

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 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
2	Origin and Spread of the Dengue Virus Type 1, Genotype V in Senegal, 2015â€“2019. <i>Viruses</i> , 2021, 13, 57.	1.5	24
3	Field Deployment of a Mobile Biosafety Laboratory Reveals the Co-Circulation of Dengue Viruses Serotype 1 and Serotype 2 in Louga City, Senegal, 2017. <i>Journal of Tropical Medicine</i> , 2021, 2021, 1-10.	0.6	11
4	Systemic dengue infection associated with a new dengue virus type 2 introduction in Brazil â€“ a case report. <i>BMC Infectious Diseases</i> , 2021, 21, 311.	1.3	8
5	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
6	Biological Characteristics and Patterns of Codon Usage Evolution for the African Genotype Zika Virus. <i>Viruses</i> , 2020, 12, 1306.	1.5	2
7	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
8	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
9	Systems analysis of subjects acutely infected with the Chikungunya virus. <i>PLoS Pathogens</i> , 2019, 15, e1007880.	2.1	33
10	Yellow fever and orthotopic liver transplantation: new insights from the autopsy room for an old but reâ€emerging disease. <i>Histopathology</i> , 2019, 75, 638-648.	1.6	29
11	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
12	Origin, tempo, and mode of the spread of DENV-4 Genotype IIB across the state of SÃ£o Paulo, Brazil during the 2012-2013 outbreak. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e180251.	0.8	12
13	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
14	Usutu Virus Isolated from Rodents in Senegal. <i>Viruses</i> , 2019, 11, 181.	1.5	37
15	Origin of the SÃ£o Paulo Yellow Fever epidemic of 2017â€“2018 revealed through molecular epidemiological analysis of fatal cases. <i>Scientific Reports</i> , 2019, 9, 20418.	1.6	46
16	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
17	An Outbreak of Human Parvovirus B19 Hidden by Dengue Fever. <i>Clinical Infectious Diseases</i> , 2019, 68, 810-817.	2.9	11
18	Complete Genome Sequences of Five Human Respiratory Syncytial Virus Isolates Collected in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	0

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19	Complete Genome Sequence of a Human Metapneumovirus Isolate Collected in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
20	Characterisation of Zika virus infection in primary human astrocytes. <i>BMC Neuroscience</i> , 2018, 19, 5.	0.8	55
21	Modeling neuro-immune interactions during Zika virus infection. <i>Human Molecular Genetics</i> , 2018, 27, 41-52.	1.4	50
22	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
23	The Challenges Imposed by Dengue, Zika, and Chikungunya to Brazil. <i>Frontiers in Immunology</i> , 2018, 9, 1964.	2.2	52
24	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
25	NS1 codon usage adaptation to humans in pandemic Zika virus. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, e170385.	0.8	11
26	Does adaptation to vertebrate codon usage relate to flavivirus emergence potential?. <i>PLoS ONE</i> , 2018, 13, e0191652.	1.1	11
27	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
28	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
29	Complete Genome Sequences of Two Human Parainfluenza Virus Type 3 Isolates Collected in Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
30	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
31	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
32	Biological and phylogenetic characteristics of West African lineages of West Nile virus. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006078.	1.3	83
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	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
35	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
36	The Brazilian Zika virus strain causes birth defects in experimental models. <i>Nature</i> , 2016, 534, 267-271.	13.7	1,132

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37	Protective efficacy of multiple vaccine platforms against Zika virus challenge in rhesus monkeys. <i>Science</i> , 2016, 353, 1129-1132.	6.0	461
38	A betabaculovirus encoding a gp64 homolog. <i>BMC Genomics</i> , 2016, 17, 94.	1.2	8
39	The Pangenome of the <i>Anticarsia gemmatalis</i> Multiple Nucleopolyhedrovirus (AgMNPV). <i>Genome Biology and Evolution</i> , 2016, 8, 94-108.	1.1	25
40	Vaccine protection against Zika virus from Brazil. <i>Nature</i> , 2016, 536, 474-478.	13.7	460
41	Epidemiological dynamics of an urban Dengue 4 outbreak in São Paulo, Brazil. <i>PeerJ</i> , 2016, 4, e1892.	0.9	13
42	A deep phylogeny of viral and cellular right-hand polymerases. <i>Infection, Genetics and Evolution</i> , 2015, 36, 275-286.	1.0	10
43	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
44	Reemergence of Rift Valley Fever, Mauritania, 2010. <i>Emerging Infectious Diseases</i> , 2014, 20, 300-303.	2.0	35
45	Molecular Evolution of Zika Virus during Its Emergence in the 20th Century. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2636.	1.3	659
46	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
47	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
48	Genomic mosaicism in two strains of dengue virus type 3. <i>Infection, Genetics and Evolution</i> , 2013, 18, 202-212.	1.0	6
49	Molecular phylogeography of tick-borne encephalitis virus in central Europe. <i>Journal of General Virology</i> , 2013, 94, 2129-2139.	1.3	35
50	Modularity and evolutionary constraints in a baculovirus gene regulatory network. <i>BMC Systems Biology</i> , 2013, 7, 87.	3.0	12
51	Dengue Virus Type 3 Adaptive Changes during Epidemics in São Jose de Rio Preto, Brazil, 2006-2007. <i>PLoS ONE</i> , 2013, 8, e63496.	1.1	14
52	Tracing the Origin and Northward Dissemination Dynamics of HIV-1 Subtype C in Brazil. <i>PLoS ONE</i> , 2013, 8, e74072.	1.1	23
53	Worldwide Spread of Dengue Virus Type 1. <i>PLoS ONE</i> , 2013, 8, e62649.	1.1	69
54	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

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55	Phylodynamics and movement of Phycodnaviruses among aquatic environments. <i>ISME Journal</i> , 2012, 6, 237-247.	4.4	19
56	First Identification of <i>Culex flavivirus</i> (Flaviviridae) in Brazil. <i>Intervirology</i> , 2012, 55, 475-483.	1.2	35
57	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
58	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
59	Phylogeographic Analysis of HIV-1 Subtype C Dissemination in Southern Brazil. <i>PLoS ONE</i> , 2012, 7, e35649.	1.1	24
60	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
61	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
62	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
63	Evolutionary history of Dengue virus type 4: Insights into genotype phylodynamics. <i>Infection, Genetics and Evolution</i> , 2011, 11, 878-885.	1.0	35
64	Social Networks Shape the Transmission Dynamics of Hepatitis C Virus. <i>PLoS ONE</i> , 2010, 5, e11170.	1.1	48
65	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
66	Hantavirus Pulmonary Syndrome, Central Plateau, Southeastern, and Southern Brazil. <i>Emerging Infectious Diseases</i> , 2009, 15, 561-567.	2.0	69
67	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
68	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
69	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
70	Phylogeography and evolutionary history of dengue virus type 3. <i>Infection, Genetics and Evolution</i> , 2009, 9, 716-725.	1.0	70
71	Structural and phylogenetic relationship of ORF 31 from the <i>Anticarsia gemmatilis</i> MNPV to poly (ADP-ribose) polymerases (PARP). <i>Virus Genes</i> , 2008, 37, 177-184.	0.7	2
72	Bayesian Coalescent Analysis Reveals a High Rate of Molecular Evolution in GB Virus C. <i>Journal of Molecular Evolution</i> , 2008, 66, 292-297.	0.8	10

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73	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
74	Boosting Virology in Brazil. <i>PLoS Biology</i> , 2008, 6, e57.	2.6	3
75	High Rates of Molecular Evolution in Hantaviruses. <i>Molecular Biology and Evolution</i> , 2008, 25, 1488-1492.	3.5	117
76	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
77	Complete Genome Viral Phylogenies Suggests the Concerted Evolution of Regulatory Cores and Accessory Satellites. <i>PLoS ONE</i> , 2008, 3, e3500.	1.1	15
78	Viral Individuality and Limitations of the Life Concept. , 2008, , 513-536.		2
79	Expression and diversity of <i>Echinococcus multilocularis</i> AgB genes in secondarily infected mice: evaluating the influence of T-cell immune selection on antigenic variation. <i>Gene</i> , 2007, 392, 98-105.	1.0	11
80	The "pressure pan" evolution of human erythrovirus B19 in the Amazon, Brazil. <i>Virology</i> , 2007, 369, 281-287.	1.1	12
81	Demographic Histories of ERV-K in Humans, Chimpanzees and Rhesus Monkeys. <i>PLoS ONE</i> , 2007, 2, e1026.	1.1	15
82	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
83	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
84	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
85	Tempo and mode of ERV-K evolution in human and chimpanzee genomes. <i>Archives of Virology</i> , 2006, 151, 2215-2228.	0.9	24
86	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
87	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
88	Sequence Analysis of the Genome of the <i>Neodiprion sertifer</i> Nucleopolyhedrovirus. <i>Journal of Virology</i> , 2004, 78, 7036-7051.	1.5	104
89	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
90	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

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91	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
92	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
93	Identification and characterization of a baculovirus from <i>Lonomia obliqua</i> (Lepidoptera: Saturniidae). <i>Journal of Invertebrate Pathology</i> , 2002, 79, 137-145.	1.5	12
94	Molecular Epidemiology, Evolution and Dispersal of the Genus <i>Flavivirus</i> . , 2002, , 167-195.		5
95	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
96	Construction of a recombinant <i>Anticarsia gemmatalis</i> nucleopolyhedrovirus (AgMNPV-2D) harbouring the β -galactosidase gene. <i>Archives of Virology</i> , 2001, 146, 1355-1367.	0.9	13
97	Evolution, epidemiology, and dispersal of flaviviruses revealed by molecular phylogenies. <i>Advances in Virus Research</i> , 2001, 57, 71-103.	0.9	89
98	Lack of Evidence for Cospeciation Between Retroelements and Their Hosts. <i>Journal of Molecular Evolution</i> , 2000, 50, 194-201.	0.8	5
99	Viral diseases and human evolution. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2000, 95, 193-200.	0.8	21
100	Physical maps and virulence of <i>Anticarsia gemmatalis</i> nucleopolyhedrovirus genomic variants. <i>Archives of Virology</i> , 1999, 144, 1991-2006.	0.9	22
101	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
102	Genealogical Evidence for Positive Selection in the <i>nef</i> Gene of HIV-1. <i>Genetics</i> , 1999, 153, 1077-1089.	1.2	113
103	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
104	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
105	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
106	Origin of 1997-98 Rift Valley fever outbreak in East Africa. <i>Lancet</i> , The, 1998, 352, 1596-1597.	6.3	29
107	Genetic Drift of Human Immunodeficiency Virus Type 1?. <i>Journal of Virology</i> , 1998, 72, 886-887.	1.5	7
108	Molecular Epidemiology and Emergence of Rift Valley Fever. <i>Memorias Do Instituto Oswaldo Cruz</i> , 1998, 93, 609-614.	0.8	14

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109	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
110	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
111	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
112	Phylogenesis of prion protein. <i>Nature</i> , 1996, 380, 675-675.	13.7	43
113	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
114	Phylogenetic Interrelationships among Baculoviruses: Evolutionary Rates and Host Associations. <i>Journal of Invertebrate Pathology</i> , 1993, 62, 147-164.	1.5	249