

Philippe Lemey

List of Publications by Year in descending order

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317
papers

33,614
citations

6495

79
h-index

5645

160
g-index

402
all docs

402
docs citations

402
times ranked

38637
citing authors

#	ARTICLE	IF	CITATIONS
1	Many-core algorithms for high-dimensional gradients on phylogenetic trees. <i>Bioinformatics</i> , 2024, 40, .	4.2	2
2	Revisiting the origins of the Sobemovirus genus: A case for ancient origins of plant viruses. <i>PLoS Pathogens</i> , 2024, 20, e1011911.	4.0	0
3	Contemporary and historical human migration patterns shape hepatitis B virus diversity. <i>Virus Evolution</i> , 2024, 10, .	4.9	0
4	Synchrony of Bird Migration with Global Dispersal of Avian Influenza Reveals Exposed Bird Orders. <i>Nature Communications</i> , 2024, 15, .	13.0	2
5	Dispersion patterns of SARS-CoV-2 variants Gamma, Lambda and Mu in Latin America and the Caribbean. <i>Nature Communications</i> , 2024, 15, .	13.0	2
6	Drivers and impact of the early silent invasion of SARS-CoV-2 Alpha. <i>Nature Communications</i> , 2024, 15, .	13.0	0
7	The genomic evolutionary dynamics and global circulation patterns of respiratory syncytial virus. <i>Nature Communications</i> , 2024, 15, .	13.0	1
8	Mapping Transmission Dynamics and Drug Resistance Surveillance in the Cyprus HIV-1 Epidemic (2017â€“2021). <i>Viruses</i> , 2024, 16, 1449.	3.4	0
9	Accelerated evolution of SARS-CoV-2 in free-ranging white-tailed deer. <i>Nature Communications</i> , 2023, 14, .	13.0	14
10	Newly identified lineages ofÂporcine hemagglutinating encephalomyelitis virus exhibit respiratory phenotype. <i>Virus Evolution</i> , 2023, 9, .	4.9	3
11	Renaming of the genus <i>Flavivirus</i> to <i>Orthoflavivirus</i> and extension of binomial species names within the family <i>Flaviviridae</i> . <i>Archives of Virology</i> , 2023, 168, .	1.9	42
12	Shrinkage-based Random Local Clocks with Scalable Inference. <i>Molecular Biology and Evolution</i> , 2023, 40, .	9.1	2
13	Inferring Phenotypic Trait Evolution on Large Trees With Many Incomplete Measurements. <i>Journal of the American Statistical Association</i> , 2022, 117, 678-692.	3.4	11
14	A systematic review on global RSV genetic data: Identification of knowledge gaps. <i>Reviews in Medical Virology</i> , 2022, 32, e2284.	8.4	30
15	Phylogeography Reveals Association between Swine Trade and the Spread of Porcine Epidemic Diarrhea Virus in China and across the World. <i>Molecular Biology and Evolution</i> , 2022, 39, .	9.1	40
16	Phycova â€” a tool for exploring covariates of pathogen spread. <i>Virus Evolution</i> , 2022, 8, veac015.	4.9	4
17	Quantifying rates of HIV-1 flow between risk groups and geographic locations in Kenya: A country-wide phylogenetic study. <i>Virus Evolution</i> , 2022, 8, veac016.	4.9	7
18	Virome characterization of game animals in China reveals a spectrum of emerging pathogens. <i>Cell</i> , 2022, 185, 1117-1129.e8.	27.7	133

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19	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. <i>Molecular Biology and Evolution</i> , 2022, 39, .	9.1	92
20	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.4	40
21	Reconstruction of the origin and dispersal of the worldwide dominant Hepatitis B Virus subgenotype D1. <i>Virus Evolution</i> , 2022, 8, .	4.9	5
22	The role of high-risk geographies in the perpetuation of the HIV epidemic in rural South Africa: A spatial molecular epidemiology study. <i>PLOS Global Public Health</i> , 2022, 2, e0000105.	1.5	5
23	Global spatial dynamics and vaccine-induced fitness changes of <i>Bordetella pertussis</i> . <i>Science Translational Medicine</i> , 2022, 14, eabn3253.	13.3	29
24	Spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals. <i>Nature Medicine</i> , 2022, 28, 1476-1485.	29.9	29
25	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. <i>Nature Communications</i> , 2022, 13, 2314.	13.0	30
26	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017â€“2019. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010255.	2.4	12
27	Accommodating sampling location uncertainty in continuous phylogeography. <i>Virus Evolution</i> , 2022, 8, .	4.9	10
28	The phylodynamics of SARS-CoV-2 during 2020 in Finland. <i>Communications Medicine</i> , 2022, 2, .	4.2	6
29	Detection of Marburg Virus Disease in Guinea. <i>New England Journal of Medicine</i> , 2022, 386, 2528-2530.	29.7	30
30	The Huanan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic. <i>Science</i> , 2022, 377, 951-959.	19.8	222
31	SPREAD 4: online visualisation of pathogen phylogeographic reconstructions. <i>Virus Evolution</i> , 2022, 8, .	4.9	13
32	Endogenous Viral Elements in Shrew Genomes Provide Insights into <i>Pestivirus</i> Ancient History. <i>Molecular Biology and Evolution</i> , 2022, 39, .	9.1	10
33	Predicting the evolution of the Lassa virus endemic area and population at risk over the next decades. <i>Nature Communications</i> , 2022, 13, .	13.0	40
34	Updated vaccine protects against SARS-CoV-2 variants including Omicron (B.1.1.529) and prevents transmission in hamsters. <i>Nature Communications</i> , 2022, 13, .	13.0	15
35	Markov-Modulated Continuous-Time Markov Chains to Identify Site- and Branch-Specific Evolutionary Variation in BEAST. <i>Systematic Biology</i> , 2021, 70, 181-189.	5.9	13
36	Massive Parallelization Boosts Big Bayesian Multidimensional Scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021, 30, 11-24.	1.8	16

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37	Relaxed Random Walks at Scale. <i>Systematic Biology</i> , 2021, 70, 258-267.	5.9	20
38	Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , 2021, 7, veab036.	4.9	11
39	Relax, Keep Walking – A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021, 38, 3486-3493.	9.1	40
40	Large-scale inference of correlation among mixed-type biological traits with phylogenetic multivariate probit models. <i>Annals of Applied Statistics</i> , 2021, 15, .	1.1	11
41	Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. <i>PLoS Biology</i> , 2021, 19, e3001115.	5.4	185
42	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	19.8	1,197
43	Genome Sequence of Ruloma Virus, a Novel Paramyxovirus Clustering Basally to Members of the Genus <i>Jeilongvirus</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	1.1	13
44	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021, 595, 713-717.	35.8	144
45	Context-dependent modulation of aggressiveness of pediatric tumors by individual oncogenic RAS isoforms. <i>Oncogene</i> , 2021, 40, 4955-4966.	5.9	5
46	Efficient Bayesian inference of general Gaussian models on large phylogenetic trees. <i>Annals of Applied Statistics</i> , 2021, 15, .	1.1	10
47	A Comprehensive Molecular Epidemiological Analysis of SARS-CoV-2 Infection in Cyprus from April 2020 to January 2021: Evidence of a Highly Polyphyletic and Evolving Epidemic. <i>Viruses</i> , 2021, 13, 1098.	3.4	13
48	A Novel Series of Indole Alkaloid Derivatives Inhibit Dengue and Zika Virus Infection by Interference with the Viral Replication Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0234920.	3.4	14
49	<i>In Vivo</i> Therapy with M2e-Specific IgG Selects for an Influenza A Virus Mutant with Delayed Matrix Protein 2 Expression. <i>MBio</i> , 2021, 12, e0074521.	4.3	4
50	Rivers and landscape ecology of a plant virus, Rice yellow mottle virus along the Niger Valley. <i>Virus Evolution</i> , 2021, 7, .	4.9	10
51	Genomic population structure associated with repeated escape of <i>Salmonella enterica</i> ATCC14028s from the laboratory into nature. <i>PLoS Genetics</i> , 2021, 17, e1009820.	3.3	8
52	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	27.7	215
53	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	35.8	119
54	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. <i>Viruses</i> , 2021, 13, 1842.	3.4	5

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55	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference “Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , 2020, 36, 2098-2104.	4.2	14
56	Towards a unified classification for human respiratory syncytial virus genotypes. <i>Virus Evolution</i> , 2020, 6, veaa052.	4.9	38
57	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020, 6, veaa061.	4.9	341
58	Rational design of a microbial consortium of mucosal sugar utilizers reduces <i>Clostridiodes difficile</i> colonization. <i>Nature Communications</i> , 2020, 11, 5104.	13.0	200
59	Air conditioning system usage and SARS-CoV-2 transmission dynamics in Iran. <i>Medical Hypotheses</i> , 2020, 143, 110164.	1.5	3
60	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 3363-3379.	9.1	92
61	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620.	13.0	42
62	An endoribonuclease-based feedforward controller for decoupling resource-limited genetic modules in mammalian cells. <i>Nature Communications</i> , 2020, 11, 5690.	13.0	77
63	HIV-1 p24Gag adaptation to modern and archaic HLA-allele frequency differences in ethnic groups contributes to viral subtype diversification. <i>Virus Evolution</i> , 2020, 6, veaa085.	4.9	8
64	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	12.9	820
65	Nanotechnology-based disinfectants and sensors for SARS-CoV-2. <i>Nature Nanotechnology</i> , 2020, 15, 618-621.	30.1	282
66	Pathogenic mosaic variants in congenital hypogonadotropic hypogonadism. <i>Genetics in Medicine</i> , 2020, 22, 1759-1767.	2.4	7
67	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110.	13.0	128
68	Globally altered epigenetic landscape and delayed osteogenic differentiation in H3.3-G34W-mutant giant cell tumor of bone. <i>Nature Communications</i> , 2020, 11, 5414.	13.0	33
69	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020, 370, 564-570.	19.8	346
70	Determinants of dengue virus dispersal in the Americas. <i>Virus Evolution</i> , 2020, 6, veaa074.	4.9	5
71	A near full-length HIV-1 genome from 1966 recovered from formalin-fixed paraffin-embedded tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12222-12229.	7.5	33
72	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.5	70

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73	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020, 37, 2641-2654.	9.1	86
74	Gradients Do Grow on Trees: A Linear-Time $O(N)$ -Dimensional Gradient for Statistical Phylogenetics. <i>Molecular Biology and Evolution</i> , 2020, 37, 3047-3060.	9.1	24
75	nosoi: A stochastic agent-based transmission chain simulation framework in R. <i>Methods in Ecology and Evolution</i> , 2020, 11, 1002-1007.	5.2	23
76	Assessing the role of live poultry trade in community-structured transmission of avian influenza in China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5949-5954.	7.5	45
77	DEAD-Box Helicases: Sensors, Regulators, and Effectors for Antiviral Defense. <i>Viruses</i> , 2020, 12, 181.	3.4	83
78	In Search of Covariates of HIV-1 Subtype B Spread in the United States—A Cautionary Tale of Large-Scale Bayesian Phylogeography. <i>Viruses</i> , 2020, 12, 182.	3.4	18
79	Evaluating predictive markers for viral rebound and safety assessment in blood and lumbar fluid during HIV-1 treatment interruption. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1311-1320.	3.2	17
80	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020, 37, 1832-1842.	9.1	28
81	Polygenic Patterns of Adaptive Introgression in Modern Humans Are Mainly Shaped by Response to Pathogens. <i>Molecular Biology and Evolution</i> , 2020, 37, 1420-1433.	9.1	46
82	Hamiltonian Monte Carlo sampling to estimate past population dynamics using the skygrid coalescent model in a Bayesian phylogenetics framework. <i>Wellcome Open Research</i> , 2020, 5, 53.	1.9	18
83	Genomic Epidemiology of 2015–2016 Zika Virus Outbreak in Cape Verde. <i>Emerging Infectious Diseases</i> , 2020, 26, 1084-1090.	4.3	26
84	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020, 9, .	5.9	17
85	Comparing patterns and scales of plant virus phylogeography: Rice yellow mottle virus in Madagascar and in continental Africa. <i>Virus Evolution</i> , 2019, 5, vez023.	4.9	23
86	Phylogeography of Lassa Virus in Nigeria. <i>Journal of Virology</i> , 2019, 93, .	3.4	55
87	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019, 7, 208.	2.8	17
88	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. <i>Methods in Molecular Biology</i> , 2019, 1910, 691-722.	0.7	13
89	A6—Quantifying the dynamics of evolutionary rates through time. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
90	A4—An amplicon-based approach for universal amplification, sequencing, and assembly of full-length HIV-1 samples from the DRC. <i>Virus Evolution</i> , 2019, 5, .	4.9	0

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91	Using phylogeographic approaches to analyse the dispersal history, velocity and direction of viral lineages—Application to rabies virus spread in Iran. <i>Molecular Ecology</i> , 2019, 28, 4335-4350.	3.6	37
92	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019, 5, vez009.	4.9	19
93	HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. <i>Cell Host and Microbe</i> , 2019, 26, 347-358.e7.	11.0	127
94	Divergence dating using mixed effects clock modelling: An application to HIV-1. <i>Virus Evolution</i> , 2019, 5, vez036.	4.9	25
95	Earlier Initiation of Antiretroviral Treatment Coincides With an Initial Control of the HIV-1 Sub-Subtype F1 Outbreak Among Men-Having-Sex-With-Men in Flanders, Belgium. <i>Frontiers in Microbiology</i> , 2019, 10, 613.	3.5	21
96	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. <i>Molecular Biology and Evolution</i> , 2019, 36, 1793-1803.	9.1	43
97	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019, 68, 1052-1061.	5.9	159
98	Mass migration to Europe: an opportunity for elimination of hepatitis B virus?. <i>The Lancet Gastroenterology and Hepatology</i> , 2019, 4, 315-323.	8.2	27
99	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , 2019, 220, 233-243.	3.9	26
100	Disentangling the role of Africa in the global spread of H5 highly pathogenic avian influenza. <i>Nature Communications</i> , 2019, 10, 5310.	13.0	68
101	Limited evolution of the yellow fever virus 17d in a mouse infection model. <i>Emerging Microbes and Infections</i> , 2019, 8, 1734-1746.	6.5	20
102	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019, 15, e1007976.	4.0	40
103	Low Postseroconversion CD4 + T-cell Level Is Associated with Faster Disease Progression and Higher Viral Evolutionary Rate in HIV-2 Infection. <i>MBio</i> , 2019, 10, .	4.3	8
104	Pneumococcal quorum sensing drives an asymmetric owner–intruder competitive strategy during carriage via the competence regulon. <i>Nature Microbiology</i> , 2019, 4, 198-208.	12.9	44
105	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	12.9	333
106	APOBEC restriction goes nuclear. <i>Nature Microbiology</i> , 2019, 4, 6-7.	12.9	2
107	Global origins of African highly pathogenic avian influenza H5Nx viruses and intracontinental spread. <i>International Journal of Infectious Diseases</i> , 2019, 79, 9-10.	3.3	2
108	Increasing importance of European lineages in seeding the hepatitis C virus subtype 1a epidemic in Spain. <i>Eurosurveillance</i> , 2019, 24, .	7.3	15

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109	Viral Characteristics Associated with the Clinical Nonprogressor Phenotype Are Inherited by Viruses from a Cluster of HIV-1 Elite Controllers. <i>MBio</i> , 2018, 9, .	4.3	41
110	Proposal for a new subtype of the zoonotic genotype 3 Hepatitis E virus: HEV-3I. <i>Virus Research</i> , 2018, 248, 1-4.	2.3	22
111	A novel hepatitis B virus species discovered in capuchin monkeys sheds new light on the evolution of primate hepadnaviruses. <i>Journal of Hepatology</i> , 2018, 68, 1114-1122.	3.9	57
112	Landscape attributes governing local transmission of an endemic zoonosis: Rabies virus in domestic dogs. <i>Molecular Ecology</i> , 2018, 27, 773-788.	3.6	53
113	Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. <i>Statistics in Medicine</i> , 2018, 37, 195-206.	1.7	4
114	Phylogenetic Factor Analysis. <i>Systematic Biology</i> , 2018, 67, 384-399.	5.9	18
115	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018, 14, e1007392.	4.0	43
116	Viral attenuation by engineered protein fragmentation. <i>Virus Evolution</i> , 2018, 4, vey017.	4.9	2
117	Iran's hepatitis elimination programme is under threat. <i>Lancet, The</i> , 2018, 392, 1009.	12.1	19
118	Whole genome analysis of local Kenyan and global sequences unravels the epidemiological and molecular evolutionary dynamics of RSV genotype ON1 strains. <i>Virus Evolution</i> , 2018, 4, vey027.	4.9	30
119	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018, 31, 24-32.	5.5	52
120	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. <i>BMC Genomics</i> , 2018, 19, 617.	2.9	39
121	Geographical and Historical Patterns in the Emergences of Novel Highly Pathogenic Avian Influenza (HPAI) H5 and H7 Viruses in Poultry. <i>Frontiers in Veterinary Science</i> , 2018, 5, 84.	2.3	80
122	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	19.8	292
123	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018, 4, vey023.	4.9	30
124	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018, 4, vey016.	4.9	2,634
125	Polyvalent Detection of Members of the Genus <i>Potyvirus</i> by Molecular Hybridization Using a Genus-Probe. <i>Phytopathology</i> , 2018, 108, 1522-1529.	2.3	8
126	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222.	13.0	61

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127	A Relaxed Directional Random Walk Model for Phylogenetic Trait Evolution. <i>Systematic Biology</i> , 2017, 66, syw093.	5.9	25
128	Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017, 66, syw054.	5.9	88
129	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	35.8	367
130	The multi-faceted dynamics of HIV-1 transmission in Northern Alberta: A combined analysis of virus genetic and public health data. <i>Infection, Genetics and Evolution</i> , 2017, 52, 100-105.	2.3	25
131	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. <i>Bioinformatics</i> , 2017, 33, 1798-1805.	4.2	39
132	The epidemic dynamics of hepatitis C virus subtypes 4a and 4d in Saudi Arabia. <i>Scientific Reports</i> , 2017, 7, 44947.	3.4	22
133	Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics. <i>Molecular Biology and Evolution</i> , 2017, 34, 2563-2571.	9.1	70
134	Differential Infection Patterns and Recent Evolutionary Origins of Equine Hepaciviruses in Donkeys. <i>Journal of Virology</i> , 2017, 91, .	3.4	46
135	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. <i>Genome Biology and Evolution</i> , 2017, 9, 3202-3213.	2.6	19
136	Genetic Diversity of Highly Pathogenic Avian Influenza A(H5N8/H5N5) Viruses in Italy, 2016-17. <i>Emerging Infectious Diseases</i> , 2017, 23, 1543-1547.	4.3	66
137	A21- HIV-1 sub-subtype F1 outbreak among MSM in Belgium. <i>Virus Evolution</i> , 2017, 3, .	4.9	6
138	Accurate quantification of within- and between-host HBV evolutionary rates requires explicit transmission chain modelling. <i>Virus Evolution</i> , 2017, 3, vex028.	4.9	16
139	Phylogenetic relationships of the HA and NA genes between vaccine and seasonal influenza A(H3N2) strains in Korea. <i>PLoS ONE</i> , 2017, 12, e0172059.	2.5	11
140	The geography of earth building. , 2017, , 9-14.		1
141	Genetically Different Highly Pathogenic Avian Influenza A(H5N1) Viruses in West Africa, 2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 2132-2136.	4.3	20
142	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016, 8, 12.	3.4	14
143	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. <i>PLoS Pathogens</i> , 2016, 12, e1005525.	4.0	66
144	Understanding Past Population Dynamics: Bayesian Coalescent-Based Modeling with Covariates. <i>Systematic Biology</i> , 2016, 65, 1041-1056.	5.9	61

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145	Spred3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2167-2169.	9.1	439
146	Distinct Effects of T-705 (Favipiravir) and Ribavirin on Influenza Virus Replication and Viral RNA Synthesis. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6679-6691.	3.4	92
147	1970s and "Patient 0"™ HIV-1 genomes illuminate early HIV/AIDS history in North America. <i>Nature</i> , 2016, 539, 98-101.	35.8	184
148	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016, 2, vew023.	4.9	13
149	Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. <i>Molecular Ecology</i> , 2016, 25, 5994-6008.	3.6	29
150	Successful Conservative Treatment of a Kommerell Aneurysm Associated With Right-Sided Aortic Arch. <i>Vascular and Endovascular Surgery</i> , 2016, 50, 458-459.	0.7	5
151	The recent ancestry of Middle East respiratory syndrome coronavirus in Korea has been shaped by recombination. <i>Scientific Reports</i> , 2016, 6, 18825.	3.4	26
152	Reassortment compatibility between PB1, PB2, and HA genes of the two influenza B virus lineages in mammalian cells. <i>Scientific Reports</i> , 2016, 6, 27480.	3.4	11
153	Spain: trusts and taxes. <i>Trusts & Trustees</i> , 2016, 22, 37-42.	0.0	1
154	Shared Drivers but Divergent Ecological Responses: Insights from Long-Term Experiments in Mesic Savanna Grasslands. <i>BioScience</i> , 2016, 66, 666-682.	4.8	21
155	Genealogical Working Distributions for Bayesian Model Testing with Phylogenetic Uncertainty. <i>Systematic Biology</i> , 2016, 65, 250-264.	5.9	106
156	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. <i>Microbial Genomics</i> , 2016, 2, e000057.	2.1	5
157	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2016, 12, e1005894.	4.0	31
158	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016, 5, e12217.	5.9	153
159	Simultaneously estimating evolutionary history and repeated traits phylogenetic signal: applications to viral and host phenotypic evolution. <i>Methods in Ecology and Evolution</i> , 2015, 6, 67-82.	5.2	23
160	Assessing phenotypic correlation through the multivariate phylogenetic latent liability model. <i>Annals of Applied Statistics</i> , 2015, 9, 969-991.	1.1	31
161	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. <i>Aids</i> , 2015, 29, 1549-1556.	2.1	16
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