Jayna Raghwani

List of Publications by Year in Descending Order

38 papers	**3,605** citations	**18** h-index	**47** g-index
47 ext. papers	**4,543** ext. citations	**12.8** avg, IF	**4.62** L-index

#	Paper	IF	Citations
38	Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza.. *Molecular Biology and Evolution*, **2022**,	8.3	5
37	Discovery of a Novel Coronavirus in Swedish Bank Voles (Myodes glareolus). *Viruses*, **2022**, 14, 1205	6.2	0
36	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. **2021**,		3
35	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. *Cell*, **2021**, 184, 64-75.e11	56.2	518
34	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. *Science*, **2021**, 371, 708-712	33.3	159
33	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. **2021**,		2
32	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. *Cell*, **2020**, 181, 997-1003.e9	56.2	175
31	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. *Nature Communications*, **2020**, 11, 2688	17.4	174
30	A de novo approach to inferring within-host fitness effects during untreated HIV-1 infection. *PLoS Pathogens*, **2020**, 16, e1008171	7.6	1
29	Link between the numbers of particles and variants founding new HIV-1 infections depends on the timing of transmission. *Virus Evolution*, **2019**, 5, vey038	3.7	6
28	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. *PLoS Pathogens*, **2019**, 15, e1007976	7.6	25
27	High-Resolution Evolutionary Analysis of Within-Host Hepatitis C Virus Infection. *Journal of Infectious Diseases*, **2019**, 219, 1722-1729	7	8
26	Evolution of HIV-1 within untreated individuals and at the population scale in Uganda. *PLoS Pathogens*, **2018**, 14, e1007167	7.6	15
25	A Protective Monoclonal Antibody Targets a Site of Vulnerability on the Surface of Rift Valley Fever Virus. *Cell Reports*, **2018**, 25, 3750-3758.e4	10.6	29
24	Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. *Emerging Infectious Diseases*, **2018**, 24, 1795-1805	10.2	22
23	Where do all the subtypes go? Temporal dynamics of H8-H12 influenza A viruses in waterfowl. *Virus Evolution*, **2018**, 4, vey025	3.7	14
22	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

#	Reference	IF	Cit
21	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. *Journal of Virology*, **2017**, 91,	6.6	12
20	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. *Nature*, **2017**, 546, 406-410	40.4	366
19	Role of HIV-specific CD8 T cells in pediatric HIV cure strategies after widespread early viral escape. *Journal of Experimental Medicine*, **2017**, 214, 3239-3261	16.6	15
18	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. *PLoS Pathogens*, **2017**, 13, e1006749	7.6	55
17	Selection on non-antigenic gene segments of seasonal influenza A virus and its impact on adaptive evolution. *Virus Evolution*, **2017**, 3, vex034	3.7	8
16	The Evolution and Transmission of Epidemic GII.17 Noroviruses. *Journal of Infectious Diseases*, **2016**, 214, 556-64	7	50
15	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intrahost HIV Infection. *Genetics*, **2016**, 202, 1449-72	4	8
14	Venue-Based Networks May Underpin HCV Transmissions amongst HIV-Infected Gay and Bisexual Men. *PLoS ONE*, **2016**, 11, e0162002	3.7	6
13	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. *PLoS Pathogens*, **2016**, 12, e1005894	7.6	25
12	Faster Adaptation in Smaller Populations: Counterintuitive Evolution of HIV during Childhood Infection. *PLoS Computational Biology*, **2016**, 12, e1004694	5	6
11	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. *Emerging Infectious Diseases*, **2016**, 22, 2104-2112	10.2	22
10	A Molecular-Level Account of the Antigenic Hantaviral Surface. *Cell Reports*, **2016**, 15, 959-967	10.6	39
9	Transmission of hepatitis C virus infection among younger and older people who inject drugs in Vancouver, Canada. *Journal of Hepatology*, **2016**, 64, 1247-55	13.4	18
8	Occurrence and reassortment of avian influenza A (H7N9) viruses derived from coinfected birds in China. *Journal of Virology*, **2014**, 88, 13344-51	6.6	13
7	Phylogeography and epidemic history of hepatitis C virus genotype 4 in Africa. *Virology*, **2014**, 464-465, 233-243	3.6	57
6	Intercontinental dispersal of HIV-1 subtype B associated with transmission among men who have sex with men in Japan. *Journal of Virology*, **2014**, 88, 9864-76	6.6	18
5	Origin and evolution of the unique hepatitis C virus circulating recombinant form 2k/1b. *Journal of Virology*, **2012**, 86, 2212-20	6.6	46
4	Endemic dengue associated with the co-circulation of multiple viral lineages and localized density-dependent transmission. *PLoS Pathogens*, **2011**, 7, e1002064	7.6	74

3 Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. *Nature*, **2009**, 459, 1122-5   50.4   1535

2 Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza   1

1 Genomic epidemiology of early SARS-CoV-2 transmission dynamics in Gujarat, India   2