

Jemma L Geoghegan

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,542
citations

331642

21
h-index

361001

35
g-index

50
all docs

50
docs citations

50
times ranked

2695
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. <i>PLoS Pathogens</i> , 2017, 13, e1006215.	4.7	224
2	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. <i>Nature Communications</i> , 2020, 11, 6351.	12.8	100
3	Population-epigenetic models of selection. <i>Theoretical Population Biology</i> , 2012, 81, 232-242.	1.1	87
4	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	5.3	59
5	Virome composition in marine fish revealed by meta-transcriptomics. <i>Virus Evolution</i> , 2021, 7, veab005.	4.9	58
6	Genomic Evidence of In-Flight Transmission of SARS-CoV-2 Despite Predeparture Testing. <i>Emerging Infectious Diseases</i> , 2021, 27, 687-693.	4.3	58
7	How accurately can we assess zoonotic risk?. <i>PLoS Biology</i> , 2021, 19, e3001135.	5.6	56
8	Hidden diversity and evolution of viruses in market fish. <i>Virus Evolution</i> , 2018, 4, vey031.	4.9	54
9	Phylogenetics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015, 89, 8871-8879.	3.4	51
10	Evolutionary Virology at 40. <i>Genetics</i> , 2018, 210, 1151-1162.	2.9	51
11	Virological Sampling of Inaccessible Wildlife with Drones. <i>Viruses</i> , 2018, 10, 300.	3.3	49
12	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.	2.6	46
13	Contact Heterogeneity, Rather Than Transmission Efficiency, Limits the Emergence and Spread of Canine Influenza Virus. <i>PLoS Pathogens</i> , 2014, 10, e1004455.	4.7	43
14	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.	3.4	42
15	Estimating evolutionary rates using time-structured data: a general comparison of phylogenetic methods. <i>Bioinformatics</i> , 2016, 32, 3375-3379.	4.1	38
16	Continental synchronicity of human influenza virus epidemics despite climactic variation. <i>PLoS Pathogens</i> , 2018, 14, e1006780.	4.7	38
17	Seasonal Drivers of the Epidemiology of Arthropod-Borne Viruses in Australia. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3325.	3.0	37
18	Phylogenetics 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.	4.9	35

#	ARTICLE	IF	CITATIONS
19	Exploring epiallele stability in a population-epigenetic model. <i>Theoretical Population Biology</i> , 2013, 83, 136-144.	1.1	33
20	Transcriptome Mining Expands Knowledge of RNA Viruses across the Plant Kingdom. <i>Journal of Virology</i> , 2022, 96, .	3.4	32
21	A generic assay for whole-genome amplification and deep sequencing of enterovirus A71. <i>Journal of Virological Methods</i> , 2015, 215-216, 30-36.	2.1	28
22	Evolution of Human Respiratory Syncytial Virus (RSV) over Multiple Seasons in New South Wales, Australia. <i>Viruses</i> , 2018, 10, 476.	3.3	28
23	Red fox viromes in urban and rural landscapes. <i>Virus Evolution</i> , 2020, 6, veaa065.	4.9	27
24	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.	4.9	27
25	New Zealandâ€™s science-led response to the SARS-CoV-2 pandemic. <i>Nature Immunology</i> , 2021, 22, 262-263.	14.5	24
26	Divergent Influenza-Like Viruses of Amphibians and Fish Support an Ancient Evolutionary Association. <i>Viruses</i> , 2020, 12, 1042.	3.3	23
27	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.	4.9	23
28	Molecular evolution and antigenic variation of European brown hare syndrome virus (EBHSV). <i>Virology</i> , 2014, 468-470, 104-112.	2.4	21
29	The adaptive invasion of epialleles in a heterogeneous environment. <i>Theoretical Population Biology</i> , 2013, 88, 1-8.	1.1	19
30	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016, 16, 115.	3.2	19
31	The evolutionary potential of paramutation: A population-epigenetic model. <i>Theoretical Population Biology</i> , 2013, 88, 9-19.	1.1	16
32	Meta-Transcriptomic Identification of Divergent Amnoonviridae in Fish. <i>Viruses</i> , 2020, 12, 1254.	3.3	16
33	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.	3.3	12
34	Viromes of Freshwater Fish with Lacustrine and Diadromous Life Histories Differ in Composition. <i>Viruses</i> , 2022, 14, 257.	3.3	8
35	Subtypeâ€“specific differences in transmission cluster dynamics of HIVâ€“1 B and CRF01_â€“AE in New South Wales, Australia. <i>Journal of the International AIDS Society</i> , 2021, 24, e25655.	3.0	7
36	Inheritance of Epigenome Variants Across Generations and its Implications on the Emergence of Phenotypic Novelty During Evolution. , 2014, , 187-194.		1