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	Detection of a SARS-CoV-2 variant of concern in South Africa. Nature, 2021, 592, 438-443.	27.8	1,381
2	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 2022, 603, 679-686.	27.8	1,210
3	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
4	SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma. Nature Medicine, 2021, 27, 622-625.	30.7	984
5	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization. Nature, 2022, 602, 654-656.	27.8	928
6	The biological and clinical significance of emerging SARS-CoV-2 variants. Nature Reviews Genetics, 2021, 22, 757-773.	16.3	778
7	New SARS-CoV-2 Variants â€” Clinical, Public Health, and Vaccine Implications. New England Journal of Medicine, 2021, 384, 1866-1868.	27.0	581
8	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma. Nature, 2021, 593, 142-146.	27.8	574
9	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
10	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. Nature Medicine, 2022, 28, 1785-1790.	30.7	456
11	T cell responses to SARS-CoV-2 spike cross-recognize Omicron. Nature, 2022, 603, 488-492.	27.8	430
12	Sixteen novel lineages of SARS-CoV-2 in South Africa. Nature Medicine, 2021, 27, 440-446.	30.7	326
13	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
14	Genome Detective: an automated system for virus identification from high-throughput sequencing data. Bioinformatics, 2019, 35, 871-873.	4.1	254
15	Microbial genome-wide association studies: lessons from human GWAS. Nature Reviews Genetics, 2017, 18, 41-50.	16.3	239
16	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. Nature Microbiology, 2021, 6, 821-823.	13.3	221
17	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
18	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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19	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	5.6	200
20	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
21	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. Cell, 2021, 184, 5189-5200.e7.	28.9	186
22	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
23	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
24	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
25	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431.	12.6	144
26	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. Bioinformatics, 2020, 36, 3552-3555.	4.1	129
27	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
28	Omicron extensively but incompletely escapes Pfizer BNT162b2 neutralization. Nature, 0, , .	27.8	104
29	Declines in HIV incidence among men and women in a South African population-based cohort. Nature Communications, 2019, 10, 5482.	12.8	102
30	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
31	Phylogenetic Studies of Transmission Dynamics in Generalized HIV Epidemics. Journal of Acquired Immune Deficiency Syndromes (1999), 2014, 67, 181-195.	2.1	80
32	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
33	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
34	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
35	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
36	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

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37	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
38	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 0, , .	27.8	61
39	Effect of population viral load on prospective HIV incidence in a hyperendemic rural African community. Science Translational Medicine, 2017, 9, .	12.4	60
40	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
41	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
42	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
43	Reduced efficacy of HIV-1 integrase inhibitors in patients with drug resistance mutations in reverse transcriptase. Nature Communications, 2020, 11, 5922.	12.8	55
44	Current Affairs of Microbial Genome-Wide Association Studies: Approaches, Bottlenecks and Analytical Pitfalls. Frontiers in Microbiology, 2019, 10, 3119.	3.5	54
45	PANGEA-HIV: phylogenetics for generalised epidemics in Africa. Lancet Infectious Diseases, The, 2015, 15, 259-261.	9.1	51
46	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
47	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
48	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
49	Unlocking the efficiency of genomics laboratories with robotic liquid-handling. BMC Genomics, 2020, 21, 729.	2.8	50
50	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
51	An early warning system for emerging SARS-CoV-2 variants. Nature Medicine, 2022, 28, 1110-1115.	30.7	47
52	A genomics network established to respond rapidly to public health threats in South Africa. Lancet Microbe, The, 2020, 1, e229-e230.	7.3	46
53	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
54	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

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55	Reduced antibody cross-reactivity following infection with B.1.1.7 than with parental SARS-CoV-2 strains. ELife, 2021, 10, .	6.0	42
56	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
57	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
58	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. Cell Reports, 2020, 30, 2275-2283.e7.	6.4	37
59	The political theatre of the UK's travel ban on South Africa. Lancet, The, 2021, 398, 2211-2213.	13.7	37
60	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
61	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. Emerging Infectious Diseases, 2019, 25, 784-787.	4.3	36
62	Africa: tackle HIV and COVID-19 together. Nature, 2021, 600, 33-36.	27.8	35
63	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
64	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
65	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. PLoS ONE, 2019, 14, e0217871.	2.5	31
66	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
67	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. Nature Communications, 2021, 12, 2296.	12.8	29
68	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
69	HIV status alters disease severity and immune cell responses in Beta variant SARS-CoV-2 infection wave. ELife, 2021, 10, .	6.0	28
70	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
71	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. Nature Communications, 2022, 13, 1976.	12.8	27
72	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

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73	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. Scientific Reports, 2016, 6, 39489.	3.3	23
74	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
75	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
76	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
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	Multiple Early Introductions of SARS-CoV-2 to Cape Town, South Africa. Viruses, 2021, 13, 526.	3.3	20
79	Genome-Wide Association Study of HIV Whole Genome Sequences Validated using Drug Resistance. PLoS ONE, 2016, 11, e0163746.	2.5	20
80	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
81	Comparison of SARS-CoV-2 sequencing using the ONT GridION and the Illumina MiSeq. BMC Genomics, 2022, 23, 319.	2.8	19
82	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
83	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
84	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
85	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
86	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
87	Sociobehavioral and community predictors of unsuppressed HIV viral load. Aids, 2019, 33, 559-569.	2.2	14
88	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
89	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. Emerging Infectious Diseases, 2021, 27, 1393-1404.	4.3	13
90	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

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91	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. PLoS Computational Biology, 2016, 12, e1004395.	3.2	12
92	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
93	Community engagement with HIV drug adherence in rural South Africa: a transdisciplinary approach. Medical Humanities, 2018, 44, 239-246.	1.2	12
94	Persistent SARS-CoV-2 Infection with Accumulation of Mutations in a Patient with Poorly Controlled HIV Infection. SSRN Electronic Journal, 0, , .	0.4	12
95	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
96	Ethical issues associated with HIV molecular epidemiology: a qualitative exploratory study using inductive analytic approaches. BMC Medical Ethics, 2019, 20, 67.	2.4	11
97	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
98	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
99	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
100	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
101	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
102	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
103	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. Virus Evolution, 2020, 6, veaa004.	4.9	9
104	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
105	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
106	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
107	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
108	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

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109	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
110	Implementation of an efficient SARS-CoV-2 specimen pooling strategy for high throughput diagnostic testing. Scientific Reports, 2021, 11, 17793.	3.3	5
111	HIV-1 Evolutionary Dynamics under Nonsuppressive Antiretroviral Therapy. MBio, 2022, 13, e0026922.	4.1	5
112	Adding a Voice to the Unique Ethical Considerations in Molecular HIV Surveillance. American Journal of Bioethics, 2020, 20, 34-36.	0.9	4
113	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil. Microbiology Spectrum, 2022, 10, e0015522.	3.0	4
114	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
115	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
116	Infectious diseases science in Africa takes a leading place in the world. Lancet, The, 2022, , .	13.7	1
117	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