

William T Harvey

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

5,709
citations

516710

16
h-index

526287

27
g-index

40
all docs

40
docs citations

40
times ranked

9539
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutations that adapt SARS-CoV-2 to mink or ferret do not increase fitness in the human airway. <i>Cell Reports</i> , 2022, 38, 110344.	6.4	46
2	Population genomics of <i>Bacillus anthracis</i> from an anthrax hyperendemic area reveals transmission processes across spatial scales and unexpected within-host diversity. <i>Microbial Genomics</i> , 2022, 8, .	2.0	5
3	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. <i>Virus Evolution</i> , 2022, 8, veac023.	4.9	19
4	Familial long-read sequencing increases yield of de novo mutations. <i>American Journal of Human Genetics</i> , 2022, 109, 631-646.	6.2	32
5	Segmental duplications and their variation in a complete human genome. <i>Science</i> , 2022, 376, eabj6965.	12.6	130
6	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. <i>Cell</i> , 2022, 185, 1986-2005.e26.	28.9	67
7	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 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. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 152-167.	3.0	7
9	Genetic Determinants of Receptor-Binding Preference and Zoonotic Potential of H9N2 Avian Influenza Viruses. <i>Journal of Virology</i> , 2021, 95, .	3.4	14
10	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. <i>Nature Biotechnology</i> , 2021, 39, 302-308.	17.5	127
11	Spatiotemporal reconstruction and transmission dynamics during the 2016â€“17 H5N8 highly pathogenic avian influenza epidemic in Italy. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 37-50.	3.0	7
12	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021, 593, 136-141.	27.8	648
13	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , 2021, 593, 101-107.	27.8	221
14	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	12.6	358
15	A high-quality bonobo genome refines the analysis of hominid evolution. <i>Nature</i> , 2021, 594, 77-81.	27.8	39
16	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 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. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
18	Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination. <i>PLoS Pathogens</i> , 2021, 17, e1010022.	4.7	139

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19	Genetic Basis of Antigenic Variation of SAT3 Foot-And-Mouth Disease Viruses in Southern Africa. <i>Frontiers in Veterinary Science</i> , 2020, 7, 568.	2.2	1
20	Genomic and Immunogenic Protein Diversity of <i>Erysipelothrix rhusiopathiae</i> Isolated From Pigs in Great Britain: Implications for Vaccine Protection. <i>Frontiers in Microbiology</i> , 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. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 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. <i>Microbial Genomics</i> , 2018, 4, .	2.0	12
23	The molecular basis of antigenic variation among A(H9N2) avian influenza viruses. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	6.5	24
24	A sparse hierarchical Bayesian model for detecting relevant antigenic sites in virus evolution. <i>Computational Statistics</i> , 2017, 32, 803-843.	1.5	8
25	Selecting Random Effect Components in a Sparse Hierarchical Bayesian Model for Identifying Antigenic Variability. <i>Lecture Notes in Computer Science</i> , 2016, , 14-27.	1.3	1
26	Tracking the Antigenic Evolution of Foot-and-Mouth Disease Virus. <i>PLoS ONE</i> , 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. <i>PLoS Pathogens</i> , 2016, 12, e1005526.	4.7	58