

Aris Katzourakis

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

3,366
citations

236925

25
h-index

168389

53
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68
all docs

68
docs citations

68
times ranked

4455
citing authors

#	ARTICLE	IF	CITATIONS
1	Paleovirology of the DNA viruses of eukaryotes. <i>Trends in Microbiology</i> , 2022, 30, 281-292.	7.7	20
2	Purifying Selection Determines the Short-Term Time Dependency of Evolutionary Rates in SARS-CoV-2 and pH1N1 Influenza. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	42
3	Antigenic evolution will lead to new SARS-CoV-2 variants with unpredictable severity. <i>Nature Reviews Microbiology</i> , 2022, 20, 251-252.	28.6	96
4	Target Enrichment Metagenomics Reveals Human Pegivirus-1 in Pediatric Hematopoietic Stem Cell Transplantation Recipients. <i>Viruses</i> , 2022, 14, 796.	3.3	1
5	A framework for reconstructing SARS-CoV-2 transmission dynamics using excess mortality data. <i>Nature Communications</i> , 2022, 13, .	12.8	10
6	Tilapia lake virus (TiLV): Genomic epidemiology and its early origin. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 435-444.	3.0	18
7	Estimates of anti-SARS-CoV-2 antibody seroprevalence in Iran. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 602-603.	9.1	11
8	Excess deaths associated with the Iranian COVID-19 epidemic: A province-level analysis. <i>International Journal of Infectious Diseases</i> , 2021, 107, 101-115.	3.3	24
9	A mechanistic evolutionary model explains the time-dependent pattern of substitution rates in viruses. <i>Current Biology</i> , 2021, 31, 4689-4696.e5.	3.9	30
10	Lessons for preparedness and reasons for concern from the early COVID-19 epidemic in Iran. <i>Epidemics</i> , 2021, 36, 100472.	3.0	17
11	Phylogenomics of the <i>Maverick</i> Virus-Like Mobile Genetic Elements of Vertebrates. <i>Molecular Biology and Evolution</i> , 2021, 38, 1731-1743.	8.9	22
12	Rapid evidence review to inform safe return to campus in the context of coronavirus disease 2019 (COVID-19). <i>Wellcome Open Research</i> , 2021, 6, 282.	1.8	6
13	Diversity, taxonomy, and evolution of archaeal viruses of the class Caudoviricetes. <i>PLoS Biology</i> , 2021, 19, e3001442.	5.6	44
14	SARS-CoV-2 genetic variations associated with COVID-19 pathogenicity. <i>Microbial Genomics</i> , 2021, 7, .	2.0	10
15	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	27.8	210
16	HIV-1 p24Gag adaptation to modern and archaic HLA-allele frequency differences in ethnic groups contributes to viral subtype diversification. <i>Virus Evolution</i> , 2020, 6, veaa085.	4.9	7
17	Host or pathogen-related factors in COVID-19 severity? – Authors' reply. <i>Lancet</i> , The, 2020, 396, 1397.	13.7	3
18	The Potential Role of Endogenous Viral Elements in the Evolution of Bats as Reservoirs for Zoonotic Viruses. <i>Annual Review of Virology</i> , 2020, 7, 103-119.	6.7	34

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19	The First Co-Opted Endogenous Foamy Viruses and the Evolutionary History of Reptilian Foamy Viruses. <i>Viruses</i> , 2019, 11, 641.	3.3	13
20	The evolution of endogenous retroviral envelope genes in bats and their potential contribution to host biology. <i>Virus Research</i> , 2019, 270, 197645.	2.2	10
21	Modular nature of simian foamy virus genomes and their evolutionary history. <i>Virus Evolution</i> , 2019, 5, vez032.	4.9	14
22	Interferon-Inducible Protein 16 (IFI16) Has a Broad-Spectrum Binding Ability Against ssDNA Targets: An Evolutionary Hypothesis for Antiretroviral Checkpoint. <i>Frontiers in Microbiology</i> , 2019, 10, 1426.	3.5	18
23	The Exaptation of HERV-H: Evolutionary Analyses Reveal the Genomic Features of Highly Transcribed Elements. <i>Frontiers in Immunology</i> , 2019, 10, 1339.	4.8	18
24	Reply to “Evolutionary stasis of viruses”. <i>Nature Reviews Microbiology</i> , 2019, 17, 329-330.	28.6	3
25	Prisoners of war “ host adaptation and its constraints on virus evolution. <i>Nature Reviews Microbiology</i> , 2019, 17, 321-328.	28.6	117
26	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	7.8	124
27	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.	7.1	65
28	Human Endogenous Retrovirus-K HML-2 integration within <i>RASGRF2</i> is associated with intravenous drug abuse and modulates transcription in a cell-line model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10434-10439.	7.1	18
29	Cell-Derived Viral Genes Evolve under Stronger Purifying Selection in Rhadinoviruses. <i>Journal of Virology</i> , 2018, 92, .	3.4	3
30	Marine origin of retroviruses in the early Palaeozoic Era. <i>Nature Communications</i> , 2017, 8, 13954.	12.8	104
31	Roles of Endogenous Retroviruses in Early Life Events. <i>Trends in Microbiology</i> , 2017, 25, 876-877.	7.7	14
32	Editorial overview: Paleovirology: the genomic fossil record, and consequences of ancient viral infections. <i>Current Opinion in Virology</i> , 2017, 25, ix-xi.	5.4	3
33	A novel viral lineage distantly related to herpesviruses discovered within fish genome sequence data. <i>Virus Evolution</i> , 2017, 3, vex016.	4.9	20
34	Disentangling the origins of virophages and polintons. <i>Current Opinion in Virology</i> , 2017, 25, 59-65.	5.4	16
35	STEAK: A specific tool for transposable elements and retrovirus detection in high-throughput sequencing data. <i>Virus Evolution</i> , 2017, 3, vex023.	4.9	21
36	De Novo Assembly of Human Herpes Virus Type 1 (HHV-1) Genome, Mining of Non-Canonical Structures and Detection of Novel Drug-Resistance Mutations Using Short- and Long-Read Next Generation Sequencing Technologies. <i>PLoS ONE</i> , 2016, 11, e0157600.	2.5	43

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37	A contaminant-free assessment of Endogenous Retroviral RNA in human plasma. <i>Scientific Reports</i> , 2016, 6, 33598.	3.3	15
38	Evolution: Endogenous Viruses Provide Shortcuts in Antiviral Immunity. <i>Current Biology</i> , 2016, 26, R427-R429.	3.9	16
39	The global spread of HIV-1 subtype B epidemic. <i>Infection, Genetics and Evolution</i> , 2016, 46, 169-179.	2.3	60
40	Time-Dependent Rate Phenomenon in Viruses. <i>Journal of Virology</i> , 2016, 90, 7184-7195.	3.4	128
41	Human endogenous retrovirus (HERV) expression is not induced by treatment with the histone deacetylase (HDAC) inhibitors in cellular models of HIV-1 latency. <i>Retrovirology</i> , 2016, 13, 10.	2.0	25
42	Phylogenetic Analysis Reveals That ERVs "Die Young" but HERV-H Is Unusually Conserved. <i>PLoS Computational Biology</i> , 2016, 12, e1004964.	3.2	22
43	HIV-infected sex workers with beneficial HLA-variants are potential hubs for selection of HIV-1 recombinants that may affect disease progression. <i>Scientific Reports</i> , 2015, 5, 11253.	3.3	5
44	Orthologous endogenous retroviruses exhibit directional selection since the chimp-human split. <i>Retrovirology</i> , 2015, 12, 52.	2.0	17
45	Wide distribution and ancient evolutionary history of simian foamy viruses in New World primates. <i>Retrovirology</i> , 2015, 12, 89.	2.0	26
46	Convergent capture of retroviral superantigens by mammalian herpesviruses. <i>Nature Communications</i> , 2015, 6, 8299.	12.8	14
47	Endogenous retroviruses. <i>Current Biology</i> , 2015, 25, R644-R646.	3.9	17
48	Endogenous viruses: Connecting recent and ancient viral evolution. <i>Virology</i> , 2015, 479-480, 26-37.	2.4	152
49	Time dependency of foamy virus evolutionary rate estimates. <i>BMC Evolutionary Biology</i> , 2015, 15, 119.	3.2	28
50	Larger Mammalian Body Size Leads to Lower Retroviral Activity. <i>PLoS Pathogens</i> , 2014, 10, e1004214.	4.7	47
51	The First Endogenous Herpesvirus, Identified in the Tarsier Genome, and Novel Sequences from Primate Rhadinoviruses and Lymphocryptoviruses. <i>PLoS Genetics</i> , 2014, 10, e1004332.	3.5	47
52	Discovery of prosimian and afrotherian foamy viruses and potential cross species transmissions amidst stable and ancient mammalian co-evolution. <i>Retrovirology</i> , 2014, 11, 61.	2.0	45
53	Sex-specific aspects of endogenous retroviral insertion and deletion. <i>BMC Evolutionary Biology</i> , 2013, 13, 243.	3.2	2
54	Paleovirology: inferring viral evolution from host genome sequence data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120493.	4.0	53

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55	The mode and tempo of hepatitis C virus evolution within and among hosts. <i>BMC Evolutionary Biology</i> , 2011, 11, 131.	3.2	122
56	Phylogenetic Analysis of Murine Leukemia Virus Sequences from Longitudinally Sampled Chronic Fatigue Syndrome Patients Suggests PCR Contamination Rather than Viral Evolution. <i>Journal of Virology</i> , 2011, 85, 10909-10913.	3.4	15
57	Endogenous Viral Elements in Animal Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001191.	3.5	565
58	Macroevolution of Complex Retroviruses. <i>Science</i> , 2009, 325, 1512-1512.	12.6	146
59	HLA Footprints on Human Immunodeficiency Virus Type 1 Are Associated with Interclade Polymorphisms and Intraclade Phylogenetic Clustering. <i>Journal of Virology</i> , 2009, 83, 4605-4615.	3.4	40
60	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
61	Effects of Recombination Rate on Human Endogenous Retrovirus Fixation and Persistence. <i>Journal of Virology</i> , 2007, 81, 10712-10717.	3.4	39
62	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
63	The evolutionary dynamics of endogenous retroviruses. <i>Trends in Microbiology</i> , 2005, 13, 463-468.	7.7	84
64	A Mechanistic Evolutionary Model Explains the Time-Dependent Pattern of Substitution Rates in Viruses. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1