

Julien ThÃ©zÃ©

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

4,544
citations

186265

28
h-index

197818

49
g-index

61
all docs

61
docs citations

61
times ranked

7907
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017–2019. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010255.	3.0	9
2	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021, 27, 1393-1404.	4.3	13
3	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. <i>Virus Evolution</i> , 2021, 7, veab065.	4.9	0
4	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 – 2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	4.7	39
5	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
6	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008405.	3.0	17
7	Parallel evolution in the emergence of highly pathogenic avian influenza A viruses. <i>Nature Communications</i> , 2020, 11, 5511.	12.8	23
8	Transmission of hepatitis C virus in HIV-positive and PrEP-using MSM in England. <i>Journal of Viral Hepatitis</i> , 2020, 27, 721-730.	2.0	16
9	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
10	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	13.3	114
11	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.	1.6	30
12	Characterising West Nile virus epidemiology in Israel using a transmission suitability index. <i>Eurosurveillance</i> , 2020, 25, .	7.0	15
13	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	17
14	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016–2019. <i>Journal of Virology</i> , 2019, 94, .	3.4	62
15	A60–f Revealing the evolution of virulence in RNA viruses. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
16	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1138-1147.	9.1	63
17	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019, 14, e0217871.	2.5	31
18	<sc>MVSE</sc>: An R package that estimates a climate-driven mosquito-borne viral suitability index. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1357-1370.	5.2	35

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19	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 784-787.	4.3	36
20	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	3.0	75
21	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	7.8	124
22	Molecular epidemiology reveals the role of war in the spread of HIV in Ukraine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1051-1056.	7.1	65
23	Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. <i>Emerging Infectious Diseases</i> , 2018, 24, 1795-1805.	4.3	26
24	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018, 23, 855-864.e7.	11.0	82
25	Biodiversity, Evolution and Ecological Specialization of Baculoviruses: A Treasure Trove for Future Applied Research. <i>Viruses</i> , 2018, 10, 366.	3.3	33
26	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	12.6	279
27	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
28	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	27.8	515
29	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017, 7, 15216.	3.3	40
30	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017, 23, 1742-1744.	4.3	69
31	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016, 22, 1788-1792.	4.3	45
32	Birth of a W sex chromosome by horizontal transfer of <i>Wolbachia</i> bacterial symbiont genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15036-15041.	7.1	83
33	Genome Sequence of a Candidate World Health Organization Reference Strain of Zika Virus for Nucleic Acid Testing. <i>Genome Announcements</i> , 2016, 4, .	0.8	20
34	Hepacivirus cross-species transmission and the origins of the hepatitis C virus. <i>Current Opinion in Virology</i> , 2016, 16, 1-7.	5.4	66
35	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016, 352, 345-349.	12.6	877
36	Genetic diversity and phenotypic associations of feline caliciviruses from cats in Switzerland. <i>Journal of General Virology</i> , 2016, 97, 3253-3266.	2.9	10

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37	Evolutionary and Phylogenetic Analysis of the Hepaciviruses and Pegiviruses. <i>Genome Biology and Evolution</i> , 2015, 7, 2996-3008.	2.5	57
38	The Genome of the Nucleopolyhedrosis-Causing Virus from <i>Tipula oleracea</i> Sheds New Light on the Nudiviridae Family. <i>Journal of Virology</i> , 2015, 89, 3008-3025.	3.4	49
39	Gene Acquisition Convergence between Entomopoxviruses and Baculoviruses. <i>Viruses</i> , 2015, 7, 1960-1974.	3.3	41
40	Recurrent DNA virus domestication leading to different parasite virulence strategies. <i>Science Advances</i> , 2015, 1, e1501150.	10.3	88
41	Remarkable Diversity of Endogenous Viruses in a Crustacean Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 2129-2140.	2.5	50
42	Genomic diversity in European <i>Spodoptera exigua</i> multiple nucleopolyhedrovirus isolates. <i>Journal of General Virology</i> , 2014, 95, 2297-2309.	2.9	29
43	Functional Annotation of <i>Cotesia congregata</i> Bracovirus: Identification of Viral Genes Expressed in Parasitized Host Immune Tissues. <i>Journal of Virology</i> , 2014, 88, 8795-8812.	3.4	56
44	When parasitic wasps hijacked viruses: genomic and functional evolution of polydnaviruses. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130051.	4.0	150
45	Functional endogenous viral elements in the genome of the parasitoid wasp <i>Cotesia congregata</i> : insights into the evolutionary dynamics of bracoviruses. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130047.	4.0	68
46	New Insights into the Evolution of Entomopoxvirinae from the Complete Genome Sequences of Four Entomopoxviruses Infecting <i>Adoxophyes honmai</i> , <i>Choristoneura biennis</i> , <i>Choristoneura rosaceana</i> , and <i>Mythimna separata</i> . <i>Journal of Virology</i> , 2013, 87, 7992-8003.	3.4	43
47	Paleozoic origin of insect large dsDNA viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15931-15935.	7.1	136
48	Revisiting the missing protein-coding gene catalog of the domestic dog. <i>BMC Genomics</i> , 2009, 10, 62.	2.8	18