Tulio de Oliveira

List of Publications by Year
in descending order

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117	17,094	61984 43	26613 107
papers	citations	h-index	g-index
164	164	164	19996
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	HIV-1 drug resistance in adults and adolescents on protease inhibitor-based antiretroviral therapy in KwaZulu-Natal Province, South Africa. Journal of Global Antimicrobial Resistance, 2022, 29, 468-475.	2.2	6
2	Hypermethylation at the <i>CXCR5</i> gene locus limits trafficking potential of CD8+ T cells into B-cell follicles during HIV-1 infection. Blood Advances, 2022, 6, 1904-1916.	5.2	6
3	T cell responses to SARS-CoV-2 spike cross-recognize Omicron. Nature, 2022, 603, 488-492.	27.8	430
4	SARS-CoV-2 prolonged infection during advanced HIV disease evolves extensive immune escape. Cell Host and Microbe, 2022, 30, 154-162.e5.	11.0	153
5	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 2022, 603, 679-686.	27.8	1,210
6	Reduced amplification efficiency of the RNA-dependent-RNA-polymerase target enables tracking of the Delta SARS-CoV-2 variant using routine diagnostic tests. Journal of Virological Methods, 2022, 302, 114471.	2.1	8
7	Escape from recognition of SARS-CoV-2 variant spike epitopes but overall preservation of T cell immunity. Science Translational Medicine, 2022, 14, .	12.4	77
8	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization. Nature, 2022, 602, 654-656.	27.8	928
9	Replacement of the Gamma by the Delta variant in Brazil: Impact of lineage displacement on the ongoing pandemic. Virus Evolution, 2022, 8, veac024.	4.9	37
10	The geography and inter-community configuration of new sexual partnership formation in a rural South African population over fourteen years (2003â€“2016). PLOS Global Public Health, 2022, 2, e0000055.	1.6	0
11	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. Lancet, The, 2022, 399, 1141-1153.	13.7	51
12	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. Molecular Biology and Evolution, 2022, 39, .	8.9	84
13	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil. Microbiology Spectrum, 2022, 10, e0015522.	3.0	4
14	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. Nature Communications, 2022, 13, 1976.	12.8	27
15	Immunogenicity of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection and Ad26.CoV2.S Vaccination in People Living With Human Immunodeficiency Virus (HIV). Clinical Infectious Diseases, 2022, 75, e857-e864.	5.8	30
16	Identification of SARSâ€CoVâ€2 Omicron variant using spike gene target failure and genotyping assays, Gauteng, South Africa, 2021. Journal of Medical Virology, 2022, 94, 3676-3684.	5.0	23
17	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy. MBio, 2022, 13, e0026922.	4.1	5
18	Comparison of SARS-CoV-2 sequencing using the ONT GridION and the Illumina MiSeq. BMC Genomics, 2022, 23, 319.	2.8	19

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19	Infectious diseases science in Africa takes a leading place in the world. Lancet, The, 2022, , .	13.7	1
20	An early warning system for emerging SARS-CoV-2 variants. Nature Medicine, 2022, 28, 1110-1115.	30.7	47
21	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. Nature Medicine, 2022, 28, 1785-1790.	30.7	456
22	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report. International Journal of Infectious Diseases, 2021, 103, 234-241.	3.3	63
23	Sixteen novel lineages of SARS-CoV-2 in South Africa. Nature Medicine, 2021, 27, 440-446.	30.7	326
24	Using the Emanuel Framework to Explore the Ethical Issues Raised in a Participatory Visual Research Project in Rural South Africa. Journal of Empirical Research on Human Research Ethics, 2021, 16, 3-14.	1.3	1
25	Multiple Early Introductions of SARS-CoV-2 to Cape Town, South Africa. Viruses, 2021, 13, 526.	3.3	20
26	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma. Nature, 2021, 593, 142-146.	27.8	574
27	Detection of a SARS-CoV-2 variant of concern in South Africa. Nature, 2021, 592, 438-443.	27.8	1,381
28	SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma. Nature Medicine, 2021, 27, 622-625.	30.7	984
29	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. BMJ Open, 2021, 11, e041083.	1.9	8
30	Short report: Introduction of chikungunya virus ECSA genotype into the Brazilian Midwest and its dispersion through the Americas. PLoS Neglected Tropical Diseases, 2021, 15, e0009290.	3.0	17
31	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. Nature Communications, 2021, 12, 2296.	12.8	29
32	Efficacy of NVX-CoV2373 Covid-19 Vaccine against the B.1.351 Variant. New England Journal of Medicine, 2021, 384, 1899-1909.	27.0	541
33	New SARS-CoV-2 Variants â€" Clinical, Public Health, and Vaccine Implications. New England Journal of Medicine, 2021, 384, 1866-1868.	27.0	581
34	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. Emerging Infectious Diseases, 2021, 27, 1393-1404.	4.3	13
35	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	5.6	200
36	Efficacy of the ChAdOx1 nCoV-19 Covid-19 Vaccine against the B.1.351 Variant. New England Journal of Medicine, 2021, 384, 1885-1898.	27.0	1,077

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37	Cross-Reactive Neutralizing Antibody Responses Elicited by SARS-CoV-2 501Y.V2 (B.1.351). New England Journal of Medicine, 2021, 384, 2161-2163.	27.0	111
38	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. Nature Microbiology, 2021, 6, 821-823.	13.3	221
39	Reduced antibody cross-reactivity following infection with B.1.1.7 than with parental SARS-CoV-2 strains. ELife, 2021, 10, .	6.0	42
40	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. Cell Host and Microbe, 2021, 29, 1093-1110.	11.0	73
41	Short Report: Early genomic detection of SARS-CoV-2 P.1 variant in Northeast Brazil. PLoS Neglected Tropical Diseases, 2021, 15, e0009591.	3.0	13
42	Two doses of SARS-CoV-2 vaccination induce robust immune responses to emerging SARS-CoV-2 variants of concern. Nature Communications, 2021, 12, 5061.	12.8	150
43	Implementation of an efficient SARS-CoV-2 specimen pooling strategy for high throughput diagnostic testing. Scientific Reports, 2021, 11, 17793.	3.3	5
44	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. Cell, 2021, 184, 5189-5200.e7.	28.9	186
45	The biological and clinical significance of emerging SARS-CoV-2 variants. Nature Reviews Genetics, 2021, 22, 757-773.	16.3	778
46	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431.	12.6	144
47	HIV status alters disease severity and immune cell responses in Beta variant SARS-CoV-2 infection wave. ELife, 2021, 10, .	6.0	28
48	Acquired HIV drug resistance and virologic monitoring in a HIV hyper-endemic setting in KwaZulu-Natal Province, South Africa. AIDS Research and Therapy, 2021, 18, 74.	1.7	2
49	The political theatre of the UK's travel ban on South Africa. Lancet, The, 2021, 398, 2211-2213.	13.7	37
50	Africa: tackle HIV and COVID-19 together. Nature, 2021, 600, 33-36.	27.8	35
51	Escape from recognition of SARS-CoV-2 Beta variant spike epitopes but overall preservation of T cell immunity.. Science Translational Medicine, 2021, , eabj6824.	12.4	11
52	Return of the founder Chikungunya virus to its place of introduction into Brazil is revealed by genomic characterization of exanthematic disease cases. Emerging Microbes and Infections, 2020, 9, 53-57.	6.5	11
53	Adding a Voice to the Unique Ethical Considerations in Molecular HIV Surveillance. American Journal of Bioethics, 2020, 20, 34-36.	0.9	4
54	Unlocking the efficiency of genomics laboratories with robotic liquid-handling. BMC Genomics, 2020, 21, 729.	2.8	50

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55	Reduced efficacy of HIV-1 integrase inhibitors in patients with drug resistance mutations in reverse transcriptase. Nature Communications, 2020, 11, 5922.	12.8	55
56	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing. Emerging Microbes and Infections, 2020, 9, 1824-1834.	6.5	42
57	Impact of pretreatment low-abundance HIV-1 drug-resistant variants on virological failure among HIV-1/TB-co-infected individuals. Journal of Antimicrobial Chemotherapy, 2020, 75, 3319-3326.	3.0	9
58	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. Genes, 2020, 11, 949.	2.4	65
59	A genomics network established to respond rapidly to public health threats in South Africa. Lancet Microbe, The, 2020, 1, e229-e230.	7.3	46
60	New Genomes from the Congo Basin Expand History of CRF01_AE Origin and Dissemination. AIDS Research and Human Retroviruses, 2020, 36, 574-582.	1.1	7
61	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523.	7.1	68
62	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. Virus Evolution, 2020, 6, veaa004.	4.9	9
63	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. Bioinformatics, 2020, 36, 3552-3555.	4.1	129
64	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. Cell Reports, 2020, 30, 2275-2283.e7.	6.4	37
65	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. Lancet HIV,the, 2020, 7, e173-e183.	4.7	59
66	Genome Detective: an automated system for virus identification from high-throughput sequencing data. Bioinformatics, 2019, 35, 871-873.	4.1	254
67	Ethical issues associated with HIV molecular epidemiology: a qualitative exploratory study using inductive analytic approaches. BMC Medical Ethics, 2019, 20, 67.	2.4	11
68	Trends in HIV Prevention, Treatment, and Incidence in a Hyperendemic Area of KwaZulu-Natal, South Africa. JAMA Network Open, 2019, 2, e1914378.	5.9	33
69	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. PLoS ONE, 2019, 14, e0217871.	2.5	31
70	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. PLoS Neglected Tropical Diseases, 2019, 13, e0007231.	3.0	44
71	Trends in Pretreatment HIV-1 Drug Resistance in Antiretroviral Therapy-naive Adults in South Africa, 2000â€“2016: A Pooled Sequence Analysis. EClinicalMedicine, 2019, 9, 26-34.	7.1	51
72	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. Emerging Infectious Diseases, 2019, 25, 784-787.	4.3	36

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73	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. Nature Communications, 2019, 10, 1411.	12.8	50
74	The effect of interventions on the transmission and spread of HIV in South Africa: a phylodynamic analysis. Scientific Reports, 2019, 9, 2640.	3.3	9
75	Declines in HIV incidence among men and women in a South African population-based cohort. Nature Communications, 2019, 10, 5482.	12.8	102
76	Sociobehavioral and community predictors of unsuppressed HIV viral load. Aids, 2019, 33, 559-569.	2.2	14
77	Moderate-to-High Levels of Pretreatment HIV Drug Resistance in KwaZulu-Natal Province, South Africa. AIDS Research and Human Retroviruses, 2019, 35, 129-138.	1.1	21
78	Expertsâ€™ Perspectives on Key Ethical Issues Associated With HIV Phylogenetics as Applied in HIV Transmission Dynamics Research. Journal of Empirical Research on Human Research Ethics, 2019, 14, 61-77.	1.3	16
79	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. Journal of Antimicrobial Chemotherapy, 2019, 74, 473-479.	3.0	15
80	Impact of Next-generation Sequencing Defined Human Immunodeficiency Virus Pretreatment Drug Resistance on Virological Outcomes in the ANRS 12249 Treatment-as-Prevention Trial. Clinical Infectious Diseases, 2019, 69, 207-214.	5.8	48
81	Ethical issues associated with <scp>HIV</scp> phylogenetics in <scp>HIV</scp> transmission dynamics research: A review of the literature using the Emanuel Framework. Developing World Bioethics, 2019, 19, 25-35.	0.9	14
82	Current Affairs of Microbial Genome-Wide Association Studies: Approaches, Bottlenecks and Analytical Pitfalls. Frontiers in Microbiology, 2019, 10, 3119.	3.5	54
83	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. Lancet Infectious Diseases, The, 2018, 18, 346-355.	9.1	290
84	Universal test and treat and the HIV epidemic in rural South Africa: a phase 4, open-label, community cluster randomised trial. Lancet HIV,the, 2018, 5, e116-e125.	4.7	187
85	Longitudinal Trends in the Prevalence of Detectable HIV Viremia: Population-Based Evidence From Rural KwaZulu-Natal, South Africa. Clinical Infectious Diseases, 2018, 66, 1254-1260.	5.8	12
86	High percentage of undiagnosed HIV cases within a hyperendemic South African community: a population-based study. Journal of Epidemiology and Community Health, 2018, 72, 168-172.	3.7	25
87	Community engagement with HIV drug adherence in rural South Africa: a transdisciplinary approach. Medical Humanities, 2018, 44, 239-246.	1.2	12
88	Combining Phylogenetic and Network Approaches to Identify HIV-1 Transmission Links in San Mateo County, California. Frontiers in Microbiology, 2018, 9, 2799.	3.5	9
89	Incidence rate estimation, periodic testing and the limitations of the mid-point imputation approach. International Journal of Epidemiology, 2018, 47, 236-245.	1.9	60
90	Dolutegravir for first-line antiretroviral therapy in low-income and middle-income countries: uncertainties and opportunities for implementation and research. Lancet HIV,the, 2018, 5, e400-e404.	4.7	75

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91	HTLV-1aA introduction into Brazil and its association with the trans-Atlantic slave trade. Infection, Genetics and Evolution, 2017, 48, 95-101.	2.3	9
92	Sensitive Next-Generation Sequencing Method Reveals Deep Genetic Diversity of HIV-1 in the Democratic Republic of the Congo. Journal of Virology, 2017, 91, .	3.4	39
93	Transmission networks and risk of HIV infection in KwaZulu-Natal, South Africa: a community-wide phylogenetic study. Lancet HIV,the, 2017, 4, e41-e50.	4.7	220
94	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. AIDS Research and Human Retroviruses, 2017, 33, 1083-1098.	1.1	18
95	Mutational Correlates of Virological Failure in Individuals Receiving a WHO-Recommended Tenofovir-Containing First-Line Regimen: An International Collaboration. EBioMedicine, 2017, 18, 225-235.	6.1	28
96	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. Lancet Infectious Diseases, The, 2017, 17, 296-304.	9.1	58
97	Spread of yellow fever virus outbreak in Angola and the Democratic Republic of the Congo 2015â€“16: a modelling study. Lancet Infectious Diseases, The, 2017, 17, 330-338.	9.1	185
98	Rates of virological suppression and drug resistance in adult HIV-1-positive patients attending primary healthcare facilities in KwaZulu-Natal, South Africa. Journal of Antimicrobial Chemotherapy, 2017, 72, 3141-3148.	3.0	23
99	Social Disequilibrium and the Risk of HIV Acquisition: A Multilevel Study in Rural KwaZulu-Natal Province, South Africa. Journal of Acquired Immune Deficiency Syndromes (1999), 2017, 75, 164-174.	2.1	19
100	Effect of population viral load on prospective HIV incidence in a hyperendemic rural African community. Science Translational Medicine, 2017, 9, .	12.4	60
101	Microbial genome-wide association studies: lessons from human GWAS. Nature Reviews Genetics, 2017, 18, 41-50.	16.3	239
102	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. Clinical Infectious Diseases, 2017, 64, 1092-1097.	5.8	11
103	Virological Outcomes of Second-line Protease Inhibitorâ€“Based Treatment for Human Immunodeficiency Virus Type 1 in a High-Prevalence Rural South African Setting: A Competing-Risks Prospective Cohort Analysis. Clinical Infectious Diseases, 2017, 64, 1006-1016.	5.8	37
104	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. PLoS Computational Biology, 2016, 12, e1004395.	3.2	12
105	Increasing HIV-1 Drug Resistance Between 2010 and 2012 in Adults Participating in Population-Based HIV Surveillance in Rural KwaZulu-Natal, South Africa. AIDS Research and Human Retroviruses, 2016, 32, 763-769.	1.1	32
106	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. Scientific Reports, 2016, 6, 39489.	3.3	23
107	Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. Infection, Genetics and Evolution, 2016, 46, 200-208.	2.3	23
108	Global epidemiology of drug resistance after failure of WHO recommended first-line regimens for adult HIV-1 infection: a multicentre retrospective cohort study. Lancet Infectious Diseases, The, 2016, 16, 565-575.	9.1	217

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109	Understanding Specific Contexts of Antiretroviral Therapy Adherence in Rural South Africa: A Thematic Analysis of Digital Stories from a Community with High HIV Prevalence. PLoS ONE, 2016, 11, e0148801.	2.5	17
110	Genome-Wide Association Study of HIV Whole Genome Sequences Validated using Drug Resistance. PLoS ONE, 2016, 11, e0163746.	2.5	20
111	PANGEA-HIV: phylogenetics for generalised epidemics in Africa. Lancet Infectious Diseases, The, 2015, 15, 259-261.	9.1	51
112	Phylogenetic Studies of Transmission Dynamics in Generalized HIV Epidemics. Journal of Acquired Immune Deficiency Syndromes (1999), 2014, 67, 181-195.	2.1	80
113	Detection of Transmission Clusters of HIV-1 Subtype C over a 21-Year Period in Cape Town, South Africa. PLoS ONE, 2014, 9, e109296.	2.5	9
114	Implementing HIV-1 genotypic resistance testing in antiretroviral therapy programs in Africa: needs, opportunities, and challenges. AIDS Reviews, 2013, 15, 221-9.	1.0	28
115	Persistent SARS-CoV-2 Infection with Accumulation of Mutations in a Patient with Poorly Controlled HIV Infection. SSRN Electronic Journal, 0, , .	0.4	12
116	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 0, , .	27.8	61
117	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization. Nature, 0, , .	27.8	104