Sharon J Peacock

List of Publications by Citations

438 papers	30,611 citations	78 h-index	161 g-index
466 ext. papers	37,925 ext. citations	9 avg, IF	7.39 L-index

#	Paper	IF	Citations
438	Multilocus sequence typing for characterization of methicillin-resistant and methicillin-susceptible clones of Staphylococcus aureus. *Journal of Clinical Microbiology*, **2000**, 38, 1008-15	9.7	2450
437	Pathophysiology, Transmission, Diagnosis, and Treatment of Coronavirus Disease 2019 (COVID-19): A Review. *JAMA - Journal of the American Medical Association*, **2020**, 324, 782-793	27.4	1978
436	SARS-CoV-2 variants, spike mutations and immune escape. *Nature Reviews Microbiology*, **2021**, 19, 409-424	24.2	873
435	Evolution of MRSA during hospital transmission and intercontinental spread. *Science*, **2010**, 327, 469-74	33.3	858
434	Complete genomes of two clinical Staphylococcus aureus 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, 9786-91	11.5	717
433	Meticillin-resistant Staphylococcus aureus with a novel mecA homologue in human and bovine populations in the UK and Denmark: a descriptive study. *Lancet Infectious Diseases, The*, **2011**, 11, 595-603	25.5	617
432	Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 14240-5	11.5	569
431	Melioidosis. *New England Journal of Medicine*, **2012**, 367, 1035-44	59.2	527
430	Emergence and global spread of epidemic healthcare-associated Clostridium difficile. *Nature Genetics*, **2013**, 45, 109-13	36.3	509
429	How clonal is Staphylococcus aureus?. *Journal of Bacteriology*, **2003**, 185, 3307-16	3.5	499
428	Rapid whole-genome sequencing for investigation of a neonatal MRSA outbreak. *New England Journal of Medicine*, **2012**, 366, 2267-75	59.2	480
427	Virulent combinations of adhesin and toxin genes in natural populations of Staphylococcus aureus. *Infection and Immunity*, **2002**, 70, 4987-96	3.7	466
426	Predicted global distribution of and burden of melioidosis. *Nature Microbiology*, **2016**, 1,	26.6	463
425	Whole-genome sequencing to identify transmission of Mycobacterium abscessus between patients with cystic fibrosis: a retrospective cohort study. *Lancet, The*, **2013**, 381, 1551-60	40	449
424	Melioidosis: insights into the pathogenicity of Burkholderia pseudomallei. *Nature Reviews Microbiology*, **2006**, 4, 272-82	22.2	445
423	Whole-genome sequencing for analysis of an outbreak of meticillin-resistant Staphylococcus aureus: a descriptive study. *Lancet Infectious Diseases, The*, **2013**, 13, 130-6	25.5	414
422	Routine use of microbial whole genome sequencing in diagnostic and public health microbiology. *PLoS Pathogens*, **2012**, 8, e1002824	7.6	358

421	Human placenta has no microbiome but can contain potential pathogens. *Nature*, **2019**, 572, 329-334	50.4	323
420	Increasing incidence of human melioidosis in Northeast Thailand. *American Journal of Tropical Medicine and Hygiene*, **2010**, 82, 1113-7	3.2	287
419	Microarrays reveal that each of the ten dominant lineages of Staphylococcus aureus has a unique combination of surface-associated and regulatory genes. *Journal of Bacteriology*, **2006**, 188, 669-76	3.5	271
418	Mechanisms of Methicillin Resistance in Staphylococcus aureus. *Annual Review of Biochemistry*, **2015**, 84, 577-601	29.1	268
417	What determines nasal carriage of Staphylococcus aureus?. *Trends in Microbiology*, **2001**, 9, 605-10	12.4	261
416	Melioidosis. *Nature Reviews Disease Primers*, **2018**, 4, 17107	51.1	236
415	Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. *Lancet Infectious Diseases, The*, **2020**, 20, 1263-1272	25.5	200
414	MntR modulates expression of the PerR regulon and superoxide resistance in Staphylococcus aureus through control of manganese uptake. *Molecular Microbiology*, **2002**, 44, 1269-86	4.1	197
413	Risk factors for hematogenous complications of intravascular catheter-associated Staphylococcus aureus bacteremia. *Clinical Infectious Diseases*, **2005**, 40, 695-703	11.6	197
412	The cluster 1 type VI secretion system is a major virulence determinant in Burkholderia pseudomallei. *Infection and Immunity*, **2011**, 79, 1512-25	3.7	188
411	Staphylococcus aureus clumping factor B (ClfB) promotes adherence to human type I cytokeratin 10: implications for nasal colonization. *Cellular Microbiology*, **2002**, 4, 759-70	3.9	178
410	Identification of in vivo-expressed antigens of Staphylococcus aureus and their use in vaccinations for protection against nasal carriage. *Journal of Infectious Diseases*, **2006**, 193, 1098-108	7	171
409	Melioidosis: a clinical overview. *British Medical Bulletin*, **2011**, 99, 125-39	5.4	170
408	Bacterial fibronectin-binding proteins and endothelial cell surface fibronectin mediate adherence of Staphylococcus aureus to resting human endothelial cells. *Microbiology (United Kingdom)*, **1999**, 145 (Pt 12), 3477-3486	2.9	170
407	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus Leptospira. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004403	4.8	170
406	Whole-genome sequencing for rapid susceptibility testing of M. tuberculosis. *New England Journal of Medicine*, **2013**, 369, 290-2	59.2	167
405	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel mecA homologue mecC. *EMBO Molecular Medicine*, **2013**, 5, 509-15	12	166
404	Improved multilocus sequence typing scheme for Staphylococcus epidermidis. *Journal of Clinical Microbiology*, **2007**, 45, 616-9	9.7	166

403	Recognizing the reagent microbiome. *Nature Microbiology*, **2018**, 3, 851-853	26.6	161
402	Characterization of novel LPXTG-containing proteins of Staphylococcus aureus identified from genome sequences. *Microbiology (United Kingdom)*, **2003**, 149, 643-654	2.9	161
401	Whole-genome sequencing to control antimicrobial resistance. *Trends in Genetics*, **2014**, 30, 401-7	8.5	158
400	Determinants of acquisition and carriage of Staphylococcus aureus in infancy. *Journal of Clinical Microbiology*, **2003**, 41, 5718-25	9.7	154
399	Rapid bacterial whole-genome sequencing to enhance diagnostic and public health microbiology. *JAMA Internal Medicine*, **2013**, 173, 1397-404	11.5	152
398	Fibronectin-binding protein A of Staphylococcus aureus has multiple, substituting, binding regions that mediate adherence to fibronectin and invasion of endothelial cells. *Cellular Microbiology*, **2001**, 3, 839-51	3.9	149
397	Fools gold: Why imperfect reference tests are undermining the evaluation of novel diagnostics: a reevaluation of 5 diagnostic tests for leptospirosis. *Clinical Infectious Diseases*, **2012**, 55, 322-31	11.6	139
396	A Burkholderia pseudomallei protein microarray reveals serodiagnostic and cross-reactive antigens. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 13499-504	11.5	139
395	Epidemiology and burden of multidrug-resistant bacterial infection in a developing country. *ELife*, **2016**, 5,	8.9	138
394	A dominant clone of Leptospira interrogans associated with an outbreak of human leptospirosis in Thailand. *PLoS Neglected Tropical Diseases*, **2007**, 1, e56	4.8	133
393	Identification and preliminary characterization of cell-wall-anchored proteins of Staphylococcus epidermidis. *Microbiology (United Kingdom)*, **2005**, 151, 1453-1464	2.9	132
392	Antibody response to SARS-CoV-2 infection in humans: A systematic review. *PLoS ONE*, **2020**, 15, e0244126	3.7	130
391	IFN-gamma at the site of infection determines rate of clearance of infection in cryptococcal meningitis. *Journal of Immunology*, **2005**, 174, 1746-50	5.3	129
390	Workshop on treatment of and postexposure prophylaxis for Burkholderia pseudomallei and B. mallei Infection, 2010. *Emerging Infectious Diseases*, **2012**, 18, e2	10.2	128
389	Predicting the virulence of MRSA from its genome sequence. *Genome Research*, **2014**, 24, 839-49	9.7	126
388	Systematic longitudinal survey of invasive in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. *Genome Research*, **2017**,	9.7	122
387	Molecular tracing of the emergence, diversification, and transmission of S. aureus sequence type 8 in a New York community. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6738-43	11.5	121
386	A single multilocus sequence typing (MLST) scheme for seven pathogenic Leptospira species. *PLoS Neglected Tropical Diseases*, **2013**, 7, e1954	4.8	118

385	Toll-like receptor 2 impairs host defense in gram-negative sepsis caused by Burkholderia pseudomallei (Melioidosis). *PLoS Medicine*, **2007**, 4, e248	11.6	118
384	Doxycycline versus azithromycin for treatment of leptospirosis and scrub typhus. *Antimicrobial Agents and Chemotherapy*, **2007**, 51, 3259-63	5.9	112
383	Activities of daily living associated with acquisition of melioidosis in northeast Thailand: a matched case-control study. *PLoS Neglected Tropical Diseases*, **2013**, 7, e2072	4.8	109
382	Biological relevance of colony morphology and phenotypic switching by Burkholderia pseudomallei. *Journal of Bacteriology*, **2007**, 189, 807-17	3.5	108
381	Phenotypic switching of antibiotic resistance circumvents permanent costs in Staphylococcus aureus. *Current Biology*, **2001**, 11, 1810-4	6.3	103
380	Risk factors for recurrent melioidosis in northeast Thailand. *Clinical Infectious Diseases*, **2006**, 43, 979-86	11.6	99
379	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, 308-14	11.6	98
378	Defining the true sensitivity of culture for the diagnosis of melioidosis using Bayesian latent class models. *PLoS ONE*, **2010**, 5, e12485	3.7	96
377	Melioidosis in 6 tsunami survivors in southern Thailand. *Clinical Infectious Diseases*, **2005**, 41, 982-90	11.6	92
376	Management of accidental laboratory exposure to Burkholderia pseudomallei and B. mallei. *Emerging Infectious Diseases*, **2008**, 14, e2	10.2	91
375	A link between virulence and ecological abundance in natural populations of Staphylococcus aureus. *Science*, **2001**, 292, 114-6	33.3	90
374	Trimethoprim-sulfamethoxazole versus trimethoprim-sulfamethoxazole plus doxycycline as oral eradicative treatment for melioidosis (MERTH): a multicentre, double-blind, non-inferiority, randomised controlled trial. *Lancet, The*, **2014**, 383, 807-14	40	89
373	Glyburide is anti-inflammatory and associated with reduced mortality in melioidosis. *Clinical Infectious Diseases*, **2011**, 52, 717-25	11.6	89
372	Global and regional dissemination and evolution of Burkholderia pseudomallei. *Nature Microbiology* , **2017**, 2, 16263	26.6	87
371	Management of melioidosis. *Expert Review of Anti-Infective Therapy*, **2006**, 4, 445-55	5.5	87
370	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. *Nature Communications*, **2015**, 6, 6560	17.4	83
369	Evolution of Burkholderia pseudomallei in recurrent melioidosis. *PLoS ONE*, **2012**, 7, e36507	3.7	83
368	Systematic review and consensus guidelines for environmental sampling of Burkholderia pseudomallei. *PLoS Neglected Tropical Diseases*, **2013**, 7, e2105	4.8	82

367	Association of high Orientia tsutsugamushi DNA loads with disease of greater severity in adults with scrub typhus. *Journal of Clinical Microbiology*, **2009**, 47, 430-4	9.7	82
366	Diagnostic accuracy of real-time PCR assays targeting 16S rRNA and lipL32 genes for human leptospirosis in Thailand: a case-control study. *PLoS ONE*, **2011**, 6, e16236	3.7	82
365	Gene exchange drives the ecological success of a multi-host bacterial pathogen. *Nature Ecology and Evolution*, **2018**, 2, 1468-1478	12.3	80
364	Strategies to reduce mortality from bacterial sepsis in adults in developing countries. *PLoS Medicine*, **2008**, 5, e175	11.6	80
363	Prospective Surveillance and Rapid Whole-Genome Sequencing Detects Two Unsuspected Outbreaks of Carbapenemase-Producing Klebsiella pneumoniae in a UK Teaching Hospital. *Open Forum Infectious Diseases*, **2017**, 4, S43-S44	1	78
362	The toxin/immunity network of Burkholderia pseudomallei contact-dependent growth inhibition (CDI) systems. *Molecular Microbiology*, **2012**, 84, 516-29	4.1	78
361	A pilot study of rapid whole-genome sequencing for the investigation of a Legionella outbreak. *BMJ Open*, **2013**, 3,	3	78
360	CAUSES OF COMMUNITY-ACQUIRED BACTEREMIA AND PATTERNS OF ANTIMICROBIAL RESISTANCE IN VIENTIANE, LAOS. *American Journal of Tropical Medicine and Hygiene*, **2006**, 75, 978-985	3.2	78
359	The Lancet Infectious Diseases Commission on antimicrobial resistance: 6 years later. *Lancet Infectious Diseases, The*, **2020**, 20, e51-e60	25.5	77
358	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of Staphylococcus aureus. *PLoS Biology*, **2015**, 13, e1002229	9.7	76
357	Evolutionary dynamics of methicillin-resistant Staphylococcus aureus within a healthcare system. *Genome Biology*, **2015**, 16, 81	18.3	76
356	DEVELOPMENT OF ANTIBODIES TO BURKHOLDERIA PSEUDOMALLEI DURING CHILDHOOD IN MELIOIDOSIS-ENDEMIC NORTHEAST THAILAND. *American Journal of Tropical Medicine and Hygiene*, **2006**, 74, 1074-1075	3.2	76
355	Early insights into the potential of the Oxford Nanopore MinION for the detection of antimicrobial resistance genes. *Journal of Antimicrobial Chemotherapy*, **2015**, 70, 2775-8	5.1	75
354	Genome sequencing defines phylogeny and spread of methicillin-resistant Staphylococcus aureus in a high transmission setting. *Genome Research*, **2015**, 25, 111-8	9.7	75
353	Genomic islands from five strains of Burkholderia pseudomallei. *BMC Genomics*, **2008**, 9, 566	4.5	75
352	Melioidosis vaccines: a systematic review and appraisal of the potential to exploit biodefense vaccines for public health purposes. *PLoS Neglected Tropical Diseases*, **2012**, 6, e1488	4.8	74
351	Melioidosis. *Current Opinion in Infectious Diseases*, **2006**, 19, 421-8	5.4	74
350	Antimicrobial resistance to ceftazidime involving loss of penicillin-binding protein 3 in Burkholderia pseudomallei. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 17165-70	11.5	73

349	Recurrent melioidosis in patients in northeast Thailand is frequently due to reinfection rather than relapse. *Journal of Clinical Microbiology*, **2005**, 43, 6032-4	9.7	73
348	AMR Surveillance in low and middle-income settings - A roadmap for participation in the Global Antimicrobial Surveillance System (GLASS). *Wellcome Open Research*, **2017**, 2, 92	4.8	72
347	A horizontal gene transfer event defines two distinct groups within Burkholderia pseudomallei that have dissimilar geographic distributions. *Journal of Bacteriology*, **2007**, 189, 9044-9	3.5	71
346	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. *Science Translational Medicine*, **2017**, 9,	17.5	70
345	A shared population of epidemic methicillin-resistant Staphylococcus aureus 15 circulates in humans and companion animals. *MBio*, **2014**, 5, e00985-13	7.8	70
344	Staphylococcus aureus disease and drug resistance in resource-limited countries in south and east Asia. *Lancet Infectious Diseases, The*, **2009**, 9, 130-5	25.5	70
343	Nonrandom distribution of Burkholderia pseudomallei clones in relation to geographical location and virulence. *Journal of Clinical Microbiology*, **2006**, 44, 2553-7	9.7	68
342	Trimethoprim/sulfamethoxazole resistance in clinical isolates of Burkholderia pseudomallei. *Journal of Antimicrobial Chemotherapy*, **2005**, 55, 1029-31	5.1	68
341	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, 4020-5	5.9	67
340	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, 594-7	5.1	65
339	One Health Genomic Surveillance of Escherichia coli Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. *MBio*, **2019**, 10,	7.8	64
338	Clonal differences in Staphylococcus aureus bacteraemia-associated mortality. *Nature Microbiology*, **2017**, 2, 1381-1388	26.6	64
337	The core and accessory genomes of Burkholderia pseudomallei: implications for human melioidosis. *PLoS Pathogens*, **2008**, 4, e1000178	7.6	64
336	Immunosuppression associated with interleukin-1R-associated-kinase-M upregulation predicts mortality in Gram-negative sepsis (melioidosis). *Critical Care Medicine*, **2009**, 37, 569-76	1.4	63
335	A decade of genomic history for healthcare-associated Enterococcus faecium in the United Kingdom and Ireland. *Genome Research*, **2016**, 26, 1388-1396	9.7	62
334	A novel hybrid SCCmec-mecC region in Staphylococcus sciuri. *Journal of Antimicrobial Chemotherapy*, **2014**, 69, 911-8	5.1	62
333	Epidemiology, microbiology and mortality associated with community-acquired bacteremia in northeast Thailand: a multicenter surveillance study. *PLoS ONE*, **2013**, 8, e54714	3.7	62
332	Development of a prototype lateral flow immunoassay (LFI) for the rapid diagnosis of melioidosis. *PLoS Neglected Tropical Diseases*, **2014**, 8, e2727	4.8	61

331	The microscopic agglutination test (MAT) is an unreliable predictor of infecting Leptospira serovar in Thailand. *American Journal of Tropical Medicine and Hygiene*, **2009**, 81, 695-7	3.2	61
330	Survey of antimicrobial resistance in clinical Burkholderia pseudomallei isolates over two decades in Northeast Thailand. *Antimicrobial Agents and Chemotherapy*, **2011**, 55, 5388-91	5.9	60
329	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, 1105-13	11.6	60
328	Evolution and Epidemiology of Multidrug-Resistant in the United Kingdom and Ireland. *MBio*, **2017**, 8,	7.8	59
327	Complex Routes of Nosocomial Vancomycin-Resistant Enterococcus faecium Transmission Revealed by Genome Sequencing. *Clinical Infectious Diseases*, **2017**, 64, 886-893	11.6	59
326	Staphylococcus aureus bacteraemia in a tropical setting: patient outcome and impact of antibiotic resistance. *PLoS ONE*, **2009**, 4, e4308	3.7	59
325	Causes of community-acquired bacteremia and patterns of antimicrobial resistance in Vientiane, Laos. *American Journal of Tropical Medicine and Hygiene*, **2006**, 75, 978-85	3.2	59
324	A Staphylococcus xylosus isolate with a new mecC allotype. *Antimicrobial Agents and Chemotherapy*, **2013**, 57, 1524-8	5.9	58
323	Genomic acquisition of a capsular polysaccharide virulence cluster by non-pathogenic Burkholderia isolates. *Genome Biology*, **2010**, 11, R89	18.3	58
322	What Is Resistance? Impact of Phenotypic versus Molecular Drug Resistance Testing on Therapy for Multi- and Extensively Drug-Resistant Tuberculosis. *Antimicrobial Agents and Chemotherapy*, **2018**, 62,	5.9	58
321	Leptospirosis outbreak in Sri Lanka in 2008: lessons for assessing the global burden of disease. *American Journal of Tropical Medicine and Hygiene*, **2011**, 85, 471-8	3.2	57
320	The genetic and molecular basis of O-antigenic diversity in Burkholderia pseudomallei lipopolysaccharide. *PLoS Neglected Tropical Diseases*, **2012**, 6, e1453	4.8	56
319	Rapid detection of the pandemic methicillin-resistant Staphylococcus aureus clone ST 239, a dominant strain in Asian hospitals. *Journal of Clinical Microbiology*, **2008**, 46, 1520-2	9.7	56
318	Innate immunity. A Spaetzle-like role for nerve growth factor in vertebrate immunity to Staphylococcus aureus. *Science*, **2014**, 346, 641-646	33.3	55
317	Rapid whole-genome sequencing for investigation of a suspected tuberculosis outbreak. *Journal of Clinical Microbiology*, **2013**, 51, 611-4	9.7	55
316	Accuracy of Burkholderia pseudomallei identification using the API 20NE system and a latex agglutination test. *Journal of Clinical Microbiology*, **2007**, 45, 3774-6	9.7	55
315	Baseline correlation and comparative kinetics of cerebrospinal fluid colony-forming unit counts and antigen titers in cryptococcal meningitis. *Journal of Infectious Diseases*, **2005**, 192, 681-4	7	55
314	From genotype to phenotype: can systems biology be used to predict Staphylococcus aureus virulence?. *Nature Reviews Microbiology*, **2012**, 10, 791-7	22.2	54

313	Optimization of culture of Leptospira from humans with leptospirosis. *Journal of Clinical Microbiology*, **2007**, 45, 1363-5	9.7	54
312	Clinical and molecular epidemiology of Staphylococcus argenteus infections in Thailand. *Journal of Clinical Microbiology*, **2015**, 53, 1005-8	9.7	53
311	Characterization of ceftazidime resistance mechanisms in clinical isolates of Burkholderia pseudomallei from Australia. *PLoS ONE*, **2012**, 7, e30789	3.7	53
310	Arthropod borne disease: the leading cause of fever in pregnancy on the Thai-Burmese border. *PLoS Neglected Tropical Diseases*, **2010**, 4, e888	4.8	52
309	Burkholderia pseudomallei genome plasticity associated with genomic island variation. *BMC Genomics*, **2008**, 9, 190	4.5	52
308	Activation of the coagulation cascade in patients with leptospirosis. *Clinical Infectious Diseases*, **2008**, 46, 254-60	11.6	52
307	Survival of Burkholderia pseudomallei in distilled water for 16 years. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, **2011**, 105, 598-600	2	51
306	Clinical diagnosis and geographic distribution of leptospirosis, Thailand. *Emerging Infectious Diseases*, **2007**, 13, 124-6	10.2	51
305	Genetic typing of the 56-kDa type-specific antigen gene of contemporary Orientia tsutsugamushi isolates causing human scrub typhus at two sites in north-eastern and western Thailand. *FEMS Immunology and Medical Microbiology*, **2008**, 52, 335-42		51
304	Host responses to melioidosis and tuberculosis are both dominated by interferon-mediated signaling. *PLoS ONE*, **2013**, 8, e54961	3.7	50
303	Genome-based characterization of hospital-adapted lineages. *Nature Microbiology*, **2016**, 1,	26.6	49
302	Loop-mediated isothermal amplification method targeting the TTS1 gene cluster for detection of Burkholderia pseudomallei and diagnosis of melioidosis. *Journal of Clinical Microbiology*, **2008**, 46, 568-73	9.7	49
301	Whole genome sequencing of ESBL-producing Escherichia coli isolated from patients, farm waste and canals in Thailand. *Genome Medicine*, **2017**, 9, 81	14.4	48
300	Genetic diversity and microevolution of Burkholderia pseudomallei in the environment. *PLoS Neglected Tropical Diseases*, **2008**, 2, e182	4.8	48
299	Molecular basis of rare aminoglycoside susceptibility and pathogenesis of Burkholderia pseudomallei clinical isolates from Thailand. *PLoS Neglected Tropical Diseases*, **2009**, 3, e519	4.8	47
298	Recent independent emergence of multiple multidrug-resistant Serratia marcescens clones within the United Kingdom and Ireland. *Genome Research*, **2016**, 26, 1101-9	9.7	47
297	Whole-genome sequencing reveals transmission of vancomycin-resistant Enterococcus faecium in a healthcare network. *Genome Medicine*, **2016**, 8, 4	14.4	46
296	High-throughput mRNA profiling characterizes the expression of inflammatory molecules in sepsis caused by Burkholderia pseudomallei. *Infection and Immunity*, **2007**, 75, 3074-9	3.7	46

295	Within-host evolution of Burkholderia pseudomallei in four cases of acute melioidosis. *PLoS Pathogens*, **2010**, 6, e1000725	7.6	45
294	The BpeEF-OprC efflux pump is responsible for widespread trimethoprim resistance in clinical and environmental Burkholderia pseudomallei isolates. *Antimicrobial Agents and Chemotherapy*, **2013**, 57, 4381-6	5.9	44
293	Evaluating Burkholderia pseudomallei Bip proteins as vaccines and Bip antibodies as detection agents. *FEMS Immunology and Medical Microbiology*, **2008**, 52, 78-87		44
292	Development of ceftazidime resistance in an acute Burkholderia pseudomallei infection. *Infection and Drug Resistance*, **2012**, 5, 129-32	4.2	43
291	Use of Vitek 2 antimicrobial susceptibility profile to identify mecC in methicillin-resistant Staphylococcus aureus. *Journal of Clinical Microbiology*, **2013**, 51, 2732-4	9.7	43
290	Urokinase receptor is necessary for bacterial defense against pneumonia-derived septic melioidosis by facilitating phagocytosis. *Journal of Immunology*, **2010**, 184, 3079-86	5.3	43
289	Burkholderia pseudomallei is spatially distributed in soil in northeast Thailand. *PLoS Neglected Tropical Diseases*, **2010**, 4, e694	4.8	43
288	Biogeography and virulence of Staphylococcus aureus. *PLoS ONE*, **2009**, 4, e6216	3.7	43
287	Rapid immunofluorescence microscopy for diagnosis of melioidosis. *Vaccine Journal*, **2005**, 12, 555-6		43
286	Tsunami in Thailand--disaster management in a district hospital. *New England Journal of Medicine*, **2005**, 352, 962-4	59.2	43
285	T cell response to SARS-CoV-2 infection in humans: A systematic review. *PLoS ONE*, **2021**, 16, e0245532	3.7	43
284	Rapid single-colony whole-genome sequencing of bacterial pathogens. *Journal of Antimicrobial Chemotherapy*, **2014**, 69, 1275-81	5.1	42
283	Serological and blood culture investigations of Nepalese fever patients. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, **2007**, 101, 686-90	2	42
282	Comparison of Ashdown® medium, Burkholderia cepacia medium, and Burkholderia pseudomallei selective agar for clinical isolation of Burkholderia pseudomallei. *Journal of Clinical Microbiology*, **2005**, 43, 5359-61	9.7	42
281	Improving the estimation of the global burden of antimicrobial resistant infections. *Lancet Infectious Diseases, The*, **2019**, 19, e392-e398	25.5	41
280	Molecular detection and speciation of pathogenic Leptospira spp. in blood from patients with culture-negative leptospirosis. *BMC Infectious Diseases*, **2011**, 11, 338	4	41
279	Accuracy of a commercial IgM ELISA for the diagnosis of human leptospirosis in Thailand. *American Journal of Tropical Medicine and Hygiene*, **2012**, 86, 524-527	3.2	41
278	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. *Genome Research*, **2016**, 26, 263-70	9.7	41

277	Melioidosis caused by Burkholderia pseudomallei in drinking water, Thailand, 2012. *Emerging Infectious Diseases*, **2014**, 20, 265-8	10.2	40
276	Emergence of pediatric melioidosis in Siem Reap, Cambodia. *American Journal of Tropical Medicine and Hygiene*, **2010**, 82, 1106-12	3.2	40
275	Phenotypic and functional characterization of human memory T cell responses to Burkholderia pseudomallei. *PLoS Neglected Tropical Diseases*, **2009**, 3, e407	4.8	40
274	Consensus on the development of vaccines against naturally acquired melioidosis. *Emerging Infectious Diseases*, **2015**, 21,	10.2	39
273	Accuracy of loop-mediated isothermal amplification for diagnosis of human leptospirosis in Thailand. *American Journal of Tropical Medicine and Hygiene*, **2011**, 84, 614-20	3.2	39
272	The potential emergence of leptospirosis in Sri Lanka. *Lancet Infectious Diseases, The*, **2009**, 9, 524-6	25.5	39
271	Accuracy of enzyme-linked immunosorbent assay using crude and purified antigens for serodiagnosis of melioidosis. *Vaccine Journal*, **2007**, 14, 110-3		39
270	Emergence of community-associated methicillin-resistant Staphylococcus aureus associated with pediatric infection in Cambodia. *PLoS ONE*, **2009**, 4, e6630	3.7	39
269	Reconstructing transmission trees for communicable diseases using densely sampled genetic data. *Annals of Applied Statistics*, **2016**, 10, 395-417	2.1	39
268	Development of antibodies to Burkholderia pseudomallei during childhood in melioidosis-endemic northeast Thailand. *American Journal of Tropical Medicine and Hygiene*, **2006**, 74, 1074-5	3.2	39
267	Clinical definitions of melioidosis. *American Journal of Tropical Medicine and Hygiene*, **2013**, 88, 411-413	3.2	38
266	The autopsy: a useful tool or an old relic?. *Journal of Pathology*, **1988**, 156, 9-14	9.4	38
265	Changing the paradigm for hospital outbreak detection by leading with genomic surveillance of nosocomial pathogens. *Microbiology (United Kingdom)*, **2018**, 164, 1213-1219	2.9	38
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