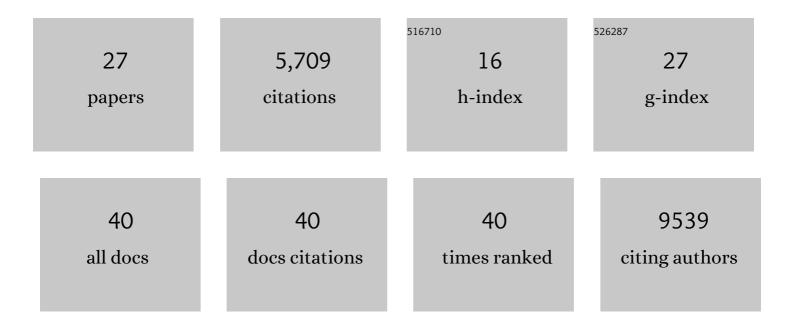
William T Harvey

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2169135/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Mutations that adapt SARS-CoV-2 to mink or ferret do not increase fitness in the human airway. Cell Reports, 2022, 38, 110344.	6.4	46
2	Population genomics of Bacillus anthracis from an anthrax hyperendemic area reveals transmission processes across spatial scales and unexpected within-host diversity. Microbial Genomics, 2022, 8, .	2.0	5
3	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. Virus Evolution, 2022, 8, veac023.	4.9	19
4	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	6.2	32
5	Segmental duplications and their variation in a complete human genome. Science, 2022, 376, eabj6965.	12.6	130
6	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
7	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. Nature Microbiology, 2022, 7, 1161-1179.	13.3	352
8	Different environmental gradients associated to the spatiotemporal and genetic pattern of the H5N8 highly pathogenic avian influenza outbreaks in poultry in Italy. Transboundary and Emerging Diseases, 2021, 68, 152-167.	3.0	7
9	Genetic Determinants of Receptor-Binding Preference and Zoonotic Potential of H9N2 Avian Influenza Viruses. Journal of Virology, 2021, 95, .	3.4	14
10	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	17.5	127
11	Spatiotemporal reconstruction and transmission dynamics during the 2016–17 H5N8 highly pathogenic avian influenza epidemic in Italy. Transboundary and Emerging Diseases, 2021, 68, 37-50.	3.0	7
12	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. Nature, 2021, 593, 136-141.	27.8	648
13	The structure, function and evolution of a complete human chromosome 8. Nature, 2021, 593, 101-107.	27.8	221
14	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
15	A high-quality bonobo genome refines the analysis of hominid evolution. Nature, 2021, 594, 77-81.	27.8	39
16	SARS-CoV-2 variants, spike mutations and immune escape. Nature Reviews Microbiology, 2021, 19, 409-424.	28.6	2,650
17	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
18	Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination. PLoS Pathogens, 2021, 17, e1010022.	4.7	139

WILLIAM T HARVEY

#	Article	IF	CITATIONS
19	Genetic Basis of Antigenic Variation of SAT3 Foot-And-Mouth Disease Viruses in Southern Africa. Frontiers in Veterinary Science, 2020, 7, 568.	2.2	1
20	Genomic and Immunogenic Protein Diversity of Erysipelothrix rhusiopathiae Isolated From Pigs in Great Britain: Implications for Vaccine Protection. Frontiers in Microbiology, 2020, 11, 418.	3.5	13
21	Improving the identification of antigenic sites in the H1N1 influenza virus through accounting for the experimental structure in a sparse hierarchical Bayesian model. Journal of the Royal Statistical Society Series C: Applied Statistics, 2019, 68, 859-885.	1.0	5
22	Integrating patient and whole-genome sequencing data to provide insights into the epidemiology of seasonal influenza A(H3N2) viruses. Microbial Genomics, 2018, 4, .	2.0	12
23	The molecular basis of antigenic variation among A(H9N2) avian influenza viruses. Emerging Microbes and Infections, 2018, 7, 1-12.	6.5	24
24	A sparse hierarchical Bayesian model for detecting relevant antigenic sites in virus evolution. Computational Statistics, 2017, 32, 803-843.	1.5	8
25	Selecting Random Effect Components in a Sparse Hierarchical Bayesian Model for Identifying Antigenic Variability. Lecture Notes in Computer Science, 2016, , 14-27.	1.3	1
26	Tracking the Antigenic Evolution of Foot-and-Mouth Disease Virus. PLoS ONE, 2016, 11, e0159360.	2.5	32
27	Identification of Low- and High-Impact Hemagglutinin Amino Acid Substitutions That Drive Antigenic Drift of Influenza A(H1N1) Viruses. PLoS Pathogens, 2016, 12, e1005526.	4.7	58