

# William L Hamilton

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3990288/publications.pdf>

Version: 2024-02-01

27  
papers

3,957  
citations

394421

19  
h-index

552781

26  
g-index

35  
all docs

35  
docs citations

35  
times ranked

7944  
citing authors

#	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. <i>Clinical Microbiology and Infection</i> , 2022, 28, 93-100.	6.0	21
2	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. <i>Lancet Microbe</i> , The, 2022, 3, e151-e158.	7.3	25
3	A2B-COVID: A Tool for Rapidly Evaluating Potential SARS-CoV-2 Transmission Events. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	12
4	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	12.8	27
5	Transmission of B.1.617.2 Delta variant between vaccinated healthcare workers. <i>Scientific Reports</i> , 2022, 12, .	3.3	9
6	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	97
7	Genomic epidemiology of COVID-19 in care homes in the east of England. <i>ELife</i> , 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. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
9	Applying prospective genomic surveillance to support investigation of hospital-onset COVID-19. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 916-917.	9.1	14
10	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	51
11	Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections. <i>ELife</i> , 2021, 10, .	6.0	34
12	Patterns of within-host genetic diversity in SARS-CoV-2. <i>ELife</i> , 2021, 10, .	6.0	110
13	SARS-CoV-2 B.1.617.2 Delta variant replication and immune evasion. <i>Nature</i> , 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. <i>Lancet Infectious Diseases</i> , 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. <i>ELife</i> , 2020, 9, .	6.0	423
16	Evolution and expansion of multidrug-resistant malaria in southeast Asia: a genomic epidemiology study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 943-951.	9.1	219
17	Determinants of dihydroartemisinin-piperazine treatment failure in <i>Plasmodium falciparum</i> malaria in Cambodia, Thailand, and Vietnam: a prospective clinical, pharmacological, and genetic study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 952-961.	9.1	252
18	Clinical predictors of specialist treatment requirements in pelvic fracture: A retrospective cohort study. <i>Trauma</i> , 2018, 20, 183-188.	0.5	0

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