abdominal abscesses in patients with melioidosis in northeast Thailand. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2012, 106, 629-631.	1.8	15
246	Effectiveness of a Simplified Method for Isolation of <i>Burkholderia pseudomallei</i> from Soil. <i>Applied and Environmental Microbiology</i> , 2012, 78, 876-877.	3.1	24
247	Melioidosis. <i>New England Journal of Medicine</i> , 2012, 367, 1035-1044.	27.0	648
248	Identification of differentially expressed proteins from <i>Burkholderia pseudomallei</i> isolated during primary and relapsing melioidosis. <i>Microbes and Infection</i> , 2012, 14, 335-340.	1.9	8
249	Proteomic analysis of colony morphology variants of <i>Burkholderia pseudomallei</i> defines a role for the arginine deiminase system in bacterial survival. <i>Journal of Proteomics</i> , 2012, 75, 1031-1042.	2.4	31
250	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.	28.6	62
251	Development of ceftazidime resistance in an acute <i>Burkholderia pseudomallei</i> infection. <i>Infection and Drug Resistance</i> , 2012, 5, 129.	2.7	60
252	Melioidosis in Animals, Thailand, 2006-2010. <i>Emerging Infectious Diseases</i> , 2012, 18, 325-327.	4.3	33

#	ARTICLE	IF	CITATIONS
253	Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak. <i>New England Journal of Medicine</i> , 2012, 366, 2267-2275.	27.0	609
254	The toxin/immunity network of <i>Burkholderia pseudomallei</i> contact-dependent growth inhibition (CDI) systems. <i>Molecular Microbiology</i> , 2012, 84, 516-529.	2.5	86
255	Feasibility of Modified Surviving Sepsis Campaign Guidelines in a Resource-Restricted Setting Based on a Cohort Study of Severe <i>S. Aureus</i> Sepsis. <i>PLoS ONE</i> , 2012, 7, e29858.	2.5	29
256	Evolution of <i>Burkholderia pseudomallei</i> in Recurrent Melioidosis. <i>PLoS ONE</i> , 2012, 7, e36507.	2.5	96
257	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.	2.5	50
258	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.	4.3	170
259	Antimicrobial resistance to ceftazidime involving loss of penicillin-binding protein 3 in <i>Burkholderia pseudomallei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17165-17170.	7.1	98
260	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.	1.8	71
261	Meticillin-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. <i>Lancet Infectious Diseases</i> , The, 2011, 11, 595-603.	9.1	751
262	Diabetes does not influence activation of coagulation, fibrinolysis or anticoagulant pathways in Gram-negative sepsis (melioidosis). <i>Thrombosis and Haemostasis</i> , 2011, 106, 1139-1148.	3.4	13
263	Diversity of 16S-23S rDNA Internal Transcribed Spacer (ITS) Reveals Phylogenetic Relationships in <i>Burkholderia pseudomallei</i> and Its Near-Neighbors. <i>PLoS ONE</i> , 2011, 6, e29323.	2.5	33
264	Microbial sequences benefit health now. <i>Nature</i> , 2011, 471, 578-578.	27.8	5
265	Molecular detection and speciation of pathogenic <i>Leptospiraspp.</i> in blood from patients with culture-negative leptospirosis. <i>BMC Infectious Diseases</i> , 2011, 11, 338.	2.9	52
266	Improved culture-based detection and quantification of <i>Burkholderia pseudomallei</i> from soil. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2011, 105, 346-351.	1.8	16
267	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.	1.4	83
268	The Use of Positive Serological Tests as Evidence of Exposure to <i>Burkholderia pseudomallei</i> . <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 1021-1022.	1.4	12
269	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.	3.2	76
270	Highly Sensitive Direct Detection and Quantification of <i>Burkholderia pseudomallei</i> Bacteria in Environmental Soil Samples by Using Real-Time PCR. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6486-6494.	3.1	44

#	ARTICLE	IF	CITATIONS
271	Identification of Circulating Bacterial Antigens by <i>In Vivo</i> Microbial Antigen Discovery. <i>MBio</i> , 2011, 2, .	4.1	35
272	Glyburide Is Anti-inflammatory and Associated with Reduced Mortality in Melioidosis. <i>Clinical Infectious Diseases</i> , 2011, 52, 717-725.	5.8	97
273	Emergence of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Carriage in Children in Cambodia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 313-317.	1.4	36
274	Melioidosis: a clinical overview. <i>British Medical Bulletin</i> , 2011, 99, 125-139.	6.9	225
275	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.	2.2	258
276	Enzyme-Linked Immunosorbent Assay for the Diagnosis of Melioidosis: Better Than We Thought. <i>Clinical Infectious Diseases</i> , 2011, 52, 1024-1028.	5.8	26
277	Comparison of Two Multilocus Sequence Based Genotyping Schemes for <i>Leptospira</i> Species. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1374.	3.0	42
278	Accuracy of Loop-Mediated Isothermal Amplification for Diagnosis of Human Leptospirosis in Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 614-620.	1.4	53
279	Melioidosis. , 2011, , 219-222.		1
280	Randomized Soil Survey of the Distribution of <i>Burkholderia pseudomallei</i> in Rice Fields in Laos. <i>Applied and Environmental Microbiology</i> , 2011, 77, 532-536.	3.1	39
281	Epidemiological Tracking and Population Assignment of the Non-Clonal Bacterium, <i>Burkholderia pseudomallei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1381.	3.0	27
282	Repeat Blood Culture Positive for <i>B. pseudomallei</i> Indicates an Increased Risk of Death from Melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 858-861.	1.4	20
283	Diagnostic Accuracy of Real-Time PCR Assays Targeting 16S rRNA and <i>lipI32</i> Genes for Human Leptospirosis in Thailand: A Case-Control Study. <i>PLoS ONE</i> , 2011, 6, e16236.	2.5	94
284	Evolution of MRSA During Hospital Transmission and Intercontinental Spread. <i>Science</i> , 2010, 327, 469-474.	12.6	1,054
285	Effect of colony morphology variation of <i>Burkholderia pseudomallei</i> on intracellular survival and resistance to antimicrobial environments in human macrophages <i>in vitro</i> . <i>BMC Microbiology</i> , 2010, 10, 303.	3.3	39
286	Defining the True Sensitivity of Culture for the Diagnosis of Melioidosis Using Bayesian Latent Class Models. <i>PLoS ONE</i> , 2010, 5, e12485.	2.5	136
287	BurkDiff: A Real-Time PCR Allelic Discrimination Assay for <i>Burkholderia Pseudomallei</i> and <i>B. mallei</i> . <i>PLoS ONE</i> , 2010, 5, e15413.	2.5	38
288	Emergence of Pediatric Melioidosis in Siem Reap, Cambodia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 1106-1112.	1.4	49

#	ARTICLE	IF	CITATIONS
289	Urokinase Receptor Is Necessary for Bacterial Defense against Pneumonia-Derived Septic Melioidosis by Facilitating Phagocytosis. <i>Journal of Immunology</i> , 2010, 184, 3079-3086.	0.8	49
290	Enhanced Determination of <i>Streptococcus pneumoniae</i> Serotypes Associated with Invasive Disease in Laos by Using a Real-Time Polymerase Chain Reaction Serotyping Assay with Cerebrospinal Fluid. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 83, 451-457.	1.4	28
291	Increasing Incidence of Human Melioidosis in Northeast Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 1113-1117.	1.4	353
292	Pathogenicity of High-Dose Enteral Inoculation of <i>Burkholderia pseudomallei</i> to Mice. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 83, 1066-1069.	1.4	27
293	Diagnostic and Treatment Difficulties of Pyelonephritis in Pregnancy in Resource-Limited Settings. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 83, 1322-1329.	1.4	16
294	High Rates of Homologous Recombination in the Mite Endosymbiont and Opportunistic Human Pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e752.	3.0	50
295	Arthropod Borne Disease: The Leading Cause of Fever in Pregnancy on the Thai-Burmese Border. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e888.	3.0	61
296	Expression and Function of Macrophage Migration Inhibitory Factor (MIF) in Melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e605.	3.0	17
297	Within-Host Evolution of <i>Burkholderia pseudomallei</i> in Four Cases of Acute Melioidosis. <i>PLoS Pathogens</i> , 2010, 6, e1000725.	4.7	50
298	Osteopontin Impairs Host Defense during Established Gram-Negative Sepsis Caused by <i>Burkholderia pseudomallei</i> (Melioidosis). <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e806.	3.0	13
299	<i>Burkholderia pseudomallei</i> Is Spatially Distributed in Soil in Northeast Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e694.	3.0	47
300	Genomic acquisition of a capsular polysaccharide virulence cluster by non-pathogenic <i>Burkholderia</i> isolates. <i>Genome Biology</i> , 2010, 11, R89.	9.6	70
301	Melioidosis. , 2010, , 1213-1217.		0
302	<i>Staphylococcus aureus</i> Bacteraemia in a Tropical Setting: Patient Outcome and Impact of Antibiotic Resistance. <i>PLoS ONE</i> , 2009, 4, e4308.	2.5	65
303	Biogeography and Virulence of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2009, 4, e6216.	2.5	51
304	Factors Predicting and Reducing Mortality in Patients with Invasive <i>Staphylococcus aureus</i> Disease in a Developing Country. <i>PLoS ONE</i> , 2009, 4, e6512.	2.5	39
305	Association of High <i>Orientia tsutsugamushi</i> DNA Loads with Disease of Greater Severity in Adults with Scrub Typhus. <i>Journal of Clinical Microbiology</i> , 2009, 47, 430-434.	3.9	106
306	Dosing Regimens of Cotrimoxazole (Trimethoprim-Sulfamethoxazole) for Melioidosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 4193-4199.	3.2	47

#	ARTICLE	IF	CITATIONS
307	Phenotypic and Functional Characterization of Human Memory T Cell Responses to <i>Burkholderia pseudomallei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e407.	3.0	53
308	Molecular Basis of Rare Aminoglycoside Susceptibility and Pathogenesis of <i>Burkholderia pseudomallei</i> Clinical Isolates from Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e519.	3.0	55
309	<i>Burkholderia pseudomallei</i> Is Genetically Diverse in Agricultural Land in Northeast Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e496.	3.0	35
310	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.	1.4	84
311	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.	7.1	171
312	<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.	9.1	80
313	The potential emergence of leptospirosis in Sri Lanka. <i>Lancet Infectious Diseases</i> , The, 2009, 9, 524-526.	9.1	52
314	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.	0.9	70
315	Emergence of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Associated with Pediatric Infection in Cambodia. <i>PLoS ONE</i> , 2009, 4, e6630.	2.5	43
316	Patterns of Organ Involvement in Recurrent Melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2009, 81, 335-337.	1.4	17
317	Intensity of exposure and incidence of melioidosis in Thai children. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2008, 102, S37-S39.	1.8	31
318	Public health impact of establishing the cause of bacterial infections in rural Asia. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2008, 102, 5-6.	1.8	34
319	Evaluating <i>Burkholderia pseudomallei</i> Bip proteins as vaccines and Bip antibodies as detection agents. <i>FEMS Immunology and Medical Microbiology</i> , 2008, 52, 78-87.	2.7	48
320	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
321	<i>Burkholderia pseudomallei</i> genome plasticity associated with genomic island variation. <i>BMC Genomics</i> , 2008, 9, 190.	2.8	66
322	Genomic islands from five strains of <i>Burkholderia pseudomallei</i> . <i>BMC Genomics</i> , 2008, 9, 566.	2.8	90
323	Application of Polysaccharide Microarray Technology for the Serodiagnosis of <i>Burkholderia pseudomallei</i> Infection (Melioidosis) in Humans. <i>Journal of Carbohydrate Chemistry</i> , 2008, 27, 32-40.	1.1	11
324	Prevalence and Sequence Diversity of a Factor Required for Actin-Based Motility in Natural Populations of <i>Burkholderia</i> Species. <i>Journal of Clinical Microbiology</i> , 2008, 46, 2418-2422.	3.9	45

#	ARTICLE	IF	CITATIONS
325	Strategies to Reduce Mortality from Bacterial Sepsis in Adults in Developing Countries. <i>PLoS Medicine</i> , 2008, 5, e175.	8.4	94
326	The Core and Accessory Genomes of <i>Burkholderia pseudomallei</i> : Implications for Human Melioidosis. <i>PLoS Pathogens</i> , 2008, 4, e1000178.	4.7	71
327	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.	3.9	67
328	Activation of the Coagulation Cascade in Patients with Leptospirosis. <i>Clinical Infectious Diseases</i> , 2008, 46, 254-260.	5.8	67
329	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.	3.9	61
330	Antimicrobial Drug Selection Markers for <i>Burkholderia pseudomallei</i> and <i>B. mallei</i> . <i>Emerging Infectious Diseases</i> , 2008, 14, 1689-1692.	4.3	16
331	Surviving sepsis in developing countries. <i>Critical Care Medicine</i> , 2008, 36, 2487.	0.9	17
332	<i>Burkholderia pseudomallei</i> Antibodies in Children, Cambodia. <i>Emerging Infectious Diseases</i> , 2008, 14, 301-303.	4.3	36
333	Genetic Diversity and Microevolution of <i>Burkholderia pseudomallei</i> in the Environment. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e182.	3.0	51
334	A Simple Scoring System to Differentiate between Relapse and Re-Infection in Patients with Recurrent Melioidosis. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e327.	3.0	27
335	Management of Accidental Laboratory Exposure to <i>Burkholderia pseudomallei</i> and <i>B. mallei</i> . <i>Emerging Infectious Diseases</i> , 2008, 14, e2-e2.	4.3	140
336	Consensus Guidelines for Dosing of Amoxicillin-Clavulanate in Melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 78, 208-209.	1.4	41
337	Consensus guidelines for dosing of amoxicillin-clavulanate in melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 78, 208-9.	1.4	11
338	Endogenous Interleukin-18 Improves the Early Antimicrobial Host Response in Severe Melioidosis. <i>Infection and Immunity</i> , 2007, 75, 3739-3746.	2.2	37
339	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.	3.9	66
340	Accuracy of Enzyme-Linked Immunosorbent Assay Using Crude and Purified Antigens for Serodiagnosis of Melioidosis. <i>Vaccine Journal</i> , 2007, 14, 110-113.	3.1	45
341	Biological Relevance of Colony Morphology and Phenotypic Switching by <i>Burkholderia pseudomallei</i> . <i>Journal of Bacteriology</i> , 2007, 189, 807-817.	2.2	124
342	Addition of Trimethoprim-Sulfamethoxazole to Ceftazidime during Parenteral Treatment of Melioidosis Is Not Associated with a Long-Term Outcome Benefit. <i>Clinical Infectious Diseases</i> , 2007, 45, 521-523.	5.8	17

#	ARTICLE	IF	CITATIONS
343	Improved Multilocus Sequence Typing Scheme for <i>Staphylococcus epidermidis</i> . <i>Journal of Clinical Microbiology</i> , 2007, 45, 616-619.	3.9	207
344	A Randomized Controlled Trial of Granulocyte Colony-Stimulating Factor for the Treatment of Severe Sepsis Due to Melioidosis in Thailand. <i>Clinical Infectious Diseases</i> , 2007, 45, 308-314.	5.8	103
345	High-Throughput mRNA Profiling Characterizes the Expression of Inflammatory Molecules in Sepsis Caused by <i>Burkholderia pseudomallei</i> . <i>Infection and Immunity</i> , 2007, 75, 3074-3079.	2.2	48
346	Expression Profile and Function of Triggering Receptor Expressed on Myeloid Cells during Melioidosis. <i>Journal of Infectious Diseases</i> , 2007, 196, 1707-1716.	4.0	37
347	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.	2.2	81
348	Simultaneous Infection with More than One Strain of <i>Burkholderia pseudomallei</i> Is Uncommon in Human Melioidosis. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3830-3832.	3.9	23
349	Doxycycline versus Azithromycin for Treatment of Leptospirosis and Scrub Typhus. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 3259-3263.	3.2	139
350	Optimization of Culture of <i>Leptospira</i> from Humans with Leptospirosis. <i>Journal of Clinical Microbiology</i> , 2007, 45, 1363-1365.	3.9	64
351	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.	3.0	167
352	Clinical Diagnosis and Geographic Distribution of Leptospirosis, Thailand. <i>Emerging Infectious Diseases</i> , 2007, 13, 124-126.	4.3	60
353	Serological and blood culture investigations of Nepalese fever patients. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2007, 101, 686-690.	1.8	49
354	Molecular typing of <i>Leptospira</i> spp. based on putative O-antigen polymerase gene (<i>wzy</i>), the benefit over 16S rRNA gene sequence. <i>FEMS Microbiology Letters</i> , 2007, 271, 170-179.	1.8	14
355	<i>Burkholderia</i> Hep_Hag autotransporter (BuHA) proteins elicit a strong antibody response during experimental glanders but not human melioidosis. <i>BMC Microbiology</i> , 2007, 7, 19.	3.3	41
356	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.	8.4	128
357	Variable Presentation of Neurological Melioidosis in Northeast Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 77, 118-120.	1.4	29
358	Quantitation of <i>B. Pseudomallei</i> in Clinical Samples. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 77, 812-813.	1.4	43
359	Prospective Clinical Evaluation of the Accuracy of 16S rRNA Real-Time PCR Assay for the Diagnosis of Melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 77, 814-817.	1.4	34
360	Patient and sample-related factors that effect the success of in vitro isolation of <i>Orientia tsutsugamushi</i> . <i>Southeast Asian Journal of Tropical Medicine and Public Health</i> , 2007, 38, 91-6.	1.0	37

#	ARTICLE	IF	CITATIONS
361	Variable presentation of neurological melioidosis in Northeast Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 77, 118-20.	1.4	14
362	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
363	Quantitation of <i>B. Pseudomallei</i> in clinical samples. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 77, 812-3.	1.4	25
364	Prospective clinical evaluation of the accuracy of 16S rRNA real-time PCR assay for the diagnosis of melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 77, 814-7.	1.4	17
365	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.	4.0	183
366	Management of melioidosis. <i>Expert Review of Anti-Infective Therapy</i> , 2006, 4, 445-455.	4.4	100
367	Meticillin-resistant <i>Staphylococcus aureus</i> in rural Asia. <i>Lancet Infectious Diseases</i> , The, 2006, 6, 70-71.	9.1	28
368	Melioidosis. <i>Current Opinion in Infectious Diseases</i> , 2006, 19, 421-428.	3.1	85
369	Melioidosis: insights into the pathogenicity of <i>Burkholderia pseudomallei</i> . <i>Nature Reviews Microbiology</i> , 2006, 4, 272-282.	28.6	526
370	Prospective evaluation of a rapid immunochromogenic cassette test for the diagnosis of melioidosis in northeast Thailand. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2006, 100, 64-67.	1.8	30
371	Pharmacokinetic and pharmacodynamic assessment of co-amoxiclav in the treatment of melioidosis. <i>Journal of Antimicrobial Chemotherapy</i> , 2006, 58, 1215-1220.	3.0	14
372	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.	3.9	73
373	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.	2.2	303
374	Serological Evidence for Increased Human Exposure to <i>Burkholderia pseudomallei</i> following the Tsunami in Southern Thailand. <i>Journal of Clinical Microbiology</i> , 2006, 44, 239-240.	3.9	23
375	Risk Factors for Recurrent Melioidosis in Northeast Thailand. <i>Clinical Infectious Diseases</i> , 2006, 43, 979-986.	5.8	124
376	Role of Selective and Nonselective Media for Isolation of <i>Burkholderia pseudomallei</i> from Throat Swabs of Patients with Melioidosis. <i>Journal of Clinical Microbiology</i> , 2006, 44, 2316-2316.	3.9	16
377	<i>Staphylococcus aureus</i> . , 2006, , 73-98.		6
378	DEVELOPMENT OF ANTIBODIES TO BURKHOLDERIA PSEUDOMALLEI DURING CHILDHOOD IN MELIOIDOSIS-ENDEMIC NORTHEAST THAILAND. <i>American Journal of Tropical Medicine and Hygiene</i> , 2006, 74, 1074-1075.	1.4	93

#	ARTICLE	IF	CITATIONS
379	PULSED-FIELD GEL ELECTROPHORESIS AS A DISCRIMINATORY TYPING TECHNIQUE FOR THE BIOTHREAT AGENT BURKHOLDERIA MALLEI. American Journal of Tropical Medicine and Hygiene, 2006, 74, 345-347.	1.4	16
380	RAPID DIAGNOSIS OF SCRUB TYPHUS IN RURAL THAILAND USING POLYMERASE CHAIN REACTION. American Journal of Tropical Medicine and Hygiene, 2006, 75, 1099-1102.	1.4	50
381	CAUSES OF COMMUNITY-ACQUIRED BACTEREMIA AND PATTERNS OF ANTIMICROBIAL RESISTANCE IN VIENTIANE, LAOS. American Journal of Tropical Medicine and Hygiene, 2006, 75, 978-985.	1.4	89
382	Causes of community-acquired bacteremia and patterns of antimicrobial resistance in Vientiane, Laos. American Journal of Tropical Medicine and Hygiene, 2006, 75, 978-85.	1.4	61
383	Pulsed-field gel electrophoresis as a discriminatory typing technique for the biothreat agent burkholderia mallei. American Journal of Tropical Medicine and Hygiene, 2006, 74, 345-7.	1.4	6
384	Development of antibodies to Burkholderia pseudomallei during childhood in melioidosis-endemic northeast Thailand. American Journal of Tropical Medicine and Hygiene, 2006, 74, 1074-5.	1.4	41
385	In vitro motility of a population of clinical Burkholderia pseudomallei isolates. Journal of the Medical Association of Thailand = Chotmaiht Thangphaet, 2006, 89, 1506-10.	0.1	3
386	Short report: Melioidosis in Myanmar: forgotten but not gone?. American Journal of Tropical Medicine and Hygiene, 2006, 75, 945-6.	1.4	15
387	Rapid diagnosis of scrub typhus in rural Thailand using polymerase chain reaction. American Journal of Tropical Medicine and Hygiene, 2006, 75, 1099-102.	1.4	29
388	Two Randomized Controlled Trials of Ceftazidime Alone versus Ceftazidime in Combination with Trimethoprim-Sulfamethoxazole for the Treatment of Severe Melioidosis. Clinical Infectious Diseases, 2005, 41, 1105-1113.	5.8	75
389	Melioidosis in 6 Tsunami Survivors in Southern Thailand. Clinical Infectious Diseases, 2005, 41, 982-990.	5.8	108
390	Recurrent Melioidosis in Patients in Northeast Thailand Is Frequently Due to Reinfection Rather than Relapse. Journal of Clinical Microbiology, 2005, 43, 6032-6034.	3.9	82
391	Risk Factors For Hematogenous Complications of Intravascular Catheter--Associated Staphylococcus aureus Bacteremia. Clinical Infectious Diseases, 2005, 40, 695-703.	5.8	235
392	Baseline Correlation and Comparative Kinetics of Cerebrospinal Fluid Colony-Forming Unit Counts and Antigen Titers in Cryptococcal Meningitis. Journal of Infectious Diseases, 2005, 192, 681-684.	4.0	59
393	Role and Significance of Quantitative Urine Cultures in Diagnosis of Melioidosis. Journal of Clinical Microbiology, 2005, 43, 2274-2276.	3.9	36
394	Rapid Immunofluorescence Microscopy for Diagnosis of Melioidosis. Vaccine Journal, 2005, 12, 555-556.	3.1	57
395	Open-Label Randomized Trial of Oral Trimethoprim-Sulfamethoxazole, Doxycycline, and Chloramphenicol Compared with Trimethoprim-Sulfamethoxazole and Doxycycline for Maintenance Therapy of Melioidosis. Antimicrobial Agents and Chemotherapy, 2005, 49, 4020-4025.	3.2	84
396	Antibodies from Patients with Melioidosis Recognize Burkholderia mallei but Not Burkholderia thailandensis Antigens in the Indirect Hemagglutination Assay. Journal of Clinical Microbiology, 2005, 43, 4872-4874.	3.9	28

#	ARTICLE	IF	CITATIONS
397	Trimethoprim/sulfamethoxazole resistance in clinical isolates of <i>Burkholderia pseudomallei</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2005, 55, 1029-1031.	3.0	78
398	Tsunami in Thailand – Disaster Management in a District Hospital. <i>New England Journal of Medicine</i> , 2005, 352, 962-964.	27.0	53
399	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.	0.8	150
400	Detection of <i>Burkholderia pseudomallei</i> in Soil within the Lao People's Democratic Republic. <i>Journal of Clinical Microbiology</i> , 2005, 43, 923-924.	3.9	42
401	Comparison of Ashdown's Medium, <i>Burkholderia cepacia</i> Medium, and <i>Burkholderia pseudomallei</i> Selective Agar for Clinical Isolation of <i>Burkholderia pseudomallei</i> . <i>Journal of Clinical Microbiology</i> , 2005, 43, 5359-5361.	3.9	56
402	Identification and preliminary characterization of cell-wall-anchored proteins of <i>Staphylococcus epidermidis</i> . <i>Microbiology (United Kingdom)</i> , 2005, 151, 1453-1464.	1.8	157
403	DISEASE SEVERITY AND OUTCOME OF MELIOIDOSIS IN HIV COINFECTED INDIVIDUALS. <i>American Journal of Tropical Medicine and Hygiene</i> , 2005, 73, 1165-1166.	1.4	41
404	THE ROLE AND SIGNIFICANCE OF SPUTUM CULTURES IN THE DIAGNOSIS OF MELIOIDOSIS. <i>American Journal of Tropical Medicine and Hygiene</i> , 2005, 73, 657-661.	1.4	13
405	The role and significance of sputum cultures in the diagnosis of melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2005, 73, 657-61.	1.4	6
406	Short report: disease severity and outcome of melioidosis in HIV coinfected individuals. <i>American Journal of Tropical Medicine and Hygiene</i> , 2005, 73, 1165-6.	1.4	16
407	Complete genomes of two clinical <i>Staphylococcus aureus</i> strains: Evidence for the rapid evolution of virulence and drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9786-9791.	7.1	830
408	Evaluation of Immunoglobulin M (IgM) and IgG Rapid Cassette Test Kits for Diagnosis of Melioidosis in an Area of Endemicity. <i>Journal of Clinical Microbiology</i> , 2004, 42, 3435-3437.	3.9	26
409	Genomic plasticity of the causative agent of melioidosis, <i>Burkholderia pseudomallei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14240-14245.	7.1	675
410	Adherence of <i>Staphylococcus aureus</i> fibronectin binding protein A mutants: an investigation using optical tweezers. <i>New Biotechnology</i> , 2004, 21, 105-111.	2.7	20
411	Characterization of novel LPXTG-containing proteins of <i>Staphylococcus aureus</i> identified from genome sequences. <i>Microbiology (United Kingdom)</i> , 2003, 149, 643-654.	1.8	184
412	How Clonal Is <i>Staphylococcus aureus</i> ?. <i>Journal of Bacteriology</i> , 2003, 185, 3307-3316.	2.2	560
413	Determinants of Acquisition and Carriage of <i>Staphylococcus aureus</i> in Infancy. <i>Journal of Clinical Microbiology</i> , 2003, 41, 5718-5725.	3.9	170
414	Virulent Combinations of Adhesin and Toxin Genes in Natural Populations of <i>Staphylococcus aureus</i> . <i>Infection and Immunity</i> , 2002, 70, 4987-4996.	2.2	539

#	ARTICLE	IF	CITATIONS
415	Functional Blocking of <i>Staphylococcus aureus</i> Adhesins following Growth in Ex Vivo Media. <i>Infection and Immunity</i> , 2002, 70, 5339-5345.	2.2	21
416	Antibiotic-resistant sub-populations of the pathogenic bacterium <i>Staphylococcus aureus</i> confer population-wide resistance. <i>Current Biology</i> , 2002, 12, R686-R687.	3.9	22
417	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.	2.5	220
418	<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.	2.1	202
419	What determines nasal carriage of <i>Staphylococcus aureus</i> ?. <i>Trends in Microbiology</i> , 2001, 9, 605-610.	7.7	290
420	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.	2.1	162
421	Phenotypic switching of antibiotic resistance circumvents permanent costs in <i>Staphylococcus aureus</i> . <i>Current Biology</i> , 2001, 11, 1810-1814.	3.9	120
422	A Link Between Virulence and Ecological Abundance in Natural Populations of <i>Staphylococcus aureus</i> . <i>Science</i> , 2001, 292, 114-116.	12.6	100
423	Multilocus Sequence Typing for Characterization of Methicillin-Resistant and Methicillin-Susceptible Clones of <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2000, 38, 1008-1015.	3.9	2,746
424	Adhesion of <i>Staphylococcus aureus</i> to Collagen Is Not a Major Virulence Determinant for Septic Arthritis, Osteomyelitis, or Endocarditis. <i>Journal of Infectious Diseases</i> , 1999, 179, 291-293.	4.0	27
425	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.	1.8	196
426	The autopsy: A useful tool or an old relic?. <i>Journal of Pathology</i> , 1988, 156, 9-14.	4.5	48
427	<i>Burkholderia</i> , <i>Stenotrophomonas</i> , <i>Ralstonia</i> , <i>Cupriavidus</i> , <i>Pandoraea</i> , <i>Brevundimonas</i> , <i>Comamonas</i> , <i>Delftia</i> , and <i>Acidovorax</i> , , 791-812.		16
428	Surveillance and Epidemiology of Drug Resistant Infections Consortium (SEDRIC): Supporting the transition from strategy to action. <i>Wellcome Open Research</i> , 0, 3, 59.	1.8	2