

Robert James Gifford

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

3,843
citations

218677

26
h-index

168389

53
g-index

71
all docs

71
docs citations

71
times ranked

5920
citing authors

#	ARTICLE	IF	CITATIONS
1	Making genomic surveillance deliver: A lineage classification and nomenclature system to inform rabies elimination. <i>PLoS Pathogens</i> , 2022, 18, e1010023.	4.7	17
2	Ancient evolution of hepadnaviral paleoviruses and their impact on host genomes. <i>Virus Evolution</i> , 2021, 7, veab012.	4.9	8
3	Mapping the evolution of bornaviruses across geological timescales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2108123118.	7.1	2
4	Reproductive and metabolic adaptation to multistressor training in women. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2021, 321, E281-E291.	3.5	13
5	No evidence of SARS-CoV-2 reverse transcription and integration as the origin of chimeric transcripts in patient tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	28
6	Amilorides inhibit SARS-CoV-2 replication in vitro by targeting RNA structures. <i>Science Advances</i> , 2021, 7, eabl6096.	10.3	31
7	Evolution of dependoparvoviruses across geological timescalesâ€™ implications for design of AAV-based gene therapy vectors. <i>Virus Evolution</i> , 2020, 6, veaa043.	4.9	10
8	Retroviruses drive the rapid evolution of mammalian <i>APOBEC3</i> genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 610-618.	7.1	77
9	Rapid in-country sequencing of whole virus genomes to inform rabies elimination programmes. <i>Wellcome Open Research</i> , 2020, 5, 3.	1.8	30
10	Rapid in-country sequencing of whole virus genomes to inform rabies elimination programmes. <i>Wellcome Open Research</i> , 2020, 5, 3.	1.8	26
11	Molecular Properties and Evolutionary Origins of a Parvovirus-Derived Myosin Fusion Gene in Guinea Pigs. <i>Journal of Virology</i> , 2019, 93, .	3.4	6
12	An Ancient Lineage of Highly Divergent Parvoviruses Infects both Vertebrate and Invertebrate Hosts. <i>Viruses</i> , 2019, 11, 525.	3.3	64
13	Derivation of simian tropic HIV-1 infectious clone reveals virus adaptation to a new host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10504-10509.	7.1	14
14	Interpreting Viral Deep Sequencing Data with GLUE. <i>Viruses</i> , 2019, 11, 323.	3.3	29
15	Origin and recent expansion of an endogenous gammaretroviral lineage in domestic and wild canids. <i>Retrovirology</i> , 2019, 16, 6.	2.0	16
16	Deltaretroviruses have circulated since at least the Paleogene and infected a broad range of mammalian species. <i>Retrovirology</i> , 2019, 16, 33.	2.0	14
17	Examination and Reconstruction of Three Ancient Endogenous Parvovirus Capsid Protein Gene Remnants Found in Rodent Genomes. <i>Journal of Virology</i> , 2019, 93, .	3.4	13
18	The evolution, distribution and diversity of endogenous circoviral elements in vertebrate genomes. <i>Virus Research</i> , 2019, 262, 15-23.	2.2	27

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19	GLUE: a flexible software system for virus sequence data. BMC Bioinformatics, 2018, 19, 532.	2.6	84
20	Endogenous amdoparvovirus-related elements reveal insights into the biology and evolution of vertebrate parvoviruses. Virus Evolution, 2018, 4, vey026.	4.9	19
21	Distribution, Diversity, and Evolution of Endogenous Retroviruses in Perissodactyl Genomes. Journal of Virology, 2018, 92, .	3.4	6
22	Nomenclature for endogenous retrovirus (ERV) loci. Retrovirology, 2018, 15, 59.	2.0	103
23	Predicting the Effectiveness of Hepatitis C Virus Neutralizing Antibodies by Bioinformatic Analysis of Conserved Epitope Residues Using Public Sequence Data. Frontiers in Immunology, 2018, 9, 1470.	4.8	11
24	Novel Parvoviruses from Wild and Domestic Animals in Brazil Provide New Insights into Parvovirus Distribution and Diversity. Viruses, 2018, 10, 143.	3.3	28
25	Remnants of an Ancient Deltaretrovirus in the Genomes of Horseshoe Bats (Rhinolophidae). Viruses, 2018, 10, 185.	3.3	14
26	Reconstruction of a replication-competent ancestral murine endogenous retrovirus-L. Retrovirology, 2018, 15, 34.	2.0	11
27	Insights into Circovirus Host Range from the Genomic Fossil Record. Journal of Virology, 2018, 92, .	3.4	39
28	Discovery of an endogenous Deltaretrovirus in the genome of long-fingered bats (Chiroptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 114, 3145-3150.	7.1	32
29	Hepatitis C and the absence of genomic data in low-income countries: a barrier on the road to elimination?. The Lancet Gastroenterology and Hepatology, 2017, 2, 700-701.	8.1	18
30	Chapparvoviruses occur in at least three vertebrate classes and have a broad biogeographic distribution. Journal of General Virology, 2017, 98, 225-229.	2.9	58
31	Fundamental properties of the mammalian innate immune system revealed by multispecies comparison of type I interferon responses. PLoS Biology, 2017, 15, e2004086.	5.6	272
32	Co-option of an endogenous retrovirus envelope for host defense in hominid ancestors. ELife, 2017, 6, .	6.0	75
33	An Intact Retroviral Gene Conserved in Spiny-Rayed Fishes for over 100ÂMy. Molecular Biology and Evolution, 2016, 34, msw262.	8.9	21
34	Late Ebola virus relapse causing meningoencephalitis: a case report. Lancet, The, 2016, 388, 498-503.	13.7	291
35	Identification and spontaneous immune targeting of an endogenous retrovirus K envelope protein in the Indian rhesus macaque model of human disease. Retrovirology, 2016, 13, 6.	2.0	9
36	A Novel Recombinant Retrovirus in the Genomes of Modern Birds Combines Features of Avian and Mammalian Retroviruses. Journal of Virology, 2014, 88, 2398-2405.	3.4	31

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37	Parvovirus-Derived Endogenous Viral Elements in Two South American Rodent Genomes. <i>Journal of Virology</i> , 2014, 88, 12158-12162.	3.4	23
38	Extreme Genetic Fragility of the HIV-1 Capsid. <i>PLoS Pathogens</i> , 2013, 9, e1003461.	4.7	178
39	The Extraordinary Evolutionary History of the Reticuloendotheliosis Viruses. <i>PLoS Biology</i> , 2013, 11, e1001642.	5.6	88
40	<i>Env</i>-less endogenous retroviruses are genomic superspreaders. <i>Proceedings of the National Academy of Sciences of the United States of America</i>, 2012, 109, 7385-7390.</i>	7.1	111
41	Vaccination with Cancer- and HIV Infection-Associated Endogenous Retrotransposable Elements Is Safe and Immunogenic. <i>Journal of Immunology</i> , 2012, 189, 1467-1479.	0.8	46
42	Viral evolution in deep time: lentiviruses and mammals. <i>Trends in Genetics</i> , 2012, 28, 89-100.	6.7	95
43	Endogenous Viral Elements in Animal Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001191.	3.5	565
44	The HIV-1 Subtype C Epidemic in South America Is Linked to the United Kingdom. <i>PLoS ONE</i> , 2010, 5, e9311.	2.5	53
45	Macroevolution of Complex Retroviruses. <i>Science</i> , 2009, 325, 1512-1512.	12.6	146
46	Demonstration of Sustained Drug-Resistant Human Immunodeficiency Virus Type 1 Lineages Circulating among Treatment-Naïve Individuals. <i>Journal of Virology</i> , 2009, 83, 2645-2654.	3.4	102
47	The calibrated population resistance tool: standardized genotypic estimation of transmitted HIV-1 drug resistance. <i>Bioinformatics</i> , 2009, 25, 1197-1198.	4.1	159
48	Phylogenetic Reconstruction of Transmission Events from Individuals with Acute HIV Infection: Toward More Rigorous Epidemiological Definitions. <i>Journal of Infectious Diseases</i> , 2009, 199, 427-431.	4.0	36
49	Sequence editing by Apolipoprotein B RNA-editing catalytic component-B and epidemiological surveillance of transmitted HIV-1 drug resistance. <i>Aids</i> , 2008, 22, 717-725.	2.2	21
50	A transitional endogenous lentivirus from the genome of a basal primate and implications for lentivirus evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20362-20367.	7.1	183
51	Phylogenetic Surveillance of Viral Genetic Diversity and the Evolving Molecular Epidemiology of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2007, 81, 13050-13056.	3.4	81
52	Discovery and analysis of the first endogenous lentivirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6261-6265.	7.1	193
53	Evolution at the host-retrovirus interface. <i>BioEssays</i> , 2006, 28, 1153-1156.	2.5	7