

Tulio de Oliveira

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Selection analysis identifies unusual clustered mutational changes in Omicron lineage BA.1 that likely impact Spike function. 2022 ,		8
149	T cell responses to SARS-CoV-2 spike cross-recognize Omicron.. <i>Nature</i> , 2022 ,	50.4	78
148	SARS-CoV-2 prolonged infection during advanced HIV disease evolves extensive immune escape.. <i>Cell Host and Microbe</i> , 2022 ,	23.4	22
147	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , 2022 ,	50.4	205
146	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
145	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
144	Genomic epidemiology reveals the impact of national and international restrictions measures on the SARS-CoV-2 epidemic in Brazil. 2022 ,		1
143	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
142	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		
141	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
140	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
139	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil.. <i>Microbiology Spectrum</i> , 2022 , e0015522	8.9	0
138	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage.. <i>Nature Communications</i> , 2022 , 13, 1976	17.4	3
137	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy.. <i>MBio</i> , 2022 , e0026922	7.8	0
136	Comparison of SARS-CoV-2 sequencing using the ONT GridION and the Illumina MiSeq.. <i>BMC Genomics</i> , 2022 , 23, 319	4.5	2
135	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization.. <i>Nature</i> , 2021 ,	50.4	209
134	SARS-CoV-2 Omicron has extensive but incomplete escape of Pfizer BNT162b2 elicited neutralization and requires ACE2 for infection. 2021 ,		130

133	Omicron infection enhances neutralizing immunity against the Delta variant. 2021 ,		15
132	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
131	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
130	The political theatre of the UK's travel ban on South Africa. <i>Lancet, The</i> , 2021 ,	4.0	12
129	Africa: tackle HIV and COVID-19 together. <i>Nature</i> , 2021 , 600, 33-36	50.4	9
128	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
127	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
126	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma. <i>Nature</i> , 2021 , 593, 142-146	50.4	344
125	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
124	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021 , 592, 438-443	50.4	685
123	SARS-CoV-2 501Y.V2 (B.1.351) elicits cross-reactive neutralizing antibodies 2021 ,		16
122	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
121	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
120	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
119	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021 , 12, 2296	17.4	3
118	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
117	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
116	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021 , 27, 1393-1404	10.2	0

115	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , 2021 , 19, e3001236	9.7	85
114	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
113	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
112	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
111	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
110	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
109	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
108	SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma 2021 ,		183
107	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021 , 27, 440-446	50.5	206
106	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
105	Multiple Early Introductions of SARS-CoV-2 to Cape Town, South Africa. <i>Viruses</i> , 2021 , 13,	6.2	9
104	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
103	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
102	Global disparities in SARS-CoV-2 genomic surveillance 2021 ,		26
101	SARS-CoV-2 evolved during advanced HIV disease immunosuppression has Beta-like escape of vaccine and Delta infection elicited immunity. 2021 ,		12
100	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
99	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021 , 184, 5189-5200.e7	56.2	61
98	The biological and clinical significance of emerging SARS-CoV-2 variants. <i>Nature Reviews Genetics</i> , 2021 , 22, 757-773	30.1	175

97	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
96	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
95	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
94	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
93	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
92	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020 , 6, veaa004	3.7	3
91	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. <i>Bioinformatics</i> , 2020 , 36, 3552-3555	7.2	89
90	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24
89	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
88	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes 2020 ,		10
87	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report 2020 ,		20
86	High Resolution analysis of Transmission Dynamics of Sars-Cov-2 in Two Major Hospital Outbreaks in South Africa Leveraging Intra-host Diversity 2020 ,		15
85	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
84	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
83	Unlocking the efficiency of genomics laboratories with robotic liquid-handling. <i>BMC Genomics</i> , 2020 , 21, 729	4.5	6
82	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
81	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
80	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

79	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
78	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019 , 14, e0217871	3.7	16
77	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
76	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
75	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
74	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
73	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
72	Current Affairs of Microbial Genome-Wide Association Studies: Approaches, Bottlenecks and Analytical Pitfalls. <i>Frontiers in Microbiology</i> , 2019 , 10, 3119	5.7	20
71	Genome Detective: an automated system for virus identification from high-throughput sequencing data. <i>Bioinformatics</i> , 2019 , 35, 871-873	7.2	109
70	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
69	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
68	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
67	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
66	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
65	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	1.6	6
64	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
63	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
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	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
60	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
59	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
58	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
57	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
56	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
55	Community engagement with HIV drug adherence in rural South Africa: a transdisciplinary approach. <i>Medical Humanities</i> , 2018 , 44, 239-246	1.4	8
54	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
53	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
52	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
51	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
50	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
49	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
48	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
47	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
46	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
45	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
44	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

43	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
42	Microbial genome-wide association studies: lessons from human GWAS. <i>Nature Reviews Genetics</i> , 2017 , 18, 41-50	30.1	137
41	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
40	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
39	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</i> , 2016 , 16, 565-575	25.5	175
38	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
37	Genome-Wide Association Study of HIV Whole Genome Sequences Validated using Drug Resistance. <i>PLoS ONE</i> , 2016 , 11, e0163746	3.7	13
36	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. <i>PLoS Computational Biology</i> , 2016 , 12, e1004395	5	9
35	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
34	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. <i>Scientific Reports</i> , 2016 , 6, 39489	4.9	20
33	PANGEA-HIV: phylogenetics for generalised epidemics in Africa. <i>Lancet Infectious Diseases</i> , 2015 , 15, 259-61	25.5	39
32	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
31	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
30	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
29	SARS-CoV-2 Genetic diversity and lineage dynamics of in Egypt		3
28	Persistent SARS-CoV-2 Infection with Accumulation of Mutations in a Patient with Poorly Controlled HIV Infection. <i>SSRN Electronic Journal</i> ,	1	5
27	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> ,	50.4	20
26	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization. <i>Nature</i> ,	50.4	31

25	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa	12
24	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
23	Immunogenicity of SARS-CoV-2 infection and Ad26.CoV2.S vaccination in people living with HIV	1
22	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing	5
21	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation During a Pandemic	4
20	Major new lineages of SARS-CoV-2 emerge and spread in South Africa during lockdown	8
19	HIV status alters disease severity and immune cell responses in Δvariant SARS-CoV-2 infection wave	15
18	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	44 ⁶
17	The CNS in the face of ART contains T cell origin HIV which can lead to drug resistance	2
16	External introductions helped drive and sustain the high incidence of HIV-1 in rural KwaZulu-Natal, South Africa	1
15	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
14	Preliminary Efficacy of the NVX-CoV2373 Covid-19 Vaccine Against the B.1.351 Variant	18
13	A novel variant of interest of SARS-CoV-2 with multiple spike mutations detected through travel surveillance in Africa	17
12	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa	3
11	Persistent SARS-CoV-2 infection and intra-host evolution in association with advanced HIV infection	32
10	Loss of recognition of SARS-CoV-2 B.1.351 variant spike epitopes but overall preservation of T cell immunity	4
9	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
8	SARS-CoV-2 cell-to-cell spread occurs rapidly and is insensitive to antibody neutralization	7

7	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma	71
6	Safety and efficacy of the ChAdOx1 nCoV-19 (AZD1222) Covid-19 vaccine against the B.1.351 variant in South Africa	25
5	Emergence and phenotypic characterization of C.1.2, a globally detected lineage that rapidly accumulated mutations of concern	23
4	Rapid replacement of the Beta variant by the Delta variant in South Africa	17
3	Continued Emergence and Evolution of Omicron in South Africa: New BA.4 and BA.5 lineages	7
2	Omicron sub-lineages BA.4/BA.5 escape BA.1 infection elicited neutralizing immunity	7
1	An early warning system for emerging SARS-CoV-2 variants. <i>Nature Medicine</i> ,	50.5 2