Jayna Raghwani

List of Publications by Citations

Source: https://exaly.com/author-pdf/1695440/jayna-raghwani-publications-by-citations.pdf

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

38
papers

3,605
citations

18
h-index

47
g-index

47
ext. papers

2.8
ext. citations

12.8
avg, IF

L-index

#	Paper	IF	Citations
38	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009 , 459, 1122-5	50.4	1535
37	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021 , 184, 64-75.e11	56.2	518
36	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017 , 546, 406-4	1 50 .4	366
35	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020 , 181, 997-1003.e9	56.2	175
34	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020 , 11, 2688	17.4	174
33	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021 , 371, 708-712	33-3	159
32	Endemic dengue associated with the co-circulation of multiple viral lineages and localized density-dependent transmission. <i>PLoS Pathogens</i> , 2011 , 7, e1002064	7.6	74
31	Structure of the Lassa virus glycan shield provides a model for immunological resistance. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7320-7325	11.5	62
30	Phylogeography and epidemic history of hepatitis C virus genotype 4 in Africa. <i>Virology</i> , 2014 , 464-465, 233-243	3.6	57
29	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017 , 13, e1006749	7.6	55
28	The Evolution and Transmission of Epidemic GII.17 Noroviruses. <i>Journal of Infectious Diseases</i> , 2016 , 214, 556-64	7	50
27	Origin and evolution of the unique hepatitis C virus circulating recombinant form 2k/1b. <i>Journal of Virology</i> , 2012 , 86, 2212-20	6.6	46
26	A Molecular-Level Account of the Antigenic Hantaviral Surface. <i>Cell Reports</i> , 2016 , 15, 959-967	10.6	39
25	A Protective Monoclonal Antibody Targets a Site of Vulnerability on the Surface of Rift Valley Fever Virus. <i>Cell Reports</i> , 2018 , 25, 3750-3758.e4	10.6	29
24	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2016 , 12, e1005894	7.6	25
23	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019 , 15, e1007976	7.6	25
22	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , 2016 , 22, 2104-2112	10.2	22

(2021-2018)

21	Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1795-1805	10.2	22
20	Intercontinental dispersal of HIV-1 subtype B associated with transmission among men who have sex with men in Japan. <i>Journal of Virology</i> , 2014 , 88, 9864-76	6.6	18
19	Transmission of hepatitis C virus infection among younger and older people who inject drugs in Vancouver, Canada. <i>Journal of Hepatology</i> , 2016 , 64, 1247-55	13.4	18
18	Role of HIV-specific CD8 T cells in pediatric HIV cure strategies after widespread early viral escape. <i>Journal of Experimental Medicine</i> , 2017 , 214, 3239-3261	16.6	15
17	Evolution of HIV-1 within untreated individuals and at the population scale in Uganda. <i>PLoS Pathogens</i> , 2018 , 14, e1007167	7.6	15
16	Where do all the subtypes go? Temporal dynamics of H8-H12 influenza A viruses in waterfowl. <i>Virus Evolution</i> , 2018 , 4, vey025	3.7	14
15	Occurrence and reassortment of avian influenza A (H7N9) viruses derived from coinfected birds in China. <i>Journal of Virology</i> , 2014 , 88, 13344-51	6.6	13
14	Characterization of Hepatitis C Virus (HCV) Envelope Diversification from Acute to Chronic Infection within a Sexually Transmitted HCV Cluster by Using Single-Molecule, Real-Time Sequencing. <i>Journal of Virology</i> , 2017 , 91,	6.6	12
13	Selection on non-antigenic gene segments of seasonal influenza A virus and its impact on adaptive evolution. <i>Virus Evolution</i> , 2017 , 3, vex034	3.7	8
12	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intrahost HIV Infection. <i>Genetics</i> , 2016 , 202, 1449-72	4	8
11	High-Resolution Evolutionary Analysis of Within-Host Hepatitis C Virus Infection. <i>Journal of Infectious Diseases</i> , 2019 , 219, 1722-1729	7	8
10	Link between the numbers of particles and variants founding new HIV-1 infections depends on the timing of transmission. <i>Virus Evolution</i> , 2019 , 5, vey038	3.7	6
9	Venue-Based Networks May Underpin HCV Transmissions amongst HIV-Infected Gay and Bisexual Men. <i>PLoS ONE</i> , 2016 , 11, e0162002	3.7	6
8	Faster Adaptation in Smaller Populations: Counterintuitive Evolution of HIV during Childhood Infection. <i>PLoS Computational Biology</i> , 2016 , 12, e1004694	5	6
7	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 ,	8.3	5
6	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		3
5	Genomic epidemiology of early SARS-CoV-2 transmission dynamics in Gujarat, India		2
4	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		2

A de novo approach to inferring within-host fitness effects during untreated HIV-1 infection. *PLoS Pathogens*, **2020**, 16, e1008171

Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza

Discovery of a Novel Coronavirus in Swedish Bank Voles (Myodes glareolus). *Viruses*, **2022**, 14, 1205

6.2 0