

Aris I Katzourakis

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

4,525
citations

134610

34
h-index

129628

63
g-index

73
all docs

73
docs citations

73
times ranked

5956
citing authors

#	ARTICLE	IF	CITATIONS
1	Paleovirology of the DNA viruses of eukaryotes. <i>Trends in Microbiology</i> , 2022, 30, 281-292.	3.5	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, .	3.5	42
3	A mechanistic evolutionary model explains the time-dependent pattern of substitution rates in viruses. <i>Current Biology</i> , 2021, 31, 4689-4696.e5.	1.8	30
4	Phylogenomics of the <i>Maverick</i> Virus-Like Mobile Genetic Elements of Vertebrates. <i>Molecular Biology and Evolution</i> , 2021, 38, 1731-1743.	3.5	22
5	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	13.7	210
6	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.	2.2	7
7	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.	3.0	34
8	The First Co-Opted Endogenous Foamy Viruses and the Evolutionary History of Reptilian Foamy Viruses. <i>Viruses</i> , 2019, 11, 641.	1.5	13
9	The evolution of endogenous retroviral envelope genes in bats and their potential contribution to host biology. <i>Virus Research</i> , 2019, 270, 197645.	1.1	10
10	Modular nature of simian foamy virus genomes and their evolutionary history. <i>Virus Evolution</i> , 2019, 5, vez032.	2.2	14
11	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.	1.5	18
12	The Exaptation of HERV-H: Evolutionary Analyses Reveal the Genomic Features of Highly Transcribed Elements. <i>Frontiers in Immunology</i> , 2019, 10, 1339.	2.2	18
13	Reply to "Evolutionary stasis of viruses". <i>Nature Reviews Microbiology</i> , 2019, 17, 329-330.	13.6	3
14	Prisoners of war " host adaptation and its constraints on virus evolution. <i>Nature Reviews Microbiology</i> , 2019, 17, 321-328.	13.6	117
15	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.	3.3	65
16	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.	3.3	18
17	Cell-Derived Viral Genes Evolve under Stronger Purifying Selection in Rhadinoviruses. <i>Journal of Virology</i> , 2018, 92, .	1.5	3
18	Marine origin of retroviruses in the early Palaeozoic Era. <i>Nature Communications</i> , 2017, 8, 13954.	5.8	104

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19	Roles of Endogenous Retroviruses in Early Life Events. <i>Trends in Microbiology</i> , 2017, 25, 876-877.	3.5	14
20	A novel viral lineage distantly related to herpesviruses discovered within fish genome sequence data. <i>Virus Evolution</i> , 2017, 3, vex016.	2.2	20
21	Disentangling the origins of virophages and polintons. <i>Current Opinion in Virology</i> , 2017, 25, 59-65.	2.6	16
22	STEAK: A specific tool for transposable elements and retrovirus detection in high-throughput sequencing data. <i>Virus Evolution</i> , 2017, 3, vex023.	2.2	21
23	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.	1.1	43
24	Evolution: Endogenous Viruses Provide Shortcuts in Antiviral Immunity. <i>Current Biology</i> , 2016, 26, R427-R429.	1.8	16
25	Reducing HIV infection in people who inject drugs is impossible without targeting recently-infected subjects. <i>Aids</i> , 2016, 30, 2885-2890.	1.0	18
26	The global spread of HIV-1 subtype B epidemic. <i>Infection, Genetics and Evolution</i> , 2016, 46, 169-179.	1.0	60
27	Time-Dependent Rate Phenomenon in Viruses. <i>Journal of Virology</i> , 2016, 90, 7184-7195.	1.5	128
28	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.	0.9	25
29	Phylogenetic Analysis Reveals That ERVs "Die Young" but HERV-H Is Unusually Conserved. <i>PLoS Computational Biology</i> , 2016, 12, e1004964.	1.5	22
30	Orthologous endogenous retroviruses exhibit directional selection since the chimp-human split. <i>Retrovirology</i> , 2015, 12, 52.	0.9	17
31	Convergent capture of retroviral superantigens by mammalian herpesviruses. <i>Nature Communications</i> , 2015, 6, 8299.	5.8	14
32	Endogenous retroviruses. <i>Current Biology</i> , 2015, 25, R644-R646.	1.8	17
33	Endogenous viruses: Connecting recent and ancient viral evolution. <i>Virology</i> , 2015, 479-480, 26-37.	1.1	152
34	Time dependency of foamy virus evolutionary rate estimates. <i>BMC Evolutionary Biology</i> , 2015, 15, 119.	3.2	28
35	Larger Mammalian Body Size Leads to Lower Retroviral Activity. <i>PLoS Pathogens</i> , 2014, 10, e1004214.	2.1	47
36	The First Endogenous Herpesvirus, Identified in the Tarsier Genome, and Novel Sequences from Primate Rhadinoviruses and Lymphocryptoviruses. <i>PLoS Genetics</i> , 2014, 10, e1004332.	1.5	47

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37	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.	0.9	45
38	The origins of giant viruses, virophages and their relatives in host genomes. <i>BMC Biology</i> , 2014, 12, 51.	1.7	25
39	Sex-specific aspects of endogenous retroviral insertion and deletion. <i>BMC Evolutionary Biology</i> , 2013, 13, 243.	3.2	2
40	“There and back again”: revisiting the pathophysiological roles of human endogenous retroviruses in the post-genomic era. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120504.	1.8	57
41	Paleovirology: inferring viral evolution from host genome sequence data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120493.	1.8	53
42	Env-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.	3.3	111
43	Paleovirology and virally derived immunity. <i>Trends in Ecology and Evolution</i> , 2012, 27, 627-636.	4.2	144
44	Phylogenetic analysis consistent with a clinical history of sexual transmission of HIV-1 from a single donor reveals transmission of highly distinct variants. <i>Retrovirology</i> , 2011, 8, 54.	0.9	18
45	The mode and tempo of hepatitis C virus evolution within and among hosts. <i>BMC Evolutionary Biology</i> , 2011, 11, 131.	3.2	122
46	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.	1.5	15
47	Detecting natural selection in RNA virus populations using sequence summary statistics. <i>Infection, Genetics and Evolution</i> , 2010, 10, 421-430.	1.0	30
48	Endogenous Viral Elements in Animal Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001191.	1.5	565
49	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010, 7, 111.	0.9	141
50	Structural and Functional Analysis of Prehistoric Lentiviruses Uncovers an Ancient Molecular Interface. <i>Cell Host and Microbe</i> , 2010, 8, 248-259.	5.1	57
51	B-cell depletion reveals a role for antibodies in the control of chronic HIV-1 infection. <i>Nature Communications</i> , 2010, 1, 102.	5.8	62
52	Prevalence of HIV type-1 drug-associated mutations in pre-therapy patients in the Free State, South Africa. <i>Antiviral Therapy</i> , 2009, 14, 975-984.	0.6	23
53	Macroevolution of Complex Retroviruses. <i>Science</i> , 2009, 325, 1512-1512.	6.0	146
54	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.	1.5	40

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55	Ancient, independent evolution and distinct molecular features of the novel human T-lymphotropic virus type 4. <i>Retrovirology</i> , 2009, 6, 9.	0.9	64
56	Conserved Footprints of APOBEC3G on Hypermutated Human Immunodeficiency Virus Type 1 and Human Endogenous Retrovirus HERV-K(HML2) Sequences. <i>Journal of Virology</i> , 2008, 82, 8743-8761.	1.5	75
57	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.	3.3	183
58	Effects of Recombination Rate on Human Endogenous Retrovirus Fixation and Persistence. <i>Journal of Virology</i> , 2007, 81, 10712-10717.	1.5	39
59	Rate of Recombinational Deletion among Human Endogenous Retroviruses. <i>Journal of Virology</i> , 2007, 81, 9437-9442.	1.5	110
60	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.	3.3	193
61	High Copy Number in Human Endogenous Retrovirus Families is Associated with Copying Mechanisms in Addition to Reinfection. <i>Molecular Biology and Evolution</i> , 2005, 22, 814-817.	3.5	132
62	BlastAlign: a program that uses blast to align problematic nucleotide sequences. <i>Bioinformatics</i> , 2005, 21, 122-123.	1.8	60
63	The evolutionary dynamics of endogenous retroviruses. <i>Trends in Microbiology</i> , 2005, 13, 463-468.	3.5	84
64	Long-term reinfection of the human genome by endogenous retroviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4894-4899.	3.3	350
65	Evaluating Phylogenetic Tree Shape: Two Modifications to Fusco & Cronk's Method. <i>Journal of Theoretical Biology</i> , 2002, 214, 99-103.	0.8	48
66	Macroevolution of hoverflies (Diptera: Syrphidae): the effect of using higher-level taxa in studies of biodiversity, and correlates of species richness. <i>Journal of Evolutionary Biology</i> , 2001, 14, 219-227.	0.8	56
67	A Mechanistic Evolutionary Model Explains the Time-Dependent Pattern of Substitution Rates in Viruses. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1