

# Justin Bahl

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

7,028  
citations

109321

35  
h-index

95266

68  
g-index

82  
all docs

82  
docs citations

82  
times ranked

8176  
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel and extendable genotyping system for human respiratory syncytial virus based on whole-genome sequence analysis. <i>Influenza and Other Respiratory Viruses</i> , 2022, 16, 492-500.	3.4	14
2	Host diversity and behavior determine patterns of interspecies transmission and geographic diffusion of avian influenza A subtypes among North American wild reservoir species. <i>PLoS Pathogens</i> , 2022, 18, e1009973.	4.7	9
3	Maintenance and dissemination of avian-origin influenza A virus within the northern Atlantic Flyway of North America. <i>PLoS Pathogens</i> , 2022, 18, e1010605.	4.7	9
4	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.	3.3	8
5	Longitudinal Assessment of Immune Responses to Repeated Annual Influenza Vaccination in a Human Cohort of Adults and Teenagers. <i>Frontiers in Immunology</i> , 2021, 12, 642791.	4.8	7
6	Quantifying the Persistence of Vaccine-Related T Cell Epitopes in Circulating Swine Influenza A Strains from 2013–2017. <i>Vaccines</i> , 2021, 9, 468.	4.4	3
7	Proposal for Human Respiratory Syncytial Virus Nomenclature below the Species Level. <i>Emerging Infectious Diseases</i> , 2021, 27, 1-9.	4.3	20
8	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566.	2.1	62
9	High-Throughput Next-Generation Sequencing Respiratory Viral Panel: A Diagnostic and Epidemiologic Tool for SARS-CoV-2 and Other Viruses. <i>Viruses</i> , 2021, 13, 2063.	3.3	9
10	Domestic ducks play a major role in the maintenance and spread of H5N8 highly pathogenic avian influenza viruses in South Korea. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 844-851.	3.0	27
11	Non-gradient and genotype-dependent patterns of RSV gene expression. <i>PLoS ONE</i> , 2020, 15, e0227558.	2.5	16
12	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072.	2.1	184
13	Migration interacts with the local transmission of HIV in developed trade areas: A molecular transmission network analysis in China. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104376.	2.3	8
14	Agricultural and geographic factors shaped the North American 2015 highly pathogenic avian influenza H5N2 outbreak. <i>PLoS Pathogens</i> , 2020, 16, e1007857.	4.7	15
15	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
16	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
17	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
18	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0

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19	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
20	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
21	Active surveillance and genetic evolution of avian influenza viruses in Egypt, 2016â€“2018. <i>Emerging Microbes and Infections</i> , 2019, 8, 1370-1382.	6.5	29
22	Global phylodynamic analysis of avian paramyxovirus-1 provides evidence of inter-host transmission and intercontinental spatial diffusion. <i>BMC Evolutionary Biology</i> , 2019, 19, 108.	3.2	38
23	Computational Approaches and Challenges to Developing Universal Influenza Vaccines. <i>Vaccines</i> , 2019, 7, 45.	4.4	10
24	Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. <i>Infection, Genetics and Evolution</i> , 2019, 74, 103917.	2.3	227
25	Geochemical discrimination and petrogenetic affinities of dykes intruding the Ladakh batholith, NW India. <i>Geological Society Special Publication</i> , 2019, 481, 231-250.	1.3	3
26	Isolation and Characterization of a Distinct Influenza A Virus from Egyptian Bats. <i>Journal of Virology</i> , 2019, 93, .	3.4	42
27	Circulation of influenza in backyard productive systems in central Chile and evidence of spillover from wild birds. <i>Preventive Veterinary Medicine</i> , 2018, 153, 1-6.	1.9	20
28	Transmission Dynamics of Highly Pathogenic Avian Influenza Virus A(H5Nx) Clade 2.3.4.4, North America, 2014â€“2015. <i>Emerging Infectious Diseases</i> , 2018, 24, 1840-1848.	4.3	41
29	The influenza virus hemagglutinin head evolves faster than the stalk domain. <i>Scientific Reports</i> , 2018, 8, 10432.	3.3	171
30	Lineageâ€“specific epitope profiles for <scp>HPAI</scp> H5 preâ€“pandemic vaccine selection and evaluation. <i>Influenza and Other Respiratory Viruses</i> , 2017, 11, 445-456.	3.4	7
31	Assessment of contemporary genetic diversity and inter-taxa/inter-region exchange of avian paramyxovirus serotype 1 in wild birds sampled in North America. <i>Virology Journal</i> , 2017, 14, 43.	3.4	17
32	Highly Pathogenic Avian Influenza Viruses and Generation of Novel Reassortants, United States, 2014â€“2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 1283-1285.	4.3	132
33	Broadly-Reactive Neutralizing and Non-neutralizing Antibodies Directed against the H7 Influenza Virus Hemagglutinin Reveal Divergent Mechanisms of Protection. <i>PLoS Pathogens</i> , 2016, 12, e1005578.	4.7	124
34	Ecosystem Interactions Underlie the Spread of Avian Influenza A Viruses with Pandemic Potential. <i>PLoS Pathogens</i> , 2016, 12, e1005620.	4.7	48
35	Viral deep sequencing needs an adaptive approach: IRMA, the iterative refinement meta-assembler. <i>BMC Genomics</i> , 2016, 17, 708.	2.8	134
36	A point mutation in the polymerase protein PB2 allows a reassortant H9N2 influenza isolate of wild-bird origin to replicate in human cells. <i>Infection, Genetics and Evolution</i> , 2016, 41, 279-288.	2.3	4

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37	Inference of Japanese encephalitis virus ecological and evolutionary dynamics from passive and active virus surveillance. <i>Virus Evolution</i> , 2016, 2, vew009.	4.9	6
38	Temporal, geographic, and host distribution of avian paramyxovirus 1 (Newcastle disease virus). <i>Infection, Genetics and Evolution</i> , 2016, 39, 22-34.	2.3	216
39	Influenza A Virus Diversity and Transmission in Exhibition Swine. <i>Journal of Infectious Diseases</i> , 2016, 213, 169-170.	4.0	1
40	Evidence for common ancestry among viruses isolated from wild birds in Beringia and highly pathogenic intercontinental reassortant H5N1 and H5N2 influenza A viruses. <i>Infection, Genetics and Evolution</i> , 2016, 40, 176-185.	2.3	66
41	Genetic diversity and evolutionary insights of respiratory syncytial virus A ON1 genotype: global and local transmission dynamics. <i>Scientific Reports</i> , 2015, 5, 14268.	3.3	104
42	Adaptation of Pandemic H2N2 Influenza A Viruses in Humans. <i>Journal of Virology</i> , 2015, 89, 2442-2447.	3.4	29
43	Influenza A viruses of swine circulating in the United States during 2009–2014 are susceptible to neuraminidase inhibitors but show lineage-dependent resistance to adamantanes. <i>Antiviral Research</i> , 2015, 117, 10-19.	4.1	15
44	Dengue subgenomic RNA binds TRIM25 to inhibit interferon expression for epidemiological fitness. <i>Science</i> , 2015, 350, 217-221.	12.6	338
45	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. <i>Nature Communications</i> , 2015, 6, 6553.	12.8	90
46	Influenza A virus evolution and spatio-temporal dynamics in Eurasian wild birds: a phylogenetic and phylogeographical study of whole-genome sequence data. <i>Journal of General Virology</i> , 2015, 96, 2050-2060.	2.9	23
47	Phylodynamics of H1N1/2009 influenza reveals the transition from host adaptation to immune-driven selection. <i>Nature Communications</i> , 2015, 6, 7952.	12.8	107
48	Genomewide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011. <i>Journal of Virology</i> , 2014, 88, 2844-2857.	3.4	137
49	Epistatic interactions between neuraminidase mutations facilitated the emergence of the oseltamivir-resistant H1N1 influenza viruses. <i>Nature Communications</i> , 2014, 5, 5029.	12.8	51
50	LABEL: Fast and Accurate Lineage Assignment with Assessment of H5N1 and H9N2 Influenza A Hemagglutinins. <i>PLoS ONE</i> , 2014, 9, e86921.	2.5	31
51	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	4.7	83
52	Genetic Structure of <i>Culex erraticus</i> Populations Across the Americas. <i>Journal of Medical Entomology</i> , 2012, 49, 522-534.	1.8	9
53	Genetic Analysis. <i>Methods in Molecular Biology</i> , 2012, 865, 207-227.	0.9	2
54	Continued evolution of highly pathogenic avian influenza A (H5N1): updated nomenclature. <i>Influenza and Other Respiratory Viruses</i> , 2012, 6, 1-5.	3.4	214

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55	Feasibility of reconstructed ancestral H5N1 influenza viruses for cross-clade protective vaccine development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 349-354.	7.1	52
56	Ancient origins determine global biogeography of hot and cold desert cyanobacteria. <i>Nature Communications</i> , 2011, 2, 163.	12.8	203
57	Long-term evolution and transmission dynamics of swine influenza A virus. <i>Nature</i> , 2011, 473, 519-522.	27.8	219
58	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19359-19364.	7.1	146
59	Genetic Characterization and Epidemiology of Helicobacters in Non-domestic Animals. <i>Helicobacter</i> , 2010, 15, 126-142.	3.5	20
60	The emergence of pandemic influenza viruses. <i>Protein and Cell</i> , 2010, 1, 9-13.	11.0	140
61	Establishment of an H6N2 Influenza Virus Lineage in Domestic Ducks in Southern China. <i>Journal of Virology</i> , 2010, 84, 6978-6986.	3.4	83
62	Dating the emergence of pandemic influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11709-11712.	7.1	387
63	Characterization of Avian Influenza Viruses A (H5N1) from Wild Birds, Hong Kong, 2004-2008. <i>Emerging Infectious Diseases</i> , 2009, 15, 402-407.	4.3	94
64	Gene flow and competitive exclusion of avian influenza A virus in natural reservoir hosts. <i>Virology</i> , 2009, 390, 289-297.	2.4	108
65	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009, 459, 1122-1125.	27.8	1,870
66	The development and genetic diversity of H5N1 influenza virus in China, 1996-2006. <i>Virology</i> , 2008, 380, 243-254.	2.4	140
67	Identification of the Progenitors of Indonesian and Vietnamese Avian Influenza A (H5N1) Viruses from Southern China. <i>Journal of Virology</i> , 2008, 82, 3405-3414.	3.4	81
68	Evolutionary Dynamics and Emergence of Panzootic H5N1 Influenza Viruses. <i>PLoS Pathogens</i> , 2008, 4, e1000161.	4.7	143
69	Avian Influenza A Virus (H5N1) Outbreaks, Kuwait, 2007. <i>Emerging Infectious Diseases</i> , 2008, 14, 958-961.	4.3	20
70	Establishment of Influenza A Virus (H6N1) in Minor Poultry Species in Southern China. <i>Journal of Virology</i> , 2007, 81, 10402-10412.	3.4	106
71	The Genesis and Evolution of H9N2 Influenza Viruses in Poultry from Southern China, 2000 to 2005. <i>Journal of Virology</i> , 2007, 81, 10389-10401.	3.4	214
72	Phylogeny of <i>Rosellinia capetribulensis</i> sp. nov. and its allies (Xylariaceae). <i>Mycologia</i> , 2005, 97, 1102-1110.	1.9	14