

Justin Bahl

List of Publications by Year in descending order

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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	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009, 459, 1122-1125.	27.8	1,870
2	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
3	Dengue subgenomic RNA binds TRIM25 to inhibit interferon expression for epidemiological fitness. <i>Science</i> , 2015, 350, 217-221.	12.6	338
4	Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. <i>Infection, Genetics and Evolution</i> , 2019, 74, 103917.	2.3	227
5	Long-term evolution and transmission dynamics of swine influenza A virus. <i>Nature</i> , 2011, 473, 519-522.	27.8	219
6	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
7	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
8	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
9	Ancient origins determine global biogeography of hot and cold desert cyanobacteria. <i>Nature Communications</i> , 2011, 2, 163.	12.8	203
10	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
11	The influenza virus hemagglutinin head evolves faster than the stalk domain. <i>Scientific Reports</i> , 2018, 8, 10432.	3.3	171
12	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
13	Evolutionary Dynamics and Emergence of Panzootic H5N1 Influenza Viruses. <i>PLoS Pathogens</i> , 2008, 4, e1000161.	4.7	143
14	The development and genetic diversity of H5N1 influenza virus in China, 1996–2006. <i>Virology</i> , 2008, 380, 243-254.	2.4	140
15	The emergence of pandemic influenza viruses. <i>Protein and Cell</i> , 2010, 1, 9-13.	11.0	140
16	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
17	Viral deep sequencing needs an adaptive approach: IRMA, the iterative refinement meta-assembler. <i>BMC Genomics</i> , 2016, 17, 708.	2.8	134
18	Highly Pathogenic Avian Influenza Viruses and Generation of Novel Reassortants, United States, 2014–2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 1283-1285.	4.3	132

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19	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
20	Gene flow and competitive exclusion of avian influenza A virus in natural reservoir hosts. <i>Virology</i> , 2009, 390, 289-297.	2.4	108
21	Phylogenetics of H1N1/2009 influenza reveals the transition from host adaptation to immune-driven selection. <i>Nature Communications</i> , 2015, 6, 7952.	12.8	107
22	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
23	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
24	Characterization of Avian Influenza Viruses A (H5N1) from Wild Birds, Hong Kong, 2004â€“2008. <i>Emerging Infectious Diseases</i> , 2009, 15, 402-407.	4.3	94
25	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. <i>Nature Communications</i> , 2015, 6, 6553.	12.8	90
26	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
27	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	4.7	83
28	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
29	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
30	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
31	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
32	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
33	Ecosystem Interactions Underlie the Spread of Avian Influenza A Viruses with Pandemic Potential. <i>PLoS Pathogens</i> , 2016, 12, e1005620.	4.7	48
34	Isolation and Characterization of a Distinct Influenza A Virus from Egyptian Bats. <i>Journal of Virology</i> , 2019, 93, .	3.4	42
35	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
36	Global phylogenetic 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

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37	LABEL: Fast and Accurate Lineage Assignment with Assessment of H5N1 and H9N2 Influenza A Hemagglutinins. PLoS ONE, 2014, 9, e86921.	2.5	31
38	Adaptation of Pandemic H2N2 Influenza A Viruses in Humans. Journal of Virology, 2015, 89, 2442-2447.	3.4	29
39	Active surveillance and genetic evolution of avian influenza viruses in Egypt, 2016â€“2018. Emerging Microbes and Infections, 2019, 8, 1370-1382.	6.5	29
40	Domestic ducks play a major role in the maintenance and spread of H5N8 highly pathogenic avian influenza viruses in South Korea. Transboundary and Emerging Diseases, 2020, 67, 844-851.	3.0	27
41	Influenza A virus evolution and spatio-temporal dynamics in Eurasian wild birds: a phylogenetic and phylogeographical study of whole-genome sequence data. Journal of General Virology, 2015, 96, 2050-2060.	2.9	23
42	Avian Influenza A Virus (H5N1) Outbreaks, Kuwait, 2007. Emerging Infectious Diseases, 2008, 14, 958-961.	4.3	20
43	Genetic Characterization and Epidemiology of Helicobacters in Non-domestic Animals. Helicobacter, 2010, 15, 126-142.	3.5	20
44	Circulation of influenza in backyard productive systems in central Chile and evidence of spillover from wild birds. Preventive Veterinary Medicine, 2018, 153, 1-6.	1.9	20
45	Proposal for Human Respiratory Syncytial Virus Nomenclature below the Species Level. Emerging Infectious Diseases, 2021, 27, 1-9.	4.3	20
46	Assessment of contemporary genetic diversity and inter-taxa/inter-region exchange of avian paramyxovirus serotype 1 in wild birds sampled in North America. Virology Journal, 2017, 14, 43.	3.4	17
47	Non-gradient and genotype-dependent patterns of RSV gene expression. PLoS ONE, 2020, 15, e0227558.	2.5	16
48	Influenza A viruses of swine circulating in the United States during 2009â€“2014 are susceptible to neuraminidase inhibitors but show lineage-dependent resistance to adamantanes. Antiviral Research, 2015, 117, 10-19.	4.1	15
49	Agricultural and geographic factors shaped the North American 2015 highly pathogenic avian influenza H5N2 outbreak. PLoS Pathogens, 2020, 16, e1007857.	4.7	15
50	Phylogeny of Rosellinia capetribulensis sp. nov. and its allies (Xylariaceae). Mycologia, 2005, 97, 1102-1110.	1.9	14
51	Novel and extendable genotyping system for human respiratory syncytial virus based on whole-genome sequence analysis. Influenza and Other Respiratory Viruses, 2022, 16, 492-500.	3.4	14
52	Computational Approaches and Challenges to Developing Universal Influenza Vaccines. Vaccines, 2019, 7, 45.	4.4	10
53	Genetic Structure of Culex erraticus Populations Across the Americas. Journal of Medical Entomology, 2012, 49, 522-534.	1.8	9
54	High-Throughput Next-Generation Sequencing Respiratory Viral Panel: A Diagnostic and Epidemiologic Tool for SARS-CoV-2 and Other Viruses. Viruses, 2021, 13, 2063.	3.3	9

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55	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
56	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
57	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
58	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
59	Lineage-specific epitope profiles for <scp>HPAI</scp> H5 pre-pandemic vaccine selection and evaluation. <i>Influenza and Other Respiratory Viruses</i> , 2017, 11, 445-456.	3.4	7
60	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
61	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
62	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
63	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
64	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
65	Genetic Analysis. <i>Methods in Molecular Biology</i> , 2012, 865, 207-227.	0.9	2
66	Influenza A Virus Diversity and Transmission in Exhibition Swine. <i>Journal of Infectious Diseases</i> , 2016, 213, 169-170.	4.0	1
67	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
68	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
69	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
70	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
71	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0
72	Non-gradient and genotype-dependent patterns of RSV gene expression. , 2020, 15, e0227558.		0