

# Jayna Raghwani

## List of Publications by Year in descending order

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36  
papers

5,070  
citations

331670

21  
h-index

345221

36  
g-index

47  
all docs

47  
docs citations

47  
times ranked

10149  
citing authors

#	ARTICLE	IF	CITATIONS
1	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, .	8.9	42
2	Genomic Epidemiology of Early SARS-CoV-2 Transmission Dynamics, Gujarat, India. <i>Emerging Infectious Diseases</i> , 2022, 28, 751-758.	4.3	4
3	Discovery of a Novel Coronavirus in Swedish Bank Voles ( <i>Myodes glareolus</i> ). <i>Viruses</i> , 2022, 14, 1205.	3.3	2
4	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
5	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
6	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	28.9	236
7	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020, 11, 2688.	12.8	304
8	A de novo approach to inferring within-host fitness effects during untreated HIV-1 infection. <i>PLoS Pathogens</i> , 2020, 16, e1008171.	4.7	4
9	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.	4.9	13
10	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019, 15, e1007976.	4.7	37
11	High-Resolution Evolutionary Analysis of Within-Host Hepatitis C Virus Infection. <i>Journal of Infectious Diseases</i> , 2019, 219, 1722-1729.	4.0	11
12	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.	6.4	41
13	Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. <i>Emerging Infectious Diseases</i> , 2018, 24, 1795-1805.	4.3	26
14	Where do all the subtypes go? Temporal dynamics of H8â€“H12 influenza A viruses in waterfowl. <i>Virus Evolution</i> , 2018, 4, vey025.	4.9	23
15	Structure of the Lassa virus glycan shield provides a model for immunological resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7320-7325.	7.1	95
16	Evolution of HIV-1 within untreated individuals and at the population scale in Uganda. <i>PLoS Pathogens</i> , 2018, 14, e1007167.	4.7	27
17	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, .	3.4	17
18	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	27.8	515

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19	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.	8.5	31
20	The evolution and molecular epidemiology of epidemic GII.17 noroviruses. <i>Virus Evolution</i> , 2017, 3, .	4.9	0
21	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017, 13, e1006749.	4.7	78
22	Selection on non-antigenic gene segments of seasonal influenza A virus and its impact on adaptive evolution. <i>Virus Evolution</i> , 2017, 3, vex034.	4.9	9
23	Faster Adaptation in Smaller Populations: Counterintuitive Evolution of HIV during Childhood Infection. <i>PLoS Computational Biology</i> , 2016, 12, e1004694.	3.2	8
24	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , 2016, 22, 2104-2112.	4.3	33
25	A Molecular-Level Account of the Antigenic Hantaviral Surface. <i>Cell Reports</i> , 2016, 15, 959-967.	6.4	57
26	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.	3.7	18
27	The Evolution and Transmission of Epidemic GII.17 Noroviruses. <i>Journal of Infectious Diseases</i> , 2016, 214, 556-564.	4.0	61
28	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intra-host HIV Infection. <i>Genetics</i> , 2016, 202, 1449-1472.	2.9	11
29	Venue-Based Networks May Underpin HCV Transmissions amongst HIV-Infected Gay and Bisexual Men. <i>PLoS ONE</i> , 2016, 11, e0162002.	2.5	8
30	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2016, 12, e1005894.	4.7	31
31	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, 9864-9876.	3.4	18
32	Occurrence and Reassortment of Avian Influenza A (H7N9) Viruses Derived from Coinfected Birds in China. <i>Journal of Virology</i> , 2014, 88, 13344-13351.	3.4	20
33	Phylogeography and epidemic history of hepatitis C virus genotype 4 in Africa. <i>Virology</i> , 2014, 464-465, 233-243.	2.4	62
34	Origin and Evolution of the Unique Hepatitis C Virus Circulating Recombinant Form 2k/1b. <i>Journal of Virology</i> , 2012, 86, 2212-2220.	3.4	56
35	Endemic Dengue Associated with the Co-Circulation of Multiple Viral Lineages and Localized Density-Dependent Transmission. <i>PLoS Pathogens</i> , 2011, 7, e1002064.	4.7	86
36	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009, 459, 1122-1125.	27.8	1,870