

Ken J Forbes

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,082
citations

394421

19
h-index

501196

28
g-index

32
all docs

32
docs citations

32
times ranked

1481
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic diversity and antimicrobial resistance of <i>Campylobacter</i> spp. from humans and livestock in Nigeria. <i>Journal of Biomedical Science</i> , 2022, 29, 7.	7.0	6
2	Estimated Dissemination Ratio—A Practical Alternative to the Reproduction Number for Infectious Diseases. <i>Frontiers in Public Health</i> , 2021, 9, 675065.	2.7	0
3	Importance of untested infectious individuals for interventions to suppress COVID-19. <i>Scientific Reports</i> , 2021, 11, 20728.	3.3	4
4	Reply to Baba and Kanamori. <i>Clinical Infectious Diseases</i> , 2020, 71, 1353-1355.	5.8	0
5	Mining whole genome sequence data to efficiently attribute individuals to source populations. <i>Scientific Reports</i> , 2020, 10, 12124.	3.3	10
6	Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11018-11028.	7.1	50
7	Variability in growth responses of non-O157 EHEC isolates in leafy vegetables, sprouted seeds and soil extracts occurs at the isolate level. <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	6
8	Increasing prevalence of a fluoroquinolone resistance mutation amongst <i>Campylobacter jejuni</i> isolates from four human infectious intestinal disease studies in the United Kingdom. <i>PLoS ONE</i> , 2020, 15, e0227535.	2.5	9
9	Challenges of biofilm control and utilization: lessons from mathematical modelling. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20190042.	3.4	36
10	Influence of Plant Species, Tissue Type, and Temperature on the Capacity of Shiga-Toxigenic <i>Escherichia coli</i> To Colonize, Grow, and Be Internalized by Plants. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	23
11	Climate, human behaviour or environment: individual-based modelling of <i>Campylobacter</i> seasonality and strategies to reduce disease burden. <i>Journal of Translational Medicine</i> , 2019, 17, 34.	4.4	11
12	Phylogeographic Analysis Reveals Multiple International transmission Events Have Driven the Global Emergence of <i>Escherichia coli</i> O157:H7. <i>Clinical Infectious Diseases</i> , 2019, 69, 428-437.	5.8	26
13	LiSEQ—whole-genome sequencing of a cross-sectional survey of <i>Listeria monocytogenes</i> in ready-to-eat foods and human clinical cases in Europe. <i>Microbial Genomics</i> , 2019, 5, .	2.0	64
14	Domestication of <i>Campylobacter jejuni</i> NCTC 11168. <i>Microbial Genomics</i> , 2019, 5, .	2.0	26
15	Novel Sampling Method for Assessing Human-Pathogen Interactions in the Natural Environment Using Boot Socks and Citizen Scientists, with Application to <i>Campylobacter</i> Seasonality. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	12
16	Genomic plasticity and rapid host switching can promote the evolution of generalism: a case study in the zoonotic pathogen <i>Campylobacter</i> . <i>Scientific Reports</i> , 2017, 7, 9650.	3.3	34
17	Comparative Genomic Analysis Identifies a <i>Campylobacter</i> Clade Deficient in Selenium Metabolism. <i>Genome Biology and Evolution</i> , 2017, 9, 1843-1858.	2.5	20
18	Proteomic variation and diversity in clinical <i>Streptococcus pneumoniae</i> isolates from invasive and non-invasive sites. <i>PLoS ONE</i> , 2017, 12, e0179075.	2.5	5

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19	Comparative Genomics of <i>Campylobacter fetus</i> from Reptiles and Mammals Reveals Divergent Evolution in Host-Associated Lineages. <i>Genome Biology and Evolution</i> , 2016, 8, 2006-2019.	2.5	25
20	Comparative genomic analysis of novel <i>Acinetobacter</i> symbionts: A combined systems biology and genomics approach. <i>Scientific Reports</i> , 2016, 6, 29043.	3.3	33
21	Whole genome sequence analysis indicates recent diversification of mammal-associated <i>Campylobacter fetus</i> and implicates a genetic factor associated with H ₂ S production. <i>BMC Genomics</i> , 2016, 17, 713.	2.8	18
22	<i>Campylobacter fetus</i> Subspecies Contain Conserved Type IV Secretion Systems on Multiple Genomic Islands and Plasmids. <i>PLoS ONE</i> , 2016, 11, e0152832.	2.5	30
23	Whole Genome Sequencing demonstrates that Geographic Variation of <i>Escherichia coli</i> O157 Genotypes Dominates Host Association. <i>Scientific Reports</i> , 2015, 5, 14145.	3.3	49
24	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	3.9	131
25	Exploiting the explosion of information associated with whole genome sequencing to tackle Shiga toxin-producing <i>Escherichia coli</i> (STEC) in global food production systems. <i>International Journal of Food Microbiology</i> , 2014, 187, 57-72.	4.7	83
26	The Heterogeneity, Distribution, and Environmental Associations of <i>Borrelia burgdorferi</i> Sensu Lato, the Agent of Lyme Borreliosis, in Scotland. <i>Frontiers in Public Health</i> , 2014, 2, 129.	2.7	30
27	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013, 22, 1051-1064.	3.9	128
28	Niche segregation and genetic structure of <i>Campylobacter jejuni</i> populations from wild and agricultural host species. <i>Molecular Ecology</i> , 2011, 20, 3484-3490.	3.9	105
29	The importance of passerine birds as tick hosts and in the transmission of <i>Borrelia burgdorferi</i> , the agent of Lyme disease: a case study from Scotland. <i>Ibis</i> , 2011, 153, 293-302.	1.9	27
30	Evolution of an Agriculture-Associated Disease Causing <i>Campylobacter coli</i> Clade: Evidence from National Surveillance Data in Scotland. <i>PLoS ONE</i> , 2010, 5, e15708.	2.5	75