

Luiz C J Alcantara

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

139
papers

5,398
citations

28
h-index

72
g-index

153
ext. papers

7,301
ext. citations

7.5
avg. IF

5.29
L-index

#	Paper	IF	Citations
139	METAVIROME COMPOSITION OF BRAZILIAN BLOOD DONORS POSITIVE FOR THE ROUTINELY TESTED BLOOD-BORNE INFECTIONS.. <i>Virus Research</i> , 2022 , 311, 198689	6.4	0
138	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil.. <i>Microbiology Spectrum</i> , 2022 , e0015522	8.9	0
137	SARS-CoV-2 epidemic in Brazil: how variants displacement have driven distinct epidemic waves.. <i>Virus Research</i> , 2022 , 198785	6.4	4
136	SARS-CoV-2 SEROLOGICAL CROSS-REACTIVITY TESTING IN BRAZILIAN BLOOD DONORS, OCTOBER-DECEMBER, 2019.. <i>Journal of Infection</i> , 2021 ,	18.9	
135	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021 , 592, 438-443	50.4	685
134	Untargeted Metabolomics Insights into Newborns with Congenital Zika Infection. <i>Pathogens</i> , 2021 , 10,	4.5	1
133	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	4.8	2
132	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021 , 12, 2296	17.4	3
131	Plasma lipidome profiling of newborns with antenatal exposure to Zika virus. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009388	4.8	1
130	Chikungunya virus ECSA lineage reintroduction in the northeasternmost region of Brazil. <i>International Journal of Infectious Diseases</i> , 2021 , 105, 120-123	10.5	0
129	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	6.7	13
128	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021 , 27, 1393-1404	10.2	0
127	West Nile Virus in Brazil. <i>Pathogens</i> , 2021 , 10,	4.5	3
126	Epidemiology and evolution of Zika virus in Minas Gerais, Southeast Brazil. <i>Infection, Genetics and Evolution</i> , 2021 , 91, 104785	4.5	4
125	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	10.5	37
124	Multi-epitope based vaccine against yellow fever virus applying immunoinformatics approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 219-235	3.6	21
123	Classification of Zika virus sequences with respect to their species and subspecies 2021 , 29-37		

122	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021 , 27, 440-446	50.5	206
121	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	6	1
120	Short Report: Early genomic detection of SARS-CoV-2 P.1 variant in Northeast Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009591	4.8	5
119	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	18.9	7
118	Molecular surveillance of the on-going SARS-COV-2 epidemic in Ribeirao Preto City, Brazil. <i>Infection, Genetics and Evolution</i> , 2021 , 93, 104976	4.5	2
117	Mosquito-Borne Viral Diseases: Control and Prevention in the Genomics Era 2020 ,		1
116	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. <i>Bioinformatics</i> , 2020 , 36, 3552-3555	7.2	89
115	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24
114	The global spread of 2019-nCoV: a molecular evolutionary analysis. <i>Pathogens and Global Health</i> , 2020 , 114, 64-67	3.1	102
113	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil. <i>PLoS ONE</i> , 2020 , 15, e0226098	3.7	3
112	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 Suppl 2, 9-14	4	9
111	Pan-omics focused to Crick's central dogma 2020 , 1-41		1
110	Pan-genomics of virus and its applications 2020 , 237-250		
109	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. <i>F1000Research</i> , 2020 , 9, 514	3.6	7
108	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	2.6	10
107	Severe airport sanitarian control could slow down the spreading of COVID-19 pandemics in Brazil. <i>PeerJ</i> , 2020 , 8, e9446	3.1	14
106	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	1.5	0
105	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	4.5	2

104	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	18.9	7
103	Genomic Surveillance of Yellow Fever Virus Epizootic in S̃ Paulo, Brazil, 2016 - 2018. <i>PLoS Pathogens</i> , 2020 , 16, e1008699	7.6	18
102	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	18.9	26
101	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008405	4.8	6
100	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. <i>Genes</i> , 2020 , 11,	4.2	39
99	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,	4.5	2
98	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil 2020 , 15, e0226098		
97	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil 2020 , 15, e0226098		
96	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil 2020 , 15, e0226098		
95	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil 2020 , 15, e0226098		
94	Anti-ganglioside antibodies in patients with Zika virus infection-associated Guillain-Barré Syndrome in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007695	4.8	23
93	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , 2019 , 19, 1138-1147	25.5	40
92	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019 , 14, e0217871	3.7	16
91	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	1.6	2
90	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007231	4.8	17
89	Lipidomic Analysis Reveals Serum Alteration of Plasmalogens in Patients Infected With ZIKA Virus. <i>Frontiers in Microbiology</i> , 2019 , 10, 753	5.7	22
88	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007065	4.8	37
87	Genome Detective: an automated system for virus identification from high-throughput sequencing data. <i>Bioinformatics</i> , 2019 , 35, 871-873	7.2	109

86	Acute Vector-Borne Viral Infection: Zika and MinION Surveillance. <i>Microbiology Spectrum</i> , 2019 , 7,	8.9	9
85	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016-2019. <i>Journal of Virology</i> , 2019 , 94,	6.6	29
84	Neurodevelopmental delay in normocephalic children with in utero exposure to Zika virus. <i>BMJ Paediatrics Open</i> , 2019 , 3, e000486	2.4	24
83	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	2	6
82	First detection of human T-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	
81	Opsoclonus-myoclonus-ataxia syndrome associated with chikungunya and dengue virus co-infection. <i>International Journal of Infectious Diseases</i> , 2018 , 75, 11-14	10.5	5
80	Genomic Comparison Among Global Isolates of Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018 , 8, 193	5.9	18
79	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
78	Measuring Mosquito-borne Viral Suitability in Myanmar and Implications for Local Zika Virus Transmission. <i>PLOS Currents</i> , 2018 , 10,		5
77	Time to Harmonize Dengue Nomenclature and Classification. <i>Viruses</i> , 2018 , 10,	6.2	8
76	Reversible sensory polyneuropathy during an arboviral outbreak in Salvador, Bahia, Brazil. <i>Journal of the Neurological Sciences</i> , 2018 , 391, 3-4	3.2	1
75	HTLV-1aA introduction into Brazil and its association with the trans-Atlantic slave trade. <i>Infection, Genetics and Evolution</i> , 2017 , 48, 95-101	4.5	6
74	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017 , 546, 406-410.	10.4	366
73	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	18.8	529
72	Molecular Epidemiology Database for Sequence Management and Data Mining. <i>Methods in Molecular Biology</i> , 2017 , 1582, 25-31	1.4	1
71	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	1.3	13
70	Deep Sequencing Analysis of Human T Cell Lymphotropic Virus Type 1 Long Terminal Repeat 5R 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, 279-83	1.6	3
69	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	4.5	9

68	Guillain-Barré Syndrome After Zika Virus Infection in Brazil. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016 , 95, 1157-1160	3.2	69
67	Emergence of Congenital Zika Syndrome: Viewpoint From the Front Lines. <i>Annals of Internal Medicine</i> , 2016 , 164, 689-91	8	70
66	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016 , 352, 345-349	33.3	703
65	Zika Virus spreading in South America: Evolutionary analysis of emerging neutralizing resistant Phe279Ser strains. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016 , 9, 445-52	2.1	12
64	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , 2016 , 8,		48
63	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016 , 8, 97	14.4	130
62	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016 , 41, 142-145	1.5	20
61	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	4	26
60	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, 913-20	1.6	1
59	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, 685-91	1.6	
58	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, 1046-51	1.6	4
57	The origin of HTLV-1 in southern Bahia by phylogenetic, mtDNA and HbA1c analysis. <i>Virology Reports</i> , 2015 , 5, 63-74		5
56	Palmitoylation and p8-mediated human T-cell leukemia virus type 1 transmission. <i>Journal of Virology</i> , 2014 , 88, 2319-22	6.6	9
55	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, 92-6	1.6	4
54	HTLV-1 in pregnant women from the Southern Bahia, Brazil: a neglected condition despite the high prevalence. <i>Virology Journal</i> , 2014 , 11, 28	6.1	33
53	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, 856-62	1.6	8
52	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, 448-51	2.6	3
51	Genetic characterisation of Langerin gene in human immunodeficiency virus-1-infected women from Bahia, Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2014 , 109, 250-5	2.6	

50	Co-dependence of HTLV-1 p12 and p8 functions in virus persistence. <i>PLoS Pathogens</i> , 2014 , 10, e1004454	4.6	30
49	Molecular characterization of HTLV-1 gp46 glycoprotein from health carriers and HAM/TSP infected individuals. <i>Virology Journal</i> , 2013 , 10, 75	6.1	8
48	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, 1370-2	1.6	5
47	Human Retrovirus Codon Usage from tRNA Point of View: Therapeutic Insights. <i>Bioinformatics and Biology Insights</i> , 2013 , 7, 335-45	5.3	4
46	RegaDB: community-driven data management and analysis for infectious diseases. <i>Bioinformatics</i> , 2013 , 29, 1477-80	7.2	25
45	Molecular characterization of long terminal repeat sequences from Brazilian human immunodeficiency virus type 1 isolates. <i>AIDS Research and Human Retroviruses</i> , 2013 , 29, 837-41	1.6	3
44	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, 1428-36	19.7	7
43	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	4.8	18
42	A public HTLV-1 molecular epidemiology database for sequence management and data mining. <i>PLoS ONE</i> , 2012 , 7, e42123	3.7	11
41	Detection of distinct human immunodeficiency virus type 1 circulating recombinant forms in northeast Brazil. <i>Journal of Medical Virology</i> , 2011 , 83, 2066-72	19.7	14
40	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, 623-31	1.6	11
39	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, 1333-9	1.6	14
38	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, 1249-54	1.6	13
37	Frequency distribution of XbaIG > T and HaellIT > C GLUT1 polymorphisms among different Brazilian ethnic groups. <i>Molecular Biology Reports</i> , 2010 , 37, 75-9	2.8	1
36	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, 391-9	19.7	17
35	Polymorphisms at GLUT1 gene are not associated with the development of TSP/HAM in Brazilian HTLV-1 infected individuals and the discovery of a new polymorphism at GLUT1 gene. <i>Journal of Medical Virology</i> , 2009 , 81, 552-7	19.7	5
34	A standardized framework for accurate, high-throughput genotyping of recombinant and non-recombinant viral sequences. <i>Nucleic Acids Research</i> , 2009 , 37, W634-42	20.1	128
33	Fas 670 promoter polymorphism is associated to susceptibility, clinical presentation, and survival in adult T cell leukemia. <i>Journal of Leukocyte Biology</i> , 2008 , 83, 220-2	6.5	40

32	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, 673-7	1.6	15
31	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, 2040-5	19.7	24
30	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, 1966-71	19.7	7
29	Correlation between polymorphisms at interleukin-6 but not at interleukin-10 promoter and the risk of human T lymphotropic virus type I-associated myelopathy/tropical spastic paraparesis in Brazilian individuals. <i>Journal of Medical Virology</i> , 2008 , 80, 2141-6	19.7	18
28	Genetic and biologic characterization of HIV type 1 subtype C isolates from south Brazil. <i>AIDS Research and Human Retroviruses</i> , 2007 , 23, 135-43	1.6	9
27	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, 133-138	2.6	5
26	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	2.8	
25	Molecular epidemiology of HIV-1 in Santa Catarina State confirms increases of subtype C in Southern Brazil. <i>Journal of Medical Virology</i> , 2007 , 79, 1455-63	19.7	37
24	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, 503-7	1.6	13
23	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	2.6	2
22	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, 741-9	2.6	2
21	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, 953-9	1.6	22
20	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		12
19	Tracing the origin of Brazilian HTLV-1 as determined by analysis of host and viral genes. <i>Aids</i> , 2006 , 20, 780-2	3.5	22
18	HTLV in the Americas: challenges and perspectives. <i>Revista Panamericana De Salud Publica/Pan American Journal of Public Health</i> , 2006 , 19, 44-53	4.1	59
17	Ethnic differences in the distribution of interleukin-6 polymorphisms among three Brazilian ethnic groups. <i>Human Biology</i> , 2005 , 77, 509-14	1.2	8
16	HTLV-1 modifies the clinical and immunological response to schistosomiasis. <i>Clinical and Experimental Immunology</i> , 2004 , 137, 424-9	6.2	24
15	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> , 2004 , 21, 603-11	8.3	46

14	Globin haplotypes of human T-cell lymphotropic virus type I-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, 536-42	3.1	19
13	HTLV-I in the general population of Salvador, Brazil: a city with African ethnic and sociodemographic characteristics. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2003 , 34, 527-31	3.1	142
12	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, 519-23	1.6	27
11	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, 71-7	1.6	44
10	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples		6
9	Severe airport sanitarian control could slow down the spreading of COVID-19 pandemics in Brazil		8
8	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing		5
7	Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa		44 ⁶
6	Emergence of the Zika virus Asian lineage in Angola		1
5	Genomic Surveillance of Yellow Fever Virus Epizootic in Sã Paulo, Brazil, 2016-2018		4
4	Yellow fever virus spread in Rio de Janeiro and Espıto Santo, 2016-2019: Phylodynamic assessment to improve intervention strategies		1
3	Application of high-throughput serological tests for controlling zoonotic viral infection in Amazon rainforest and as a strategy to prevent future pandemics (Preprint)		1
2	Rapid replacement of the Beta variant by the Delta variant in South Africa		17
1	Dengue-2 Cosmopolitan genotype detection and emergence in South America		1