

# Tiago Graf

## List of Publications by Year in descending order

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Version: 2024-02-01

55  
papers

1,806  
citations

394286

19  
h-index

345118

36  
g-index

72  
all docs

72  
docs citations

72  
times ranked

3382  
citing authors

#	ARTICLE	IF	CITATIONS
1	Spread of Gamma (P.1) Sub-Lineages Carrying Spike Mutations Close to the Furin Cleavage Site and Deletions in the N-Terminal Domain Drives Ongoing Transmission of SARS-CoV-2 in Amazonas, Brazil. <i>Microbiology Spectrum</i> , 2022, 10, e0236621.	1.2	28
2	Dissemination Dynamics of HIV-1 Subtype B Pandemic and Non-pandemic Lineages Circulating in Amazonas, Brazil. <i>Frontiers in Microbiology</i> , 2022, 13, 835443.	1.5	0
3	Phylogenetic-based inference reveals distinct transmission dynamics of SARS-CoV-2 lineages Gamma and P.2 in Brazil. <i>IScience</i> , 2022, 25, 104156.	1.9	16
4	Unusual SARS-CoV-2 intrahost diversity reveals lineage superinfection. <i>Microbial Genomics</i> , 2022, 8, .	1.0	18
5	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
6	A Potential SARS-CoV-2 Variant of Interest (VOI) Harboring Mutation E484K in the Spike Protein Was Identified within Lineage B.1.1.33 Circulating in Brazil. <i>Viruses</i> , 2021, 13, 724.	1.5	38
7	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021, 12, 2296.	5.8	29
8	COVID-19 in Amazonas, Brazil, was driven by the persistence of endemic lineages and P.1 emergence. <i>Nature Medicine</i> , 2021, 27, 1230-1238.	15.2	279
9	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021, 27, 1393-1404.	2.0	13
10	Genomic Evidence of SARS-CoV-2 Reinfection Involving E484K Spike Mutation, Brazil. <i>Emerging Infectious Diseases</i> , 2021, 27, 1522-1524.	2.0	181
11	Dynamic Dispersion of HIV-1 Subtype C Toward Brazilian Northeastern Region. <i>AIDS Research and Human Retroviruses</i> , 2021, 37, 913-921.	0.5	1
12	Early detection of P.1 variant of SARS-CoV-2 in a cluster of cases in Salvador, Brazil. <i>International Journal of Infectious Diseases</i> , 2021, 108, 252-255.	1.5	17
13	HIV-1 molecular diversity in Brazil unveiled by 10 years of sampling by the national genotyping network. <i>Scientific Reports</i> , 2021, 11, 15842.	1.6	9
14	Transmission dynamics and molecular characterization of HIV-1 epidemic among therapeutic failure patients in Santa Catarina state, southern Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104854.	1.0	0
15	The ongoing evolution of variants of concern and interest of SARS-CoV-2 in Brazil revealed by convergent indels in the amino (N)-terminal domain of the spike protein. <i>Virus Evolution</i> , 2021, 7, veab069.	2.2	31
16	SARS-CoV-2 variant of concern P.1 (Gamma) infection in young and middle-aged patients admitted to the intensive care units of a single hospital in Salvador, Northeast Brazil, February 2021. <i>International Journal of Infectious Diseases</i> , 2021, 111, 47-54.	1.5	46
17	New Insights on the Zika Virus Arrival in the Americas and Spatiotemporal Reconstruction of the Epidemic Dynamics in Brazil. <i>Viruses</i> , 2021, 13, 12.	1.5	20
18	Re-emergence of Gamma-like-II and emergence of Gamma-S:E661D SARS-CoV-2 lineages in the south of Brazil after the 2021 outbreak. <i>Virology Journal</i> , 2021, 18, 222.	1.4	8

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19	Identification of a novel SARS-CoV-2 P.1 sub-lineage in Brazil provides new insights about the mechanisms of emergence of variants of concern. <i>Virus Evolution</i> , 2021, 7, veab091.	2.2	28
20	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.	3.0	11
21	Genotypic characterization and molecular evolution of avian reovirus in poultry flocks from Brazil. <i>Avian Pathology</i> , 2020, 49, 611-620.	0.8	10
22	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008405.	1.3	17
23	Multiple Introductions Followed by Ongoing Community Spread of SARS-CoV-2 at One of the Largest Metropolitan Areas of Northeast Brazil. <i>Viruses</i> , 2020, 12, 1414.	1.5	47
24	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	2.9	37
25	Evolutionary Dynamics and Dissemination Pattern of the SARS-CoV-2 Lineage B.1.1.33 During the Early Pandemic Phase in Brazil. <i>Frontiers in Microbiology</i> , 2020, 11, 615280.	1.5	62
26	Phylogenetics applied to the human immunodeficiency virus type 1 (HIV-1): from the cross-species transmissions to the contact network inferences. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e190461.	0.8	5
27	Tracking the onset date of the community spread of SARS-CoV-2 in western countries. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e200183.	0.8	18
28	Diversidade dos coronavírus, origem e evolução do SARS-CoV-2. , 2020, , .		0
29	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016–2019. <i>Journal of Virology</i> , 2019, 94, .	1.5	62
30	Identification of a novel alphavirus related to the encephalitis complexes circulating in southern Brazil. <i>Emerging Microbes and Infections</i> , 2019, 8, 920-933.	3.0	6
31	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019, 14, e0217871.	1.1	31
32	Phylogenetic analyses of Brazilian antigenic variants of infectious bursal disease virus. <i>Infection, Genetics and Evolution</i> , 2019, 73, 159-166.	1.0	9
33	Genetic clusters and transmission in transgender women. <i>Lancet HIV</i> , 2019, 6, e143-e144.	2.1	3
34	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.	0.5	21
35	Spatiotemporal and demographic history of the HIV-1 circulating recombinant form CRF31_BC in Brazil. <i>Infection, Genetics and Evolution</i> , 2018, 61, 113-118.	1.0	3
36	Phylogenetic analysis and molecular diversity of the avian infectious bronchitis virus of chickens in Brazil. <i>Infection, Genetics and Evolution</i> , 2018, 61, 77-83.	1.0	15

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37	Inferring population dynamics of HIV-1 subtype C epidemics in Eastern Africa and Southern Brazil applying different Bayesian phylodynamics approaches. <i>Scientific Reports</i> , 2018, 8, 8778.	1.6	11
38	Transmission networks and risk of HIV infection in KwaZulu-Natal, South Africa: a community-wide phylogenetic study. <i>Lancet HIV</i> , 2017, 4, e41-e50.	2.1	220
39	Spatiotemporal dynamics of influenza A(H1N1)pdm09 in Brazil during the pandemic and post-pandemic periods. <i>Virus Research</i> , 2017, 238, 69-74.	1.1	2
40	Molecular and phylogenetic analyses of <i>Salmonella Gallinarum</i> trace the origin and diversification of recent outbreaks of fowl typhoid in poultry farms. <i>Veterinary Microbiology</i> , 2017, 212, 80-86.	0.8	16
41	Comprehensive Characterization of HIV-1 Molecular Epidemiology and Demographic History in the Brazilian Region Most Heavily Affected by AIDS. <i>Journal of Virology</i> , 2016, 90, 8160-8168.	1.5	17
42	Phylogenetic analysis of canine distemper virus in South America clade 1 reveals unique molecular signatures of the local epidemic. <i>Infection, Genetics and Evolution</i> , 2016, 41, 135-141.	1.0	22
43	Draft Genome Sequence of a <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar <i>Gallinarum</i> bv. <i>Gallinarum</i> Isolate Associated with Fowl Typhoid Outbreaks in Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
44	Rapid and Slow Progressors Show Increased IL-6 and IL-10 Levels in the Pre-AIDS Stage of HIV Infection. <i>PLoS ONE</i> , 2016, 11, e0156163.	1.1	19
45	Short-Term Dynamic and Local Epidemiological Trends in the South American HIV-1B Epidemic. <i>PLoS ONE</i> , 2016, 11, e0156712.	1.1	19
46	HIV-1 epidemiology and circulating subtypes in the countryside of South Brazil. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2015, 48, 249-257.	0.4	10
47	Contribution of Epidemiological Predictors in Unraveling the Phylogeographic History of HIV-1 Subtype C in Brazil. <i>Journal of Virology</i> , 2015, 89, 12341-12348.	1.5	28
48	Analysis of Immunological, Viral, Genetic, and Environmental Factors That Might Be Associated with Decreased Susceptibility to HIV Infection in Serodiscordant Couples in Florianópolis, Southern Brazil. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 1116-1125.	0.5	6
49	The increasing prevalence of HIV-1 subtype C in Southern Brazil and its dispersion through the continent. <i>Virology</i> , 2013, 435, 170-178.	1.1	48
50	Detection of the B"-CWGR variant in the southernmost region of Brazil: unveiling the complexity of the human immunodeficiency virus-1 subtype B epidemic. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2013, 108, 735-740.	0.8	5
51	Temporal dynamics of HIV-1 circulating subtypes in distinct exposure categories in southern Brazil. <i>Virology Journal</i> , 2012, 9, 306.	1.4	17
52	Case report of a haemovigilance investigation using phylogenetic analysis of HIV-1 in Brazil. <i>Transfusion Medicine</i> , 2012, 22, 57-62.	0.5	4
53	Phylogeographic Analysis of HIV-1 Subtype C Dissemination in Southern Brazil. <i>PLoS ONE</i> , 2012, 7, e35649.	1.1	24
54	HIV-1 genetic diversity and drug resistance among treatment naïve patients from Southern Brazil: An association of HIV-1 subtypes with exposure categories. <i>Journal of Clinical Virology</i> , 2011, 51, 186-191.	1.6	35

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55	Spread of Metallo- $\beta$ -lactamases: screening reveals the presence of a BLA SPM-1 gene in hospital sewage in southern Brazil. Brazilian Journal of Microbiology, 2009, 40, 82-85.	0.8	13