

Stephen Baker

List of Publications by Year in descending order

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356
papers

27,352
citations

15504

65
h-index

9345

143
g-index

409
all docs

409
docs citations

409
times ranked

26034
citing authors

#	ARTICLE	IF	CITATIONS
1	Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. Lancet, The, 2022, 399, 629-655.	13.7	4,915
2	SARS-CoV-2 B.1.617.2 Delta variant replication and immune evasion. Nature, 2021, 599, 114-119.	27.8	1,041
3	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3574-81.	7.1	942
4	Rapid Pneumococcal Evolution in Response to Clinical Interventions. Science, 2011, 331, 430-434.	12.6	828
5	The multidrug-resistant human pathogen <i>Clostridium difficile</i> has a highly mobile, mosaic genome. Nature Genetics, 2006, 38, 779-786.	21.4	821
6	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. Nature, 2022, 603, 706-714.	27.8	756
7	Drug-resistant enteric fever worldwide, 1990 to 2018: a systematic review and meta-analysis. BMC Medicine, 2020, 18, 1.	5.5	660
8	Age-related immune response heterogeneity to SARS-CoV-2 vaccine BNT162b2. Nature, 2021, 596, 417-422.	27.8	549
9	High-throughput sequencing provides insights into genome variation and evolution in <i>Salmonella</i> Typhi. Nature Genetics, 2008, 40, 987-993.	21.4	453
10	Emergence of an Extensively Drug-Resistant <i>Salmonella enterica</i> Serovar Typhi Clone Harboring a Promiscuous Plasmid Encoding Resistance to Fluoroquinolones and Third-Generation Cephalosporins. MBio, 2018, 9, .	4.1	434
11	Screening of healthcare workers for SARS-CoV-2 highlights the role of asymptomatic carriage in COVID-19 transmission. ELife, 2020, 9, .	6.0	423
12	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. Nature Genetics, 2015, 47, 632-639.	21.4	403
13	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, 1263-1271.	9.1	352
14	Evolutionary History of <i>Salmonella</i> Typhi. Science, 2006, 314, 1301-1304.	12.6	349
15	Detection of Vi-Negative <i>Salmonella enterica</i> Serovar Typhi in the Peripheral Blood of Patients with Typhoid Fever in the Faisalabad Region of Pakistan. Journal of Clinical Microbiology, 2005, 43, 4418-4425.	3.9	333
16	Vi Antigen Expression in <i>Salmonella enterica</i> Serovar Typhi Clinical Isolates from Pakistan. Journal of Clinical Microbiology, 2005, 43, 1158-1165.	3.9	327
17	<i>Shigella sonnei</i> genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. Nature Genetics, 2012, 44, 1056-1059.	21.4	278
18	A thermostable, closed SARS-CoV-2 spike protein trimer. Nature Structural and Molecular Biology, 2020, 27, 934-941.	8.2	261

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19	<i>Salmonella enterica</i> Serovar Typhi and the Pathogenesis of Typhoid Fever. Annual Review of Microbiology, 2014, 68, 317-336.	7.3	254
20	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. Science, 2018, 360, 733-738.	12.6	254
21	Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. PLoS Pathogens, 2016, 12, e1005763.	4.7	244
22	Longitudinal analysis reveals that delayed bystander CD8+ T cell activation and early immune pathology distinguish severe COVID-19 from mild disease. Immunity, 2021, 54, 1257-1275.e8.	14.3	230
23	Salmonella chronic carriage: epidemiology, diagnosis, and gallbladder persistence. Trends in Microbiology, 2014, 22, 648-655.	7.7	227
24	Incidence of invasive salmonella disease in sub-Saharan Africa: a multicentre population-based surveillance study. The Lancet Global Health, 2017, 5, e310-e323.	6.3	223
25	Ventilator-associated pneumonia in critically ill patients with COVID-19. Critical Care, 2021, 25, 25.	5.8	217
26	Genomic Comparison of <i>Salmonella enterica</i> Serovars and <i>Salmonella bongori</i> by Use of an <i>S. enterica</i> Serovar Typhimurium DNA Microarray. Journal of Bacteriology, 2003, 185, 553-563.	2.2	211
27	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. Lancet Infectious Diseases, The, 2015, 15, 913-921.	9.1	204
28	Genomic surveillance for hypervirulence and multi-drug resistance in invasive <i>Klebsiella pneumoniae</i> from South and Southeast Asia. Genome Medicine, 2020, 12, 11.	8.2	178
29	<i>Salmonella enterica</i> Serovar Typhi Possesses a Unique Repertoire of Fimbrial Gene Sequences. Infection and Immunity, 2001, 69, 2894-2901.	2.2	166
30	Use of Colistin and Other Critical Antimicrobials on Pig and Chicken Farms in Southern Vietnam and Its Association with Resistance in Commensal <i>Escherichia coli</i> Bacteria. Applied and Environmental Microbiology, 2016, 82, 3727-3735.	3.1	150
31	Phase 3 Efficacy Analysis of a Typhoid Conjugate Vaccine Trial in Nepal. New England Journal of Medicine, 2019, 381, 2209-2218.	27.0	147
32	An extended genotyping framework for <i>Salmonella enterica</i> serovar Typhi, the cause of human typhoid. Nature Communications, 2016, 7, 12827.	12.8	145
33	The utility of diagnostic tests for enteric fever in endemic locations. Expert Review of Anti-Infective Therapy, 2011, 9, 711-725.	4.4	143
34	Composition, Acquisition, and Distribution of the Vi Exopolysaccharide-Encoding <i>Salmonella enterica</i> Pathogenicity Island SPI-7. Journal of Bacteriology, 2003, 185, 5055-5065.	2.2	142
35	The genomic signatures of <i>Shigella</i> evolution, adaptation and geographical spread. Nature Reviews Microbiology, 2016, 14, 235-250.	28.6	142
36	The Rising Dominance of <i>Shigella sonnei</i> : An Intercontinental Shift in the Etiology of Bacillary Dysentery. PLoS Neglected Tropical Diseases, 2015, 9, e0003708.	3.0	140

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37	A current perspective on antimicrobial resistance in Southeast Asia. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2963-2972.	3.0	139
38	Recent insights into <i>Shigella</i> : a major contributor to the global diarrhoeal disease burden. <i>Current Opinion in Infectious Diseases</i> , 2018, 31, 449-454.	3.1	134
39	Tracking the establishment of local endemic populations of an emergent enteric pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17522-17527.	7.1	124
40	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015, 6, 6740.	12.8	124
41	The global burden and epidemiology of invasive non-typhoidal <i>Salmonella</i> infections. <i>Human Vaccines and Immunotherapeutics</i> , 2019, 15, 1421-1426.	3.3	118
42	Whole-genome sequences of <i>Chlamydia trachomatis</i> directly from clinical samples without culture. <i>Genome Research</i> , 2013, 23, 855-866.	5.5	115
43	Emergence of a Globally Dominant IncHI1 Plasmid Type Associated with Multiple Drug Resistant Typhoid. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1245.	3.0	114
44	Combined high-resolution genotyping and geospatial analysis reveals modes of endemic urban typhoid fever transmission. <i>Open Biology</i> , 2011, 1, 110008.	3.6	112
45	The Role of Prophage-like Elements in the Diversity of <i>Salmonella enterica</i> Serovars. <i>Journal of Molecular Biology</i> , 2004, 339, 279-300.	4.2	111
46	A changing picture of shigellosis in southern Vietnam: shifting species dominance, antimicrobial susceptibility and clinical presentation. <i>BMC Infectious Diseases</i> , 2009, 9, 204.	2.9	111
47	A novel ciprofloxacin-resistant subclade of H58 <i>Salmonella</i> Typhi is associated with fluoroquinolone treatment failure. <i>ELife</i> , 2016, 5, e14003.	6.0	111
48	A high-resolution genomic analysis of multidrug-resistant hospital outbreaks of <i>Klebsiella pneumoniae</i> . <i>EMBO Molecular Medicine</i> , 2015, 7, 227-239.	6.9	104
49	Fitness benefits in fluoroquinolone-resistant <i>Salmonella</i> Typhi in the absence of antimicrobial pressure. <i>ELife</i> , 2013, 2, e01229.	6.0	103
50	Extensive Capsule Locus Variation and Large-Scale Genomic Recombination within the <i>Klebsiella pneumoniae</i> Clonal Group 258. <i>Genome Biology and Evolution</i> , 2015, 7, 1267-1279.	2.5	99
51	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	12.8	98
52	The sensitivity of real-time PCR amplification targeting invasive <i>Salmonella</i> serovars in biological specimens. <i>BMC Infectious Diseases</i> , 2010, 10, 125.	2.9	94
53	Species-wide whole genome sequencing reveals historical global spread and recent local persistence in <i>Shigella flexneri</i> . <i>ELife</i> , 2015, 4, e07335.	6.0	94
54	A return to the pre-antimicrobial era?. <i>Science</i> , 2015, 347, 1064-1066.	12.6	91

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55	Searching for the elusive typhoid diagnostic. BMC Infectious Diseases, 2010, 10, 45.	2.9	89
56	Predicting the Impact of Vaccination on the Transmission Dynamics of Typhoid in South Asia: A Mathematical Modeling Study. PLoS Neglected Tropical Diseases, 2014, 8, e2642.	3.0	88
57	The induction and identification of novel Colistin resistance mutations in <i>Acinetobacter baumannii</i> and their implications. Scientific Reports, 2016, 6, 28291.	3.3	88
58	Immune profiling with a <i>Salmonella</i> Typhi antigen microarray identifies new diagnostic biomarkers of human typhoid. Scientific Reports, 2013, 3, 1043.	3.3	87
59	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	21.4	85
60	South Asia as a Reservoir for the Global Spread of Ciprofloxacin-Resistant <i>Shigella sonnei</i> : A Cross-Sectional Study. PLoS Medicine, 2016, 13, e1002055.	8.4	84
61	A Clinical and Epidemiological Investigation of the First Reported Human Infection With the Zoonotic Parasite <i>Trypanosoma evansi</i> in Southeast Asia. Clinical Infectious Diseases, 2016, 62, 1002-1008.	5.8	83
62	Inducible colistin resistance via a disrupted plasmid-borne <i>mcr-1</i> gene in a 2008 Vietnamese <i>Shigella sonnei</i> isolate. Journal of Antimicrobial Chemotherapy, 2016, 71, 2314-2317.	3.0	82
63	Deep Sequencing of Norovirus Genomes Defines Evolutionary Patterns in an Urban Tropical Setting. Journal of Virology, 2014, 88, 11056-11069.	3.4	78
64	The Genome of <i>Salmonella enterica</i> Serovar Typhi. Clinical Infectious Diseases, 2007, 45, S29-S33.	5.8	75
65	The evolution of antimicrobial resistance in <i>Salmonella</i> Typhi. Current Opinion in Gastroenterology, 2018, 34, 25-30.	2.3	73
66	Current perspectives on invasive nontyphoidal <i>Salmonella</i> disease. Current Opinion in Infectious Diseases, 2017, 30, 498-503.	3.1	71
67	The Ecological Dynamics of Fecal Contamination and <i>Salmonella</i> Typhi and <i>Salmonella</i> Paratyphi A in Municipal Kathmandu Drinking Water. PLoS Neglected Tropical Diseases, 2016, 10, e0004346.	3.0	70
68	High-Throughput Genotyping of <i>Salmonella enterica</i> Serovar Typhi Allowing Geographical Assignment of Haplotypes and Pathotypes within an Urban District of Jakarta, Indonesia. Journal of Clinical Microbiology, 2008, 46, 1741-1746.	3.9	69
69	High prevalence of plasmid-mediated quinolone resistance determinants in commensal members of the Enterobacteriaceae in Ho Chi Minh City, Vietnam. Journal of Medical Microbiology, 2009, 58, 1585-1592.	1.8	69
70	High-throughput bacterial SNP typing identifies distinct clusters of <i>Salmonella</i> Typhi causing typhoid in Nepalese children. BMC Infectious Diseases, 2010, 10, 144.	2.9	68
71	Typhoid conjugate vaccines: a new tool in the fight against antimicrobial resistance. Lancet Infectious Diseases, The, 2019, 19, e26-e30.	9.1	67
72	The Influence of Reduced Susceptibility to Fluoroquinolones in <i>Salmonella enterica</i> Serovar Typhi on the Clinical Response to Ofloxacin Therapy. PLoS Neglected Tropical Diseases, 2011, 5, e1163.	3.0	66

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73	Assessing gut microbiota perturbations during the early phase of infectious diarrhea in Vietnamese children. <i>Gut Microbes</i> , 2018, 9, 38-54.	9.8	66
74	The Relationship Between Blood Sample Volume and Diagnostic Sensitivity of Blood Culture for Typhoid and Paratyphoid Fever: A Systematic Review and Meta-Analysis. <i>Journal of Infectious Diseases</i> , 2018, 218, S255-S267.	4.0	66
75	The Typhoid Fever Surveillance in Africa Program (TSAP): Clinical, Diagnostic, and Epidemiological Methodologies. <i>Clinical Infectious Diseases</i> , 2016, 62, S9-S16.	5.8	65
76	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2021, 12, 2684.	12.8	65
77	Repeated local emergence of carbapenem-resistant <i>Acinetobacter baumannii</i> in a single hospital ward. <i>Microbial Genomics</i> , 2016, 2, e000050.	2.0	65
78	A Novel Linear Plasmid Mediates Flagellar Variation in <i>Salmonella Typhi</i> . <i>PLoS Pathogens</i> , 2007, 3, e59.	4.7	64
79	The Relationship Between Invasive Nontyphoidal <i>Salmonella</i> Disease, Other Bacterial Bloodstream Infections, and Malaria in Sub-Saharan Africa. <i>Clinical Infectious Diseases</i> , 2016, 62, S23-S31.	5.8	63
80	The STRATAA study protocol: a programme to assess the burden of enteric fever in Bangladesh, Malawi and Nepal using prospective population census, passive surveillance, serological studies and healthcare utilisation surveys. <i>BMJ Open</i> , 2017, 7, e016283.	1.9	61
81	Combined Point-of-Care Nucleic Acid and Antibody Testing for SARS-CoV-2 following Emergence of D614G Spike Variant. <i>Cell Reports Medicine</i> , 2020, 1, 100099.	6.5	61
82	The decline of typhoid and the rise of non-typhoid salmonellae and fungal infections in a changing HIV landscape: bloodstream infection trends over 15 years in southern Vietnam. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2012, 106, 26-34.	1.8	60
83	Invasive Non-typhoidal <i>Salmonella</i> Infections in Asia: Clinical Observations, Disease Outcome and Dominant Serovars from an Infectious Disease Hospital in Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004857.	3.0	60
84	Evaluation of the Clinical and Microbiological Response to <i>Salmonella Paratyphi A</i> Infection in the First Paratyphoid Human Challenge Model. <i>Clinical Infectious Diseases</i> , 2017, 64, 1066-1073.	5.8	60
85	Differential Epidemiology of <i>Salmonella Typhi</i> and <i>Paratyphi A</i> in Kathmandu, Nepal: A Matched Case Control Investigation in a Highly Endemic Enteric Fever Setting. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2391.	3.0	59
86	A Phylogenetic and Phenotypic Analysis of <i>Salmonella enterica</i> Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004446.	3.0	59
87	The Burden and Characteristics of Enteric Fever at a Healthcare Facility in a Densely Populated Area of Kathmandu. <i>PLoS ONE</i> , 2010, 5, e13988.	2.5	58
88	A Prospective Multi-Center Observational Study of Children Hospitalized with Diarrhea in Ho Chi Minh City, Vietnam. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 92, 1045-1052.	1.4	56
89	Identification and characterization of <i>Coronaviridae</i> genomes from Vietnamese bats and rats based on conserved protein domains. <i>Virus Evolution</i> , 2018, 4, vey035.	4.9	56
90	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella Typhi</i> at pathogenwatch. <i>Nature Communications</i> , 2021, 12, 2879.	12.8	56

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91	The Microbiological and Clinical Characteristics of Invasive Salmonella in Gallbladders from Cholecystectomy Patients in Kathmandu, Nepal. PLoS ONE, 2012, 7, e47342.	2.5	56
92	Undifferentiated Febrile Illness in Kathmandu, Nepal. American Journal of Tropical Medicine and Hygiene, 2015, 92, 875-878.	1.4	55
93	Navigating the future of bacterial molecular epidemiology. Current Opinion in Microbiology, 2010, 13, 640-645.	5.1	54
94	Gatifloxacin versus ceftriaxone for uncomplicated enteric fever in Nepal: an open-label, two-centre, randomised controlled trial. Lancet Infectious Diseases, The, 2016, 16, 535-545.	9.1	54
95	Evaluation of Luminex xTAG Gastrointestinal Pathogen Panel Assay for Detection of Multiple Diarrheal Pathogens in Fecal Samples in Vietnam. Journal of Clinical Microbiology, 2016, 54, 1094-1100.	3.9	53
96	New Variant of Multidrug-Resistant <i>Salmonella enterica</i> Serovar Typhimurium Associated with Invasive Disease in Immunocompromised Patients in Vietnam. MBio, 2018, 9, .	4.1	53
97	The Co-Selection of Fluoroquinolone Resistance Genes in the Gut Flora of Vietnamese Children. PLoS ONE, 2012, 7, e42919.	2.5	52
98	Unbiased whole-genome deep sequencing of human and porcine stool samples reveals circulation of multiple groups of rotaviruses and a putative zoonotic infection. Virus Evolution, 2016, 2, vew027.	4.9	52
99	The Removal of Airborne Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and Other Microbial Bioaerosols by Air Filtration on Coronavirus Disease 2019 (COVID-19) Surge Units. Clinical Infectious Diseases, 2022, 75, e97-e101.	5.8	52
100	Identification of Core and Variable Components of the Salmonella enterica Subspecies I Genome by Microarray. Infection and Immunity, 2005, 73, 7894-7905.	2.2	51
101	One hypervirulent clone, sequence type 283, accounts for a large proportion of invasive Streptococcus agalactiae isolated from humans and diseased tilapia in Southeast Asia. PLoS Neglected Tropical Diseases, 2019, 13, e0007421.	3.0	51
102	Kathmandu, Nepal: Still an enteric fever capital of the world. Journal of Infection in Developing Countries, 2008, 2, 461-5.	1.2	51
103	Interaction of Salmonella enterica serovar Typhi with cultured epithelial cells: roles of surface structures in adhesion and invasion. Microbiology (United Kingdom), 2008, 154, 1914-1926.	1.8	50
104	Analysis of the Hypervariable Region of the Salmonella enterica Genome Associated with tRNA leuX. Journal of Bacteriology, 2005, 187, 2469-2482.	2.2	49
105	Gatifloxacin versus chloramphenicol for uncomplicated enteric fever: an open-label, randomised, controlled trial. Lancet Infectious Diseases, The, 2011, 11, 445-454.	9.1	49
106	Identification of Possible Virulence Marker from Campylobacter jejuni isolates. Emerging Infectious Diseases, 2014, 20, 1026-1029.	4.3	49
107	Emergence of carbapenem-resistant Acinetobacter baumannii as the major cause of ventilator-associated pneumonia in intensive care unit patients at an infectious disease hospital in southern Vietnam. Journal of Medical Microbiology, 2014, 63, 1386-1394.	1.8	49
108	The Sudden Dominance of bla _{CTX-M} Harboring Plasmids in Shigella spp. Circulating in Southern Vietnam. PLoS Neglected Tropical Diseases, 2010, 4, e702.	3.0	48

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109	Efficacy of typhoid conjugate vaccine in Nepal: final results of a phase 3, randomised, controlled trial. <i>The Lancet Global Health</i> , 2021, 9, e1561-e1568.	6.3	48
110	<i>Salmonella</i> Typhi sense host neuroendocrine stress hormones and release the toxin haemolysin E. <i>EMBO Reports</i> , 2011, 12, 252-258.	4.5	47
111	Temporal Fluctuation of Multidrug Resistant <i>Salmonella</i> Typhi Haplotypes in the Mekong River Delta Region of Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e929.	3.0	47
112	The Vietnam Initiative on Zoonotic Infections (VIZIONS): A Strategic Approach to Studying Emerging Zoonotic Infectious Diseases. <i>EcoHealth</i> , 2015, 12, 726-735.	2.0	47
113	Point of Care Nucleic Acid Testing for SARS-CoV-2 in Hospitalized Patients: A Clinical Validation Trial and Implementation Study. <i>Cell Reports Medicine</i> , 2020, 1, 100062.	6.5	47
114	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004781.	3.0	46
115	Suitable Disk Antimicrobial Susceptibility Breakpoints Defining <i>Salmonella enterica</i> Serovar Typhi Isolates with Reduced Susceptibility to Fluoroquinolones. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 5201-5208.	3.2	45
116	Structure, Diversity, and Mobility of the <i>Salmonella</i> Pathogenicity Island 7 Family of Integrative and Conjugative Elements within Enterobacteriaceae. <i>Journal of Bacteriology</i> , 2012, 194, 1494-1504.	2.2	45
117	<i>Salmonella</i> Typhi and <i>Salmonella</i> Paratyphi A elaborate distinct systemic metabolite signatures during enteric fever. <i>ELife</i> , 2014, 3, .	6.0	45
118	Comparative genomics of <i>Cryptococcus neoformans</i> var. <i>grubii</i> associated with meningitis in HIV infected and uninfected patients in Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005628.	3.0	45
119	Clinically and Microbiologically Derived Azithromycin Susceptibility Breakpoints for <i>Salmonella enterica</i> Serovars Typhi and Paratyphi A. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2756-2764.	3.2	44
120	Commensal <i>Escherichia coli</i> are a reservoir for the transfer of XDR plasmids into epidemic fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Microbiology</i> , 2020, 5, 256-264.	13.3	43
121	The validation and utility of a quantitative one-step multiplex RT real-time PCR targeting Rotavirus A and Norovirus. <i>Journal of Virological Methods</i> , 2013, 187, 138-143.	2.1	42
122	Burden of enteric fever at three urban sites in Africa and Asia: a multicentre population-based study. <i>The Lancet Global Health</i> , 2021, 9, e1688-e1696.	6.3	42
123	Molecular Characterization of the <i>Salmonella enterica</i> Serovar Typhi Vi-Typing Bacteriophage E1. <i>Journal of Bacteriology</i> , 2008, 190, 2580-2587.	2.2	41
124	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	12.8	41
125	Most Cases of Cryptococcal Meningitis in HIV-Uninfected Patients in Vietnam Are Due to a Distinct Amplified Fragment Length Polymorphism-Defined Cluster of <i>Cryptococcus neoformans</i> var. <i>grubii</i> VN1. <i>Journal of Clinical Microbiology</i> , 2011, 49, 658-664.	3.9	40
126	The Molecular and Spatial Epidemiology of Typhoid Fever in Rural Cambodia. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004785.	3.0	40

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127	Treatment Response in Enteric Fever in an Era of Increasing Antimicrobial Resistance: An Individual Patient Data Analysis of 2092 Participants Enrolled into 4 Randomized, Controlled Trials in Nepal. <i>Clinical Infectious Diseases</i> , 2017, 64, 1522-1531.	5.8	40
128	Effective control of SARS-CoV-2 transmission between healthcare workers during a period of diminished community prevalence of COVID-19. <i>ELife</i> , 2020, 9, .	6.0	40
129	Identification of Immunogenic <i>Salmonella enterica</i> Serotype Typhi Antigens Expressed in Chronic Biliary Carriers of <i>S. Typhi</i> in Kathmandu, Nepal. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2335.	3.0	39
130	Prevalence, genetic diversity and recombination of species G enteroviruses infecting pigs in Vietnam. <i>Journal of General Virology</i> , 2014, 95, 549-556.	2.9	39
131	Risk factors for the development of severe typhoid fever in Vietnam. <i>BMC Infectious Diseases</i> , 2014, 14, 73.	2.9	39
132	Spontaneous Emergence of Azithromycin Resistance in Independent Lineages of <i>Salmonella</i> Typhi in Northern India. <i>Clinical Infectious Diseases</i> , 2021, 72, e120-e127.	5.8	39
133	Enteric fever in Cambodian children is dominated by multidrug-resistant H58 <i>Salmonella enterica</i> serovar Typhi with intermediate susceptibility to ciprofloxacin. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2012, 106, 718-724.	1.8	38
134	The international and intercontinental spread and expansion of antimicrobial-resistant <i>Salmonella</i> Typhi: a genomic epidemiology study. <i>Lancet Microbe</i> , The, 2022, 3, e567-e577.	7.3	38
135	Genomic Epidemiology of <i>Vibrio cholerae</i> O1 Associated with Floods, Pakistan, 2010. <i>Emerging Infectious Diseases</i> , 2014, 20, 13-20.	4.3	37
136	The epidemiology and aetiology of diarrhoeal disease in infancy in southern Vietnam: a birth cohort study. <i>International Journal of Infectious Diseases</i> , 2015, 35, 3-10.	3.3	37
137	Azithromycin Resistance in <i>Shigella</i> spp. in Southeast Asia. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	37
138	Detection and Characterization of Homologues of Human Hepatitis Viruses and Pegiviruses in Rodents and Bats in Vietnam. <i>Viruses</i> , 2018, 10, 102.	3.3	37
139	Immunoproteomic Analysis of Antibody in Lymphocyte Supernatant in Patients with Typhoid Fever in Bangladesh. <i>Vaccine Journal</i> , 2014, 21, 280-285.	3.1	36
140	The Surveillance for Enteric Fever in Asia Project (SEAP), Severe Typhoid Fever Surveillance in Africa (SETA), Surveillance of Enteric Fever in India (SEFI), and Strategic Typhoid Alliance Across Africa and Asia (STRATAA) Population-based Enteric Fever Studies: A Review of Methodological Similarities and Differences. <i>Clinical Infectious Diseases</i> , 2020, 71, S102-S110.	5.8	36
141	No Clinical Benefit of Empirical Antimicrobial Therapy for Pediatric Diarrhea in a High-Usage, High-Resistance Setting. <i>Clinical Infectious Diseases</i> , 2018, 66, 504-511.	5.8	35
142	Evaluating PCR-Based Detection of <i>Salmonella</i> Typhi and Paratyphi A in the Environment as an Enteric Fever Surveillance Tool. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019, 100, 43-46.	1.4	35
143	Evaluation of the Diagnostic Accuracy of a Typhoid IgM Flow Assay for the Diagnosis of Typhoid Fever in Cambodian Children Using a Bayesian Latent Class Model Assuming an Imperfect Gold Standard. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014, 90, 114-120.	1.4	34
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