Robert James Gifford

List of Publications by Year
in descending order

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	Endogenous Viral Elements in Animal Genomes. PLoS Genetics, 2010, 6, e1001191.	3.5	565
2	Late Ebola virus relapse causing meningoencephalitis: a case report. Lancet, The, 2016, 388, 498-503.	13.7	291
3	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
4	Discovery and analysis of the first endogenous lentivirus. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6261-6265.	7.1	193
5	A transitional endogenous lentivirus from the genome of a basal primate and implications for lentivirus evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20362-20367.	7.1	183
6	Extreme Genetic Fragility of the HIV-1 Capsid. PLoS Pathogens, 2013, 9, e1003461.	4.7	178
7	The calibrated population resistance tool: standardized genotypic estimation of transmitted HIV-1 drug resistance. Bioinformatics, 2009, 25, 1197-1198.	4.1	159
8	Macroevolution of Complex Retroviruses. Science, 2009, 325, 1512-1512.	12.6	146
9	Env -less endogenous retroviruses are genomic superspreaders. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7385-7390.	7.1	111
10	Nomenclature for endogenous retrovirus (ERV) loci. Retrovirology, 2018, 15, 59.	2.0	103
11	Demonstration of Sustained Drug-Resistant Human Immunodeficiency Virus Type 1 Lineages Circulating among Treatment-Naîve Individuals. Journal of Virology, 2009, 83, 2645-2654.	3.4	102
12	Viral evolution in deep time: lentiviruses and mammals. Trends in Genetics, 2012, 28, 89-100.	6.7	95
13	The Extraordinary Evolutionary History of the Reticuloendotheliosis Viruses. PLoS Biology, 2013, 11, e1001642.	5.6	88
14	GLUE: a flexible software system for virus sequence data. BMC Bioinformatics, 2018, 19, 532.	2.6	84
15	Phylogenetic Surveillance of Viral Genetic Diversity and the Evolving Molecular Epidemiology of Human Immunodeficiency Virus Type 1. Journal of Virology, 2007, 81, 13050-13056.	3.4	81
16	Retroviruses drive the rapid evolution of mammalian APOBEC3 genes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 610-618.	7.1	77
17	Co-option of an endogenous retrovirus envelope for host defense in hominid ancestors. ELife, 2017, 6, .	6.0	75
18	An Ancient Lineage of Highly Divergent Parvoviruses Infects both Vertebrate and Invertebrate Hosts. Viruses, 2019, 11, 525.	3.3	64

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19	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
20	The HIV-1 Subtype C Epidemic in South America Is Linked to the United Kingdom. PLoS ONE, 2010, 5, e9311.	2.5	53
21	Vaccination with Cancer- and HIV Infection-Associated Endogenous Retrotransposable Elements Is Safe and Immunogenic. Journal of Immunology, 2012, 189, 1467-1479.	0.8	46
22	Insights into Circovirus Host Range from the Genomic Fossil Record. Journal of Virology, 2018, 92, .	3.4	39
23	Phylogenetic Reconstruction of Transmission Events from Individuals with Acute HIV Infection: Toward Moreâ€Rigorous Epidemiological Definitions. Journal of Infectious Diseases, 2009, 199, 427-431.	4.0	36
24	Discovery of an endogenous Deltaretrovirus in the genome of long-fingered bats (Chiroptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 114, 3145-3150.	7.1	32
25	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
26	Amilorides inhibit SARS-CoV-2 replication in vitro by targeting RNA structures. Science Advances, 2021, 7, eabl6096.	10.3	31
27	Rapid in-country sequencing of whole virus genomes to inform rabies elimination programmes. Wellcome Open Research, 2020, 5, 3.	1.8	30
28	Interpreting Viral Deep Sequencing Data with GLUE. Viruses, 2019, 11, 323.	3.3	29
29	Novel Parvoviruses from Wild and Domestic Animals in Brazil Provide New Insights into Parvovirus Distribution and Diversity. Viruses, 2018, 10, 143.	3.3	28
30	No evidence of SARS-CoV-2 reverse transcription and integration as the origin of chimeric transcripts in patient tissues. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	28
31	The evolution, distribution and diversity of endogenous circoviral elements in vertebrate genomes. Virus Research, 2019, 262, 15-23.	2.2	27
32	Rapid in-country sequencing of whole virus genomes to inform rabies elimination programmes. Wellcome Open Research, 2020, 5, 3.	1.8	26
33	Parvovirus-Derived Endogenous Viral Elements in Two South American Rodent Genomes. Journal of Virology, 2014, 88, 12158-12162.	3.4	23
34	Sequence editing by Apolipoprotein B RNA-editing catalytic component-B and epidemiological surveillance of transmitted HIV-1 drug resistance. Aids, 2008, 22, 717-725.	2.2	21
35	An Intact Retroviral Gene Conserved in Spiny-Rayed Fishes for over 100ÂMy. Molecular Biology and Evolution, 2016, 34, msw262.	8.9	21
36	Endogenous amdoparvovirus-related elements reveal insights into the biology and evolution of vertebrate parvoviruses. Virus Evolution, 2018, 4, vey026.	4.9	19

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37	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
38	Making genomic surveillance deliver: A lineage classification and nomenclature system to inform rabies elimination. PLoS Pathogens, 2022, 18, e1010023.	4.7	17
39	Origin and recent expansion of an endogenous gammaretroviral lineage in domestic and wild canids. Retrovirology, 2019, 16, 6.	2.0	16
40	Remnants of an Ancient Deltaretrovirus in the Genomes of Horseshoe Bats (Rhinolophidae). Viruses, 2018, 10, 185.	3.3	14
41	Derivation of simian tropic HIV-1 infectious clone reveals virus adaptation to a new host. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10504-10509.	7.1	14
42	Deltaretroviruses have circulated since at least the Paleogene and infected a broad range of mammalian species. Retrovirology, 2019, 16, 33.	2.0	14
43	Examination and Reconstruction of Three Ancient Endogenous Parvovirus Capsid Protein Gene Remnants Found in Rodent Genomes. Journal of Virology, 2019, 93, .	3.4	13
44	Reproductive and metabolic adaptation to multistressor training in women. American Journal of Physiology - Endocrinology and Metabolism, 2021, 321, E281-E291.	3.5	13
45	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
46	Reconstruction of a replication-competent ancestral murine endogenous retrovirus-L. Retrovirology, 2018, 15, 34.	2.0	11
47	Evolution of dependoparvoviruses across geological timescalesâ€”implications for design of AAV-based gene therapy vectors. Virus Evolution, 2020, 6, veaa043.	4.9	10
48	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
49	Ancient evolution of hepadnaviral paleoviruses and their impact on host genomes. Virus Evolution, 2021, 7, veab012.	4.9	8
50	Evolution at the hostâ€“retrovirus interface. BioEssays, 2006, 28, 1153-1156.	2.5	7
51	Distribution, Diversity, and Evolution of Endogenous Retroviruses in Perissodactyl Genomes. Journal of Virology, 2018, 92, .	3.4	6
52	Molecular Properties and Evolutionary Origins of a Parvovirus-Derived Myosin Fusion Gene in Guinea Pigs. Journal of Virology, 2019, 93, .	3.4	6
53	Mapping the evolution of bornaviruses across geological timescales. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2108123118.	7.1	2