

Tulio de Oliveira

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150
papers

8,012
citations

38
h-index

87
g-index

164
ext. papers

13,863
ext. citations

16.3
avg, IF

6.86
L-index

#	Paper	IF	Citations
150	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021 , 592, 438-443	50.4	685
149	SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma. <i>Nature Medicine</i> , 2021 , 27, 622-625	50.5	670
148	Efficacy of the ChAdOx1 nCoV-19 Covid-19 Vaccine against the B.1.351 Variant. <i>New England Journal of Medicine</i> , 2021 , 384, 1885-1898	59.2	639
147	Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa		446
146	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma. <i>Nature</i> , 2021 , 593, 142-146	50.4	344
145	New SARS-CoV-2 Variants - Clinical, Public Health, and Vaccine Implications. <i>New England Journal of Medicine</i> , 2021 , 384, 1866-1868	59.2	340
144	Efficacy of NVX-CoV2373 Covid-19 Vaccine against the B.1.351 Variant. <i>New England Journal of Medicine</i> , 2021 , 384, 1899-1909	59.2	293
143	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization.. <i>Nature</i> , 2021 ,	50.4	209
142	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021 , 27, 440-446	50.5	206
141	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , 2022 ,	50.4	205
140	HIV-1 drug resistance before initiation or re-initiation of first-line antiretroviral therapy in low-income and middle-income countries: a systematic review and meta-regression analysis. <i>Lancet Infectious Diseases, The</i> , 2018 , 18, 346-355	25.5	200
139	SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma 2021 ,		183
138	Global epidemiology of drug resistance after failure of WHO recommended first-line regimens for adult HIV-1 infection: a multicentre retrospective cohort study. <i>Lancet Infectious Diseases, The</i> , 2016 , 16, 565-575	25.5	175
137	The biological and clinical significance of emerging SARS-CoV-2 variants. <i>Nature Reviews Genetics</i> , 2021 , 22, 757-773	30.1	175
136	Transmission networks and risk of HIV infection in KwaZulu-Natal, South Africa: a community-wide phylogenetic study. <i>Lancet HIV,the</i> , 2017 , 4, e41-e50	7.8	158
135	Spread of yellow fever virus outbreak in Angola and the Democratic Republic of the Congo 2015-16: a modelling study. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 330-338	25.5	140
134	Universal test and treat and the HIV epidemic in rural South Africa: a phase 4, open-label, community cluster randomised trial. <i>Lancet HIV,the</i> , 2018 , 5, e116-e125	7.8	140

133	Microbial genome-wide association studies: lessons from human GWAS. <i>Nature Reviews Genetics</i> , 2017 , 18, 41-50	30.1	137
132	SARS-CoV-2 Omicron has extensive but incomplete escape of Pfizer BNT162b2 elicited neutralization and requires ACE2 for infection. 2021 ,		130
131	Genome Detective: an automated system for virus identification from high-throughput sequencing data. <i>Bioinformatics</i> , 2019 , 35, 871-873	7.2	109
130	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021 , 6, 821-823	26.6	91
129	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. <i>Bioinformatics</i> , 2020 , 36, 3552-3555	7.2	89
128	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , 2021 , 19, e3001236	9.7	85
127	T cell responses to SARS-CoV-2 spike cross-recognize Omicron.. <i>Nature</i> , 2022 ,	50.4	78
126	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma		71
125	Phylogenetic studies of transmission dynamics in generalized HIV epidemics: an essential tool where the burden is greatest?. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014 , 67, 181-95 ^{3.1}		68
124	Cross-Reactive Neutralizing Antibody Responses Elicited by SARS-CoV-2 501Y.V2 (B.1.351). <i>New England Journal of Medicine</i> , 2021 , 384, 2161-2163	59.2	63
123	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021 , 184, 5189-5200.e7	56.2	61
122	Occult HIV-1 drug resistance to thymidine analogues following failure of first-line tenofovir combined with a cytosine analogue and nevirapine or efavirenz in sub Saharan Africa: a retrospective multi-centre cohort study. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 296-304	25.5	46
121	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 12522-12523	11.5	46
120	The emergence and ongoing convergent evolution of the N501Y lineages coincides with a major global shift in the SARS-CoV-2 selective landscape 2021 ,		46
119	Dolutegravir for first-line antiretroviral therapy in low-income and middle-income countries: uncertainties and opportunities for implementation and research. <i>Lancet HIV,the</i> , 2018 , 5, e400-e404	7.8	44
118	Declines in HIV incidence among men and women in a South African population-based cohort. <i>Nature Communications</i> , 2019 , 10, 5482	17.4	43
117	Two doses of SARS-CoV-2 vaccination induce robust immune responses to emerging SARS-CoV-2 variants of concern. <i>Nature Communications</i> , 2021 , 12, 5061	17.4	42
116	Effect of population viral load on prospective HIV incidence in a hyperendemic rural African community. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	41

115	PANGEA-HIV: phylogenetics for generalised epidemics in Africa. <i>Lancet Infectious Diseases, The</i> , 2015 , 15, 259-61	25.5	39
114	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. <i>Genes</i> , 2020 , 11,	4.2	39
113	Impact of Next-generation Sequencing Defined Human Immunodeficiency Virus Pretreatment Drug Resistance on Virological Outcomes in the ANRS 12249 Treatment-as-Prevention Trial. <i>Clinical Infectious Diseases</i> , 2019 , 69, 207-214	11.6	38
112	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	10.5	37
111	Incidence rate estimation, periodic testing and the limitations of the mid-point imputation approach. <i>International Journal of Epidemiology</i> , 2018 , 47, 236-245	7.8	36
110	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021 , 374, 423-431	33.3	35
109	Persistent SARS-CoV-2 infection and intra-host evolution in association with advanced HIV infection		32
108	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization. <i>Nature</i> ,	50.4	31
107	A genomics network established to respond rapidly to public health threats in South Africa. <i>Lancet Microbe, The</i> , 2020 , 1, e229-e230	22.2	30
106	Trends in Pretreatment HIV-1 Drug Resistance in Antiretroviral Therapy-naive Adults in South Africa, 2000-2016: A Pooled Sequence Analysis. <i>EclinicalMedicine</i> , 2019 , 9, 26-34	11.3	29
105	Increasing HIV-1 Drug Resistance Between 2010 and 2012 in Adults Participating in Population-Based HIV Surveillance in Rural KwaZulu-Natal, South Africa. <i>AIDS Research and Human Retroviruses</i> , 2016 , 32, 763-9	1.6	28
104	Sensitive Next-Generation Sequencing Method Reveals Deep Genetic Diversity of HIV-1 in the Democratic Republic of the Congo. <i>Journal of Virology</i> , 2017 , 91,	6.6	26
103	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019 , 10, 1411	17.4	26
102	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV,the</i> , 2020 , 7, e173-e183	7.8	26
101	Virological Outcomes of Second-line Protease Inhibitor-Based Treatment for Human Immunodeficiency Virus Type 1 in a High-Prevalence Rural South African Setting: A Competing-Risks Prospective Cohort Analysis. <i>Clinical Infectious Diseases</i> , 2017 , 64, 1006-1016	11.6	26
100	Implementing HIV-1 genotypic resistance testing in antiretroviral therapy programs in Africa: needs, opportunities, and challenges. <i>AIDS Reviews</i> , 2013 , 15, 221-9	1.5	26
99	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing. <i>Emerging Microbes and Infections</i> , 2020 , 9, 1824-1834	18.9	26
98	Reduced antibody cross-reactivity following infection with B.1.1.7 than with parental SARS-CoV-2 strains. <i>ELife</i> , 2021 , 10,	8.9	26

97	Global disparities in SARS-CoV-2 genomic surveillance 2021 ,		26
96	Mutational Correlates of Virological Failure in Individuals Receiving a WHO-Recommended Tenofovir-Containing First-Line Regimen: An International Collaboration. <i>EBioMedicine</i> , 2017 , 18, 225-235	8.8	25
95	Safety and efficacy of the ChAdOx1 nCoV-19 (AZD1222) Covid-19 vaccine against the B.1.351 variant in South Africa		25
94	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24
93	Emergence and phenotypic characterization of C.1.2, a globally detected lineage that rapidly accumulated mutations of concern		23
92	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	4.5	22
91	SARS-CoV-2 prolonged infection during advanced HIV disease evolves extensive immune escape.. <i>Cell Host and Microbe</i> , 2022 ,	23.4	22
90	Reduced efficacy of HIV-1 integrase inhibitors in patients with drug resistance mutations in reverse transcriptase. <i>Nature Communications</i> , 2020 , 11, 5922	17.4	22
89	High percentage of undiagnosed HIV cases within a hyperendemic South African community: a population-based study. <i>Journal of Epidemiology and Community Health</i> , 2018 , 72, 168-172	5.1	21
88	Current Affairs of Microbial Genome-Wide Association Studies: Approaches, Bottlenecks and Analytical Pitfalls. <i>Frontiers in Microbiology</i> , 2019 , 10, 3119	5.7	20
87	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> ,	50.4	20
86	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report 2020 ,		20
85	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. <i>Scientific Reports</i> , 2016 , 6, 39489	4.9	20
84	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021 , 29, 1093-1110	23.4	19
83	Preliminary Efficacy of the NVX-CoV2373 Covid-19 Vaccine Against the B.1.351 Variant		18
82	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007231	4.8	17
81	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019 , 25, 784-787	10.2	17
80	Trends in HIV Prevention, Treatment, and Incidence in a Hyperendemic Area of KwaZulu-Natal, South Africa. <i>JAMA Network Open</i> , 2019 , 2, e1914378	10.4	17

79	A novel variant of interest of SARS-CoV-2 with multiple spike mutations detected through travel surveillance in Africa		17
78	Rapid replacement of the Beta variant by the Delta variant in South Africa		17
77	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019 , 14, e0217871	3.7	16
76	Rates of virological suppression and drug resistance in adult HIV-1-positive patients attending primary healthcare facilities in KwaZulu-Natal, South Africa. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 3141-3148	5.1	16
75	SARS-CoV-2 501Y.V2 (B.1.351) elicits cross-reactive neutralizing antibodies 2021 ,		16
74	Social Disequilibrium and the Risk of HIV Acquisition: A Multilevel Study in Rural KwaZulu-Natal Province, South Africa. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2017 , 75, 164-174	3.1	15
73	Omicron infection enhances neutralizing immunity against the Delta variant. 2021 ,		15
72	High Resolution analysis of Transmission Dynamics of Sars-Cov-2 in Two Major Hospital Outbreaks in South Africa Leveraging Intra-host Diversity 2020 ,		15
71	HIV status alters disease severity and immune cell responses in Δvariant SARS-CoV-2 infection wave		15
70	Moderate-to-High Levels of Pretreatment HIV Drug Resistance in KwaZulu-Natal Province, South Africa. <i>AIDS Research and Human Retroviruses</i> , 2019 , 35, 129-138	1.6	15
69	Escape from recognition of SARS-CoV-2 variant spike epitopes but overall preservation of T cell immunity. <i>Science Translational Medicine</i> , 2022 , 14,	17.5	14
68	Understanding Specific Contexts of Antiretroviral Therapy Adherence in Rural South Africa: A Thematic Analysis of Digital Stories from a Community with High HIV Prevalence. <i>PLoS ONE</i> , 2016 , 11, e0148801	3.7	14
67	HIV-1 full-genome phylogenetics of generalized epidemics in sub-Saharan Africa: impact of missing nucleotide characters in next-generation sequences. <i>AIDS Research and Human Retroviruses</i> , 2017 , 33, 1083-1098	1.6	13
66	Genome-Wide Association Study of HIV Whole Genome Sequences Validated using Drug Resistance. <i>PLoS ONE</i> , 2016 , 11, e0163746	3.7	13
65	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa		12
64	The political theatre of the UK's travel ban on South Africa. <i>Lancet, The</i> , 2021 ,	4.0	12
63	SARS-CoV-2 evolved during advanced HIV disease immunosuppression has Beta-like escape of vaccine and Delta infection elicited immunity. 2021 ,		12
62	Ethical issues associated with HIV phylogenetics in HIV transmission dynamics research: A review of the literature using the Emanuel Framework. <i>Developing World Bioethics</i> , 2019 , 19, 25-35	2.6	11

61	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes 2020 ,		10
60	Predicted antiviral activity of tenofovir versus abacavir in combination with a cytosine analogue and the integrase inhibitor dolutegravir in HIV-1-infected South African patients initiating or failing first-line ART. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 473-479	5.1	10
59	Selection analysis identifies clusters of unusual mutational changes in Omicron lineage BA.1 that likely impact Spike function.. <i>Molecular Biology and Evolution</i> , 2022 ,	8.3	10
58	Longitudinal Trends in the Prevalence of Detectable HIV Viremia: Population-Based Evidence From Rural KwaZulu-Natal, South Africa. <i>Clinical Infectious Diseases</i> , 2018 , 66, 1254-1260	11.6	9
57	Africa: tackle HIV and COVID-19 together. <i>Nature</i> , 2021 , 600, 33-36	50.4	9
56	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. <i>PLoS Computational Biology</i> , 2016 , 12, e1004395	5	9
55	Multiple Early Introductions of SARS-CoV-2 to Cape Town, South Africa. <i>Viruses</i> , 2021 , 13,	6.2	9
54	Selection analysis identifies unusual clustered mutational changes in Omicron lineage BA.1 that likely impact Spike function. 2022 ,		8
53	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	3.7	8
52	HIV status alters disease severity and immune cell responses in beta variant SARS-CoV-2 infection wave. <i>ELife</i> , 2021 , 10,	8.9	8
51	Major new lineages of SARS-CoV-2 emerge and spread in South Africa during lockdown		8
50	Community engagement with HIV drug adherence in rural South Africa: a transdisciplinary approach. <i>Medical Humanities</i> , 2018 , 44, 239-246	1.4	8
49	High Rates of Transmission of Drug-resistant HIV in Aruba Resulting in Reduced Susceptibility to the WHO Recommended First-line Regimen in Nearly Half of Newly Diagnosed HIV-infected Patients. <i>Clinical Infectious Diseases</i> , 2017 , 64, 1092-1097	11.6	7
48	Return of the founder Chikungunya virus to its place of introduction into Brazil is revealed by genomic characterization of exanthematic disease cases. <i>Emerging Microbes and Infections</i> , 2020 , 9, 53-57	18.9	7
47	Two doses of SARS-CoV-2 vaccination induce more robust immune responses to emerging SARS-CoV-2 variants of concern than does natural infection.		7
46	SARS-CoV-2 cell-to-cell spread occurs rapidly and is insensitive to antibody neutralization		7
45	Effectiveness of the Ad26.COV2.S vaccine in health-care workers in South Africa (the Sisonke study): results from a single-arm, open-label, phase 3B, implementation study.. <i>Lancet, The</i> , 2022 , 399, 1141-1153	40	7
44	Continued Emergence and Evolution of Omicron in South Africa: New BA.4 and BA.5 lineages		7

43	Omicron sub-lineages BA.4/BA.5 escape BA.1 infection elicited neutralizing immunity		7
42	HTLV-1aA introduction into Brazil and its association with the trans-Atlantic slave trade. <i>Infection, Genetics and Evolution</i> , 2017 , 48, 95-101	4.5	6
41	Ethical issues associated with HIV molecular epidemiology: a qualitative exploratory study using inductive analytic approaches. <i>BMC Medical Ethics</i> , 2019 , 20, 67	2.9	6
40	Unlocking the efficiency of genomics laboratories with robotic liquid-handling. <i>BMC Genomics</i> , 2020 , 21, 729	4.5	6
39	Sociobehavioral and community predictors of unsuppressed HIV viral load: multilevel results from a hyperendemic rural South African population. <i>Aids</i> , 2019 , 33, 559-569	3.5	6
38	Experts' Perspectives on Key Ethical Issues Associated With HIV Phylogenetics as Applied in HIV Transmission Dynamics Research. <i>Journal of Empirical Research on Human Research Ethics</i> , 2019 , 14, 61-77	4.6	6
37	Immunogenicity of SARS-CoV-2 infection and Ad26.CoV2.S vaccination in people living with HIV. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	6
36	The effect of interventions on the transmission and spread of HIV in South Africa: a phylodynamic analysis. <i>Scientific Reports</i> , 2019 , 9, 2640	4.9	5
35	Persistent SARS-CoV-2 Infection with Accumulation of Mutations in a Patient with Poorly Controlled HIV Infection. <i>SSRN Electronic Journal</i> ,	1	5
34	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing		5
33	Genomic epidemiology of SARS-CoV-2 in Mauritius reveals a new wave of infections dominated by the B.1.1.318, a variant under investigation		5
32	Combining Phylogenetic and Network Approaches to Identify HIV-1 Transmission Links in San Mateo County, California. <i>Frontiers in Microbiology</i> , 2018 , 9, 2799	5.7	5
31	Short Report: Early genomic detection of SARS-CoV-2 P.1 variant in Northeast Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009591	4.8	5
30	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation During a Pandemic		4
29	Loss of recognition of SARS-CoV-2 B.1.351 variant spike epitopes but overall preservation of T cell immunity		4
28	Escape from recognition of SARS-CoV-2 Beta variant spike epitopes but overall preservation of T cell immunity.. <i>Science Translational Medicine</i> , 2021 , eabj6824	17.5	4
27	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020 , 6, veaa004	3.7	3
26	SARS-CoV-2 Genetic diversity and lineage dynamics of in Egypt		3

25	Reduced amplification efficiency of the RNA-dependent-RNA-polymerase target enables tracking of the Delta SARS-CoV-2 variant using routine diagnostic tests.. <i>Journal of Virological Methods</i> , 2022 , 302, 114471	2.6	3
24	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021 , 12, 2296	17.4	3
23	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa		3
22	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage.. <i>Nature Communications</i> , 2022 , 13, 1976	17.4	3
21	New Genomes from the Congo Basin Expand History of CRF01_AE Origin and Dissemination. <i>AIDS Research and Human Retroviruses</i> , 2020 , 36, 574-582	1.6	2
20	The CNS in the face of ART contains T cell origin HIV which can lead to drug resistance		2
19	Impact of pretreatment low-abundance HIV-1 drug-resistant variants on virological failure among HIV-1/TB-co-infected individuals. <i>Journal of Antimicrobial Chemotherapy</i> , 2020 , 75, 3319-3326	5.1	2
18	Peer-mediated HIV assisted partner services to identify and link to care HIV-positive and HCV-positive people who inject drugs: a cohort study protocol. <i>BMJ Open</i> , 2021 , 11, e041083	3	2
17	Short report: Introduction of chikungunya virus ECSA genotype into the Brazilian Midwest and its dispersion through the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009290	4.8	2
16	Implementation of an efficient SARS-CoV-2 specimen pooling strategy for high throughput diagnostic testing. <i>Scientific Reports</i> , 2021 , 11, 17793	4.9	2
15	Comparison of SARS-CoV-2 sequencing using the ONT GridION and the Illumina MiSeq.. <i>BMC Genomics</i> , 2022 , 23, 319	4.5	2
14	An early warning system for emerging SARS-CoV-2 variants. <i>Nature Medicine</i> ,	50.5	2
13	HIV-1 drug resistance in adults and adolescents on protease inhibitor-based antiretroviral treatment in KwaZulu-Natal Province, South Africa. <i>Journal of Global Antimicrobial Resistance</i> , 2021 ,	3.4	1
12	Reduced amplification efficiency of the RNA-dependent-RNA-polymerase (RdRp) target enables tracking of the Delta SARS-CoV-2 variant using routine diagnostic tests		1
11	Genomic epidemiology reveals the impact of national and international restrictions measures on the SARS-CoV-2 epidemic in Brazil. 2022 ,		1
10	Immunogenicity of SARS-CoV-2 infection and Ad26.CoV2.S vaccination in people living with HIV		1
9	External introductions helped drive and sustain the high incidence of HIV-1 in rural KwaZulu-Natal, South Africa		1
8	Adding a Voice to the Unique Ethical Considerations in Molecular HIV Surveillance. <i>American Journal of Bioethics</i> , 2020 , 20, 34-36	1.1	1

7	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	3.7	1
6	Acquired HIV drug resistance and virologic monitoring in a HIV hyper-endemic setting in KwaZulu-Natal Province, South Africa. <i>AIDS Research and Therapy</i> , 2021 , 18, 74	3	0
5	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021 , 27, 1393-1404	10.2	0
4	Using the Emanuel Framework to Explore the Ethical Issues Raised in a Participatory Visual Research Project in Rural South Africa. <i>Journal of Empirical Research on Human Research Ethics</i> , 2021 , 16, 3-14	1.6	0
3	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil.. <i>Microbiology Spectrum</i> , 2022 , e0015522	8.9	0
2	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy.. <i>MBio</i> , 2022 , e0026922	7.8	0
1	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		