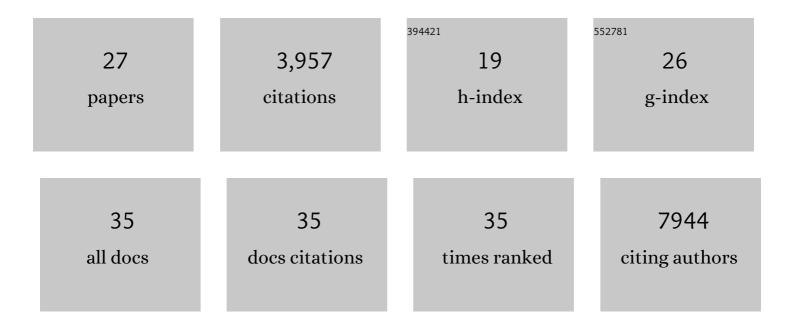
William L Hamilton

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3990288/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. Clinical Microbiology and Infection, 2022, 28, 93-100.	6.0	21
2	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. Lancet Microbe, The, 2022, 3, e151-e158.	7.3	25
3	A2B-COVID: A Tool for Rapidly Evaluating Potential SARS-CoV-2 Transmission Events. Molecular Biology and Evolution, 2022, 39, .	8.9	12
4	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. Nature Communications, 2022, 13, 751.	12.8	27
5	Transmission of B.1.617.2 Delta variant between vaccinated healthcare workers. Scientific Reports, 2022, 12, .	3.3	9
6	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	97
7	Genomic epidemiology of COVID-19 in care homes in the east of England. ELife, 2021, 10, .	6.0	20
8	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. Cell Reports, 2021, 35, 109292.	6.4	375
9	Applying prospective genomic surveillance to support investigation of hospital-onset COVID-19. Lancet Infectious Diseases, The, 2021, 21, 916-917.	9.1	14
10	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	51
11	Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections. ELife, 2021, 10, .	6.0	34
12	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	6.0	110
13	SARS-CoV-2 B.1.617.2 Delta variant replication and immune evasion. Nature, 2021, 599, 114-119.	27.8	1,041
14	Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. Lancet Infectious Diseases, The, 2020, 20, 1263-1271.	9.1	352
15	Screening of healthcare workers for SARS-CoV-2 highlights the role of asymptomatic carriage in COVID-19 transmission. ELife, 2020, 9, .	6.0	423
16	Evolution and expansion of multidrug-resistant malaria in southeast Asia: a genomic epidemiology study. Lancet Infectious Diseases, The, 2019, 19, 943-951.	9.1	219
17	Determinants of dihydroartemisinin-piperaquine treatment failure in Plasmodium falciparum malaria in Cambodia, Thailand, and Vietnam: a prospective clinical, pharmacological, and genetic study. Lancet Infectious Diseases, The, 2019, 19, 952-961.	9.1	252
18	Clinical predictors of specialist treatment requirements in pelvic fracture: A retrospective cohort study. Trauma, 2018, 20, 183-188.	0.5	0

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#	Article	IF	CITATIONS
19	Imported gnathostomiasis manifesting as cutaneous larva migrans and Löffler's syndrome. BMJ Case Reports, 2018, 2018, bcr-2017-223132.	0.5	4
20	Long read assemblies of geographically dispersed Plasmodium falciparum isolates reveal highly structured subtelomeres. Wellcome Open Research, 2018, 3, 52.	1.8	114
21	Extreme mutation bias and high AT content in <i>Plasmodium falciparum</i> . Nucleic Acids Research, 2017, 45, gkw1259.	14.5	89
22	Whole genome sequencing of Plasmodium falciparum from dried blood spots using selective whole genome amplification. Malaria Journal, 2016, 15, 597.	2.3	129
23	Public health interventions to protect against falsified medicines: a systematic review of international, national and local policies. Health Policy and Planning, 2016, 31, 1448-1466.	2.7	83
24	Shiga Toxin–Producing <i>Escherichia coli</i> Infection, Antibiotics, and Risk of Developing Hemolytic Uremic Syndrome: A Meta-analysis. Clinical Infectious Diseases, 2016, 62, 1251-1258.	5.8	194
25	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. DNA Research, 2014, 21, 661-671.	3.4	27
26	Generation of Antigenic Diversity in Plasmodium falciparum by Structured Rearrangement of Var Genes During Mitosis. PLoS Genetics, 2014, 10, e1004812.	3.5	171
27	TRIM15 is a focal adhesion protein that regulates focal adhesion disassembly. Journal of Cell Science, 2014, 127, 3928-42.	2.0	31