

Luiz C J Alcantara

List of Publications by Year in descending order

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136
papers

8,434
citations

136885

32
h-index

64755

79
g-index

153
all docs

153
docs citations

153
times ranked

14854
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	13.7	1,381
2	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017, 12, 1261-1276.	5.5	898
3	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016, 352, 345-349.	6.0	877
4	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	13.7	515
5	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	15.2	326
6	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	6.0	279
7	Genome Detective: an automated system for virus identification from high-throughput sequencing data. <i>Bioinformatics</i> , 2019, 35, 871-873.	1.8	254
8	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016, 8, 97.	3.6	182
9	HTLV-I in the General Population of Salvador, Brazil. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2003, 34, 527-531.	0.9	171
10	The global spread of 2019-nCoV: a molecular evolutionary analysis. <i>Pathogens and Global Health</i> , 2020, 114, 64-67.	1.0	161
11	A standardized framework for accurate, high-throughput genotyping of recombinant and non-recombinant viral sequences. <i>Nucleic Acids Research</i> , 2009, 37, W634-W642.	6.5	142
12	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. <i>Bioinformatics</i> , 2020, 36, 3552-3555.	1.8	129
13	Guillain-Barré Syndrome After Zika Virus Infection in Brazil. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 1157-1160.	0.6	92
14	Emergence of Congenital Zika Syndrome: Viewpoint From the Front Lines. <i>Annals of Internal Medicine</i> , 2016, 164, 689.	2.0	84
15	HTLV in the Americas: challenges and perspectives. <i>Revista Panamericana De Salud Publica/Pan American Journal of Public Health</i> , 2006, 19, 44-53.	0.6	79
16	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	1.3	75
17	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. <i>Genes</i> , 2020, 11, 949.	1.0	65
18	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , 2016, 8, .	1.4	64

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19	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1138-1147.	4.6	63
20	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report. <i>International Journal of Infectious Diseases</i> , 2021, 103, 234-241.	1.5	63
21	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016â€“2019. <i>Journal of Virology</i> , 2019, 94, .	1.5	62
22	Human Retroviruses (HIV and HTLV) in Brazilian Indians: Seroepidemiological Study and Molecular Epidemiology of HTLV Type 2 Isolates. <i>AIDS Research and Human Retroviruses</i> , 2002, 18, 71-77.	0.5	57
23	The Low Evolutionary Rate of Human T-Cell Lymphotropic Virus Type-1 Confirmed by Analysis of Vertical Transmission Chains. <i>Molecular Biology and Evolution</i> , 2003, 21, 603-611.	3.5	56
24	Neurodevelopmental delay in normocephalic children with in utero exposure to Zika virus. <i>BMJ Paediatrics Open</i> , 2019, 3, e000486.	0.6	51
25	Fasâ€™670 promoter polymorphism is associated to susceptibility, clinical presentation, and survival in adult T cell leukemia. <i>Journal of Leukocyte Biology</i> , 2008, 83, 220-222.	1.5	45
26	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007231.	1.3	44
27	HTLV-1 in pregnant women from the Southern Bahia, Brazil: a neglected condition despite the high prevalence. <i>Virology Journal</i> , 2014, 11, 28.	1.4	43
28	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing. <i>Emerging Microbes and Infections</i> , 2020, 9, 1824-1834.	3.0	42
29	Genomic Comparison Among Global Isolates of <i>L. interrogans</i> Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 193.	1.8	39
30	Lipidomic Analysis Reveals Serum Alteration of Plasmalogens in Patients Infected With ZIKA Virus. <i>Frontiers in Microbiology</i> , 2019, 10, 753.	1.5	39
31	Genomic Surveillance of Yellow Fever Virus Epizootic in SÃ£o Paulo, Brazil, 2016 â€“ 2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	2.1	39
32	Molecular epidemiology of HIVâ€”1 in Santa Catarina State confirms increases of subtype C in Southern Brazil. <i>Journal of Medical Virology</i> , 2007, 79, 1455-1463.	2.5	38
33	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	2.9	37
34	Co-dependence of HTLV-1 p12 and p8 Functions in Virus Persistence. <i>PLoS Pathogens</i> , 2014, 10, e1004454.	2.1	36
35	Sickle red cells as danger signals on proinflammatory gene expression, leukotriene B4 and interleukin-1 beta production in peripheral blood mononuclear cell. <i>Cytokine</i> , 2016, 83, 75-84.	1.4	36
36	Multi-epitope based vaccine against yellow fever virus applying immunoinformatics approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 219-235.	2.0	34

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37	Anti-ganglioside antibodies in patients with Zika virus infection-associated Guillain-Barré Syndrome in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007695.	1.3	33
38	Brazilian HTLV Type 2a Strains from Intravenous Drug Users (IDUs) Appear to Have Originated from Two Sources: Brazilian Amerindians and European/North American IDUs. <i>AIDS Research and Human Retroviruses</i> , 2003, 19, 519-523.	0.5	31
39	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019, 14, e0217871.	1.1	31
40	Genomic detection of a virus lineage replacement event of dengue virus serotype 2 in Brazil, 2019. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e190423.	0.8	30
41	Phylogenetic and molecular analysis of HTLV-1 isolates from a medium sized town in Northern of Brazil: Tracing a common origin of the virus from the most endemic city in the country. <i>Journal of Medical Virology</i> , 2008, 80, 2040-2045.	2.5	29
42	RegaDB: community-driven data management and analysis for infectious diseases. <i>Bioinformatics</i> , 2013, 29, 1477-1480.	1.8	29
43	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021, 12, 2296.	5.8	29
44	Severe airport sanitarian control could slow down the spreading of COVID-19 pandemics in Brazil. <i>PeerJ</i> , 2020, 8, e9446.	0.9	28
45	Globin Haplotypes of Human T-Cell Lymphotropic Virus Type 1 Infected Individuals in Salvador, Bahia, Brazil, Suggest a Post-Columbian African Origin of This Virus. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2003, 33, 536-542.	0.9	27
46	HTLV-1 modifies the clinical and immunological response to schistosomiasis. <i>Clinical and Experimental Immunology</i> , 2004, 137, 424-429.	1.1	26
47	SARS-CoV-2 epidemic in Brazil: how the displacement of variants has driven distinct epidemic waves. <i>Virus Research</i> , 2022, 315, 198785.	1.1	26
48	Tracing the origin of Brazilian HTLV-1 as determined by analysis of host and viral genes. <i>Aids</i> , 2006, 20, 780-782.	1.0	24
49	Distribution of Human T Cell Lymphotropic Virus Type 1 (HTLV-1) Subtypes in Brazil: Genetic Characterization of LTR and Tax Region. <i>AIDS Research and Human Retroviruses</i> , 2006, 22, 953-959.	0.5	24
50	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016, 41, 142-145.	1.0	24
51	Genetic variability of human immunodeficiency virus-1 in Bahia state, Northeast, Brazil: High diversity of HIV genotypes. <i>Journal of Medical Virology</i> , 2009, 81, 391-399.	2.5	23
52	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021, 4, 489.	2.0	23
53	Molecular Epidemiology of Endemic Human T-Lymphotropic Virus Type 1 in a Rural Community in Guinea-Bissau. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1690.	1.3	22
54	Correlation between polymorphisms at interleukin-6 but not at interleukin-10 promoter and the risk of human T lymphotropic virus type 1-associated myelopathy/tropical spastic paraparesis in Brazilian individuals. <i>Journal of Medical Virology</i> , 2008, 80, 2141-2146.	2.5	21

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55	HTLV Type 1 Molecular Study in Brazilian Villages with African Characteristics Giving Support to the Post-Columbian Introduction Hypothesis. <i>AIDS Research and Human Retroviruses</i> , 2008, 24, 673-677.	0.5	19
56	Lower Prevalence of Human Immunodeficiency Virus Type 1 Brazilian Subtype B Found in Northeastern Brazil with Slower Progression to AIDS. <i>AIDS Research and Human Retroviruses</i> , 2010, 26, 1249-1254.	0.5	17
57	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008405.	1.3	17
58	Short report: Introduction of chikungunya virus ECSA genotype into the Brazilian Midwest and its dispersion through the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009290.	1.3	17
59	CD4+ T-cell Count may not be a Useful Strategy to Monitor Antiretroviral Therapy Response in HTLV-1/HIV Co-infected Patients. <i>Current HIV Research</i> , 2017, 15, 225-231.	0.2	17
60	A case-control study of HTLV-infection among blood donors in Salvador, Bahia, Brazil - associated risk factors and trend towards declining prevalence. <i>Revista Brasileira De Hematologia E Hemoterapia</i> , 2006, 28, 120.	0.7	16
61	Seroprevalence and Molecular Epidemiology of HTLV-1 Isolates from HIV-1 Co-Infected Women in Feira de Santana, Bahia, Brazil. <i>AIDS Research and Human Retroviruses</i> , 2010, 26, 1333-1339.	0.5	16
62	Detection of distinct human immunodeficiency virus Type 1 circulating recombinant forms in Northeast Brazil. <i>Journal of Medical Virology</i> , 2011, 83, 2066-2072.	2.5	16
63	Lack of High-Level Resistance Mutations in HIV Type 1 BF Recombinant Strains Circulating in Northeast Brazil. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 623-631.	0.5	16
64	A Public HTLV-1 Molecular Epidemiology Database for Sequence Management and Data Mining. <i>PLoS ONE</i> , 2012, 7, e42123.	1.1	16
65	The Close Relationship between South African and Latin American HTLV Type 1 Strains Corroborated in a Molecular Epidemiological Study of the HTLV Type 1 Isolates from a Blood Donor Cohort. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 503-507.	0.5	15
66	Chikungunya virus ECSA lineage reintroduction in the northeasternmost region of Brazil. <i>International Journal of Infectious Diseases</i> , 2021, 105, 120-123.	1.5	15
67	Zika Virus spreading in South America: Evolutionary analysis of emerging neutralizing resistant Phe279Ser strains. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 445-452.	0.4	14
68	Time to Harmonize Dengue Nomenclature and Classification. <i>Viruses</i> , 2018, 10, 569.	1.5	14
69	Acute Vector-Borne Viral Infection: Zika and MinION Surveillance. <i>Microbiology Spectrum</i> , 2019, 7, .	1.2	14
70	West Nile Virus in Brazil. <i>Pathogens</i> , 2021, 10, 896.	1.2	14
71	Oral health profile in patients infected with HTLV-1: Clinical findings, proviral load, and molecular analysis from HTLV-1 in saliva. <i>Journal of Medical Virology</i> , 2012, 84, 1428-1436.	2.5	13
72	Opsoclonus-myoclonus-ataxia syndrome associated with chikungunya and dengue virus co-infection. <i>International Journal of Infectious Diseases</i> , 2018, 75, 11-14.	1.5	13

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73	Co-Circulation of Two Independent Clades and Persistence of CHIKV-ECSA Genotype during Epidemic Waves in Rio de Janeiro, Southeast Brazil. <i>Pathogens</i> , 2020, 9, 984.	1.2	13
74	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021, 27, 1393-1404.	2.0	13
75	Short Report: Early genomic detection of SARS-CoV-2 P.1 variant in Northeast Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009591.	1.3	13
76	Analyses of HTLV-1 sequences suggest interaction between ORF-I mutations and HAM/TSP outcome. <i>Infection, Genetics and Evolution</i> , 2016, 45, 420-425.	1.0	12
77	Neonatal surveillance for congenital Zika infection during the 2016 microcephaly outbreak in Salvador, Brazil: Zika virus detection in asymptomatic newborns. <i>International Journal of Gynecology and Obstetrics</i> , 2020, 148, 9-14.	1.0	12
78	Genomic evidence of SARS-CoV-2 reinfection case with the emerging B.1.2 variant in Brazil. <i>Journal of Infection</i> , 2021, 83, 237-279.	1.7	12
79	Paraprobiotics and Postbiotics of <i>Lactobacillus delbrueckii</i> CIDCA 133 Mitigate 5-FU-Induced Intestinal Inflammation. <i>Microorganisms</i> , 2022, 10, 1418.	1.6	12
80	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
81	Structural Transformation to Attain Responsible BIOSciences (STARBIOS2): Protocol for a Horizon 2020 Funded European Multicenter Project to Promote Responsible Research and Innovation. <i>JMIR Research Protocols</i> , 2019, 8, e11745.	0.5	11
82	Ethnic Differences in the Distribution of Interleukin-6 Polymorphisms Among Three Brazilian Ethnic Groups. <i>Human Biology</i> , 2005, 77, 509-514.	0.4	10
83	Genetic and Biologic Characterization of HIV Type 1 Subtype C Isolates from South Brazil. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 135-143.	0.5	10
84	Molecular characterization of HTLV-1 gp46 glycoprotein from health carriers and HAM/TSP infected individuals. <i>Virology Journal</i> , 2013, 10, 75.	1.4	10
85	Molecular Epidemiology and Clinical Features of Human T Cell Lymphotropic Virus Type 1 Infection in Spain. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 856-862.	0.5	10
86	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. <i>F1000Research</i> , 2020, 9, 514.	0.8	10
87	Measuring Mosquito-borne Viral Suitability in Myanmar and Implications for Local Zika Virus Transmission. <i>PLOS Currents</i> , 2018, 10, .	1.4	10
88	Palmitoylation and p8-Mediated Human T-Cell Leukemia Virus Type 1 Transmission. <i>Journal of Virology</i> , 2014, 88, 2319-2322.	1.5	9
89	HTLV-1aA introduction into Brazil and its association with the trans-Atlantic slave trade. <i>Infection, Genetics and Evolution</i> , 2017, 48, 95-101.	1.0	9
90	Re-mapping the molecular features of the human immunodeficiency virus type 1 and human T-cell lymphotropic virus type 1 Brazilian sequences using a bioinformatics unit established in Salvador, Bahia, Brazil, to give support to the viral epidemiology studies. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2007, 102, 133-139.	0.8	8

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91	HTLV-1 infection in blood donors from the Western Brazilian Amazon region: Seroprevalence and molecular study of viral isolates. <i>Journal of Medical Virology</i> , 2008, 80, 1966-1971.	2.5	7
92	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil. <i>PLoS ONE</i> , 2020, 15, e0226098.	1.1	7
93	Untargeted Metabolomics Insights into Newborns with Congenital Zika Infection. <i>Pathogens</i> , 2021, 10, 468.	1.2	7
94	Molecular surveillance of the on-going SARS-COV-2 epidemic in Ribeirao Preto City, Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104976.	1.0	7
95	Polymorphisms at <i>GLUT1</i> gene are not associated with the development of TSP/HAM in Brazilian HTLV-1 infected individuals and the discovery of a new polymorphism at <i>GLUT1</i> gene. <i>Journal of Medical Virology</i> , 2009, 81, 552-557.	2.5	6
96	Complete genome sequence of human T-cell lymphotropic type 1 from patients with different clinical profiles, including infective dermatitis. <i>Infection, Genetics and Evolution</i> , 2020, 79, 104166.	1.0	6
97	Plasma lipidome profiling of newborns with antenatal exposure to Zika virus. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009388.	1.3	6
98	Molecular Study of HBZ and gp21 Human T Cell Leukemia Virus Type 1 Proteins Isolated from Different Clinical Profile Infected Individuals. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 1370-1372.	0.5	5
99	Human Retrovirus Codon Usage from tRNA Point of View: Therapeutic Insights. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S12093.	1.0	5
100	The origin of HTLV-1 in southern Bahia by phylogenetic, mtDNA and β -globin analysis. <i>Virology Reports</i> , 2015, 5, 63-74.	0.4	5
101	Molecular Characterization of the Human Immunodeficiency Virus Type 1 in Women and Their Vertically Infected Children. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 1046-1051.	0.5	5
102	Epidemiology and evolution of Zika virus in Minas Gerais, Southeast Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104785.	1.0	5
103	Molecular Characterization of the Human T Cell Lymphotropic Virus Type 2 Long Terminal Repeat Region: A Discussion about Possible Influences at Viral Gene Expression. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 92-96.	0.5	4
104	Deep Sequencing Analysis of Human T Cell Lymphotropic Virus Type 1 Long Terminal Repeat 5' Region from Patients with Tropical Spastic Paraparesis/Human T Cell Lymphotropic Virus Type 1-Associated Myelopathy and Asymptomatic Carriers. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 279-283.	0.5	4
105	Promoting Responsible Research and Innovation (RRI) During Brazilian Activities of Genomic and Epidemiological Surveillance of Arboviruses. <i>Frontiers in Public Health</i> , 2021, 9, 693743.	1.3	4
106	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil. <i>Microbiology Spectrum</i> , 2022, 10, e0015522.	1.2	4
107	Molecular Characterization of Long Terminal Repeat Sequences from Brazilian Human Immunodeficiency Virus Type 1 Isolates. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 837-841.	0.5	3
108	Inferences about the global scenario of human T-cell lymphotropic virus type 1 infection using data mining of viral sequences. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2014, 109, 448-451.	0.8	3

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109	Assessment of Genetic Diversity of HTLV-1 ORF-I Sequences Collected from Patients with Different Clinical Profiles. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 881-884.	0.5	3
110	Pan-omics focused to Crick's central dogma. , 2020, , 1-41.		3
111	The obscurance of the greatest sylvatic yellow fever epidemic and the cooperation of the Pan American Health Organization during the COVID-19 pandemic. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2020, 53, e20200787.	0.4	3
112	Metavirome composition of Brazilian blood donors positive for the routinely tested blood-borne infections. <i>Virus Research</i> , 2022, 311, 198689.	1.1	3
113	Mapping the molecular characteristics of Brazilian human T-cell lymphotropic virus type 1 Env (gp46) and Pol amino acid sequences for vaccine design. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2007, 102, 741-749.	0.8	2
114	Mapping the molecular characteristics of Brazilian human T-cell lymphotropic virus type 1 Env (gp46) and Pol amino acid sequences for vaccine design. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2007, 102, 741-749.	0.8	2
115	Dynamics and Determinants of SARS-CoV-2 RT-PCR Testing on Symptomatic Individuals Attending Healthcare Centers during 2020 in Bahia, Brazil. <i>Viruses</i> , 2022, 14, 1549.	1.5	2
116	Frequency distribution of XbaI G A T and HaeIII T A C GLUT1 polymorphisms among different Brazilian ethnic groups. <i>Molecular Biology Reports</i> , 2010, 37, 75-79.	1.0	1
117	Short Communication: Phylodynamics Analysis of the Human Immunodeficiency Virus Type 1 Envelope Gene in Mother and Child Pairs. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 913-920.	0.5	1
118	Molecular Epidemiology Database for Sequence Management and Data Mining. <i>Methods in Molecular Biology</i> , 2017, 1582, 25-31.	0.4	1
119	Reversible sensory polyneuropathy during an arboviral outbreak in Salvador, Bahia, Brazil. <i>Journal of the Neurological Sciences</i> , 2018, 391, 3-4.	0.3	1
120	Mosquito-Borne Viral Diseases: Control and Prevention in the Genomics Era. , 2020, , .		1
121	In silico analysis of human T-lymphotropic virus type 1 complete genomes from patients with different clinical outcomes. <i>Future Virology</i> , 0, , .	0.9	1
122	Guillain-Barré Syndrome and Miller Fisher Syndrome in Association With an Arboviral Outbreak: A Brazilian Case Series. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	1
123	Retrospective Investigation in Horses with Encephalitis Reveals Unnoticed Circulation of West Nile Virus in Brazil. <i>Viruses</i> , 2022, 14, 1540.	1.5	1
124	The Divergent Pattern of SARS-CoV-2 Variant Predominance and Transmission Dynamics in the Brazilian Island of Ilhabela. <i>Viruses</i> , 2022, 14, 1481.	1.5	1
125	Identification and characterization of previously described epitopes in HIV-1 subtypes B, C, F and BF in Brazil. <i>Brazilian Journal of Infectious Diseases</i> , 2007, 11, 27-30.	0.3	0
126	Genetic characterisation of Langerin gene in human immunodeficiency virus-1-infected women from Bahia, Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2014, 109, 250-255.	0.8	0

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127	Amino- and Carboxyl-Terminal CCR5 Mutations in Brazilian HIV-1-Infected Women and Homology Model of p.L55Q CCR5 Mutant. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 685-691.	0.5	0
128	First detection of human T-cell lymphotropic virus in blood donors in Benin shows that testing is required to improve blood safety. <i>ISBT Science Series</i> , 2019, 14, 163-168.	1.1	0
129	Pan-genomics of virus and its applications. , 2020, , 237-250.		0
130	Classification of Zika virus sequences with respect to their species and subspecies. , 2021, , 29-37.		0
131	SARS-CoV-2 serological cross-reactivity testing in Brazilian blood donors, October-December, 2019. <i>Journal of Infection</i> , 2022, , .	1.7	0
132	Distribui�o espacial de dengue, chikungunya e Zika e os determinantes socioeconomicos em um municpio da Bahia. <i>Revista De Cincias Mdicas E Biolgicas</i> , 2022, 20, 551-559.	0.0	0
133	Title is missing!. , 2020, 15, e0226098.		0
134	Title is missing!. , 2020, 15, e0226098.		0
135	Title is missing!. , 2020, 15, e0226098.		0
136	Title is missing!. , 2020, 15, e0226098.		0