

# Gkikas Magiorkinis

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

2,406  
citations

212478

28  
h-index

252626

46  
g-index

73  
all docs

73  
docs citations

73  
times ranked

4308  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dating the Origin and Estimating the Transmission Rates of the Major HIV-1 Clusters in Greece: Evidence about the Earliest Subtype A1 Epidemic in Europe. <i>Viruses</i> , 2022, 14, 101.	1.5	2
2	Editorial: Unravelling the Role of HERVs in Cancer: Insights and New Targets for Therapy. <i>Frontiers in Oncology</i> , 2022, 12, 874245.	1.3	1
3	Systematic review with meta-analysis: COVID-19 outcomes in patients receiving anti-TNF treatments. <i>Alimentary Pharmacology and Therapeutics</i> , 2022, 55, 154-167.	1.9	42
4	BreakAlign: a Perl program to align chimaeric (split) genomic NGS reads and allow visual confirmation of novel retroviral integrations. <i>BMC Bioinformatics</i> , 2022, 23, 134.	1.2	2
5	Prolonged Cardiac Monitoring and Stroke Recurrence. <i>Neurology</i> , 2022, 98, .	1.5	37
6	Earlier treatment initiation is associated with a decreased number of HIV-1 subtype A1 transmissions in Greece. <i>Sexually Transmitted Infections</i> , 2021, 97, 232-237.	0.8	2
7	Classification, Genetic Diversity and Global Distribution of Hepatitis C Virus (HCV) Genotypes and Subtypes. , 2021, , 55-69.		1
8	SARS-CoV-2 Molecular Transmission Clusters and Containment Measures in Ten European Regions during the First Pandemic Wave. <i>Life</i> , 2021, 11, 219.	1.1	7
9	Molecular Epidemiology of SARS-CoV-2 in Greece Reveals Low Rates of Onward Virus Transmission after Lifting of Travel Restrictions Based on Risk Assessment during Summer 2020. <i>MSphere</i> , 2021, 6, e0018021.	1.3	8
10	Validation of molecular clock inferred HIV infection ages: Evidence for accurate estimation of infection dates. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104799.	1.0	4
11	Comparative Immunogenicity of BNT162b2 mRNA Vaccine with Natural SARS-CoV-2 Infection. <i>Vaccines</i> , 2021, 9, 1017.	2.1	10
12	Efficient and targeted COVID-19 border testing via reinforcement learning. <i>Nature</i> , 2021, 599, 108-113.	13.7	51
13	Upregulation of Human Endogenous Retroviruses in Bronchoalveolar Lavage Fluid of COVID-19 Patients. <i>Microbiology Spectrum</i> , 2021, 9, e0126021.	1.2	30
14	Viral Causality of Human Cancer and Potential Roles of Human Endogenous Retroviruses in the Multi-Omics Era: An Evolutionary Epidemiology Review. <i>Frontiers in Oncology</i> , 2021, 11, 687631.	1.3	9
15	Satellite Earth Observation Data in Epidemiological Modeling of Malaria, Dengue and West Nile Virus: A Scoping Review. <i>Remote Sensing</i> , 2019, 11, 1862.	1.8	50
16	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
17	Editorial: The Past and the Future of Human Immunity Under Viral Evolutionary Pressure. <i>Frontiers in Immunology</i> , 2019, 10, 2340.	2.2	4
18	Potential for diagnosis of infectious disease from the 100,000 Genomes Project Metagenomic Dataset: Recommendations for reporting results. <i>Wellcome Open Research</i> , 2019, 4, 155.	0.9	9

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19	Spatiotemporal Characteristics of the HIV-1 CRF02_AG/CRF63_02A1 Epidemic in Russia and Central Asia. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 415-420.	0.5	19
20	Molecular Analysis of Human Immunodeficiency Virus Type 1 (HIV-1)â€“Infected Individuals in a Network-Based Intervention (Transmission Reduction Intervention Project): Phylogenetics Identify HIV-1â€“Infected Individuals With Social Links. <i>Journal of Infectious Diseases</i> , 2018, 218, 707-715.	1.9	18
21	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
22	Multiplexed Targeted Sequencing for Oxford Nanopore MinION: A Detailed Library Preparation Procedure. <i>Methods in Molecular Biology</i> , 2018, 1712, 43-51.	0.4	34
23	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
24	Nanopore sequencing and full genome de novo assembly of human cytomegalovirus TB40/E reveals clonal diversity and structural variations. <i>BMC Genomics</i> , 2018, 19, 577.	1.2	17
25	An Innovative Study Design to Assess the Community Effect of Interventions to Mitigate HIV Epidemics Using Transmission-Chain Phylodynamics. <i>American Journal of Epidemiology</i> , 2018, 187, 2615-2622.	1.6	7
26	Transcriptional Modulation of Human Endogenous Retroviruses in Primary CD4+ T Cells Following Vorinostat Treatment. <i>Frontiers in Immunology</i> , 2018, 9, 603.	2.2	22
27	Impact of Interferon-Î± Receptor-1 Promoter Polymorphisms on the Transcriptome of the Hepatitis B Virus-Associated Hepatocellular Carcinoma. <i>Frontiers in Immunology</i> , 2018, 9, 777.	2.2	8
28	Detailed Molecular Surveillance of the HIV-1 Outbreak Among People who Inject Drugs (PWID) in Athens During a Period of Four Years. <i>Current HIV Research</i> , 2018, 15, 396-404.	0.2	20
29	Roles of Endogenous Retroviruses in Early Life Events. <i>Trends in Microbiology</i> , 2017, 25, 876-877.	3.5	14
30	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
31	Epigenetic Control of Human Endogenous Retrovirus Expression: Focus on Regulation of Long-Terminal Repeats (LTRs). <i>Viruses</i> , 2017, 9, 130.	1.5	104
32	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
33	A contaminant-free assessment of Endogenous Retroviral RNA in human plasma. <i>Scientific Reports</i> , 2016, 6, 33598.	1.6	15
34	A network intervention that locates and intervenes with recently HIV-infected persons: The Transmission Reduction Intervention Project (TRIP). <i>Scientific Reports</i> , 2016, 6, 38100.	1.6	60
35	Transmission of hepatitis C virus infection among younger and older people who inject drugs in Vancouver, Canada. <i>Journal of Hepatology</i> , 2016, 64, 1247-1255.	1.8	18
36	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

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37	The global spread of HIV-1 subtype B epidemic. <i>Infection, Genetics and Evolution</i> , 2016, 46, 169-179.	1.0	60
38	Integrating molecular epidemiology and social network analysis to study infectious diseases: Towards a socio-molecular era for public health. <i>Infection, Genetics and Evolution</i> , 2016, 46, 248-255.	1.0	37
39	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
40	The interferon receptor $\alpha 1$ promoter polymorphisms affect the outcome of Caucasians with HBsAg-negative chronic HBV infection. <i>Liver International</i> , 2015, 35, 2506-2513.	1.9	12
41	Prevention of early HIV transmissions might be more important in emerging or generalizing epidemics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1515-E1515.	3.3	3
42	Activation of the innate immune response by endogenous retroviruses. <i>Journal of General Virology</i> , 2015, 96, 1207-1218.	1.3	105
43	The decline of human endogenous retroviruses: extinction and survival. <i>Retrovirology</i> , 2015, 12, 8.	0.9	49
44	Dating the origin of hepatitis B virus reveals higher substitution rate and adaptation on the branch leading to F/H genotypes. <i>Molecular Phylogenetics and Evolution</i> , 2015, 93, 44-54.	1.2	43
45	A novel method for the multiplexed target enrichment of MinION next generation sequencing libraries using PCR-generated baits. <i>Nucleic Acids Research</i> , 2015, 43, e152-e152.	6.5	44
46	Enhanced HIV-1 surveillance using molecular epidemiology to study and monitor HIV-1 outbreaks among intravenous drug users (IDUs) in Athens and Bucharest. <i>Infection, Genetics and Evolution</i> , 2015, 35, 109-121.	1.0	36
47	Global Dispersal Pattern of HIV Type 1 Subtype CRF01_AE: A Genetic Trace of Human Mobility Related to Heterosexual Sexual Activities Centralized in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 1735-1744.	1.9	62
48	Larger Mammalian Body Size Leads to Lower Retroviral Activity. <i>PLoS Pathogens</i> , 2014, 10, e1004214.	2.1	47
49	Phylogenetic clustering of hepatitis C virus among people who inject drugs in Vancouver, Canada. <i>Hepatology</i> , 2014, 60, 1571-1580.	3.6	59
50	Unfixed Endogenous Retroviral Insertions in the Human Population. <i>Journal of Virology</i> , 2014, 88, 9529-9537.	1.5	118
51	Socially-Integrated Transdisciplinary HIV Prevention. <i>AIDS and Behavior</i> , 2014, 18, 1821-1834.	1.4	39
52	HIV-1 epidemic in Russia: an evolutionary epidemiology analysis. <i>Lancet, The</i> , 2014, 383, S71.	6.3	3
53	Neanderthal and Denisovan retroviruses in modern humans. <i>Current Biology</i> , 2013, 23, R994-R995.	1.8	17
54	Dating the origin and dispersal of hepatitis B virus infection in humans and primates. <i>Hepatology</i> , 2013, 57, 908-916.	3.6	131

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55	Viral Proteins Originated De Novo by Overprinting Can Be Identified by Codon Usage: Application to the "Gene Nursery" of Deltaretroviruses. PLoS Computational Biology, 2013, 9, e1003162.	1.5	61
56	Integrating Phylodynamics and Epidemiology to Estimate Transmission Diversity in Viral Epidemics. PLoS Computational Biology, 2013, 9, e1002876.	1.5	57
57	"There and back again"™: revisiting the pathophysiological roles of human endogenous retroviruses in the post-genomic era. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120504.	1.8	57
58	<i>Env</i>-less endogenous retroviruses are genomic superspreaders. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7385-7390.	3.3	111
59	Assessment of phylogenetic sensitivity for reconstructing HIV-1 epidemiological relationships. Virus Research, 2012, 166, 54-60.	1.1	11
60	Molecular typing of the recently expanding subtype B HIV-1 epidemic in Romania: Evidence for local spread among MSMs in Bucharest area. Infection, Genetics and Evolution, 2012, 12, 1052-1057.	1.0	19
61	Appearance of a Single Amino Acid Insertion at Position 33 in HIV Type 1 Protease Under a Lopinavir-Containing Regimen, Associated with Reduced Protease Inhibitor Susceptibility. AIDS Research and Human Retroviruses, 2011, 27, 1223-1229.	0.5	0
62	The Global Spread of Hepatitis C Virus 1a and 1b: A Phylodynamic and Phylogeographic Analysis. PLoS Medicine, 2009, 6, e1000198.	3.9	177
63	Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. Retrovirology, 2009, 6, 49.	0.9	114
64	Comments on "The distribution of HIV-1 recombination breakpoints" by Jun Fan, Matteo Negroni, David L. Robertson. Infection, Genetics and Evolution, 2008, 8, 527-528.	1.0	2
65	The phylogenetic information profile of HIV-1 and the degradation effect of recombination. Infection, Genetics and Evolution, 2008, 8, 139-145.	1.0	0
66	Phylogenetic Reconstruction of a Known HIV-1 CRF04_cpx Transmission Network Using Maximum Likelihood and Bayesian Methods. Journal of Molecular Evolution, 2004, 59, 709-717.	0.8	26
67	In vivo characteristics of human immunodeficiency virus type 1 intersubtype recombination: determination of hot spots and correlation with sequence similarity. Journal of General Virology, 2003, 84, 2715-2722.	1.3	63