

Philippe Lemey

List of Publications by Year in descending order

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293
papers

30,526
citations

7568

77
h-index

6996

154
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all docs

325
docs citations

325
times ranked

31727
citing authors

#	ARTICLE	IF	CITATIONS
1	Inferring Phenotypic Trait Evolution on Large Trees With Many Incomplete Measurements. <i>Journal of the American Statistical Association</i> , 2022, 117, 678-692.	3.1	10
2	A systematic review on global RSV genetic data: Identification of knowledge gaps. <i>Reviews in Medical Virology</i> , 2022, 32, e2284.	8.3	19
3	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, .	8.9	35
4	Phycova – a tool for exploring covariates of pathogen spread. <i>Virus Evolution</i> , 2022, 8, veac015.	4.9	3
5	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	6
6	Virome characterization of game animals in China reveals a spectrum of emerging pathogens. <i>Cell</i> , 2022, 185, 1117-1129.e8.	28.9	106
7	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, .	8.9	84
8	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
9	Reconstruction of the origin and dispersal of the worldwide dominant Hepatitis B Virus subgenotype D1. <i>Virus Evolution</i> , 2022, 8, .	4.9	4
10	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.	1.6	3
11	Global spatial dynamics and vaccine-induced fitness changes of <i>Bordetella pertussis</i> . <i>Science Translational Medicine</i> , 2022, 14, eabn3253.	12.4	22
12	Spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals. <i>Nature Medicine</i> , 2022, 28, 1476-1485.	30.7	24
13	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. <i>Nature Communications</i> , 2022, 13, 2314.	12.8	25
14	The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022, 14, 973.	3.3	3
15	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017–2019. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010255.	3.0	9
16	Accommodating sampling location uncertainty in continuous phylogeography. <i>Virus Evolution</i> , 2022, 8, .	4.9	8
17	The phylodynamics of SARS-CoV-2 during 2020 in Finland. <i>Communications Medicine</i> , 2022, 2, .	4.2	5
18	Detection of Marburg Virus Disease in Guinea. <i>New England Journal of Medicine</i> , 2022, 386, 2528-2530.	27.0	26

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19	Markov-Modulated Continuous-Time Markov Chains to Identify Site- and Branch-Specific Evolutionary Variation in BEAST. <i>Systematic Biology</i> , 2021, 70, 181-189.	5.6	11
20	Massive Parallelization Boosts Big Bayesian Multidimensional Scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021, 30, 11-24.	1.7	15
21	Relaxed Random Walks at Scale. <i>Systematic Biology</i> , 2021, 70, 258-267.	5.6	19
22	Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , 2021, 7, veab036.	4.9	11
23	Relax, Keep Walking – A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021, 38, 3486-3493.	8.9	31
24	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	10
25	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.	5.6	172
26	Bayesian Phylogeographic Analysis Incorporating Predictors and Individual Travel Histories in BEAST. <i>Current Protocols</i> , 2021, 1, e98.	2.9	14
27	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	12.6	1,125
28	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, .	0.6	11
29	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021, 595, 713-717.	27.8	133
30	Efficient Bayesian inference of general Gaussian models on large phylogenetic trees. <i>Annals of Applied Statistics</i> , 2021, 15, .	1.1	7
31	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.	3.3	11
32	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.	3.2	13
33	<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.	4.1	4
34	Rivers and landscape ecology of a plant virus, Rice yellow mottle virus along the Niger Valley. <i>Virus Evolution</i> , 2021, 7, .	4.9	9
35	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.	3.5	8
36	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	28.9	186

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37	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	27.8	113
38	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. <i>Viruses</i> , 2021, 13, 1842.	3.3	4
39	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference “Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , 2020, 36, 2098-2104.	4.1	11
40	Towards a unified classification for human respiratory syncytial virus genotypes. <i>Virus Evolution</i> , 2020, 6, veaa052.	4.9	31
41	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020, 6, veaa061.	4.9	317
42	Air conditioning system usage and SARS-CoV-2 transmission dynamics in Iran. <i>Medical Hypotheses</i> , 2020, 143, 110164.	1.5	3
43	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 3363-3379.	8.9	81
44	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620.	12.8	35
45	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	7
46	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
47	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	13.3	772
48	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110.	12.8	118
49	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020, 370, 564-570.	12.6	331
50	Determinants of dengue virus dispersal in the Americas. <i>Virus Evolution</i> , 2020, 6, veaa074.	4.9	5
51	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.	7.1	31
52	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.	7.1	68
53	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020, 37, 2641-2654.	8.9	76
54	Gradients Do Grow on Trees: A Linear-Time N -Dimensional Gradient for Statistical Phylogenetics. <i>Molecular Biology and Evolution</i> , 2020, 37, 3047-3060.	8.9	22

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55	nosoi: A stochastic agent-based transmission chain simulation framework in <sc>r</sc>. <i>Methods in Ecology and Evolution</i> , 2020, 11, 1002-1007.	5.2	19
56	Measles virus and rinderpest virus divergence dated to the sixth century BCE. <i>Science</i> , 2020, 368, 1367-1370.	12.6	102
57	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.	7.1	43
58	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.	3.3	15
59	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.	3.0	15
60	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020, 37, 1832-1842.	8.9	25
61	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.	1.8	15
62	Genomic Epidemiology of 2015–2016 Zika Virus Outbreak in Cape Verde. <i>Emerging Infectious Diseases</i> , 2020, 26, 1084-1090.	4.3	24
63	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020, 9, .	6.0	13
64	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	22
65	Phylogeography of Lassa Virus in Nigeria. <i>Journal of Virology</i> , 2019, 93, .	3.4	49
66	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019, 7, 208.	2.7	15
67	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. <i>Methods in Molecular Biology</i> , 2019, 1910, 691-722.	0.9	11
68	A6—Quantifying the dynamics of evolutionary rates through time. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
69	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
70	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.	3.9	34
71	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019, 5, vez009.	4.9	16
72	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	117

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73	Divergence dating using mixed effects clock modelling: An application to HIV-1. <i>Virus Evolution</i> , 2019, 5, vez036.	4.9	24
74	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
75	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. <i>Molecular Biology and Evolution</i> , 2019, 36, 1793-1803.	8.9	39
76	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019, 68, 1052-1061.	5.6	139
77	Mass migration to Europe: an opportunity for elimination of hepatitis B virus?. <i>The Lancet Gastroenterology and Hepatology</i> , 2019, 4, 315-323.	8.1	25
78	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.	4.0	23
79	Disentangling the role of Africa in the global spread of H5 highly pathogenic avian influenza. <i>Nature Communications</i> , 2019, 10, 5310.	12.8	61
80	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	18
81	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
82	Metagenomic sequencing at the epicenter of the Nigeria 2018 Lassa fever outbreak. <i>Science</i> , 2019, 363, 74-77.	12.6	201
83	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, .	4.1	7
84	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	13.3	305
85	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
86	Increasing importance of European lineages in seeding the hepatitis C virus subtype 1a epidemic in Spain. <i>Eurosurveillance</i> , 2019, 24, .	7.0	14
87	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, .	4.1	37
88	Proposal for a new subtype of the zoonotic genotype 3 Hepatitis E virus: HEV-3I. <i>Virus Research</i> , 2018, 248, 1-4.	2.2	21
89	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.	3.7	56
90	Landscape attributes governing local transmission of an endemic zoonosis: Rabies virus in domestic dogs. <i>Molecular Ecology</i> , 2018, 27, 773-788.	3.9	50

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91	Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. <i>Statistics in Medicine</i> , 2018, 37, 195-206.	1.6	4
92	Phylogenetic Factor Analysis. <i>Systematic Biology</i> , 2018, 67, 384-399.	5.6	16
93	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018, 14, e1007392.	4.7	35
94	Iran's hepatitis elimination programme is under threat. <i>Lancet</i> , The, 2018, 392, 1009.	13.7	19
95	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	27
96	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018, 31, 24-32.	5.4	45
97	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.	2.8	35
98	Phylogenetic analysis of two genotype 3 Hepatitis E viruses from wild boar, Italy. <i>Virus Genes</i> , 2018, 54, 812-817.	1.6	11
99	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.	2.2	72
100	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	12.6	279
101	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018, 4, vey023.	4.9	29
102	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018, 4, vey016.	4.9	2,401
103	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222.	12.8	59
104	HIV-2, Phylogeographic Insights into the Origins and Epidemic History. , 2018, , 970-978.		0
105	A Relaxed Directional Random Walk Model for Phylogenetic Trait Evolution. <i>Systematic Biology</i> , 2017, 66, syw093.	5.6	25
106	Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017, 66, syw054.	5.6	87
107	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
108	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	24

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109	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. <i>Bioinformatics</i> , 2017, 33, 1798-1805.	4.1	35
110	The epidemic dynamics of hepatitis C virus subtypes 4a and 4d in Saudi Arabia. <i>Scientific Reports</i> , 2017, 7, 44947.	3.3	22
111	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.	8.9	64
112	Differential Infection Patterns and Recent Evolutionary Origins of Equine Hepaciviruses in Donkeys. <i>Journal of Virology</i> , 2017, 91, .	3.4	45
113	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. <i>Genome Biology and Evolution</i> , 2017, 9, 3202-3213.	2.5	19
114	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	62
115	A21 HIV-1 sub-subtype F1 outbreak among MSM in Belgium. <i>Virus Evolution</i> , 2017, 3, .	4.9	6
116	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
117	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	10
118	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
119	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016, 8, 12.	3.3	13
120	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. <i>PLoS Pathogens</i> , 2016, 12, e1005525.	4.7	65
121	Understanding Past Population Dynamics: Bayesian Coalescent-Based Modeling with Covariates. <i>Systematic Biology</i> , 2016, 65, 1041-1056.	5.6	60
122	Spred3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2167-2169.	8.9	413
123	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.	3.2	86
124	1970s and 1980s Patient 0 HIV-1 genomes illuminate early HIV/AIDS history in North America. <i>Nature</i> , 2016, 539, 98-101.	27.8	177
125	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016, 2, vew023.	4.9	13
126	Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. <i>Molecular Ecology</i> , 2016, 25, 5994-6008.	3.9	28

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127	The recent ancestry of Middle East respiratory syndrome coronavirus in Korea has been shaped by recombination. <i>Scientific Reports</i> , 2016, 6, 18825.	3.3	26
128	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.	3.3	10
129	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016, 32, 3204-3206.	4.1	124
130	Genealogical Working Distributions for Bayesian Model Testing with Phylogenetic Uncertainty. <i>Systematic Biology</i> , 2016, 65, 250-264.	5.6	101
131	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. <i>Microbial Genomics</i> , 2016, 2, e000057.	2.0	4
132	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2016, 12, e1005894.	4.7	31
133	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016, 5, e12217.	6.0	146
134	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	22
135	Assessing phenotypic correlation through the multivariate phylogenetic latent liability model. <i>Annals of Applied Statistics</i> , 2015, 9, 969-991.	1.1	30
136	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. <i>Aids</i> , 2015, 29, 1549-1556.	2.2	16
137	Enzootic Transmission of Yellow Fever Virus, Venezuela. <i>Emerging Infectious Diseases</i> , 2015, 21, 99-102.	4.3	22
138	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015, 523, 217-220.	27.8	445
139	The global distribution of Banana bunchy top virus reveals little evidence for frequent recent, human-mediated long distance dispersal events. <i>Virus Evolution</i> , 2015, 1, vev009.	4.9	58
140	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015, 1, vev016.	4.9	59
141	Virus evolution and transmission in an ever more connected world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142878.	2.6	96
142	Longitudinal Genetic Characterization Reveals That Cell Proliferation Maintains a Persistent HIV Type 1 DNA Pool During Effective HIV Therapy. <i>Journal of Infectious Diseases</i> , 2015, 212, 596-607.	4.0	138
143	Geographic and Temporal Trends in the Molecular Epidemiology and Genetic Mechanisms of Transmitted HIV-1 Drug Resistance: An Individual-Patient- and Sequence-Level Meta-Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001810.	8.4	188
144	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015, 12, 18.	2.0	90

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145	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015, 6, 6696.	12.8	128
146	Contribution of Epidemiological Predictors in Unraveling the Phylogeographic History of HIV-1 Subtype C in Brazil. <i>Journal of Virology</i> , 2015, 89, 12341-12348.	3.4	28
147	Synonymous and nonsynonymous distances help untangle convergent evolution and recombination. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 375-89.	0.6	5
148	Genome-Wide Evolutionary Analyses of G1P[8] Strains Isolated Before and After Rotavirus Vaccine Introduction. <i>Genome Biology and Evolution</i> , 2015, 7, 2473-2483.	2.5	43
149	Bayesian Inference Reveals Host-Specific Contributions to the Epidemic Expansion of Influenza A H5N1. <i>Molecular Biology and Evolution</i> , 2015, 32, msv185.	8.9	46
150	Ecuador Paraiso Escondido Virus, a New Flavivirus Isolated from New World Sand Flies in Ecuador, Is the First Representative of a Novel Clade in the Genus Flavivirus. <i>Journal of Virology</i> , 2015, 89, 11773-11785.	3.4	31
151	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , 2015, 63, 38-41.	3.1	7
152	Combining phylogeography and spatial epidemiology to uncover predictors of H5N1 influenza A virus diffusion. <i>Archives of Virology</i> , 2015, 160, 215-224.	2.1	28
153	New Insights into Flavivirus Evolution, Taxonomy and Biogeographic History, Extended by Analysis of Canonical and Alternative Coding Sequences. <i>PLoS ONE</i> , 2015, 10, e0117849.	2.5	139
154	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014, 3, e01914.	6.0	299
155	The Genealogical Population Dynamics of HIV-1 in a Large Transmission Chain: Bridging within and among Host Evolutionary Rates. <i>PLoS Computational Biology</i> , 2014, 10, e1003505.	3.2	79
156	Air Travel Is Associated with Intracontinental Spread of Dengue Virus Serotypes 1-3 in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2769.	3.0	91
157	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. <i>PLoS Pathogens</i> , 2014, 10, e1003932.	4.7	330
158	On the Biogeography of Centipeda: A Species-Tree Diffusion Approach. <i>Systematic Biology</i> , 2014, 63, 178-191.	5.6	43
159	A uniquely prevalent nonnucleoside reverse transcriptase inhibitor resistance mutation in Russian subtype A HIV-1 viruses. <i>Aids</i> , 2014, 28, F1-F8.	2.2	32
160	Inferring Heterogeneous Evolutionary Processes Through Time: from Sequence Substitution to Phylogeography. <i>Systematic Biology</i> , 2014, 63, 493-504.	5.6	75
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