

Paolo Marinho de Andrade Zanotto

List of Publications by Year in descending order

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114
papers

6,664
citations

117453

34
h-index

66788

78
g-index

117
all docs

117
docs citations

117
times ranked

8777
citing authors

#	ARTICLE	IF	CITATIONS
1	The Brazilian Zika virus strain causes birth defects in experimental models. <i>Nature</i> , 2016, 534, 267-271.	13.7	1,132
2	Molecular Evolution of Zika Virus during Its Emergence in the 20th Century. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2636.	1.3	659
3	Protective efficacy of multiple vaccine platforms against Zika virus challenge in rhesus monkeys. <i>Science</i> , 2016, 353, 1129-1132.	6.0	461
4	Vaccine protection against Zika virus from Brazil. <i>Nature</i> , 2016, 536, 474-478.	13.7	460
5	Population dynamics of flaviviruses revealed by molecular phylogenies.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 548-553.	3.3	300
6	Phylogenetic Interrelationships among Baculoviruses: Evolutionary Rates and Host Associations. <i>Journal of Invertebrate Pathology</i> , 1993, 62, 147-164.	1.5	249
7	Origins, evolution, and vector-host coadaptations within the Genus <i>Flavivirus</i> . <i>Advances in Virus Research</i> , 2003, 59, 277-314.	0.9	163
8	Identification and Preliminary Characterization of a Chitinase Gene in the <i>Autographa californica</i> Nuclear Polyhedrosis Virus Genome. <i>Virology</i> , 1995, 212, 673-685.	1.1	130
9	Complete sequence of two tick-borne flaviviruses isolated from Siberia and the UK: analysis and significance of the 5' and 3'-UTRs. <i>Virus Research</i> , 1997, 49, 27-39.	1.1	124
10	Positive Selection Results in Frequent Reversible Amino Acid Replacements in the G Protein Gene of Human Respiratory Syncytial Virus. <i>PLoS Pathogens</i> , 2009, 5, e1000254.	2.1	121
11	High Rates of Molecular Evolution in Hantaviruses. <i>Molecular Biology and Evolution</i> , 2008, 25, 1488-1492.	3.5	117
12	Genealogical Evidence for Positive Selection in the <i>nef</i> Gene of HIV-1. <i>Genetics</i> , 1999, 153, 1077-1089.	1.2	113
13	Sequence Analysis of the Genome of the Neodiprion sertifer Nucleopolyhedrovirus. <i>Journal of Virology</i> , 2004, 78, 7036-7051.	1.5	104
14	Evolution of Base Composition and Codon Usage Bias in the Genus <i>Flavivirus</i> . <i>Journal of Molecular Evolution</i> , 2001, 52, 383-390.	0.8	99
15	Evolution, epidemiology, and dispersal of flaviviruses revealed by molecular phylogenies. <i>Advances in Virus Research</i> , 2001, 57, 71-103.	0.9	89
16	Biological and phylogenetic characteristics of West African lineages of West Nile virus. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006078.	1.3	83
17	Genome of the most widely used viral biopesticide: <i>Anticarsia gemmatalis</i> multiple nucleopolyhedrovirus. <i>Journal of General Virology</i> , 2006, 87, 3233-3250.	1.3	76
18	Phylogeography and evolutionary history of dengue virus type 3. <i>Infection, Genetics and Evolution</i> , 2009, 9, 716-725.	1.0	70

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19	Hantavirus Pulmonary Syndrome, Central Plateau, Southeastern, and Southern Brazil. <i>Emerging Infectious Diseases</i> , 2009, 15, 561-567.	2.0	69
20	Worldwide Spread of Dengue Virus Type 1. <i>PLoS ONE</i> , 2013, 8, e62649.	1.1	69
21	Zika Virus Impairs Neurogenesis and Synaptogenesis Pathways in Human Neural Stem Cells and Neurons. <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 64.	1.8	65
22	First report of naturally infected <i>Aedes aegypti</i> with chikungunya virus genotype ECSA in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005630.	1.3	59
23	Spatio-Temporal Tracking and Phylodynamics of an Urban Dengue 3 Outbreak in São Paulo, Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e448.	1.3	56
24	Characterisation of Zika virus infection in primary human astrocytes. <i>BMC Neuroscience</i> , 2018, 19, 5.	0.8	55
25	The Challenges Imposed by Dengue, Zika, and Chikungunya to Brazil. <i>Frontiers in Immunology</i> , 2018, 9, 1964.	2.2	52
26	Modeling neuro-immune interactions during Zika virus infection. <i>Human Molecular Genetics</i> , 2018, 27, 41-52.	1.4	50
27	Social Networks Shape the Transmission Dynamics of Hepatitis C Virus. <i>PLoS ONE</i> , 2010, 5, e11170.	1.1	48
28	Analysis of the genome of <i>Spodoptera frugiperda</i> nucleopolyhedrovirus (SfMNPV-19) and of the high genomic heterogeneity in group II nucleopolyhedroviruses. <i>Journal of General Virology</i> , 2008, 89, 1202-1211.	1.3	46
29	Origin of the São Paulo Yellow Fever epidemic of 2017–2018 revealed through molecular epidemiological analysis of fatal cases. <i>Scientific Reports</i> , 2019, 9, 20418.	1.6	46
30	Molecular characterization of human erythrovirus B19 strains obtained from patients with several clinical presentations in the Amazon region of Brazil. <i>Journal of Clinical Virology</i> , 2008, 43, 60-65.	1.6	45
31	Phylogenesis of prion protein. <i>Nature</i> , 1996, 380, 675-675.	13.7	43
32	Detection Of Four Dengue Serotypes Suggests Rise In Hyperendemicity In Urban Centers Of Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2620.	1.3	42
33	Laboratory strains of <i>Aedes aegypti</i> are competent to Brazilian Zika virus. <i>PLoS ONE</i> , 2017, 12, e0171951.	1.1	42
34	Ultrasound-guided minimally invasive autopsy as a tool for rapid post-mortem diagnosis in the 2018 Sao Paulo yellow fever epidemic: Correlation with conventional autopsy. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007625.	1.3	37
35	Usutu Virus Isolated from Rodents in Senegal. <i>Viruses</i> , 2019, 11, 181.	1.5	37
36	Evolutionary history of Dengue virus type 4: Insights into genotype phylodynamics. <i>Infection, Genetics and Evolution</i> , 2011, 11, 878-885.	1.0	35

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37	First Identification of <i>Culex flavivirus</i> (Flaviviridae) in Brazil. <i>Intervirology</i> , 2012, 55, 475-483.	1.2	35
38	Molecular phylogeography of tick-borne encephalitis virus in central Europe. <i>Journal of General Virology</i> , 2013, 94, 2129-2139.	1.3	35
39	Reemergence of Rift Valley Fever, Mauritania, 2010. <i>Emerging Infectious Diseases</i> , 2014, 20, 300-303.	2.0	35
40	Introduction of Dengue Virus 4 (DENV-4) Genotype I into Brazil from Asia?. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e390.	1.3	34
41	Genomic comparison of <i>Neodiprion sertifer</i> and <i>Neodiprion lecontei</i> nucleopolyhedroviruses and identification of potential hymenopteran baculovirus-specific open reading frames. <i>Journal of General Virology</i> , 2006, 87, 1477-1489.	1.3	33
42	Systems analysis of subjects acutely infected with the Chikungunya virus. <i>PLoS Pathogens</i> , 2019, 15, e1007880.	2.1	33
43	GenSeed-HMM: A Tool for Progressive Assembly Using Profile HMMs as Seeds and its Application in <i>Alpavirinae</i> Viral Discovery from Metagenomic Data. <i>Frontiers in Microbiology</i> , 2016, 7, 269.	1.5	30
44	Persistence and Intra-Host Genetic Evolution of Zika Virus Infection in Symptomatic Adults: A Special View in the Male Reproductive System. <i>Viruses</i> , 2018, 10, 615.	1.5	30
45	Origin of 1997-1998 Rift Valley fever outbreak in East Africa. <i>Lancet, The</i> , 1998, 352, 1596-1597.	6.3	29
46	Identification, sequence analysis and phylogeny of the <i>lef-2</i> gene of <i>Helicoverpa armigera</i> single-nucleocapsid baculovirus. <i>Virus Research</i> , 1999, 65, 21-32.	1.1	29
47	Relation of genetic phylogeny and geographical distance of tick-borne encephalitis virus in central Europe. <i>Journal of General Virology</i> , 2011, 92, 1906-1916.	1.3	29
48	Yellow fever and orthotopic liver transplantation: new insights from the autopsy room for an old but re-emerging disease. <i>Histopathology</i> , 2019, 75, 638-648.	1.6	29
49	Distinct patterns of natural selection in the reverse transcriptase gene of HIV-1 in the presence and absence of antiretroviral therapy. <i>Virology</i> , 2004, 325, 181-191.	1.1	27
50	Phylogeography of Rift Valley Fever Virus in Africa Reveals Multiple Introductions in Senegal and Mauritania. <i>PLoS ONE</i> , 2012, 7, e35216.	1.1	27
51	Searching for antigen B genes and their adaptive sites in distinct strains and species of the helminth <i>Echinococcus</i> . <i>Infection, Genetics and Evolution</i> , 2006, 6, 251-261.	1.0	26
52	Prion's Progress: Patterns and Rates of Molecular Evolution in Relation to Spongiform Disease. <i>Journal of Molecular Evolution</i> , 1998, 47, 133-145.	0.8	25
53	Production of a Recombinant Dengue Virus 2 NS5 Protein and Potential Use as a Vaccine Antigen. <i>Vaccine Journal</i> , 2016, 23, 460-469.	3.2	25
54	The Pangenome of the <i>Anticarsia gemmatalis</i> Multiple Nucleopolyhedrovirus (AgMNPV). <i>Genome Biology and Evolution</i> , 2016, 8, 94-108.	1.1	25

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55	Outbreak of chikungunya virus in a vulnerable population of Sergipe, Brazil—A molecular and serological survey. <i>Journal of Clinical Virology</i> , 2017, 97, 44-49.	1.6	25
56	Tempo and mode of ERV-K evolution in human and chimpanzee genomes. <i>Archives of Virology</i> , 2006, 151, 2215-2228.	0.9	24
57	Origin and Spread of the Dengue Virus Type 1, Genotype V in Senegal, 2015–2019. <i>Viruses</i> , 2021, 13, 57.	1.5	24
58	Phylogeographic Analysis of HIV-1 Subtype C Dissemination in Southern Brazil. <i>PLoS ONE</i> , 2012, 7, e35649.	1.1	24
59	Tracing the Origin and Northward Dissemination Dynamics of HIV-1 Subtype C in Brazil. <i>PLoS ONE</i> , 2013, 8, e74072.	1.1	23
60	Physical maps and virulence of <i>Anticarsia gemmatalis</i> nucleopolyhedrovirus genomic variants. <i>Archives of Virology</i> , 1999, 144, 1991-2006.	0.9	22
61	Viral diseases and human evolution. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2000, 95, 193-200.	0.8	21
62	Rapid Molecular Detection of Zika Virus in Acute-Phase Urine Samples Using the Recombinase Polymerase Amplification Assay. <i>PLOS Currents</i> , 2017, 9, .	1.4	20
63	Phylodynamics and movement of Phycodnaviruses among aquatic environments. <i>ISME Journal</i> , 2012, 6, 237-247.	4.4	19
64	Proteomic analyses of baculovirus <i>Anticarsia gemmatalis</i> multiple nucleopolyhedrovirus budded and occluded virus. <i>Journal of General Virology</i> , 2014, 95, 980-989.	1.3	19
65	The complete sequence of four major structural proteins of African horse sickness virus serotype 6: evolutionary relationships within and between the orbiviruses. <i>Virus Research</i> , 1998, 53, 53-73.	1.1	18
66	High Prevalence of GB Virus C in Brazil and Molecular Evidence for Intrafamilial Transmission. <i>Journal of Clinical Microbiology</i> , 1999, 37, 1634-1637.	1.8	18
67	Phylodynamics and Dispersal of HRSV Entails Its Permanence in the General Population in between Yearly Outbreaks in Children. <i>PLoS ONE</i> , 2012, 7, e41953.	1.1	18
68	Genetic diversity of environmental <i>Aspergillus flavus</i> strains in the state of São Paulo, Brazil by random amplified polymorphic DNA. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2007, 102, 687-692.	0.8	18
69	Sequence analysis of a 5.1 kbp region of the <i>Spodoptera frugiperda</i> multicapsid nucleopolyhedrovirus genome that comprises a functional ecdysteroid UDP-glucosyltransferase (egt) gene. <i>Virus Genes</i> , 2003, 27, 137-144.	0.7	17
70	Complete Genome Viral Phylogenies Suggests the Concerted Evolution of Regulatory Cores and Accessory Satellites. <i>PLoS ONE</i> , 2008, 3, e3500.	1.1	15
71	One-step protocol for amplification of near full-length cDNA of the rabies virus genome. <i>Journal of Virological Methods</i> , 2011, 174, 1-6.	1.0	15
72	Association of Malaria Infection During Pregnancy With Head Circumference of Newborns in the Brazilian Amazon. <i>JAMA Network Open</i> , 2019, 2, e193300.	2.8	15

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73	Demographic Histories of ERV-K in Humans, Chimpanzees and Rhesus Monkeys. PLoS ONE, 2007, 2, e1026.	1.1	15
74	Dengue Virus Type 3 Adaptive Changes during Epidemics in São Jose de Rio Preto, Brazil, 2006–2007. PLoS ONE, 2013, 8, e63496.	1.1	14
75	Molecular Epidemiology and Emergence of Rift Valley Fever. Memórias Do Instituto Oswaldo Cruz, 1998, 93, 609-614.	0.8	14
76	Construction of a recombinant Anticarsia gemmatalis nucleopolyhedrovirus (AgMNPV-2D) harbouring the β -galactosidase gene. Archives of Virology, 2001, 146, 1355-1367.	0.9	13
77	Epidemiological dynamics of an urban Dengue 4 outbreak in São Paulo, Brazil. PeerJ, 2016, 4, e1892.	0.9	13
78	Identification and characterization of a baculovirus from Lonomia obliqua (Lepidoptera: Saturniidae). Journal of Invertebrate Pathology, 2002, 79, 137-145.	1.5	12
79	The α -pressure pan-evolution of human erythrovirus B19 in the Amazon, Brazil. Virology, 2007, 369, 281-287.	1.1	12
80	Modularity and evolutionary constraints in a baculovirus gene regulatory network. BMC Systems Biology, 2013, 7, 87.	3.0	12
81	Origin, tempo, and mode of the spread of DENV-4 Genotype IIB across the state of São Paulo, Brazil during the 2012-2013 outbreak. Memórias Do Instituto Oswaldo Cruz, 2019, 114, e180251.	0.8	12
82	Expression and diversity of Echinococcus multilocularis AgB genes in secondarily infected mice: evaluating the influence of T-cell immune selection on antigenic variation. Gene, 2007, 392, 98-105.	1.0	11
83	NS1 codon usage adaptation to humans in pandemic Zika virus. Memórias Do Instituto Oswaldo Cruz, 2018, 113, e170385.	0.8	11
84	An Outbreak of Human Parvovirus B19 Hidden by Dengue Fever. Clinical Infectious Diseases, 2019, 68, 810-817.	2.9	11
85	Field Deployment of a Mobile Biosafety Laboratory Reveals the Co-Circulation of Dengue Viruses Serotype 1 and Serotype 2 in Louga City, Senegal, 2017. Journal of Tropical Medicine, 2021, 2021, 1-10.	0.6	11
86	Does adaptation to vertebrate codon usage relate to flavivirus emergence potential?. PLoS ONE, 2018, 13, e0191652.	1.1	11
87	Bayesian Coalescent Analysis Reveals a High Rate of Molecular Evolution in GB Virus C. Journal of Molecular Evolution, 2008, 66, 292-297.	0.8	10
88	A deep phylogeny of viral and cellular right-hand polymerases. Infection, Genetics and Evolution, 2015, 36, 275-286.	1.0	10
89	A betabaculovirus encoding a gp64 homolog. BMC Genomics, 2016, 17, 94.	1.2	8
90	Systemic dengue infection associated with a new dengue virus type 2 introduction in Brazil – a case report. BMC Infectious Diseases, 2021, 21, 311.	1.3	8

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91	Genetic Drift of Human Immunodeficiency Virus Type 1?. <i>Journal of Virology</i> , 1998, 72, 886-887.	1.5	7
92	Genomic mosaicism in two strains of dengue virus type 3. <i>Infection, Genetics and Evolution</i> , 2013, 18, 202-212.	1.0	6
93	A Metagenomic Approach Identified a Novel Phasi Charoen-Like Virus Coinfecting a Chikungunya Virus-Infected <i>Aedes aegypti</i> Mosquito in Brazil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
94	Lack of Evidence for Cospeciation Between Retroelements and Their Hosts. <i>Journal of Molecular Evolution</i> , 2000, 50, 194-201.	0.8	5
95	Identification, Expression and Phylogenetic Analysis of the <i>Anticarsia gemmatalis</i> multicapsid nucleopolyhedrovirus (AgMNPV) Helicase. <i>Virus Genes</i> , 2004, 29, 345-352.	0.7	5
96	BF Integrase Genes of HIV-1 Circulating in São Paulo, Brazil, with a Recurrent Recombination Region. <i>PLoS ONE</i> , 2012, 7, e34324.	1.1	5
97	Nano-multilamellar lipid vesicles loaded with a recombinant form of the chikungunya virus E2 protein improve the induction of virus-neutralizing antibodies. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2021, 37, 102445.	1.7	5
98	Molecular Epidemiology, Evolution and Dispersal of the Genus <i>Flavivirus</i> . , 2002, , 167-195.		5
99	Characterization of Primary Isolates of HIV Type 1 CRF28_BF, CRF29_BF, and Unique BF Recombinants Circulating in São Paulo, Brazil. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1082-1088.	0.5	4
100	Codon adaptation biases among sylvatic and urban genotypes of Dengue virus type 2. <i>Infection, Genetics and Evolution</i> , 2018, 64, 207-211.	1.0	4
101	A tick homologue of the human DNA helicase II 70-kDa subunit. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1996, 1305, 120-124.	2.4	3
102	Boosting Virology in Brazil. <i>PLoS Biology</i> , 2008, 6, e57.	2.6	3
103	Variability of the conserved V3 loop tip motif in HIV-1 subtype B isolates collected from Brazilian and French patients. <i>Brazilian Journal of Microbiology</i> , 2010, 41, 720-728.	0.8	3
104	Comparison between ectodomain and G2 region of G glycoprotein for genotyping of HRSV. <i>Brazilian Journal of Microbiology</i> , 2007, 38, 413-416.	0.8	3
105	Structural and phylogenetic relationship of ORF 31 from the <i>Anticarsia gemmatalis</i> MNPV to poly (ADP-ribose) polymerases (PARP). <i>Virus Genes</i> , 2008, 37, 177-184.	0.7	2
106	Biological Characteristics and Patterns of Codon Usage Evolution for the African Genotype Zika Virus. <i>Viruses</i> , 2020, 12, 1306.	1.5	2
107	The impact of Zika virus exposure on the placental proteomic profile. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2022, 1868, 166270.	1.8	2
108	Viral Individuality and Limitations of the Life Concept. , 2008, , 513-536.		2

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109	First Genome Sequences of Dengue Virus Strains Isolated during the First DENV-4 Outbreak in São Paulo, Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
110	Complete Genome Sequences of Two Human Parainfluenza Virus Type 3 Isolates Collected in Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
111	Complete Genome Sequence of a Human Metapneumovirus Isolate Collected in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
112	Influence of the HIV GWG variant in the HIV infection progression in mono and HCV coinfecting patients. <i>Medicine (United States)</i> , 2019, 98, e16376.	0.4	1
113	Complete Genome Sequences of Five Human Respiratory Syncytial Virus Isolates Collected in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
114	Where there is no overlap, there is a gap. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2014, 47, 675-676.	0.4	0