

Eduan Wilkinson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9764794/publications.pdf>

Version: 2024-02-01

32
papers

4,901
citations

393982

19
h-index

454577

30
g-index

43
all docs

43
docs citations

43
times ranked

8104
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	13.7	1,381
2	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	13.7	1,210
3	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma. <i>Nature</i> , 2021, 593, 142-146.	13.7	574
4	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	15.2	326
5	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	13.5	186
6	SARS-CoV-2 prolonged infection during advanced HIV disease evolves extensive immune escape. <i>Cell Host and Microbe</i> , 2022, 30, 154-162.e5.	5.1	153
7	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
8	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.	5.1	73
9	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. <i>Genes</i> , 2020, 11, 949.	1.0	65
10	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report. <i>International Journal of Infectious Diseases</i> , 2021, 103, 234-241.	1.5	63
11	A genomics network established to respond rapidly to public health threats in South Africa. <i>Lancet Microbe</i> , The, 2020, 1, e229-e230.	3.4	46
12	Next Generation Sequencing and Bioinformatics Analysis of Family Genetic Inheritance. <i>Frontiers in Genetics</i> , 2020, 11, 544162.	1.1	41
13	Replacement of the Gamma by the Delta variant in Brazil: Impact of lineage displacement on the ongoing pandemic. <i>Virus Evolution</i> , 2022, 8, veac024.	2.2	37
14	Identifying Recent HIV Infections: From Serological Assays to Genomics. <i>Viruses</i> , 2015, 7, 5508-5524.	1.5	27
15	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. <i>Nature Communications</i> , 2022, 13, 1976.	5.8	27
16	History and origin of the HIV-1 subtype C epidemic in South Africa and the greater southern African region. <i>Scientific Reports</i> , 2015, 5, 16897.	1.6	26
17	Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. <i>Infection, Genetics and Evolution</i> , 2016, 46, 200-208.	1.0	23
18	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021, 4, 489.	2.0	23

#	ARTICLE	IF	CITATIONS
19	Identification of SARS-CoV-2 Omicron variant using spike gene target failure and genotyping assays, Gauteng, South Africa, 2021. <i>Journal of Medical Virology</i> , 2022, 94, 3676-3684.	2.5	23
20	Tracking external introductions of HIV using phylodynamics reveals a major source of infections in rural KwaZulu-Natal, South Africa. <i>Virus Evolution</i> , 2018, 4, vey037.	2.2	22
21	Multiple Early Introductions of SARS-CoV-2 to Cape Town, South Africa. <i>Viruses</i> , 2021, 13, 526.	1.5	20
22	Comparison of SARS-CoV-2 sequencing using the ONT GridION and the Illumina MiSeq. <i>BMC Genomics</i> , 2022, 23, 319.	1.2	19
23	Analysis of Viral Diversity in Relation to the Recency of HIV-1C Infection in Botswana. <i>PLoS ONE</i> , 2016, 11, e0160649.	1.1	14
24	Combining Phylogenetic and Network Approaches to Identify HIV-1 Transmission Links in San Mateo County, California. <i>Frontiers in Microbiology</i> , 2018, 9, 2799.	1.5	9
25	Detection of Transmission Clusters of HIV-1 Subtype C over a 21-Year Period in Cape Town, South Africa. <i>PLoS ONE</i> , 2014, 9, e109296.	1.1	9
26	Sequencing and Phylogenetic Analysis of Near Full-Length HIV-1 Subtypes A, B, G and Unique Recombinant AC and AD Viral Strains Identified in South Africa. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 412-420.	0.5	8
27	Factors influencing HIV-1 phylogenetic clustering. <i>Current Opinion in HIV and AIDS</i> , 2019, 14, 161-172.	1.5	7
28	Targeted Sanger sequencing to recover key mutations in SARS-CoV-2 variant genome assemblies produced by next-generation sequencing. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
29	High rate of occult hepatitis B virus infection in hemodialysis units of KwaZulu-Natal, South Africa. <i>Journal of Medical Virology</i> , 2019, 91, 1797-1803.	2.5	3
30	Persistent Hepatitis B Viraemia with Polymerase Mutations among HIV/HBV Co-Infected Patients on HBV-Active ART in KwaZulu-Natal, South Africa. <i>Viruses</i> , 2022, 14, 788.	1.5	3
31	The role of high-risk geographies in the perpetuation of the HIV epidemic in rural South Africa: A spatial molecular epidemiology study. <i>PLOS Global Public Health</i> , 2022, 2, e0000105.	0.5	3
32	The geography and inter-community configuration of new sexual partnership formation in a rural South African population over fourteen years (2003-2016). <i>PLOS Global Public Health</i> , 2022, 2, e0000055.	0.5	0