

Bram Vrancken

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

1,879
citations

361296

20
h-index

302012

39
g-index

66
all docs

66
docs citations

66
times ranked

3366
citing authors

#	ARTICLE	IF	CITATIONS
1	Spred3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2167-2169.	3.5	413
2	HIV persists throughout deep tissues with repopulation from multiple anatomical sources. <i>Journal of Clinical Investigation</i> , 2020, 130, 1699-1712.	3.9	140
3	HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. <i>Cell Host and Microbe</i> , 2019, 26, 347-358.e7.	5.1	117
4	Measles virus and rinderpest virus divergence dated to the sixth century BCE. <i>Science</i> , 2020, 368, 1367-1370.	6.0	102
5	Distinct Effects of T-705 (Favipiravir) and Ribavirin on Influenza Virus Replication and Viral RNA Synthesis. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6679-6691.	1.4	86
6	The Genealogical Population Dynamics of HIV-1 in a Large Transmission Chain: Bridging within and among Host Evolutionary Rates. <i>PLoS Computational Biology</i> , 2014, 10, e1003505.	1.5	79
7	Disentangling the role of Africa in the global spread of H5 highly pathogenic avian influenza. <i>Nature Communications</i> , 2019, 10, 5310.	5.8	61
8	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015, 1, vev016.	2.2	59
9	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018, 31, 24-32.	2.6	45
10	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018, 14, e1007392.	2.1	35
11	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. <i>BMC Genomics</i> , 2018, 19, 617.	1.2	35
12	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620.	5.8	35
13	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018, 4, vey023.	2.2	29
14	Contribution of Epidemiological Predictors in Unraveling the Phylogeographic History of HIV-1 Subtype C in Brazil. <i>Journal of Virology</i> , 2015, 89, 12341-12348.	1.5	28
15	Comparative Circulation Dynamics of the Five Main HIV Types in China. <i>Journal of Virology</i> , 2020, 94, .	1.5	26
16	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. <i>Nature Communications</i> , 2022, 13, 2314.	5.8	25
17	The multi-faceted dynamics of HIV-1 transmission in Northern Alberta: A combined analysis of virus genetic and public health data. <i>Infection, Genetics and Evolution</i> , 2017, 52, 100-105.	1.0	24
18	Cross-border spread, lineage displacement and evolutionary rate estimation of rabies virus in Yunnan Province, China. <i>Virology Journal</i> , 2017, 14, 102.	1.4	24

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19	Divergence dating using mixed effects clock modelling: An application to HIV-1. <i>Virus Evolution</i> , 2019, 5, vez036.	2.2	24
20	Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City. <i>PLoS Pathogens</i> , 2021, 17, e1009571.	2.1	24
21	Genomic Epidemiology of 2015â€“2016 Zika Virus Outbreak in Cape Verde. <i>Emerging Infectious Diseases</i> , 2020, 26, 1084-1090.	2.0	24
22	Covering all bases in HIV research: unveiling a hidden world of viral evolution. <i>AIDS Reviews</i> , 2010, 12, 89-102.	0.5	23
23	Simultaneously estimating evolutionary history and repeated traits phylogenetic signal: applications to viral and host phenotypic evolution. <i>Methods in Ecology and Evolution</i> , 2015, 6, 67-82.	2.2	22
24	The epidemic dynamics of hepatitis C virus subtypes 4a and 4d in Saudi Arabia. <i>Scientific Reports</i> , 2017, 7, 44947.	1.6	22
25	Comparing patterns and scales of plant virus phylogeography: Rice yellow mottle virus in Madagascar and in continental Africa. <i>Virus Evolution</i> , 2019, 5, vez023.	2.2	22
26	Implications of hepatitis C virus subtype 1a migration patterns for virus genetic sequencing policies in Italy. <i>BMC Evolutionary Biology</i> , 2017, 17, 70.	3.2	21
27	Proposal for a new subtype of the zoonotic genotype 3 Hepatitis E virus: HEV-3I. <i>Virus Research</i> , 2018, 248, 1-4.	1.1	21
28	Dynamics and Dispersal of Local Human Immunodeficiency Virus Epidemics Within San Diego and Across the San Diegoâ€“Tijuana Border. <i>Clinical Infectious Diseases</i> , 2021, 73, e2018-e2025.	2.9	19
29	Limited evolution of the yellow fever virus 17d in a mouse infection model. <i>Emerging Microbes and Infections</i> , 2019, 8, 1734-1746.	3.0	18
30	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. <i>Aids</i> , 2015, 29, 1549-1556.	1.0	16
31	Accurate quantification of within- and between-host HBV evolutionary rates requires explicit transmission chain modelling. <i>Virus Evolution</i> , 2017, 3, vex028.	2.2	16
32	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019, 5, vez009.	2.2	16
33	In Search of Covariates of HIV-1 Subtype B Spread in the United Statesâ€“A Cautionary Tale of Large-Scale Bayesian Phylogeography. <i>Viruses</i> , 2020, 12, 182.	1.5	15
34	Evaluating predictive markers for viral rebound and safety assessment in blood and lumbar fluid during HIV-1 treatment interruption. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1311-1320.	1.3	15
35	Extensive characterization of HIV-1 reservoirs reveals links to plasma viremia before and during analytical treatment interruption. <i>Cell Reports</i> , 2022, 39, 110739.	2.9	15
36	Detection of Natural Resistance-Associated Substitutions by Ion Semiconductor Technology in HCV1b Positive, Direct-Acting Antiviral Agents-Naïve Patients. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1416.	1.8	14

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37	Increasing importance of European lineages in seeding the hepatitis C virus subtype 1a epidemic in Spain. <i>Eurosurveillance</i> , 2019, 24, .	3.9	14
38	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016, 8, 12.	1.5	13
39	Drivers of HIV-1 transmission: The Portuguese case. <i>PLoS ONE</i> , 2019, 14, e0218226.	1.1	12
40	A near-full length genotypic assay for HCV1b. <i>Journal of Virological Methods</i> , 2014, 209, 126-135.	1.0	11
41	New evidence for the east-west spread of the highly pathogenic avian influenza H5N1 virus between Central Asian and east Asian-Australasian flyways in China. <i>Emerging Microbes and Infections</i> , 2019, 8, 823-826.	3.0	11
42	Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , 2021, 7, veab036.	2.2	11
43	A Comprehensive Molecular Epidemiological Analysis of SARS-CoV-2 Infection in Cyprus from April 2020 to January 2021: Evidence of a Highly Polyphyletic and Evolving Epidemic. <i>Viruses</i> , 2021, 13, 1098.	1.5	11
44	Assessing the impact of COVID-19 border restrictions on dengue transmission in Yunnan Province, China: an observational epidemiological and phylogenetic analysis. <i>The Lancet Regional Health - Western Pacific</i> , 2021, 14, 100259.	1.3	11
45	Phylogenetic relationships of the HA and NA genes between vaccine and seasonal influenza A(H3N2) strains in Korea. <i>PLoS ONE</i> , 2017, 12, e0172059.	1.1	10
46	Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008117.	1.3	8
47	HIV-1 evolution in patients undergoing immunotherapy with Tat, Rev, and Nef expressing dendritic cells followed by treatment interruption. <i>Aids</i> , 2013, 27, 2679-2689.	1.0	7
48	Cross-country migration linked to people who inject drugs challenges the long-term impact of national HCV elimination programmes. <i>Journal of Hepatology</i> , 2019, 71, 1270-1272.	1.8	7
49	A paucigranulocytic asthma host environment promotes the emergence of virulent influenza viral variants. <i>ELife</i> , 2021, 10, .	2.8	5
50	Why comprehensive datasets matter when inferring epidemic links or subgenotyping. <i>Infection, Genetics and Evolution</i> , 2018, 65, 350-351.	1.0	4
51	<i>In Vivo</i> Therapy with M2e-Specific IgG Selects for an Influenza A Virus Mutant with Delayed Matrix Protein 2 Expression. <i>MBio</i> , 2021, 12, e0074521.	1.8	4
52	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. <i>Viruses</i> , 2021, 13, 1842.	1.5	4
53	Reconstruction of the origin and dispersal of the worldwide dominant Hepatitis B Virus subgenotype D1. <i>Virus Evolution</i> , 2022, 8, .	2.2	4
54	Global origins of African highly pathogenic avian influenza H5Nx viruses and intracontinental spread. <i>International Journal of Infectious Diseases</i> , 2019, 79, 9-10.	1.5	2

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55	High-throughput HIV sequencing: evolution in 2D. <i>Future Virology</i> , 2011, 6, 417-420.	0.9	1
56	A18â€fRandom amplification with next-generation sequencing to cover HIV and HCV full-length genomes. <i>Virus Evolution</i> , 2017, 3, .	2.2	1
57	Inferring the migration routes of hepatitis C virus subtype 1a lineages identifies a need for pan-European prevention strategies. <i>Journal of Hepatology</i> , 2018, 68, S158-S159.	1.8	0
58	A4â€fAn amplicon-based approach for universal amplification, sequencing, and assembly of full-length HIV-1 samples from the DRC. <i>Virus Evolution</i> , 2019, 5, .	2.2	0