

Joel O Wertheim

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9518654/publications.pdf>

Version: 2024-02-01

96
papers

7,807
citations

101384

36
h-index

62479

80
g-index

110
all docs

110
docs citations

110
times ranked

10512
citing authors

#	ARTICLE	IF	CITATIONS
1	Accuracy in Near-Perfect Virus Phylogenies. <i>Systematic Biology</i> , 2022, 71, 426-438.	2.7	8
2	Forecasting HIV-1 Genetic Cluster Growth in Illinois, United States. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2022, 89, 49-55.	0.9	7
3	When viruses become more virulent. <i>Science</i> , 2022, 375, 493-494.	6.0	4
4	Using molecular epidemiology to trace the history of the injection-related HIV epidemic in New York City, 1985–2019. <i>Aids</i> , 2022, 36, 889-895.	1.0	1
5	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	9.0	35
6	Do partner services linked to molecular clusters yield people with viremia or new HIV?. <i>Aids</i> , 2022, 36, 845-852.	1.0	2
7	Establishing a framework towards monitoring HCV microelimination among men who have sex with men living with HIV in Germany: A modeling analysis. <i>PLoS ONE</i> , 2022, 17, e0267853.	1.1	2
8	Introduction and Establishment of SARS-CoV-2 Gamma Variant in New York City in Early 2021. <i>Journal of Infectious Diseases</i> , 2022, 226, 2142-2149.	1.9	5
9	Detection of SARS-CoV-2 intra-host recombination during superinfection with Alpha and Epsilon variants in New York City. <i>Nature Communications</i> , 2022, 13, .	5.8	22
10	Sorting by Race/Ethnicity Across HIV Genetic Transmission Networks in Three Major Metropolitan Areas in the United States. <i>AIDS Research and Human Retroviruses</i> , 2021, 37, 784-792.	0.5	5
11	Methodological synthesis of Bayesian phylodynamics, HIV-TRACE, and GEE: HIV-1 transmission epidemiology in a racially/ethnically diverse Southern U.S. context. <i>Scientific Reports</i> , 2021, 11, 3325.	1.6	8
12	Discovery of Novel Herpes Simplexviruses in Wild Gorillas, Bonobos, and Chimpanzees Supports Zoonotic Origin of HSV-2. <i>Molecular Biology and Evolution</i> , 2021, 38, 2818-2830.	3.5	13
13	Increasing Capacity to Detect Clusters of Rapid HIV Transmission in Varied Populations—United States. <i>Viruses</i> , 2021, 13, 577.	1.5	15
14	Interplay Between Geography and HIV Transmission Clusters in Los Angeles County. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab211.	0.4	2
15	Timing the SARS-CoV-2 index case in Hubei province. <i>Science</i> , 2021, 372, 412-417.	6.0	109
16	Detection and characterization of the SARS-CoV-2 lineage B.1.526 in New York. <i>Nature Communications</i> , 2021, 12, 4886.	5.8	65
17	Prevalence of resistance-associated substitutions and phylogenetic analysis of hepatitis C virus infection in Russia. <i>International Journal of Infectious Diseases</i> , 2021, 113, 36-42.	1.5	5
18	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	13.5	186

#	ARTICLE	IF	CITATIONS
19	Incorporating metadata in HIV transmission network reconstruction: A machine learning feasibility assessment. <i>PLoS Computational Biology</i> , 2021, 17, e1009336.	1.5	5
20	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021, 184, 4848-4856.	13.5	330
21	Characterization of HIV Risk Behaviors and Clusters Using HIV-Transmission Cluster Engine Among a Cohort of Persons Living with HIV in Washington, DC. <i>AIDS Research and Human Retroviruses</i> , 2021, 37, 706-715.	0.5	3
22	Characteristics and growth of the genetic HIV transmission network of Mexico City during 2020. <i>Journal of the International AIDS Society</i> , 2021, 24, e25836.	1.2	7
23	StrainHub: a phylogenetic tool to construct pathogen transmission networks. <i>Bioinformatics</i> , 2020, 36, 945-947.	1.8	30
24	Use of molecular HIV surveillance data and predictive modeling to prioritize persons for transmission-reduction interventions. <i>Aids</i> , 2020, 34, 459-467.	1.0	8
25	Incident infection in high-priority HIV molecular transmission clusters in the United States. <i>Aids</i> , 2020, 34, 1187-1193.	1.0	15
26	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020, 370, 564-570.	6.0	331
27	Brief Report: Temporal Changes in HIV Transmission Patterns Among Young Men Who Have Sex With Men, United States, 2009-2016. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2020, 84, 1-4.	0.9	6
28	A Glimpse Into the Origins of Genetic Diversity in the Severe Acute Respiratory Syndrome Coronavirus 2. <i>Clinical Infectious Diseases</i> , 2020, 71, 721-722.	2.9	14
29	The Relationship Between the Human Immunodeficiency Virus-1 Transmission Network and the HIV Care Continuum in Los Angeles County. <i>Clinical Infectious Diseases</i> , 2020, 71, e384-e391.	2.9	2
30	Analysis of Hepatitis B Virus Genotype D in Greenland Suggests the Presence of a Novel Quasi-Subgenotype. <i>Frontiers in Microbiology</i> , 2020, 11, 602296.	1.5	5
31	Hepatitis C virus genotype 1 and 2 recombinant genomes and the phylogeographic history of the 2k/1b lineage. <i>Virus Evolution</i> , 2019, 5, vez041.	2.2	5
32	Consent and criminalisation concerns over phylogenetic analysis of surveillance data – Authors' reply. <i>Lancet HIV</i> , 2019, 6, e420-e421.	2.1	6
33	HIV coinfection is associated with increased transmission risk in patients with chronic hepatitis C virus. <i>Journal of Viral Hepatitis</i> , 2019, 26, 1351-1354.	1.0	3
34	HIV transmission networks among transgender women in Los Angeles County, CA, USA: a phylogenetic analysis of surveillance data. <i>Lancet HIV</i> , 2019, 6, e164-e172.	2.1	57
35	Natural selection favoring more transmissible HIV detected in United States molecular transmission network. <i>Nature Communications</i> , 2019, 10, 5788.	5.8	22
36	Understanding disclosed and cryptic HIV transmission risk via genetic analysis. <i>Current Opinion in HIV and AIDS</i> , 2019, 14, 205-212.	1.5	11

#	ARTICLE	IF	CITATIONS
37	Characteristics of a cohort of high-risk men who have sex with men on pre-exposure prophylaxis reporting transgender sexual partners. <i>Medicine (United States)</i> , 2019, 98, e18232.	0.4	3
38	Comparative analysis of HIV sequences in real time for public health. <i>Current Opinion in HIV and AIDS</i> , 2019, 14, 213-220.	1.5	16
39	FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences. <i>Bioinformatics</i> , 2019, 35, 1852-1861.	1.8	45
40	Transmission Patterns in a Low HIV-Morbidity State – Wisconsin, 2014–2017. <i>Morbidity and Mortality Weekly Report</i> , 2019, 68, 149-152.	9.0	6
41	HIV-TRACE (TRANSMISSION Cluster Engine): a Tool for Large Scale Molecular Epidemiology of HIV-1 and Other Rapidly Evolving Pathogens. <i>Molecular Biology and Evolution</i> , 2018, 35, 1812-1819.	3.5	206
42	Maintenance and reappearance of extremely divergent intra-host HIV-1 variants. <i>Virus Evolution</i> , 2018, 4, vey030.	2.2	5
43	Identifying Clusters of Recent and Rapid HIV Transmission Through Analysis of Molecular Surveillance Data. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2018, 79, 543-550.	0.9	123
44	Ethical considerations in global HIV phylogenetic research. <i>Lancet HIV</i> , 2018, 5, e656-e666.	2.1	39
45	Growth of HIV-1 Molecular Transmission Clusters in New York City. <i>Journal of Infectious Diseases</i> , 2018, 218, 1943-1953.	1.9	75
46	Phosphoserine acidic cluster motifs bind distinct basic regions on the β subunits of clathrin adaptor protein complexes. <i>Journal of Biological Chemistry</i> , 2018, 293, 15678-15690.	1.6	10
47	Short Communication: HIV-1 Transmission Networks Across South Korea. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 827-831.	0.5	4
48	Viral Evolution: Mummy Virus Challenges Presumed History of Smallpox. <i>Current Biology</i> , 2017, 27, R119-R120.	1.8	12
49	Increasing HIV-1 subtype diversity in seven states, United States, 2006–2013. <i>Annals of Epidemiology</i> , 2017, 27, 244-251.e1.	0.9	21
50	HIV Transmission Dynamics Among Foreign-Born Persons in the United States. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2017, 76, 445-452.	0.9	21
51	No Substantial Evidence for Sexual Transmission of Minority HIV Drug Resistance Mutations in Men Who Have Sex with Men. <i>Journal of Virology</i> , 2017, 91, .	1.5	12
52	Identification of major routes of HIV transmission throughout Mesoamerica. <i>Infection, Genetics and Evolution</i> , 2017, 54, 98-107.	1.0	15
53	Identifying Transmission Clusters with Cluster Picker and HIV-TRACE. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 211-218.	0.5	66
54	A molecular transmission network of recent hepatitis C infection in people with and without Δ 169K: Implications for targeted treatment strategies. <i>Journal of Viral Hepatitis</i> , 2017, 24, 404-411.	1.0	23

#	ARTICLE	IF	CITATIONS
55	Transmission fitness of drug-resistant HIV revealed in a surveillance system transmission network. <i>Virus Evolution</i> , 2017, 3, vex008.	2.2	46
56	Evolution and spread of Venezuelan equine encephalitis complex alphavirus in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005693.	1.3	56
57	Social and Genetic Networks of HIV-1 Transmission in New York City. <i>PLoS Pathogens</i> , 2017, 13, e1006000.	2.1	157
58	HIV transmission clusters among injecting drug users in Romania. <i>Romanian Biotechnological Letters</i> , 2017, 22, 12307-12315.	0.5	3
59	Molecular epidemiology identifies HIV transmission networks associated with younger age and heterosexual exposure among Korean individuals. <i>Journal of Medical Virology</i> , 2016, 88, 1832-1835.	2.5	7
60	The Evolutionary Histories of Antiretroviral Proteins SERINC3 and SERINC5 Do Not Support an Evolutionary Arms Race in Primates. <i>Journal of Virology</i> , 2016, 90, 8085-8089.	1.5	40
61	Prevalence of Transmitted HIV Drug Resistance Among Recently Infected Persons in San Diego, CA 1996–2013. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2016, 71, 228-236.	0.9	47
62	The International Dimension of the U.S. HIV Transmission Network and Onward Transmission of HIV Recently Imported into the United States. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 1046-1053.	0.5	44
63	Using HIV Sequence and Epidemiologic Data to Assess the Effect of Self-referral Testing for Acute HIV Infection on Incident Diagnoses in San Diego, California. <i>Clinical Infectious Diseases</i> , 2016, 63, 101-107.	2.9	20
64	Assessing Host-Virus Codivergence for Close Relatives of Merkel Cell Polyomavirus Infecting African Great Apes. <i>Journal of Virology</i> , 2016, 90, 8531-8541.	1.5	21
65	Concurrency and HIV transmission network characteristics among MSM with recent HIV infection. <i>Aids</i> , 2016, 30, 2875-2883.	1.0	35
66	HIV Transmission Networks in the San Diego–Tijuana Border Region. <i>EBioMedicine</i> , 2015, 2, 1456-1463.	2.7	51
67	Molecular analysis allows inference into HIV transmission among young men who have sex with men in the United States. <i>Aids</i> , 2015, 29, 2517-2522.	1.0	47
68	Using Molecular HIV Surveillance Data to Understand Transmission Between Subpopulations in the United States. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2015, 70, 444-451.	0.9	139
69	The Sordid Affair Between Human Herpesvirus and HIV. <i>Journal of Infectious Diseases</i> , 2015, 212, 845-852.	1.9	75
70	RELAX: Detecting Relaxed Selection in a Phylogenetic Framework. <i>Molecular Biology and Evolution</i> , 2015, 32, 820-832.	3.5	535
71	Less Is More: An Adaptive Branch-Site Random Effects Model for Efficient Detection of Episodic Diversifying Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 1342-1353.	3.5	631
72	Targeting HIV Prevention Based on Molecular Epidemiology Among Deeply Sampled Subnetworks of Men Who Have Sex With Men. <i>Clinical Infectious Diseases</i> , 2015, 61, 1462-1468.	2.9	53

#	ARTICLE	IF	CITATIONS
73	Gene-Wide Identification of Episodic Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 1365-1371.	3.5	493
74	Neuropathy- and myopathy-associated mutations in human small heat shock proteins: Characteristics and evolutionary history of the mutation sites. <i>Mutation Research - Reviews in Mutation Research</i> , 2014, 761, 15-30.	2.4	52
75	The Global Transmission Network of HIV-1. <i>Journal of Infectious Diseases</i> , 2014, 209, 304-313.	1.9	194
76	Evolutionary Origins of Human Herpes Simplex Viruses 1 and 2. <i>Molecular Biology and Evolution</i> , 2014, 31, 2356-2364.	3.5	139
77	Using HIV Networks to Inform Real Time Prevention Interventions. <i>PLoS ONE</i> , 2014, 9, e98443.	1.1	158
78	Dynamics of Viral Evolution and Neutralizing Antibody Response after HIV-1 Superinfection. <i>Journal of Virology</i> , 2013, 87, 12737-12744.	1.5	22
79	A Case for the Ancient Origin of Coronaviruses. <i>Journal of Virology</i> , 2013, 87, 7039-7045.	1.5	186
80	Speedy speciation in a bacterial microcosm: new species can arise as frequently as adaptations within a species. <i>ISME Journal</i> , 2013, 7, 1080-1091.	4.4	62
81	Phylogenetic Relatedness of HIV-1 Donor and Recipient Populations. <i>Journal of Infectious Diseases</i> , 2013, 207, 1181-1182.	1.9	6
82	Detecting Individual Sites Subject to Episodic Diversifying Selection. <i>PLoS Genetics</i> , 2012, 8, e1002764.	1.5	1,455
83	Inconsistencies in Estimating the Age of HIV-1 Subtypes Due to Heterotachy. <i>Molecular Biology and Evolution</i> , 2012, 29, 451-456.	3.5	65
84	ESTIMATING DIVERSIFICATION RATES: HOW USEFUL ARE DIVERGENCE TIMES?. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 309-320.	1.1	36
85	Using phylogeography to characterize the origins of the HIV-1 subtype F epidemic in Romania. <i>Infection, Genetics and Evolution</i> , 2011, 11, 975-979.	1.0	32
86	Evolutionary History of Chimpanzees Inferred from Complete Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 615-623.	3.5	53
87	Purifying Selection Can Obscure the Ancient Age of Viral Lineages. <i>Molecular Biology and Evolution</i> , 2011, 28, 3355-3365.	3.5	186
88	Using HIV Transmission Networks to Investigate Community Effects in HIV Prevention Trials. <i>PLoS ONE</i> , 2011, 6, e27775.	1.1	34
89	The Re-Emergence of H1N1 Influenza Virus in 1977: A Cautionary Tale for Estimating Divergence Times Using Biologically Unrealistic Sampling Dates. <i>PLoS ONE</i> , 2010, 5, e11184.	1.1	26
90	Relaxed Molecular Clocks, the Bias-Variance Trade-off, and the Quality of Phylogenetic Inference. <i>Systematic Biology</i> , 2010, 59, 1-8.	2.7	71

#	ARTICLE	IF	CITATIONS
91	Dating the Age of the SIV Lineages That Gave Rise to HIV-1 and HIV-2. PLoS Computational Biology, 2009, 5, e1000377.	1.5	145
92	Relaxed Selection and the Evolution of RNA Virus Mucin-Like Pathogenicity Factors. Journal of Virology, 2009, 83, 4690-4694.	1.5	14
93	A quick fuse and the emergence of Taura syndrome virus. Virology, 2009, 390, 324-329.	1.1	22
94	When pigs fly: the avian origin of a "swine flu"™. Environmental Microbiology, 2009, 11, 2191-2192.	1.8	3
95	A Challenge to the Ancient Origin of SIVagm Based on African Green Monkey Mitochondrial Genomes. PLoS Pathogens, 2007, 3, e95.	2.1	51
96	Point, Counterpoint: The Evolution of Pathogenic Viruses and their Human Hosts. Annual Review of Ecology, Evolution, and Systematics, 2007, 38, 515-540.	3.8	22