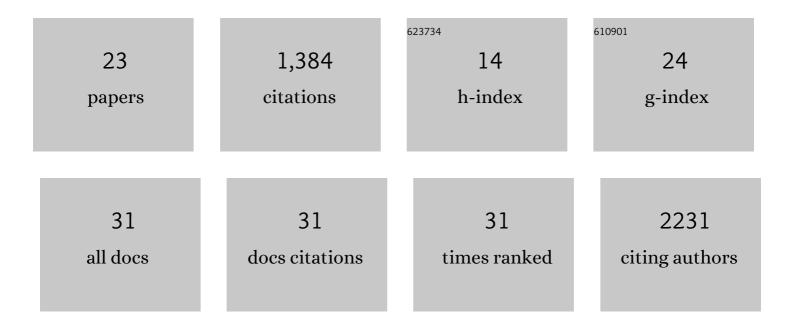
Mathew A Beale

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4664999/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	SARS-CoV-2 genomics as a springboard for future disease mitigation in LMICs. Nature Reviews Microbiology, 2022, 20, 3-3.	28.6	6
2	Trial of Three Rounds of Mass Azithromycin Administration for Yaws Eradication. New England Journal of Medicine, 2022, 386, 47-56.	27.0	9
3	Characterisation of Treponema pallidum lineages within the contemporary syphilis outbreak in Australia: a genomic epidemiological analysis. Lancet Microbe, The, 2022, 3, e417-e426.	7.3	19
4	Genomic epidemiology of COVID-19 in care homes in the east of England. ELife, 2021, 10, .	6.0	20
5	Epidemiologic and Genomic Reidentification of Yaws, Liberia. Emerging Infectious Diseases, 2021, 27, 1123-1132.	4.3	6
6	Global phylogeny of Treponema pallidum lineages reveals recent expansion and spread of contemporary syphilis. Nature Microbiology, 2021, 6, 1549-1560.	13.3	51
7	Archaeogenetics: What Can Ancient Genomes Tell Us about the Origin of Syphilis?. Current Biology, 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. Lancet Microbe, The, 2020, 1, e263-e271.	7.3	19
9	The global epidemiology of emerging Histoplasma species in recent years. Studies in Mycology, 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. Virus Evolution, 2020, 6, veaa012.	4.9	15
11	Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. Nature Communications, 2019, 10, 3255.	12.8	72
12	Identification of novel adenovirus genotype 90 in children from Bangladesh. Microbial Genomics, 2018, 4, .	2.0	10
13	Clinical and biological insights from viral genome sequencing. Nature Reviews Microbiology, 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. G3: Genes, Genomes, Genetics, 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. Genetics, 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 <scp>HIV</scp> / <scp>AIDS</scp> cohort. Molecular Ecology, 2017, 26, 1991-2005.	3.9	59
17	On the effective depth of viral sequence data. Virus Evolution, 2017, 3, vex030.	4.9	45
18	Genotypic Diversity Is Associated with Clinical Outcome and Phenotype in Cryptococcal Meningitis across Southern Africa. PLoS Neglected Tropical Diseases, 2015, 9, e0003847.	3.0	94

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