

# Edson Delatorre

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

2,467  
citations

394421

19  
h-index

265206

42  
g-index

58  
all docs

58  
docs citations

58  
times ranked

5073  
citing authors

#	ARTICLE	IF	CITATIONS
1	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016, 352, 345-349.	12.6	877
2	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	27.8	323
3	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.	30.7	279
4	Phylodynamics of Yellow Fever Virus in the Americas: new insights into the origin of the 2017 Brazilian outbreak. <i>Scientific Reports</i> , 2017, 7, 7385.	3.3	71
5	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.	3.5	62
6	Distinct YFV Lineages Co-circulated in the Central-Western and Southeastern Brazilian Regions From 2015 to 2018. <i>Frontiers in Microbiology</i> , 2019, 10, 1079.	3.5	51
7	Genomic and phylogenetic characterisation of an imported case of SARS-CoV-2 in Amazonas State, Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e200310.	1.6	44
8	Combination of surveillance tools reveals that Yellow Fever virus can remain in the same Atlantic Forest area at least for three transmission seasons. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e190076.	1.6	38
9	Emergence of the East-Central-South-African genotype of Chikungunya virus in Brazil and the city of Rio de Janeiro may have occurred years before surveillance detection. <i>Scientific Reports</i> , 2019, 9, 2760.	3.3	38
10	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.	3.3	38
11	Phylodynamics of HIV-1 Subtype C Epidemic in East Africa. <i>PLoS ONE</i> , 2012, 7, e41904.	2.5	33
12	Reduction of inflammation and T cell activation after 6 months of cART initiation during acute, but not in early chronic HIV-1 infection. <i>Retrovirology</i> , 2018, 15, 76.	2.0	32
13	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.	4.9	31
14	Phylodynamics of the HIV-1 Epidemic in Cuba. <i>PLoS ONE</i> , 2013, 8, e72448.	2.5	29
15	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.	4.9	28
16	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.	3.0	28
17	Spatiotemporal Dynamics of the HIV-1 Subtype G Epidemic in West and Central Africa. <i>PLoS ONE</i> , 2014, 9, e98908.	2.5	24
18	Phylodynamics of the major HIV-1 CRF02_AG African lineages and its global dissemination. <i>Infection, Genetics and Evolution</i> , 2016, 46, 190-199.	2.3	24

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19	Tracing the origin of the NS1 A188V substitution responsible for recent enhancement of Zika virus Asian genotype infectivity. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2017, 112, 793-795.	1.6	24
20	Tracing the Origin and Northward Dissemination Dynamics of HIV-1 Subtype C in Brazil. <i>PLoS ONE</i> , 2013, 8, e74072.	2.5	23
21	Glycine Betaine Enhances Growth of Nitrogen-Fixing Bacteria <i>Gluconacetobacter diazotrophicus</i> PAL5 Under Saline Stress Conditions. <i>Current Microbiology</i> , 2009, 59, 593-599.	2.2	19
22	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.	1.6	18
23	Unusual SARS-CoV-2 intrahost diversity reveals lineage superinfection. <i>Microbial Genomics</i> , 2022, 8, .	2.0	18
24	Phylogenetic-based inference reveals distinct transmission dynamics of SARS-CoV-2 lineages Gamma and P.2 in Brazil. <i>IScience</i> , 2022, 25, 104156.	4.1	16
25	Evidence of Multiple Introductions and Autochthonous Transmission of the HIV Type 1 CRF02_AG Clade in Brazil. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1369-1372.	1.1	14
26	High HIV-1 Diversity and Prevalence of Transmitted Drug Resistance Among Antiretroviral-Naive HIV-Infected Pregnant Women from Rio de Janeiro, Brazil. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 68-73.	1.1	14
27	Spatiotemporal dynamics of the HIV-1 CRF06_cpx epidemic in western Africa. <i>Aids</i> , 2013, 27, 1313-1320.	2.2	13
28	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.	3.3	11
29	Reduction of HIV-1 Reservoir Size and Diversity After 1 Year of cART Among Brazilian Individuals Starting Treatment During Early Stages of Acute Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 145.	3.5	11
30	An observational clinical case of Zika virus-associated neurological disease is associated with primary IgG response and enhanced TNF levels. <i>Journal of General Virology</i> , 2018, 99, 913-916.	2.9	11
31	High HIV-1 Genetic Diversity in Patients from Northern Brazil. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 918-922.	1.1	9
32	HIV-1 Genetic Diversity in Northeastern Brazil: High Prevalence of Non-B Subtypes. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 639-647.	1.1	8
33	Investigating the Role of Easter Island in Migration of Zika Virus from South Pacific to Americas. <i>Emerging Infectious Diseases</i> , 2018, 24, 2119-2121.	4.3	8
34	Short Communication: Reassessing the Origin of the HIV-1 CRF02_AG Lineages Circulating in Brazil. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 1230-1237.	1.1	7
35	Time-scale of minor HIV-1 complex circulating recombinant forms from Central and West Africa. <i>BMC Evolutionary Biology</i> , 2016, 16, 249.	3.2	7
36	HIV controllers suppress viral replication and evolution and prevent disease progression following intersubtype HIV-1 superinfection. <i>Aids</i> , 2019, 33, 399-410.	2.2	6

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37	Origin and Population Dynamics of a Novel HIV-1 Subtype G Clade Circulating in Cape Verde and Portugal. PLoS ONE, 2015, 10, e0127384.	2.5	5
38	Phylogenetics applied to the human immunodeficiency virus type 1 (HIV-1): from the cross-species transmissions to the contact network inferences. Memorias Do Instituto Oswaldo Cruz, 2020, 115, e190461.	1.6	5
39	Tracing the origin of a singular HIV-1 CRF45_cpx clade identified in Brazil. Infection, Genetics and Evolution, 2016, 46, 223-232.	2.3	3
40	Increased expression of CDKN1A/p21 in HIV-1 controllers is correlated with upregulation of ZC3H12A/MCPIP1. Retrovirology, 2020, 17, 18.	2.0	3
41	Few amino acid signatures distinguish HIV-1 subtype B pandemic and non-pandemic strains. PLoS ONE, 2020, 15, e0238995.	2.5	2
42	Proviral Quasispecies Diversity Is Not Associated With Virologic Breakthrough or CD4+ T Cell Loss in HIV-1 Elite Controllers. Frontiers in Microbiology, 2019, 10, 673.	3.5	1
43	Increasing prevalence and local transmission of non-B HIV-1 subtypes in the French Antilles and French Guiana between 1995 and 2018. Virus Evolution, 2020, 6, veaa081.	4.9	0