

Jemma L Geoghegan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7645657/publications.pdf>

Version: 2024-02-01

36
papers

1,542
citations

377584

21
h-index

406436

35
g-index

50
all docs

50
docs citations

50
times ranked

2922
citing authors

#	ARTICLE	IF	CITATIONS
1	Viromes of Freshwater Fish with Lacustrine and Diadromous Life Histories Differ in Composition. <i>Viruses</i> , 2022, 14, 257.	1.5	8
2	Transcriptome Mining Expands Knowledge of RNA Viruses across the Plant Kingdom. <i>Journal of Virology</i> , 2022, 96, .	1.5	32
3	Metagenomic sequencing reveals a lack of virus exchange between native and invasive freshwater fish across the Murrayâ€“Darling Basin, Australia. <i>Virus Evolution</i> , 2021, 7, veab034.	2.2	27
4	Virome composition in marine fish revealed by meta-transcriptomics. <i>Virus Evolution</i> , 2021, 7, veab005.	2.2	58
5	New Zealandâ€™s science-led response to the SARS-CoV-2 pandemic. <i>Nature Immunology</i> , 2021, 22, 262-263.	7.0	24
6	A Novel Rubi-Like Virus in the Pacific Electric Ray (<i>Tetronarce californica</i>) Reveals the Complex Evolutionary History of the Matonaviridae. <i>Viruses</i> , 2021, 13, 585.	1.5	12
7	Genomic Evidence of In-Flight Transmission of SARS-CoV-2 Despite Predeparture Testing. <i>Emerging Infectious Diseases</i> , 2021, 27, 687-693.	2.0	58
8	How accurately can we assess zoonotic risk?. <i>PLoS Biology</i> , 2021, 19, e3001135.	2.6	56
9	Slippery when wet: cross-species transmission of divergent coronaviruses in bony and jawless fish and the evolutionary history of the <i>Coronaviridae</i> . <i>Virus Evolution</i> , 2021, 7, veab050.	2.2	23
10	Phylodynamics reveals the role of human travel and contact tracing in controlling the first wave of COVID-19 in four island nations. <i>Virus Evolution</i> , 2021, 7, veab052.	2.2	35
11	Subtype-specific differences in transmission cluster dynamics of HIVâ€“1 B and CRF01_AE in New South Wales, Australia. <i>Journal of the International AIDS Society</i> , 2021, 24, e25655.	1.2	7
12	Red fox viromes in urban and rural landscapes. <i>Virus Evolution</i> , 2020, 6, veaa065.	2.2	27
13	Divergent Influenza-Like Viruses of Amphibians and Fish Support an Ancient Evolutionary Association. <i>Viruses</i> , 2020, 12, 1042.	1.5	23
14	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. <i>Nature Communications</i> , 2020, 11, 6351.	5.8	100
15	Meta-Transcriptomic Identification of Divergent Amnoonviridae in Fish. <i>Viruses</i> , 2020, 12, 1254.	1.5	16
16	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	2.4	59
17	Hidden diversity and evolution of viruses in market fish. <i>Virus Evolution</i> , 2018, 4, vey031.	2.2	54
18	Evolutionary Virology at 40. <i>Genetics</i> , 2018, 210, 1151-1162.	1.2	51

#	ARTICLE	IF	CITATIONS
19	Evolution of Human Respiratory Syncytial Virus (RSV) over Multiple Seasons in New South Wales, Australia. <i>Viruses</i> , 2018, 10, 476.	1.5	28
20	Virological Sampling of Inaccessible Wildlife with Drones. <i>Viruses</i> , 2018, 10, 300.	1.5	49
21	Continental synchronicity of human influenza virus epidemics despite climactic variation. <i>PLoS Pathogens</i> , 2018, 14, e1006780.	2.1	38
22	Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. <i>PLoS Pathogens</i> , 2017, 13, e1006215.	2.1	224
23	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016, 16, 115.	3.2	19
24	Pathogen population bottlenecks and adaptive landscapes: overcoming the barriers to disease emergence. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160727.	1.2	46
25	Estimating evolutionary rates using time-structured data: a general comparison of phylogenetic methods. <i>Bioinformatics</i> , 2016, 32, 3375-3379.	1.8	38
26	Fluid Spatial Dynamics of West Nile Virus in the United States: Rapid Spread in a Permissive Host Environment. <i>Journal of Virology</i> , 2016, 90, 862-872.	1.5	42
27	A generic assay for whole-genome amplification and deep sequencing of enterovirus A71. <i>Journal of Virological Methods</i> , 2015, 215-216, 30-36.	1.0	28
28	Phylogenetics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015, 89, 8871-8879.	1.5	51
29	Seasonal Drivers of the Epidemiology of Arthropod-Borne Viruses in Australia. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3325.	1.3	37
30	Contact Heterogeneity, Rather Than Transmission Efficiency, Limits the Emergence and Spread of Canine Influenza Virus. <i>PLoS Pathogens</i> , 2014, 10, e1004455.	2.1	43
31	Inheritance of Epigenome Variants Across Generations and its Implications on the Emergence of Phenotypic Novelty During Evolution. , 2014, , 187-194.		1
32	Molecular evolution and antigenic variation of European brown hare syndrome virus (EBHSV). <i>Virology</i> , 2014, 468-470, 104-112.	1.1	21
33	The evolutionary potential of paramutation: A population-epigenetic model. <i>Theoretical Population Biology</i> , 2013, 88, 9-19.	0.5	16
34	Exploring epiallele stability in a population-epigenetic model. <i>Theoretical Population Biology</i> , 2013, 83, 136-144.	0.5	33
35	The adaptive invasion of epialleles in a heterogeneous environment. <i>Theoretical Population Biology</i> , 2013, 83, 1-8.	0.5	19
36	Population-epigenetic models of selection. <i>Theoretical Population Biology</i> , 2012, 81, 232-242.	0.5	87