## Nicole Stoesser

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Symptoms and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Positivity in the General Population in the United Kingdom. Clinical Infectious Diseases, 2022, 75, e329-e337.	5.8	20
2	Tocilizumab for treatment of SARS-CoV-2 infection at home: A case report. Acute Medicine, 2022, 21, 53-55.	0.3	1
3	Antibody responses and correlates of protection in the general population after two doses of the ChAdOx1 or BNT162b2 vaccines. Nature Medicine, 2022, 28, 1072-1082.	30.7	147
4	Systematic review of wastewater surveillance of antimicrobial resistance in human populations. Environment International, 2022, 162, 107171.	10.0	29
5	Hospital outbreak of carbapenem-resistant Enterobacterales associated with a bla OXA-48 plasmid carried mostly by Escherichia coli ST399. Microbial Genomics, 2022, 8, .	2.0	3
6	Prediction of Antibiotic Resistance Evolution by Growth Measurement of All Proximal Mutants of Beta-Lactamase. Molecular Biology and Evolution, 2022, 39, .	8.9	3
7	Whole genome sequencing reveals hidden transmission of carbapenemase-producing Enterobacterales. Nature Communications, 2022, 13, .	12.8	16
8	SARS-CoV-2 antibody trajectories after a single COVID-19 vaccination with and without prior infection. Nature Communications, 2022, 13, .	12.8	6
9	Antibody Status and Incidence of SARS-CoV-2 Infection in Health Care Workers. New England Journal of Medicine, 2021, 384, 533-540.	27.0	803
10	Community prevalence of SARS-CoV-2 in England from April to November, 2020: results from the ONS Coronavirus Infection Survey. Lancet Public Health, The, 2021, 6, e30-e38.	10.0	147
11	Ten Years of Population-Level Genomic <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Serotype Surveillance Informs Vaccine Development for Invasive Infections. Clinical Infectious Diseases, 2021, 73, 2276-2282.	5.8	16
12	Stringent thresholds in SARS-CoV-2 IgG assays lead to under-detection of mild infections. BMC Infectious Diseases, 2021, 21, 187.	2.9	23
13	Amplification-Free Detection of Viruses in Minutes using Single-Particle Imaging and Machine Learning. Biophysical Journal, 2021, 120, 195a.	0.5	1
14	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2. Nature Communications, 2021, 12, 1951.	12.8	54
15	Genomic network analysis of environmental and livestock F-type plasmid populations. ISME Journal, 2021, 15, 2322-2335.	9.8	24
16	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. Science Advances, 2021, 7, .	10.3	47
17	Diagnosis of SARS-CoV-2 Infection with LamPORE, a High-Throughput Platform Combining Loop-Mediated Isothermal Amplification and Nanopore Sequencing. Journal of Clinical Microbiology, 2021, 59, .	3.9	30
18	Quantitative SARS-CoV-2 anti-spike responses to Pfizer–BioNTech and Oxford–AstraZeneca vaccines by previous infection status. Clinical Microbiology and Infection, 2021, 27, 1516.e7-1516.e14.	6.0	100

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19	Population-level faecal metagenomic profiling as a tool to predict antimicrobial resistance in Enterobacterales isolates causing invasive infections: An exploratory study across Cambodia, Kenya, and the UK. EClinicalMedicine, 2021, 36, 100910.	7.1	10
20	COVID-19: Rapid antigen detection for SARS-CoV-2 by lateral flow assay: A national systematic evaluation of sensitivity and specificity for mass-testing. EClinicalMedicine, 2021, 36, 100924.	7.1	162
21	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. Nature Medicine, 2021, 27, 1370-1378.	30.7	260
22	Ct threshold values, a proxy for viral load in community SARS-CoV-2 cases, demonstrate wide variation across populations and over time. ELife, 2021, 10, .	6.0	91
23	Antibody responses to SARS-CoV-2 vaccines in 45,965 adults from the general population of the United Kingdom. Nature Microbiology, 2021, 6, 1140-1149.	13.3	254
24	Flanker: a tool for comparative genomics of gene flanking regions. Microbial Genomics, 2021, 7, .	2.0	12
25	Ten-year longitudinal molecular epidemiology study of Escherichia coli and Klebsiella species bloodstream infections in Oxfordshire, UK. Genome Medicine, 2021, 13, 144.	8.2	35
26	Antimicrobial resistance genes and clonal success in Escherichia coli isolates causing bloodstream infection. Lancet Microbe, The, 2021, 2, e492.	7.3	2
27	Viral detection and identification in 20Âmin by rapid single-particle fluorescence in-situ hybridization of viral RNA. Scientific Reports, 2021, 11, 19579.	3.3	16
28	Epidemiological data and genome sequencing reveals that nosocomial transmission of SARS-CoV-2 is underestimated and mostly mediated by a small number of highly infectious individuals. Journal of Infection, 2021, 83, 473-482.	3.3	55
29	The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. Clinical Infectious Diseases, 2021, 73, e699-e709.	5.8	235
30	A genomic epidemiological study shows that prevalence of antimicrobial resistance in Enterobacterales is associated with the livestock host, as well as antimicrobial usage. Microbial Genomics, 2021, 7, .	2.0	20
31	Effect of Delta variant on viral burden and vaccine effectiveness against new SARS-CoV-2 infections in the UK. Nature Medicine, 2021, 27, 2127-2135.	30.7	450
32	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. Nature Communications, 2021, 12, 6250.	12.8	88
33	Frequencies and patterns of microbiology test requests from primary care in Oxfordshire, UK, 2008–2018: a retrospective cohort study of electronic health records to inform point-of-care testing. BMJ Open, 2021, 11, e048527.	1.9	2
34	Antimicrobial resistance in commensal opportunistic pathogens isolated from non-sterile sites can be an effective proxy for surveillance in bloodstream infections. Scientific Reports, 2021, 11, 23359.	3.3	2
35	Tracking the Emergence of SARS-CoV-2 Alpha Variant in the United Kingdom. New England Journal of Medicine, 2021, 385, 2582-2585.	27.0	49
36	Performance characteristics of five immunoassays for SARS-CoV-2: a head-to-head benchmark comparison. Lancet Infectious Diseases, The, 2020, 20, 1390-1400.	9.1	336

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37	Risk Factors Associated with Carbapenemase-Producing <i>Enterobacterales</i> (CPE) Positivity in the Hospital Wastewater Environment. Applied and Environmental Microbiology, 2020, 86, .	3.1	11
38	Pathogenicity of mcr-1-positive Escherichia coli from human infections. Lancet Microbe, The, 2020, 1, e195.	7.3	0
39	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne <i>bla</i> <sub>KPC</sub> Carbapenemase in <i>Enterobacterales</i> in the United Kingdom from 2009 to 2014. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	26
40	Dynamics of mcr-1 prevalence and mcr-1-positive Escherichia coli after the cessation of colistin use as a feed additive for animals in China: a prospective cross-sectional and whole genome sequencing-based molecular epidemiological study. Lancet Microbe, The, 2020, 1, e34-e43.	7.3	85
41	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism–calling pipelines. GigaScience, 2020, 9, .	6.4	92
42	Risk factors for Klebsiella pneumoniae carbapenemase (KPC) gene acquisition and clinical outcomes across multiple bacterial species. Journal of Hospital Infection, 2020, 104, 456-468.	2.9	24
43	Genomic dynamics of species and mobile genetic elements in a prolonged blaIMP-4-associated carbapenemase outbreak in an Australian hospital. Journal of Antimicrobial Chemotherapy, 2020, 75, 873-882.	3.0	31
44	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in <i>Escherichia coli</i> . Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	33
45	Cenomic surveillance of Escherichia coli and Klebsiella spp. in hospital sink drains and patients. Microbial Genomics, 2020, 6, .	2.0	26
46	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. Microbial Genomics, 2020, 6, .	2.0	14
47	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	1.8	81
48	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	1.8	122
49	SARS-CoV-2 antibody prevalence, titres and neutralising activity in an antenatal cohort, United Kingdom, 14 April to 15 June 2020. Eurosurveillance, 2020, 25, .	7.0	17
50	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. ELife, 2020, 9, .	6.0	196
51	The Role of <i>fosA</i> in Challenges with Fosfomycin Susceptibility Testing of Multispecies Klebsiella pneumoniae Carbapenemase-Producing Clinical Isolates. Journal of Clinical Microbiology, 2019, 57, .	3.9	26
52	Molecular characterization of carbapenem-resistant Escherichia coli and Acinetobacter baumannii in the Lao People's Democratic Republic. Journal of Antimicrobial Chemotherapy, 2019, 74, 2810-2821.	3.0	8
53	<i>Klebsiella quasipneumoniae</i> Provides a Window into Carbapenemase Gene Transfer, Plasmid Rearrangements, and Patient Interactions with the Hospital Environment. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	44
54	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype 078. MBio, 2019, 10, .	4.1	46

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55	Epidemiology of paediatric gastrointestinal colonisation by extended spectrum cephalosporin-resistant Escherichia coli and Klebsiella pneumoniae isolates in north-west Cambodia. BMC Microbiology, 2019, 19, 59.	3.3	17
56	Don't overlook the little guy: An evaluation of the frequency of small plasmids co-conjugating with larger carbapenemase gene containing plasmids. Plasmid, 2019, 103, 1-8.	1.4	36
57	Occurrence and characterization of Escherichia coli ST410 co-harbouring blaNDM-5, blaCMY-42 and blaTEM-190 in a dog from the UK. Journal of Antimicrobial Chemotherapy, 2019, 74, 1207-1211.	3.0	31
58	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. Environmental Microbiomes, 2019, 14, 7.	5.0	69
59	Carbapenem-resistant Enterobacteriaceae dispersal from sinks is linked to drain position and drainage ratesÂin a laboratory model system. Journal of Hospital Infection, 2019, 102, 63-69.	2.9	46
60	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. Microbial Genomics, 2019, 5, .	2.0	171
61	Panton–Valentine leucocidin is the key determinant of Staphylococcus aureus pyomyositis in a bacterial GWAS. ELife, 2019, 8, .	6.0	56
62	Transmission dynamics and control of multidrug-resistant Klebsiella pneumoniae in neonates in a developing country. ELife, 2019, 8, .	6.0	17
63	Intensive Care Unit Wastewater Interventions to Prevent Transmission of Multispecies Klebsiella pneumoniae Carbapenemase–Producing Organisms. Clinical Infectious Diseases, 2018, 67, 171-178.	5.8	74
64	Illumina short-read and MinION long-read WGS to characterize the molecular epidemiology of an NDM-1 Serratia marcescens outbreak in Romania. Journal of Antimicrobial Chemotherapy, 2018, 73, 672-679.	3.0	29
65	High Rates of Human Fecal Carriage of mcr-1–Positive Multidrug-Resistant Enterobacteriaceae Emerge in China in Association With Successful Plasmid Families. Clinical Infectious Diseases, 2018, 66, 676-685.	5.8	68
66	TETyper: a bioinformatic pipeline for classifying variation and genetic contexts of transposable elements from short-read whole-genome sequencing data. Microbial Genomics, 2018, 4, .	2.0	33
67	A Large, Refractory Nosocomial Outbreak of Klebsiella pneumoniae Carbapenemase-Producing Escherichia coli Demonstrates Carbapenemase Gene Outbreaks Involving Sink Sites Require Novel Approaches to Infection Control. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	99
68	Identification of Biomarkers for Differentiation of Hypervirulent Klebsiella pneumoniae from Classical K. pneumoniae. Journal of Clinical Microbiology, 2018, 56, .	3.9	378
69	Transmission Dynamics of Hyper-Endemic Multi-Drug Resistant Klebsiella pneumoniae in a Southeast Asian Neonatal Unit: A Longitudinal Study With Whole Genome Sequencing. Frontiers in Microbiology, 2018, 9, 1197.	3.5	24
70	Antimicrobial Resistance in Invasive Bacterial Infections in Hospitalized Children, Cambodia, 2007–2016. Emerging Infectious Diseases, 2018, 24, 841-851.	4.3	50
71	Bayesian reconstruction of transmission within outbreaks using genomic variants. PLoS Computational Biology, 2018, 14, e1006117.	3.2	69
72	Trends over time in Escherichia coli bloodstream infections, urinary tract infections, and antibiotic susceptibilities in Oxfordshire, UK, 1998–2016: a study of electronic health records. Lancet Infectious Diseases, The, 2018, 18, 1138-1149.	9.1	121

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73	Carriage of β-lactamase-producing Enterobacteriaceae by Chinese travellers. Lancet Infectious Diseases, The, 2017, 17, 138-139.	9.1	7
74	Effects of control interventions on Clostridium difficile infection in England: an observational study. Lancet Infectious Diseases, The, 2017, 17, 411-421.	9.1	269
75	IncX2 and IncX1-X2 Hybrid Plasmids Coexisting in a FosA6-Producing Escherichia coli Strain. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	14
76	Mortality risks associated with emergency admissions during weekends and public holidays: an analysis of electronic health records. Lancet, The, 2017, 390, 62-72.	13.7	114
77	The Hospital Water Environment as a Reservoir for Carbapenem-Resistant Organisms Causing Hospital-Acquired Infections—A Systematic Review of the Literature. Clinical Infectious Diseases, 2017, 64, 1435-1444.	5.8	242
78	Enhanced Klebsiella pneumoniae Carbapenemase Expression from a Novel Tn <i>4401</i> Deletion. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	64
79	Ordering the mob: Insights into replicon and MOB typing schemes from analysis of a curated dataset of publicly available plasmids. Plasmid, 2017, 91, 42-52.	1.4	89
80	Chromosomal Integration of the Klebsiella pneumoniae Carbapenemase Gene, <i>bla</i> <sub>KPC</sub> , in Klebsiella Species Is Elusive but Not Rare. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	46
81	A curated dataset of complete Enterobacteriaceae plasmids compiled from the NCBI nucleotide database. Data in Brief, 2017, 12, 423-426.	1.0	58
82	Genomic epidemiology of global Klebsiella pneumoniae carbapenemase (KPC)-producing Escherichia coli. Scientific Reports, 2017, 7, 5917.	3.3	108
83	Covert dissemination of carbapenemase-producing Klebsiella pneumoniae (KPC) in a successfully controlled outbreak: long- and short-read whole-genome sequencing demonstrate multiple genetic modes of transmission. Journal of Antimicrobial Chemotherapy, 2017, 72, 3025-3034.	3.0	73
84	Severity of illness and the weekend effect $\hat{a} \in$ "Authors' reply. Lancet, The, 2017, 390, 1735.	13.7	11
85	Mortality Risks Associated With Emergency Admissions During Weekends and Public Holidays: An Analysis of Electronic Health Records. Obstetrical and Gynecological Survey, 2017, 72, 699-701.	0.4	Ο
86	Plasmid Classification in an Era of Whole-Genome Sequencing: Application in Studies of Antibiotic Resistance Epidemiology. Frontiers in Microbiology, 2017, 8, 182.	3.5	191
87	Resolving plasmid structures in Enterobacteriaceae using the MinION nanopore sequencer: assessment of MinION and MinION/Illumina hybrid data assembly approaches. Microbial Genomics, 2017, 3, e000118.	2.0	74
88	Supporting surveillance capacity for antimicrobial resistance: Laboratory capacity strengthening for drug resistant infections in low and middle income countries. Wellcome Open Research, 2017, 2, 91.	1.8	48
89	Epidemiology of Clostridium difficile in infants in Oxfordshire, UK: Risk factors for colonization and carriage, and genetic overlap with regional C. difficile infection strains. PLoS ONE, 2017, 12, e0182307.	2.5	82
90	Complete Sequencing of Plasmids Containing <i>bla</i> <sub>OXA-163</sub> and <i>bla</i> <sub>OXA-48</sub> in Escherichia coli Sequence Type 131. Antimicrobial Agents and Chemotherapy, 2016, 60, 6948-6951.	3.2	19

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91	Characterization of a Novel IncHI2 Plasmid Carrying Tandem Copies of <i>bla</i> <sub>CTX-M-2</sub> in a <i>fosA6</i> -Harboring Escherichia coli Sequence Type 410 Strain. Antimicrobial Agents and Chemotherapy, 2016, 60, 6742-6747.	3.2	12
92	First Report of <i>bla</i> <sub>IMP-14</sub> on a Plasmid Harboring Multiple Drug Resistance Genes in Escherichia coli Sequence Type 131. Antimicrobial Agents and Chemotherapy, 2016, 60, 5068-5071.	3.2	15
93	Oral fosfomycin for treatment of urinary tract infection: a retrospective cohort study. BMC Infectious Diseases, 2016, 16, 556.	2.9	53
94	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. Nature Microbiology, 2016, 1, 16041.	13.3	247
95	Separate F-Type Plasmids Have Shaped the Evolution of the <i>H</i> 30 Subclone of Escherichia coli Sequence Type 131. MSphere, 2016, 1, .	2.9	98
96	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene <i>bla</i> <sub>KPC</sub> . Antimicrobial Agents and Chemotherapy, 2016, 60, 3767-3778.	3.2	255
97	Glutathione- <i>S</i> -transferase FosA6 of <i>Klebsiella pneumoniae</i> origin conferring fosfomycin resistance in ESBL-producing <i>Escherichia coli</i> . Journal of Antimicrobial Chemotherapy, 2016, 71, 2460-2465.	3.0	49
98	Antimicrobial susceptibility of uropathogens isolated from Cambodian children. Paediatrics and International Child Health, 2016, 36, 113-117.	1.0	24
99	Colistin resistance gene mcr-1 and pHNSHP45 plasmid in human isolates of Escherichia coli and Klebsiella pneumoniae. Lancet Infectious Diseases, The, 2016, 16, 285-286.	9.1	119
100	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	4.1	289
101	Complete Genome Sequence of KPC-Producing Klebsiella pneumoniae Strain CAV1193. Genome Announcements, 2016, 4, .	0.8	20
102	Characterisation of Invasive Streptococcus pneumoniae Isolated from Cambodian Children between 2007 – 2012. PLoS ONE, 2016, 11, e0159358.	2.5	15
103	Dynamics of MDR <i>Enterobacter cloacae</i> outbreaks in a neonatal unit in Nepal: insights using wider sampling frames and next-generation sequencing. Journal of Antimicrobial Chemotherapy, 2015, 70, 1008-1015.	3.0	45
104	Klebsiella pneumoniae Carbapenemase (KPC)-Producing K. pneumoniae at a Single Institution: Insights into Endemicity from Whole-Genome Sequencing. Antimicrobial Agents and Chemotherapy, 2015, 59, 1656-1663.	3.2	140
105	Colonization with Enterobacteriaceae producing ESBLs in children attending pre-school childcare facilities in the Lao People's Democratic Republic. Journal of Antimicrobial Chemotherapy, 2015, 70, 1893-1897.	3.0	62
106	Extensive Within-Host Diversity in Fecally Carried Extended-Spectrum-Beta-Lactamase-Producing Escherichia coli Isolates: Implications for Transmission Analyses. Journal of Clinical Microbiology, 2015, 53, 2122-2131.	3.9	84
107	Rapid Diagnostic Tests for Dengue Virus Infection in Febrile Cambodian Children: Diagnostic Accuracy and Incorporation into Diagnostic Algorithms. PLoS Neglected Tropical Diseases, 2015, 9, e0003424.	3.0	24
108	Multidrug-resistant Escherichia coli soft tissue infection investigated with bacterial whole genome sequencing. BMJ Case Reports, 2014, 2014, bcr2014207200-bcr2014207200.	0.5	4

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109	Ophthalmic infections in children presenting to Angkor Hospital for Children, Siem Reap, Cambodia. BMC Research Notes, 2014, 7, 784.	1.4	9
110	Genome Sequencing of an Extended Series of NDM-Producing Klebsiella pneumoniae Isolates from Neonatal Infections in a Nepali Hospital Characterizes the Extent of Community- versus Hospital-Associated Transmission in an Endemic Setting. Antimicrobial Agents and Chemotherapy, 2014, 58, 7347-7357.	3.2	142
111	Septic arthritis of the hip in a Cambodian child caused by multidrug-resistantSalmonella entericaserovar Typhi with intermediate susceptibility to ciprofloxacin treated with ceftriaxone and azithromycin. Paediatrics and International Child Health, 2014, 34, 227-229.	1.0	4
112	Evolutionary History of the Clostridium difficile Pathogenicity Locus. Genome Biology and Evolution, 2014, 6, 36-52.	2.5	190
113	Treatment of Suspected Hyper-Reactive Malarial Splenomegaly (HMS) in Pregnancy with Mefloquine. American Journal of Tropical Medicine and Hygiene, 2014, 90, 609-611.	1.4	6
114	Predicting antimicrobial susceptibilities for Escherichia coli and Klebsiella pneumoniae isolates using whole genomic sequence data. Journal of Antimicrobial Chemotherapy, 2013, 68, 2234-2244.	3.0	314
115	Comparison of Multilocus Variable-Number Tandem-Repeat Analysis and Whole-Genome Sequencing for Investigation of Clostridium difficile Transmission. Journal of Clinical Microbiology, 2013, 51, 4141-4149.	3.9	69
116	The Epidemiology of Pediatric Bone and Joint Infections in Cambodia, 2007-11. Journal of Tropical Pediatrics, 2013, 59, 36-42.	1.5	22
117	Risk Factors for Clostridium difficile Acquisition in Infants: Importance of Study Design. Clinical Infectious Diseases, 2013, 56, 1680-1681.	5.8	5
118	The value of intermittent point-prevalence surveys of healthcare-associated infections for evaluating infection control interventions at Angkor Hospital for Children, Siem Reap, Cambodia. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2013, 107, 248-253.	1.8	29
119	Pediatric Bloodstream Infections in Cambodia, 2007 to 2011. Pediatric Infectious Disease Journal, 2013, 32, e272-e276.	2.0	34
120	A Prospective Study of the Causes of Febrile Illness Requiring Hospitalization in Children in Cambodia. PLoS ONE, 2013, 8, e60634.	2.5	88
121	Increasing incidence of Escherichia coli bacteraemia is driven by an increase in antibiotic-resistant isolates: electronic database study in Oxfordshire 1999-2011. Journal of Antimicrobial Chemotherapy, 2012, 67, 1514-1524.	3.0	45
122	Fidaxomicin Versus Vancomycin for Clostridium difficile Infection: Meta-analysis of Pivotal Randomized Controlled Trials. Clinical Infectious Diseases, 2012, 55, S93-S103.	5.8	228
123	Changing Patterns of Gastrointestinal Parasite Infections in Cambodian Children: 2006-2011. Journal of Tropical Pediatrics, 2012, 58, 509-512.	1.5	14
124	Characteristics of CTX-M ESBL-producing Escherichia coli isolates from the Lao People's Democratic Republic, 2004-09. Journal of Antimicrobial Chemotherapy, 2012, 67, 240-242.	3.0	25
125	Paediatric Chromobacterium violaceum in Cambodia: the first documented case. Tropical Doctor, 2012, 42, 178-179.	0.5	8
126	Pediatric Suppurative Parotitis in Cambodia Between 2007 and 2011. Pediatric Infectious Disease Journal, 2012, 31, 865-868.	2.0	32

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127	Surveillance of healthcare-associated infection at Angkor Hospital for Children, Siem Reap, Cambodia. International Journal of Infectious Diseases, 2012, 16, e375.	3.3	0
128	Enteric fever in Cambodian children is dominated by multidrug resistant H58 Salmonella enterica serovar Typhi with decreased susceptibility to ciprofloxacin. International Journal of Infectious Diseases, 2012, 16, e427.	3.3	0
129	Enteric fever in Cambodian children is dominated by multidrug-resistant H58 Salmonella enterica serovar Typhi with intermediate susceptibility to ciprofloxacin. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2012, 106, 718-724.	1.8	38
130	Clinical Clostridium difficile: Clonality and Pathogenicity Locus Diversity. PLoS ONE, 2011, 6, e19993.	2.5	150
131	Molecular Epidemiology of Clostridium difficile Strains in Children Compared with That of Strains Circulating in Adults with Clostridium difficile-Associated Infection : Fig. 1 Journal of Clinical Microbiology, 2011, 49, 3994-3996.	3.9	32
132	Multilocus Sequence Typing of <i>Clostridium difficile</i> . Journal of Clinical Microbiology, 2010, 48, 770-778.	3.9	399
133	Re-visiting Clostridium difficile in children: Reservoir, victims, both or none?. Journal of Infection, 2009, 59, S429-S430.	3.3	0
134	Delayed parasite elimination in human infections treated with clindamycin parallels â€~delayed death' of Plasmodium falciparum in vitro. International Journal for Parasitology, 2007, 37, 777-785.	3.1	27
135	Treatment of enteric fever (typhoid and paratyphoid fever) with third and fourth generation cephalosporins. The Cochrane Library, 0, , .	2.8	3
136	Antimicrobial susceptibility of uropathogens isolated from Cambodian children. Paediatrics and International Child Health, 0, , 1-5.	1.0	1
137	Risk Factors Associated with Carbapenemase-Producing Enterobacterales (CPE) Positivity in the Hospital Wastewater Environment. SSRN Electronic Journal, 0, , .	0.4	0
138	Mortality risks associated with empirical antibiotic activity in <i>Escherichia coli</i> bacteraemia: an analysis of electronic health records. Journal of Antimicrobial Chemotherapy, 0, , .	3.0	3