

Julien Thz

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54
papers

3,235
citations

28
h-index

56
g-index

61
ext. papers

4,151
ext. citations

11.8
avg, IF

4.68
L-index

#	Paper	IF	Citations
54	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016 , 352, 345-349	33.3	703
53	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017 , 546, 406-410	50.4	366
52	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260	33.3	277
51	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405	50.4	235
50	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
49	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	5.8	113
48	Paleozoic origin of insect large dsDNA viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 15931-5	11.5	111
47	A60 Revealing the evolution of virulence in RNA viruses. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
46	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020 , 5, 443-454	26.6	64
45	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018 , 2, 659-668	12.3	64
44	Birth of a W sex chromosome by horizontal transfer of Wolbachia bacterial symbiont genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 15036-15041	11.5	62
43	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	23.4	60
42	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	5.8	58
41	Recurrent DNA virus domestication leading to different parasite virulence strategies. <i>Science Advances</i> , 2015 , 1, e1501150	14.3	51
40	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1742-1744	10.2	51
39	Hepacivirus cross-species transmission and the origins of the hepatitis C virus. <i>Current Opinion in Virology</i> , 2016 , 16, 1-7	7.5	50
38	Evolutionary and Phylogenetic Analysis of the Hepaciviruses and Pegiviruses. <i>Genome Biology and Evolution</i> , 2015 , 7, 2996-3008	3.9	48

37	Functional annotation of Cotesia congregata bracovirus: identification of viral genes expressed in parasitized host immune tissues. <i>Journal of Virology</i> , 2014 , 88, 8795-812	6.6	42
36	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
35	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, 3008-25	6.6	38
34	Remarkable diversity of endogenous viruses in a crustacean genome. <i>Genome Biology and Evolution</i> , 2014 , 6, 2129-40	3.9	38
33	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007065	4.8	37
32	Gene acquisition convergence between entomopoxviruses and baculoviruses. <i>Viruses</i> , 2015 , 7, 1960-74	6.2	35
31	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016 , 22, 1788-92	10.2	35
30	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017 , 7, 15216	4.9	33
29	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	11.5	32
28	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	6.6	32
27	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016-2019. <i>Journal of Virology</i> , 2019 , 94,	6.6	29
26	Genomic diversity in European <i>Spodoptera exigua</i> multiple nucleopolyhedrovirus isolates. <i>Journal of General Virology</i> , 2014 , 95, 2297-2309	4.9	25
25	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24
24	Biodiversity, Evolution and Ecological Specialization of Baculoviruses: A Treasure Trove for Future Applied Research. <i>Viruses</i> , 2018 , 10,	6.2	23
23	Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1795-1805	10.2	22
22	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 - 2018. <i>PLoS Pathogens</i> , 2020 , 16, e1008699	7.6	18
21	Genome Sequence of a Candidate World Health Organization Reference Strain of Zika Virus for Nucleic Acid Testing. <i>Genome Announcements</i> , 2016 , 4,		18
20	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019 , 25, 784-787	10.2	17

19	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019 , 14, e0217871	3.7	16
18	MVSE: An R-package that estimates a climate-driven mosquito-borne viral suitability index. <i>Methods in Ecology and Evolution</i> , 2019 , 10, 1357-1370	7.7	16
17	Revisiting the missing protein-coding gene catalog of the domestic dog. <i>BMC Genomics</i> , 2009 , 10, 62	4.5	14
16	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
15	Parallel evolution in the emergence of highly pathogenic avian influenza A viruses. <i>Nature Communications</i> , 2020 , 11, 5511	17.4	8
14	Transmission of hepatitis C virus in HIV-positive and PrEP-using MSM in England. <i>Journal of Viral Hepatitis</i> , 2020 , 27, 721-730	3.4	8
13	Genetic diversity and phenotypic associations of feline caliciviruses from cats in Switzerland. <i>Journal of General Virology</i> , 2016 , 97, 3253-3266	4.9	8
12	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,	9.7	7
11	Characterising West Nile virus epidemiology in Israel using a transmission suitability index. <i>Eurosurveillance</i> , 2020 , 25,	19.8	6
10	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
9	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008405	4.8	6
8	Parallel Evolution in the Emergence of Highly Pathogenic Avian Influenza A Viruses		2
7	Identification of site-specific evolutionary trajectories shared across human betacoronaviruses 2021 ,		2
6	Genomic epidemiology of early SARS-CoV-2 transmission dynamics in Gujarat, India		2
5	Emergence of the Zika virus Asian lineage in Angola		1
4	Yellow fever virus spread in Rio de Janeiro and Espıto Santo, 2016-2019: Phylodynamic assessment to improve intervention strategies		1
3	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	4.8	1
2	Epidemiologic History and Genetic Diversity Origins of Chikungunya and Dengue Viruses, Paraguay. <i>Emerging Infectious Diseases</i> , 2021 , 27, 1393-1404	10.2	0

- 1 Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. *Virus Evolution*, **2021**, 7, veab065 3·7