

Kate S Baker

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

2,260
citations

218677

26
h-index

243625

44
g-index

63
all docs

63
docs citations

63
times ranked

2841
citing authors

#	ARTICLE	IF	CITATIONS
1	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 913-921.	9.1	204
2	A framework for the study of zoonotic disease emergence and its drivers: spillover of bat pathogens as a case study. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 2881-2892.	4.0	156
3	Metagenomic study of the viruses of African straw-coloured fruit bats: Detection of a chiropteran poxvirus and isolation of a novel adenovirus. <i>Virology</i> , 2013, 441, 95-106.	2.4	121
4	Horizontal antimicrobial resistance transfer drives epidemics of multiple <i>Shigella</i> species. <i>Nature Communications</i> , 2018, 9, 1462.	12.8	121
5	Continent-wide panmixia of an African fruit bat facilitates transmission of potentially zoonotic viruses. <i>Nature Communications</i> , 2013, 4, 2770.	12.8	105
6	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
7	<i>Bartonella</i> species in bat flies (Diptera: Nycteribiidae) from western Africa. <i>Parasitology</i> , 2012, 139, 324-329.	1.5	82
8	Novel, Potentially Zoonotic Paramyxoviruses from the African Straw-Colored Fruit Bat <i>Eidolon helvum</i> . <i>Journal of Virology</i> , 2013, 87, 1348-1358.	3.4	75
9	Antibodies to Henipavirus or Henipa-Like Viruses in Domestic Pigs in Ghana, West Africa. <i>PLoS ONE</i> , 2011, 6, e25256.	2.5	72
10	Henipavirus Neutralising Antibodies in an Isolated Island Population of African Fruit Bats. <i>PLoS ONE</i> , 2012, 7, e30346.	2.5	71
11	Stepwise evolution of <i>Salmonella</i> Typhimurium ST313 causing bloodstream infection in Africa. <i>Nature Microbiology</i> , 2021, 6, 327-338.	13.3	68
12	Genomic epidemiology of <i>Shigella</i> in the United Kingdom shows transmission of pathogen sublineages and determinants of antimicrobial resistance. <i>Scientific Reports</i> , 2018, 8, 7389.	3.3	65
13	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
14	Search Engine for Antimicrobial Resistance: A Cloud Compatible Pipeline and Web Interface for Rapidly Detecting Antimicrobial Resistance Genes Directly from Sequence Data. <i>PLoS ONE</i> , 2015, 10, e0133492.	2.5	62
15	Co-circulation of diverse paramyxoviruses in an urban African fruit bat population. <i>Journal of General Virology</i> , 2012, 93, 850-856.	2.9	60
16	Characterization of Pre-Antibiotic Era <i>Klebsiella pneumoniae</i> Isolates with Respect to Antibiotic/Disinfectant Susceptibility and Virulence in <i>Galleria mellonella</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 3966-3972.	3.2	52
17	Use of cross-reactive serological assays for detecting novel pathogens in wildlife: Assessing an appropriate cutoff for henipavirus assays in African bats. <i>Journal of Virological Methods</i> , 2013, 193, 295-303.	2.1	50
18	Design and evaluation of consensus PCR assays for henipaviruses. <i>Journal of Virological Methods</i> , 2009, 161, 52-57.	2.1	48

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19	Persistent Transmission of Shigellosis in England Is Associated with a Recently Emerged Multidrug-Resistant Strain of <i>Shigella sonnei</i> . <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	45
20	Viral antibody dynamics in a chiropteran host. <i>Journal of Animal Ecology</i> , 2014, 83, 415-428.	2.8	43
21	Endemic Lagos bat virus infection in <i>Eidolon helvum</i> . <i>Epidemiology and Infection</i> , 2012, 140, 2163-2171.	2.1	41
22	<i>Brucella neotomae</i> Infection in Humans, Costa Rica. <i>Emerging Infectious Diseases</i> , 2017, 23, 997-1000.	4.3	40
23	The Murray collection of pre-antibiotic era Enterobacteriaceae: a unique research resource. <i>Genome Medicine</i> , 2015, 7, 97.	8.2	39
24	<i>Brucella abortus</i> Strain 2308 Wisconsin Genome: Importance of the Definition of Reference Strains. <i>Frontiers in Microbiology</i> , 2016, 7, 1557.	3.5	37
25	Whole genome sequencing of <i>Shigella sonnei</i> through PulseNet Latin America and Caribbean: advancing global surveillance of foodborne illnesses. <i>Clinical Microbiology and Infection</i> , 2017, 23, 845-853.	6.0	37
26	Support for viral persistence in bats from age-specific serology and models of maternal immunity. <i>Scientific Reports</i> , 2018, 8, 3859.	3.3	37
27	The extant World War 1 dysentery bacillus NCTC1: a genomic analysis. <i>Lancet</i> , The, 2014, 384, 1691-1697.	13.7	27
28	<i>Brucella</i> Genetic Variability in Wildlife Marine Mammals Populations Relates to Host Preference and Ocean Distribution. <i>Genome Biology and Evolution</i> , 2017, 9, 1901-1912.	2.5	26
29	Travel- and Community-Based Transmission of Multidrug-Resistant <i>Shigella sonnei</i> Lineage among International Orthodox Jewish Communities. <i>Emerging Infectious Diseases</i> , 2016, 22, 1545-1553.	4.3	23
30	How Does Africa's Most Hunted Bat Vary Across the Continent? Population Traits of the Straw-Coloured Fruit Bat (<i>Eidolon helvum</i>) and Its Interactions with Humans. <i>Acta Chiropterologica</i> , 2017, 19, 77.	0.6	23
31	Pathogenomic analyses of <i>Shigella</i> isolates inform factors limiting shigellosis prevention and control across LMICs. <i>Nature Microbiology</i> , 2022, 7, 251-261.	13.3	23
32	An accessible, efficient and global approach for the large-scale sequencing of bacterial genomes. <i>Genome Biology</i> , 2021, 22, 349.	8.8	20
33	Genetic and Phenotypic Characterization of the Etiological Agent of Canine Orchiepididymitis Smooth <i>Brucella</i> sp. BCCN84.3. <i>Frontiers in Veterinary Science</i> , 2019, 6, 175.	2.2	18
34	Poxviruses in Bats – so What?. <i>Viruses</i> , 2014, 6, 1564-1577.	3.3	17
35	Maternal antibody and the maintenance of a lyssavirus in populations of seasonally breeding African bats. <i>PLoS ONE</i> , 2018, 13, e0198563.	2.5	16
36	The diversity, evolution and ecology of <i>Salmonella</i> in venomous snakes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007169.	3.0	16

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37	Draft genome sequences of the type strains of <i>Shigella flexneri</i> held at Public Health England: comparison of classical phenotypic and novel molecular assays with whole genome sequence. <i>Gut Pathogens</i> , 2014, 6, 7.	3.4	14
38	Whole-genome sequencing revealed concurrent outbreaks of shigellosis in the English Orthodox Jewish Community caused by multiple importations of <i>Shigella sonnei</i> from Israel. <i>Microbial Genomics</i> , 2018, 4, .	2.0	14
39	Bacillary dysentery from World War 1 and NCTC1, the first bacterial isolate in the National Collection. <i>Lancet, The</i> , 2014, 384, 1720.	13.7	13
40	Demystifying <i>Escherichia coli</i> pathovars. <i>Nature Reviews Microbiology</i> , 2015, 13, 5-5.	28.6	13
41	An outbreak of a rare Shiga-toxin-producing <i>Escherichia coli</i> serotype (O117:H7) among men who have sex with men. <i>Microbial Genomics</i> , 2018, 4, .	2.0	13
42	Bat trait, genetic and pathogen data from large-scale investigations of African fruit bats, <i>Eidolon helvum</i> . <i>Scientific Data</i> , 2016, 3, 160049.	5.3	9
43	Animal infection studies of two recently discovered African bat paramyxoviruses, Achimota 1 and Achimota 2. <i>Scientific Reports</i> , 2018, 8, 12744.	3.3	9
44	Draft Genome Sequence of 24570, the Type Strain of <i>Shigella flexneri</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	7
45	Draft genomes of <i>Shigella</i> strains used by the STOPENTERICS consortium. <i>Gut Pathogens</i> , 2015, 7, 14.	3.4	7
46	Looking Backward To Move Forward: the Utility of Sequencing Historical Bacterial Genomes. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	7
47	Microbe hunting in the modern era: reflecting on a decade of microbial genomic epidemiology. <i>Current Biology</i> , 2020, 30, R1124-R1130.	3.9	7
48	Accessory Genome Dynamics and Structural Variation of <i>Shigella</i> from Persistent Infections. <i>MBio</i> , 2021, 12, .	4.1	7
49	<i>Salmonella enterica</i> Serovar Panama, an Understudied Serovar Responsible for Extraintestinal Salmonellosis Worldwide. <i>Infection and Immunity</i> , 2019, 87, .	2.2	6
50	Achimota Pararubulavirus 3: A New Bat-Derived Paramyxovirus of the Genus Pararubulavirus. <i>Viruses</i> , 2020, 12, 1236.	3.3	6
51	Travel- and Community-Based Transmission of Multidrug-Resistant <i>Shigella sonnei</i> Lineage among International Orthodox Jewish Communities. <i>Emerging Infectious Diseases</i> , 2016, 22, 1545-1553.	4.3	5
52	Demodicosis in a captive African straw-coloured fruit bat (<i>Eidolon helvum</i>). <i>Experimental and Applied Acarology</i> , 2019, 78, 547-554.	1.6	3
53	Common determinants of antimicrobial resistance in sequential episodes of sexually transmitted shigellosis in men who have sex with men: a cross-sectional study. <i>Lancet, The</i> , 2017, 389, S24.	13.7	2
54	TB or not TB? Genomic portraits provide answers. <i>Nature Reviews Microbiology</i> , 2014, 12, 398-398.	28.6	1

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55	5. Emerging risks from bat bushmeat in West Africa. , 2014, , 91-106.		0
56	Whole genome sequence analysis of Shigella from Malawi identifies fluoroquinolone resistance. Microbial Genomics, 2021, 7, .	2.0	0