Paolo Marinho de Andrade Zanotto

List of Publications by Year
in descending order

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114 papers	6,664 citations	117625 34 h-index	66911 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. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2022, 1868, 166270.	3.8	2
2	Origin and Spread of the Dengue Virus Type 1, Genotype V in Senegal, 2015â€“2019. Viruses, 2021, 13, 57.	3.3	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. Journal of Tropical Medicine, 2021, 2021, 1-10.	1.7	11
4	Systemic dengue infection associated with a new dengue virus type 2 introduction in Brazil â€“ a case report. BMC Infectious Diseases, 2021, 21, 311.	2.9	8
5	Nano-multilamellar lipid vesicles loaded with a recombinant form of the chikungunya virus E2 protein improve the induction of virus-neutralizing antibodies. Nanomedicine: Nanotechnology, Biology, and Medicine, 2021, 37, 102445.	3.3	5
6	Biological Characteristics and Patterns of Codon Usage Evolution for the African Genotype Zika Virus. Viruses, 2020, 12, 1306.	3.3	2
7	A Metagenomic Approach Identified a Novel Phasi Charoen-Like Virus Coinfecting a Chikungunya Virus-Infected Aedes aegypti Mosquito in Brazil. Microbiology Resource Announcements, 2020, 9, .	0.6	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. PLoS Neglected Tropical Diseases, 2019, 13, e0007625.	3.0	37
9	Systems analysis of subjects acutely infected with the Chikungunya virus. PLoS Pathogens, 2019, 15, e1007880.	4.7	33
10	Yellow fever and orthotopic liver transplantation: new insights from the autopsy room for an old but reâ€emerging disease. Histopathology, 2019, 75, 638-648.	2.9	29
11	Association of Malaria Infection During Pregnancy With Head Circumference of Newborns in the Brazilian Amazon. JAMA Network Open, 2019, 2, e193300.	5.9	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. Memorias Do Instituto Oswaldo Cruz, 2019, 114, e180251.	1.6	12
13	Zika Virus Impairs Neurogenesis and Synaptogenesis Pathways in Human Neural Stem Cells and Neurons. Frontiers in Cellular Neuroscience, 2019, 13, 64.	3.7	65
14	Usutu Virus Isolated from Rodents in Senegal. Viruses, 2019, 11, 181.	3.3	37
15	Origin of the SÃ£o Paulo Yellow Fever epidemic of 2017â€“2018 revealed through molecular epidemiological analysis of fatal cases. Scientific Reports, 2019, 9, 20418.	3.3	46
16	Influence of the HIV GWG variant in the HIV infection progression in mono and HCV coinfected patients. Medicine (United States), 2019, 98, e16376.	1.0	1
17	An Outbreak of Human Parvovirus B19 Hidden by Dengue Fever. Clinical Infectious Diseases, 2019, 68, 810-817.	5.8	11
18	Complete Genome Sequences of Five Human Respiratory Syncytial Virus Isolates Collected in Brazil. Genome Announcements, 2018, 6, .	0.8	0

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19	Complete Genome Sequence of a Human Metapneumovirus Isolate Collected in Brazil. Genome Announcements, 2018, 6, .	0.8	1
20	Characterisation of Zika virus infection in primary human astrocytes. BMC Neuroscience, 2018, 19, 5.	1.9	55
21	Modeling neuro-immune interactions during Zika virus infection. Human Molecular Genetics, 2018, 27, 41-52.	2.9	50
22	Persistence and Intra-Host Genetic Evolution of Zika Virus Infection in Symptomatic Adults: A Special View in the Male Reproductive System. Viruses, 2018, 10, 615.	3.3	30
23	The Challenges Imposed by Dengue, Zika, and Chikungunya to Brazil. Frontiers in Immunology, 2018, 9, 1964.	4.8	52
24	Codon adaptation biases among sylvatic and urban genotypes of Dengue virus type 2. Infection, Genetics and Evolution, 2018, 64, 207-211.	2.3	4
25	NS1 codon usage adaptation to humans in pandemic Zika virus. Memorias Do Instituto Oswaldo Cruz, 2018, 113, e170385.	1.6	11
26	Does adaptation to vertebrate codon usage relate to flavivirus emergence potential?. PLoS ONE, 2018, 13, e0191652.	2.5	11
27	First Genome Sequences of Dengue Virus Strains Isolated during the First DENV-4 Outbreak in SÃ£o Paulo, Brazil. Genome Announcements, 2017, 5, .	0.8	1
28	Outbreak of chikungunya virus in a vulnerable population of Sergipe, Brazilâ€"A molecular and serological survey. Journal of Clinical Virology, 2017, 97, 44-49.	3.1	25
29	Complete Genome Sequences of Two Human Parainfluenza Virus Type 3 Isolates Collected in Brazil. Genome Announcements, 2017, 5, .	0.8	1
30	Rapid Molecular Detection of Zika Virus in Acute-Phase Urine Samples Using the Recombinase Polymerase Amplification Assay. PLOS Currents, 2017, 9, .	1.4	20
31	First report of naturally infected Aedes aegypti with chikungunya virus genotype ECSA in the Americas. PLoS Neglected Tropical Diseases, 2017, 11, e0005630.	3.0	59
32	Biological and phylogenetic characteristics of West African lineages of West Nile virus. PLoS Neglected Tropical Diseases, 2017, 11, e0006078.	3.0	83
33	Laboratory strains of Aedes aegypti are competent to Brazilian Zika virus. PLoS ONE, 2017, 12, e0171951.	2.5	42
34	GenSeed-HMM: A Tool for Progressive Assembly Using Profile HMMs as Seeds and its Application in Alpavirinae Viral Discovery from Metagenomic Data. Frontiers in Microbiology, 2016, 7, 269.	3.5	30
35	Production of a Recombinant Dengue Virus 2 NS5 Protein and Potential Use as a Vaccine Antigen. Vaccine Journal, 2016, 23, 460-469.	3.1	25
36	The Brazilian Zika virus strain causes birth defects in experimental models. Nature, 2016, 534, 267-271.	27.8	1,132

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37	Protective efficacy of multiple vaccine platforms against Zika virus challenge in rhesus monkeys. Science, 2016, 353, 1129-1132.	12.6	461
38	A betabaculovirus encoding a gp64 homolog. BMC Genomics, 2016, 17, 94.	2.8	8
39	The Pangenome of the<i>Anticarsia gemmatalis</i>Multiple Nucleopolyhedrovirus (AgMNPV). Genome Biology and Evolution, 2016, 8, 94-108.	2.5	25
40	Vaccine protection against Zika virus from Brazil. Nature, 2016, 536, 474-478.	27.8	460
41	Epidemiological dynamics of an urban Dengue 4 outbreak in SÃ£o Paulo, Brazil. PeerJ, 2016, 4, e1892.	2.0	13
42	A deep phylogeny of viral and cellular right-hand polymerases. Infection, Genetics and Evolution, 2015, 36, 275-286.	2.3	10
43	Detection Of Four Dengue Serotypes Suggests Rise In Hyperendemicity In Urban Centers Of Brazil. PLoS Neglected Tropical Diseases, 2014, 8, e2620.	3.0	42
44	Reemergence of Rift Valley Fever, Mauritania, 2010. Emerging Infectious Diseases, 2014, 20, 300-303.	4.3	35
45	Molecular Evolution of Zika Virus during Its Emergence in the 20th Century. PLoS Neglected Tropical Diseases, 2014, 8, e2636.	3.0	659
46	Proteomic analyses of baculovirus Anticarsia gemmatalis multiple nucleopolyhedrovirus budded and occluded virus. Journal of General Virology, 2014, 95, 980-989.	2.9	19
47	Where there is no overlap, there is a gap. Revista Da Sociedade Brasileira De Medicina Tropical, 2014, 47, 675-676.	0.9	0
48	Genomic mosaicism in two strains of dengue virus type 3. Infection, Genetics and Evolution, 2013, 18, 202-212.	2.3	6
49	Molecular phylogeography of tick-borne encephalitis virus in central Europe. Journal of General Virology, 2013, 94, 2129-2139.	2.9	35
50	Modularity and evolutionary constraints in a baculovirus gene regulatory network. BMC Systems Biology, 2013, 7, 87.	3.0	12
51	Dengue Virus Type 3 Adaptive Changes during Epidemics in SÃ£o Jose de Rio Preto, Brazil, 2006â€“2007. PLoS ONE, 2013, 8, e63496.	2.5	14
52	Tracing the Origin and Northward Dissemination Dynamics of HIV-1 Subtype C in Brazil. PLoS ONE, 2013, 8, e74072.	2.5	23
53	Worldwide Spread of Dengue Virus Type 1. PLoS ONE, 2013, 8, e62649.	2.5	69
54	Characterization of Primary Isolates of HIV Type 1 CRF28_BF, CRF29_BF, and Unique BF Recombinants Circulating in SÃ£o Paulo, Brazil. AIDS Research and Human Retroviruses, 2012, 28, 1082-1088.	1.1	4

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55	Phylodynamics and movement of Phycodnaviruses among aquatic environments. ISME Journal, 2012, 6, 237-247.	9.8	19
56	First Identification of <i>Culex flavivirus</i> (Flaviviridae) in Brazil. Intervirology, 2012, 55, 475-483.	2.8	35
57	BF Integrase Genes of HIV-1 Circulating in SÃ£o Paulo, Brazil, with a Recurrent Recombination Region. PLoS ONE, 2012, 7, e34324.	2.5	5
58	Phylogeography of Rift Valley Fever Virus in Africa Reveals Multiple Introductions in Senegal and Mauritania. PLoS ONE, 2012, 7, e35216.	2.5	27
59	Phylogeographic Analysis of HIV-1 Subtype C Dissemination in Southern Brazil. PLoS ONE, 2012, 7, e35649.	2.5	24
60	Phylodynamics and Dispersal of HRSV Entails Its Permanence in the General Population in between Yearly Outbreaks in Children. PLoS ONE, 2012, 7, e41953.	2.5	18
61	One-step protocol for amplification of near full-length cDNA of the rabies virus genome. Journal of Virological Methods, 2011, 174, 1-6.	2.1	15
62	Relation of genetic phylogeny and geographical distance of tick-borne encephalitis virus in central Europe. Journal of General Virology, 2011, 92, 1906-1916.	2.9	29
63	Evolutionary history of Dengue virus type 4: Insights into genotype phylodynamics. Infection, Genetics and Evolution, 2011, 11, 878-885.	2.3	35
64	Social Networks Shape the Transmission Dynamics of Hepatitis C Virus. PLoS ONE, 2010, 5, e11170.	2.5	48
65	Variability of the conserved V3 loop tip motif in HIV-1 subtype B isolates collected from Brazilian and French patients. Brazilian Journal of Microbiology, 2010, 41, 720-728.	2.0	3
66	Hantavirus Pulmonary Syndrome, Central Plateau, Southeastern, and Southern Brazil. Emerging Infectious Diseases, 2009, 15, 561-567.	4.3	69
67	Introduction of Dengue Virus 4 (DENV-4) Genotype I into Brazil from Asia?. PLoS Neglected Tropical Diseases, 2009, 3, e390.	3.0	34
68	Spatio-Temporal Tracking and Phylodynamics of an Urban Dengue 3 Outbreak in SÃ£o Paulo, Brazil. PLoS Neglected Tropical Diseases, 2009, 3, e448.	3.0	56
69	Positive Selection Results in Frequent Reversible Amino Acid Replacements in the G Protein Gene of Human Respiratory Syncytial Virus. PLoS Pathogens, 2009, 5, e1000254.	4.7	121
70	Phylogeography and evolutionary history of dengue virus type 3. Infection, Genetics and Evolution, 2009, 9, 716-725.	2.3	70
71	Structural and phylogenetic relationship of ORF 31 from the Anticarsia gemmatalis MNPV to poly (ADP-ribose) polymerases (PARP). Virus Genes, 2008, 37, 177-184.	1.6	2
72	Bayesian Coalescent Analysis Reveals a High Rate of Molecular Evolution in GB Virus C. Journal of Molecular Evolution, 2008, 66, 292-297.	1.8	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. Journal of Clinical Virology, 2008, 43, 60-65.	3.1	45
74	Boosting Virology in Brazil. PLoS Biology, 2008, 6, e57.	5.6	3
75	High Rates of Molecular Evolution in Hantaviruses. Molecular Biology and Evolution, 2008, 25, 1488-1492.	8.9	117
76	Analysis of the genome of Spodoptera frugiperda nucleopolyhedrovirus (SfMNPV-19) and of the high genomic heterogeneity in group II nucleopolyhedroviruses. Journal of General Virology, 2008, 89, 1202-1211.	2.9	46
77	Complete Genome Viral Phylogenies Suggests the Concerted Evolution of Regulatory Cores and Accessory Satellites. PLoS ONE, 2008, 3, e3500.	2.5	15
78	Viral Individuality and Limitations of the Life Concept. , 2008, , 513-536.		2
79	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.	2.2	11
80	The â€œpressure panâ€•evolution of human erythrovirus B19 in the Amazon, Brazil. Virology, 2007, 369, 281-287.	2.4	12
81	Demographic Histories of ERV-K in Humans, Chimpanzees and Rhesus Monkeys. PLoS ONE, 2007, 2, e1026.	2.5	15
82	Genetic diversity of environmental Aspergillus flavus strains in the state of SÃ£o Paulo, Brazil by random amplified polymorphic DNA. Memorias Do Instituto Oswaldo Cruz, 2007, 102, 687-692.	1.6	18
83	Comparison between ectodomain and G2 region of G glycoprotein for genotyping of HRSV. Brazilian Journal of Microbiology, 2007, 38, 413-416.	2.0	3
84	Searching for antigen B genes and their adaptive sites in distinct strains and species of the helminth Echinococcus. Infection, Genetics and Evolution, 2006, 6, 251-261.	2.3	26
85	Tempo and mode of ERV-K evolution in human and chimpanzee genomes. Archives of Virology, 2006, 151, 2215-2228.	2.1	24
86	Genomic comparison of Neodiprion sertifer and Neodiprion lecontei nucleopolyhedroviruses and identification of potential hymenopteran baculovirus-specific open reading frames. Journal of General Virology, 2006, 87, 1477-1489.	2.9	33
87	Genome of the most widely used viral biopesticide: Anticarsia gemmatalis multiple nucleopolyhedrovirus. Journal of General Virology, 2006, 87, 3233-3250.	2.9	76
88	Sequence Analysis of the Genome of the Neodiprion sertifer Nucleopolyhedrovirus. Journal of Virology, 2004, 78, 7036-7051.	3.4	104
89	Distinct patterns of natural selection in the reverse transcriptase gene of HIV-1 in the presence and absence of antiretroviral therapy. Virology, 2004, 325, 181-191.	2.4	27
90	Identification, Expression and Phylogenetic Analysis of the Anticarsia gemmatalis multicapsid nucleopolyhedrovirus (AgMNPV) Helicase. Virus Genes, 2004, 29, 345-352.	1.6	5

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91	Sequence analysis of a 5.1 kbp region of the Spodoptera frugiperda multicapsid nucleopolyhedrovirus genome that comprises a functional ecdysteroid UDP-glucosyltransferase (egt) gene. Virus Genes, 2003, 27, 137-144.	1.6	17
92	Origins, evolution, and vectorâ§¸host coadaptations within the Genus Flavivirus. Advances in Virus Research, 2003, 59, 277-314.	2.1	163
93	Identification and characterization of a baculovirus from Lonomia obliqua (Lepidoptera: Saturniidae). Journal of Invertebrate Pathology, 2002, 79, 137-145.	3.2	12
94	Molecular Epidemiology, Evolution and Dispersal of the Genus Flavivirus. , 2002, , 167-195.		5
95	Evolution of Base Composition and Codon Usage Bias in the Genus Flavivirus. Journal of Molecular Evolution, 2001, 52, 383-390.	1.8	99
96	Construction of a recombinant Anticarsia gemmatalis nucleopolyhedrovirus (AgMNPV-2D) harbouring the Î²-galactosidase gene. Archives of Virology, 2001, 146, 1355-1367.	2.1	13
97	Evolution, epidemiology, and dispersal of flaviviruses revealed by molecular phylogenies. Advances in Virus Research, 2001, 57, 71-103.	2.1	89
98	Lack of Evidence for Cospeciation Between Retroelements and Their Hosts. Journal of Molecular Evolution, 2000, 50, 194-201.	1.8	5
99	Viral diseases and human evolution. Memorias Do Instituto Oswaldo Cruz, 2000, 95, 193-200.	1.6	21
100	Physical maps and virulence of Anticarsia gemmatalis nucleopolyhedrovirus genomic variants. Archives of Virology, 1999, 144, 1991-2006.	2.1	22
101	Identification, sequence analysis and phylogeny of the lef-2 gene of Helicoverpa armigera single-nucleocapsid baculovirus. Virus Research, 1999, 65, 21-32.	2.2	29
102	Genealogical Evidence for Positive Selection in the nef Gene of HIV-1. Genetics, 1999, 153, 1077-1089.	2.9	113
103	High Prevalence of GB Virus C in Brazil and Molecular Evidence for Intrafamilial Transmission. Journal of Clinical Microbiology, 1999, 37, 1634-1637.	3.9	18
104	Prion's Progress: Patterns and Rates of Molecular Evolution in Relation to Spongiform Disease. Journal of Molecular Evolution, 1998, 47, 133-145.	1.8	25
105	The complete sequence of four major structural proteins of African horse sickness virus serotype 6: evolutionary relationships within and between the orbiviruses. Virus Research, 1998, 53, 53-73.	2.2	18
106	Origin of 1997â€“98 Rift Valley fever outbreak in East Africa. Lancet, The, 1998, 352, 1596-1597.	13.7	29
107	Genetic Drift of Human Immunodeficiency Virus Type 1?. Journal of Virology, 1998, 72, 886-887.	3.4	7
108	Molecular Epidemiology and Emergence of Rift Valley Fever. Memorias Do Instituto Oswaldo Cruz, 1998, 93, 609-614.	1.6	14

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109	Complete sequence of two tick-borne flaviviruses isolated from Siberia and the UK: analysis and significance of the 5â€² and 3â€²-UTRs. Virus Research, 1997, 49, 27-39.	2.2	124
110	Population dynamics of flaviviruses revealed by molecular phylogenies.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 548-553.	7.1	300
111	A tick homologue of the human DNA helicase II 70-kDa subunit. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1996, 1305, 120-124.	2.4	3
112	Phylogenesis of prion protein. Nature, 1996, 380, 675-675.	27.8	43
113	Identification and Preliminary Characterization of a Chitinase Gene in the Autographa californica Nuclear Polyhedrosis Virus Genome. Virology, 1995, 212, 673-685.	2.4	130
114	Phylogenetic Interrelationships among Baculoviruses: Evolutionary Rates and Host Associations. Journal of Invertebrate Pathology, 1993, 62, 147-164.	3.2	249