

Mathew A Beale

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,384
citations

623734

14
h-index

610901

24
g-index

31
all docs

31
docs citations

31
times ranked

2231
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 genomics as a springboard for future disease mitigation in LMICs. <i>Nature Reviews Microbiology</i> , 2022, 20, 3-3.	28.6	6
2	Trial of Three Rounds of Mass Azithromycin Administration for Yaws Eradication. <i>New England Journal of Medicine</i> , 2022, 386, 47-56.	27.0	9
3	Characterisation of <i>Treponema pallidum</i> lineages within the contemporary syphilis outbreak in Australia: a genomic epidemiological analysis. <i>Lancet Microbe</i> , The, 2022, 3, e417-e426.	7.3	19
4	Genomic epidemiology of COVID-19 in care homes in the east of England. <i>ELife</i> , 2021, 10, .	6.0	20
5	Epidemiologic and Genomic Reidentification of Yaws, Liberia. <i>Emerging Infectious Diseases</i> , 2021, 27, 1123-1132.	4.3	6
6	Global phylogeny of <i>Treponema pallidum</i> lineages reveals recent expansion and spread of contemporary syphilis. <i>Nature Microbiology</i> , 2021, 6, 1549-1560.	13.3	51
7	Archaeogenetics: What Can Ancient Genomes Tell Us about the Origin of Syphilis?. <i>Current Biology</i> , 2020, 30, R1092-R1095.	3.9	8
8	Yaws re-emergence and bacterial drug resistance selection after mass administration of azithromycin: a genomic epidemiology investigation. <i>Lancet Microbe</i> , The, 2020, 1, e263-e271.	7.3	19
9	The global epidemiology of emerging <i>Histoplasma</i> species in recent years. <i>Studies in Mycology</i> , 2020, 97, 100095.	7.2	47
10	Whole genome sequencing of Herpes Simplex Virus 1 directly from human cerebrospinal fluid reveals selective constraints in neurotropic viruses. <i>Virus Evolution</i> , 2020, 6, veaa012.	4.9	15
11	Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. <i>Nature Communications</i> , 2019, 10, 3255.	12.8	72
12	Identification of novel adenovirus genotype 90 in children from Bangladesh. <i>Microbial Genomics</i> , 2018, 4, .	2.0	10
13	Clinical and biological insights from viral genome sequencing. <i>Nature Reviews Microbiology</i> , 2017, 15, 183-192.	28.6	254
14	A Population Genomics Approach to Assessing the Genetic Basis of Within-Host Microevolution Underlying Recurrent Cryptococcal Meningitis Infection. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1165-1176.	1.8	79
15	Tracing Genetic Exchange and Biogeography of <i>Cryptococcus neoformans</i> var. <i>grubii</i> at the Global Population Level. <i>Genetics</i> , 2017, 207, 327-346.	2.9	105
16	Genomic epidemiology of <i>Cryptococcus</i> yeasts identifies adaptation to environmental niches underpinning infection across an African HIV/AIDS cohort. <i>Molecular Ecology</i> , 2017, 26, 1991-2005.	3.9	59
17	On the effective depth of viral sequence data. <i>Virus Evolution</i> , 2017, 3, vex030.	4.9	45
18	Genotypic Diversity Is Associated with Clinical Outcome and Phenotype in Cryptococcal Meningitis across Southern Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003847.	3.0	94

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19	Genomic Context of Azole Resistance Mutations in <i>Aspergillus fumigatus</i> Determined Using Whole-Genome Sequencing. <i>MBio</i> , 2015, 6, e00536.	4.1	171
20	Illuminating Choices for Library Prep: A Comparison of Library Preparation Methods for Whole Genome Sequencing of <i>Cryptococcus neoformans</i> Using Illumina HiSeq. <i>PLoS ONE</i> , 2014, 9, e113501.	2.5	44
21	Efficient phagocytosis and laccase activity affect the outcome of HIV-associated cryptococcosis. <i>Journal of Clinical Investigation</i> , 2014, 124, 2000-2008.	8.2	130
22	Is there evidence of recent hepatitis E virus infection in English and North Welsh blood donors?. <i>Vox Sanguinis</i> , 2011, 100, 340-342.	1.5	88
23	The genetic backbone modulates the phenotype of hepatitis B surface antigen mutants. <i>Journal of General Virology</i> , 2010, 91, 68-73.	2.9	10