

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	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
2	Stepwise evolution of <i>Salmonella</i> Typhimurium ST313 causing bloodstream infection in Africa. <i>Nature Microbiology</i> , 2021, 6, 327-338.	13.3	68
3	Accessory Genome Dynamics and Structural Variation of <i>Shigella</i> from Persistent Infections. <i>MBio</i> , 2021, 12, .	4.1	7
4	Whole genome sequence analysis of <i>Shigella</i> from Malawi identifies fluoroquinolone resistance. <i>Microbial Genomics</i> , 2021, 7, .	2.0	0
5	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
6	An accessible, efficient and global approach for the large-scale sequencing of bacterial genomes. <i>Genome Biology</i> , 2021, 22, 349.	8.8	20
7	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
8	Achimota Pararubulavirus 3: A New Bat-Derived Paramyxovirus of the Genus Pararubulavirus. <i>Viruses</i> , 2020, 12, 1236.	3.3	6
9	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
10	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
11	The diversity, evolution and ecology of <i>Salmonella</i> in venomous snakes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007169.	3.0	16
12	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
13	<i>Salmonella enterica</i> Serovar Panama, an Understudied Serovar Responsible for Extraintestinal Salmonellosis Worldwide. <i>Infection and Immunity</i> , 2019, 87, .	2.2	6
14	Looking Backward To Move Forward: the Utility of Sequencing Historical Bacterial Genomes. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	7
15	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
16	Horizontal antimicrobial resistance transfer drives epidemics of multiple <i>Shigella</i> species. <i>Nature Communications</i> , 2018, 9, 1462.	12.8	121
17	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
18	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

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19	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
20	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
21	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
22	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
23	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
24	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</i> , The, 2017, 389, S24.	13.7	2
25	<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
26	<i>Brucella neotomae</i> Infection in Humans, Costa Rica. <i>Emerging Infectious Diseases</i> , 2017, 23, 997-1000.	4.3	40
27	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
28	<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
29	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
30	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
31	The Murray collection of pre-antibiotic era <i>Enterobacteriaceae</i> : a unique research resource. <i>Genome Medicine</i> , 2015, 7, 97.	8.2	39
32	Draft Genome Sequence of 24570, the Type Strain of <i>Shigella flexneri</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	7
33	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
34	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
35	Draft genomes of <i>Shigella</i> strains used by the STOPENTERICS consortium. <i>Gut Pathogens</i> , 2015, 7, 14.	3.4	7
36	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

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37	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
38	Demystifying <i>Escherichia coli</i> pathovars. <i>Nature Reviews Microbiology</i> , 2015, 13, 5-5.	28.6	13
39	Poxviruses in Bats – so What?. <i>Viruses</i> , 2014, 6, 1564-1577.	3.3	17
40	Viral antibody dynamics in a chiropteran host. <i>Journal of Animal Ecology</i> , 2014, 83, 415-428.	2.8	43
41	The extant World War 1 dysentery bacillus NCTC1: a genomic analysis. <i>Lancet</i> , The, 2014, 384, 1691-1697.	13.7	27
42	TB or not TB? Genomic portraits provide answers. <i>Nature Reviews Microbiology</i> , 2014, 12, 398-398.	28.6	1
43	Bacillary dysentery from World War 1 and NCTC1, the first bacterial isolate in the National Collection. <i>Lancet</i> , The, 2014, 384, 1720.	13.7	13
44	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
45	5. Emerging risks from bat bushmeat in West Africa. , 2014, , 91-106.		0
46	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
47	Continent-wide panmixia of an African fruit bat facilitates transmission of potentially zoonotic viruses. <i>Nature Communications</i> , 2013, 4, 2770.	12.8	105
48	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
49	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
50	<i>Bartonella</i> species in bat flies (Diptera: Nycteribiidae) from western Africa. <i>Parasitology</i> , 2012, 139, 324-329.	1.5	82
51	Endemic Lagos bat virus infection in <i>Eidolon helvum</i> . <i>Epidemiology and Infection</i> , 2012, 140, 2163-2171.	2.1	41
52	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
53	Henipavirus Neutralising Antibodies in an Isolated Island Population of African Fruit Bats. <i>PLoS ONE</i> , 2012, 7, e30346.	2.5	71
54	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

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55	Antibodies to Henipavirus or Henipa-Like Viruses in Domestic Pigs in Ghana, West Africa. PLoS ONE, 2011, 6, e25256.	2.5	72
56	Design and evaluation of consensus PCR assays for henipaviruses. Journal of Virological Methods, 2009, 161, 52-57.	2.1	48