

Philippe Lemey

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

300 papers	21,167 citations	71 h-index	139 g-index
324 ext. papers	27,115 ext. citations	9.4 avg, IF	7.01 L-index

#	Paper	IF	Citations
300	Phycova - a tool for exploring covariates of pathogen spread.. <i>Virus Evolution</i> , 2022 , 8, veac015	3.7	0
299	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	3.7	1
298	Virome characterization of game animals in China reveals a spectrum of emerging pathogens.. <i>Cell</i> , 2022 ,	56.2	11
297	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 ,	8.3	10
296	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		0
295	Global spatial dynamics and vaccine-induced fitness changes of .. <i>Science Translational Medicine</i> , 2022 , 14, eabn3253	17.5	2
294	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic.. <i>Nature Communications</i> , 2022 , 13, 2314	17.4	2
293	The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022 , 14, 973	6.2	0
292	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	4.8	1
291	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> , 2021 ,	8.3	3
290	Report 46: Factors driving extensive spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals 2021 ,		3
289	Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil 2021 ,		53
288	The emergence and ongoing convergent evolution of the N501Y lineages coincides with a major global shift in the SARS-CoV-2 selective landscape 2021 ,		46
287	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	9.7	88
286	Bayesian Phylogeographic Analysis Incorporating Predictors and Individual Travel Histories in BEAST. <i>Current Protocols</i> , 2021 , 1, e98		5
285	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021 , 372, 815-821	33.3	603
284	Genome Sequence of Ruloma Virus, a Novel Paramyxovirus Clustering Basally to Members of the Genus. <i>Microbiology Resource Announcements</i> , 2021 , 10,	1.3	2

283	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021 , 595, 713-717	50.4	37
282	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,	6.2	5
281	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	5.9	2
280	Markov-Modulated Continuous-Time Markov Chains to Identify Site- and Branch-Specific Evolutionary Variation in BEAST. <i>Systematic Biology</i> , 2021 , 70, 181-189	8.4	2
279	Massive parallelization boosts big Bayesian multidimensional scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021 , 30, 11-24	1.4	7
278	Relaxed Random Walks at Scale. <i>Systematic Biology</i> , 2021 , 70, 258-267	8.4	3
277	Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , 2021 , 7, veab036	3.7	2
276	SARS-CoV-2 European resurgence foretold: interplay of introductions and persistence by leveraging genomic and mobility data 2021 ,		6
275	Relax, Keep Walking - A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3486-3493	8.3	4
274	Therapy with M2e-Specific IgG Selects for an Influenza A Virus Mutant with Delayed Matrix Protein 2 Expression. <i>MBio</i> , 2021 , 12, e0074521	7.8	1
273	Genomic population structure associated with repeated escape of Salmonella enterica ATCC14028s from the laboratory into nature. <i>PLoS Genetics</i> , 2021 , 17, e1009820	6	3
272	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021 , 184, 5189-5200.e7	56.2	61
271	A systematic review on global RSV genetic data: Identification of knowledge gaps. <i>Reviews in Medical Virology</i> , 2021 , e2284	11.7	2
270	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021 , 597, 539-543	50.4	19
269	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. <i>Viruses</i> , 2021 , 13,	6.2	1
268	Determinants of dengue virus dispersal in the Americas. <i>Virus Evolution</i> , 2020 , 6, veaa074	3.7	1
267	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	11.5	18
266	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	11.5	46

265	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2641-2654	8.3	36
264	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	8.3	5
263	nosoi: A stochastic agent-based transmission chain simulation framework in r. <i>Methods in Ecology and Evolution</i> , 2020 , 11, 1002-1007	7.7	6
262	Measles virus and rinderpest virus divergence dated to the sixth century BCE. <i>Science</i> , 2020 , 368, 1367-1370	33.9	40
261	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	11.5	16
260	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,	6.2	6
259	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	5.1	9
258	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1832-1842	8.3	9
257	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	4.8	5
256	Genomic Epidemiology of 2015-2016 Zika Virus Outbreak in Cape Verde. <i>Emerging Infectious Diseases</i> , 2020 , 26, 1084-1090	10.2	11
255	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020 , 9,	8.9	9
254	The emergence of SARS-CoV-2 in Europe and the US 2020 ,		35
253	Natural selection in the evolution of SARS-CoV-2 in bats, not humans, created a highly capable human pathogen 2020 ,		28
252	Accommodating individual travel history, global mobility, and unsampled diversity in phylogeography: a SARS-CoV-2 case study 2020 ,		5
251	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference - Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , 2020 , 36, 2098-2104	7.2	4
250	Towards a unified classification for human respiratory syncytial virus genotypes. <i>Virus Evolution</i> , 2020 , 6, veaa052	3.7	8
249	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020 , 6, veaa061	3.7	147
248	Air conditioning system usage and SARS-CoV-2 transmission dynamics in Iran. <i>Medical Hypotheses</i> , 2020 , 143, 110164	3.8	2

247	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3363-3379	8.3	27
246	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020 , 11, 5620	17.4	7
245	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	3.7	3
244	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260	33.3	277
243	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020 , 5, 1408-1417	26.6	447
242	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020 , 11, 5110	17.4	49
241	Inferring Phenotypic Trait Evolution on Large Trees With Many Incomplete Measurements. <i>Journal of the American Statistical Association</i> , 2020 , 1-15	2.8	3
240	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020 , 370, 564-570	33.3	183
239	HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. <i>Cell Host and Microbe</i> , 2019 , 26, 347-358.e7	23.4	62
238	Divergence dating using mixed effects clock modelling: An application to HIV-1. <i>Virus Evolution</i> , 2019 , 5, vez036	3.7	8
237	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	5.7	8
236	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1793-1803	8.3	24
235	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019 , 68, 1052-1061	8.4	71
234	Mass migration to Europe: an opportunity for elimination of hepatitis B virus?. <i>The Lancet Gastroenterology and Hepatology</i> , 2019 , 4, 315-323	18.8	12
233	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	7	11
232	Comparing patterns and scales of plant virus phylogeography: in Madagascar and in continental Africa. <i>Virus Evolution</i> , 2019 , 5, vez023	3.7	10
231	Phylogeography of Lassa Virus in Nigeria. <i>Journal of Virology</i> , 2019 , 93,	6.6	30
230	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019 , 7, 208	6	7

229	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. <i>Methods in Molecular Biology</i> , 2019 , 1910, 691-722	1.4	3
228	A63 Quantifying the dynamics of evolutionary rates through time. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
227	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,	3.7	78
226	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	5.7	17
225	Identifying the patterns and drivers of enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019 , 5, vez009	3.7	10
224	Increasing importance of European lineages in seeding the hepatitis C virus subtype 1a epidemic in Spain. <i>Eurosurveillance</i> , 2019 , 24,	19.8	13
223	Global origins of African highly pathogenic avian influenza H5Nx viruses and intracontinental spread. <i>International Journal of Infectious Diseases</i> , 2019 , 79, 9-10	10.5	2
222	Disentangling the role of Africa in the global spread of H5 highly pathogenic avian influenza. <i>Nature Communications</i> , 2019 , 10, 5310	17.4	30
221	Limited evolution of the yellow fever virus 17d in a mouse infection model. <i>Emerging Microbes and Infections</i> , 2019 , 8, 1734-1746	18.9	11
220	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019 , 15, e1007976	7.6	25
219	Metagenomic sequencing at the epicenter of the Nigeria 2018 Lassa fever outbreak. <i>Science</i> , 2019 , 363, 74-77	33.3	130
218	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,	7.8	3
217	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019 , 4, 10-19	26.6	179
216	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,	7.8	25
215	Proposal for a new subtype of the zoonotic genotype 3 Hepatitis E virus: HEV-3I. <i>Virus Research</i> , 2018 , 248, 1-4	6.4	16
214	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	13.4	45
213	Landscape attributes governing local transmission of an endemic zoonosis: Rabies virus in domestic dogs. <i>Molecular Ecology</i> , 2018 , 27, 773-788	5.7	31
212	Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. <i>Statistics in Medicine</i> , 2018 , 37, 195-206	2.3	2

211	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	3.1	36
210	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
209	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018 , 4, vey023	3.7	18
208	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018 , 4, vey016	3.7	1199
207	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018 , 9, 2222	17.4	39
206	Phylogenetic Factor Analysis. <i>Systematic Biology</i> , 2018 , 67, 384-399	8.4	8
205	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018 , 14, e1007392	7.6	18
204	Iran's hepatitis elimination programme is under threat. <i>Lancet, The</i> , 2018 , 392, 1009	4.0	8
203	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	3.7	21
202	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018 , 31, 24-32	7.5	29
201	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	4.5	17
200	Phylogenetic analysis of two genotype 3 Hepatitis E viruses from wild boar, Italy. <i>Virus Genes</i> , 2018 , 54, 812-817	2.3	9
199	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
198	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	4.5	9
197	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. <i>Bioinformatics</i> , 2017 , 33, 1798-1805	7.2	21
196	A21 HIV-1 sub-subtype F1 outbreak among MSM in Belgium. <i>Virus Evolution</i> , 2017 , 3,	3.7	3
195	Accurate quantification of within- and between-host HBV evolutionary rates requires explicit transmission chain modelling. <i>Virus Evolution</i> , 2017 , 3, vex028	3.7	14
194	A Relaxed Directional Random Walk Model for Phylogenetic Trait Evolution. <i>Systematic Biology</i> , 2017 , 66, 299-319	8.4	16

193	Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017 , 66, e47-e64	6.4	55
192	The epidemic dynamics of hepatitis C virus subtypes 4a and 4d in Saudi Arabia. <i>Scientific Reports</i> , 2017 , 7, 44947	4.9	19
191	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	8.3	39
190	Differential Infection Patterns and Recent Evolutionary Origins of Equine Hepaciviruses in Donkeys. <i>Journal of Virology</i> , 2017 , 91,	6.6	24
189	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. <i>Genome Biology and Evolution</i> , 2017 , 9, 3202-3213	3.9	14
188	Genetic Diversity of Highly Pathogenic Avian Influenza A(H5N8/H5N5) Viruses in Italy, 2016-17. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1543-1547	10.2	52
187	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	3.7	6
186	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	5.9	57
185	1970s and 1980s Patient HIV-1 genomes illuminate early HIV/AIDS history in North America. <i>Nature</i> , 2016 , 539, 98-101	50.4	110
184	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016 , 2, vey023	9.7	9
183	Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. <i>Molecular Ecology</i> , 2016 , 25, 5994-6008	5.7	19
182	The recent ancestry of Middle East respiratory syndrome coronavirus in Korea has been shaped by recombination. <i>Scientific Reports</i> , 2016 , 6, 18825	4.9	25
181	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	4.9	8
180	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016 , 32, 3204-3206	7.2	73
179	Genealogical Working Distributions for Bayesian Model Testing with Phylogenetic Uncertainty. <i>Systematic Biology</i> , 2016 , 65, 250-64	8.4	72
178	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2016 , 12, e1005894	7.6	25
177	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016 , 5, e12217	8.9	106
176	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. <i>Microbial Genomics</i> , 2016 , 2, e000057	4.4	3

175	Genetically Different Highly Pathogenic Avian Influenza A(H5N1) Viruses in West Africa, 2015. <i>Emerging Infectious Diseases</i> , 2016 , 22, 2132-2136	10.2	17
174	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016 , 8,	6.2	11
173	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. <i>PLoS Pathogens</i> , 2016 , 12, e1005525	7.6	45
172	Understanding Past Population Dynamics: Bayesian Coalescent-Based Modeling with Covariates. <i>Systematic Biology</i> , 2016 , 65, 1041-1056	8.4	32
171	Spread3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2167-9	8.3	241
170	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	7	107
169	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	11.6	163
168	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015 , 12, 18	3.6	67
167	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015 , 6, 6696	17.4	91
166	Contribution of Epidemiological Predictors in Unraveling the Phylogeographic History of HIV-1 Subtype C in Brazil. <i>Journal of Virology</i> , 2015 , 89, 12341-8	6.6	22
165	Synonymous and nonsynonymous distances help untangle convergent evolution and recombination. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015 , 14, 375-89	1.2	3
164	Genome-Wide Evolutionary Analyses of G1P[8] Strains Isolated Before and After Rotavirus Vaccine Introduction. <i>Genome Biology and Evolution</i> , 2015 , 7, 2473-83	3.9	34
163	Bayesian Inference Reveals Host-Specific Contributions to the Epidemic Expansion of Influenza A H5N1. <i>Molecular Biology and Evolution</i> , 2015 , 32, 3264-75	8.3	34
162	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, 11773-85	6.6	27
161	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , 2015 , 63, 38-41	14.5	4
160	Combining phylogeography and spatial epidemiology to uncover predictors of H5N1 influenza A virus diffusion. <i>Archives of Virology</i> , 2015 , 160, 215-24	2.6	18
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	7.7	15
158	ASSESSING PHENOTYPIC CORRELATION THROUGH THE MULTIVARIATE PHYLOGENETIC LATENT LIABILITY MODEL. <i>Annals of Applied Statistics</i> , 2015 , 9, 969-991	2.1	23

157	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. <i>Aids</i> , 2015 , 29, 1549-56	3.5	13
156	Enzootic transmission of yellow fever virus, Venezuela. <i>Emerging Infectious Diseases</i> , 2015 , 21, 99-102	10.2	16
155	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015 , 523, 217-204	3.4	302
154	The global distribution of reveals little evidence for frequent recent, human-mediated long distance dispersal events. <i>Virus Evolution</i> , 2015 , 1, vev009	3.7	38
153	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015 , 1, vev016	3.7	43
152	Virus evolution and transmission in an ever more connected world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015 , 282, 20142878	4.4	81
151	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	3.7	97
150	Inferring heterogeneous evolutionary processes through time: from sequence substitution to phylogeography. <i>Systematic Biology</i> , 2014 , 63, 493-504	8.4	54
149	Evolutionary analysis of HBV "S" antigen genetic diversity in Iranian blood donors: a nationwide study. <i>Journal of Medical Virology</i> , 2014 , 86, 144-55	19.7	22
148	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014 , 346, 56-61	33.3	370
147	Molecular characterization of hepatitis B virus (HBV) strains circulating in the northern coast of the Persian Gulf and its comparison with worldwide distribution of HBV subgenotype D1. <i>Journal of Medical Virology</i> , 2014 , 86, 745-57	19.7	8
146	BUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. <i>BMC Bioinformatics</i> , 2014 , 15, 133	3.6	18
145	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014 , 3, e01914	8.9	213
144	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	5	66
143	Air travel is associated with intracontinental spread of dengue virus serotypes 1-3 in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2769	4.8	67
142	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. <i>PLoS Pathogens</i> , 2014 , 10, e1003932	7.6	230
141	On the biogeography of Centipeda: a species-tree diffusion approach. <i>Systematic Biology</i> , 2014 , 63, 178-814	8.1	32
140	A uniquely prevalent nonnucleoside reverse transcriptase inhibitor resistance mutation in Russian subtype A HIV-1 viruses. <i>Aids</i> , 2014 , 28, F1-8	3.5	19

139	Generalized linear models for identifying predictors of the evolutionary diffusion of viruses. <i>AMIA Summits on Translational Science Proceedings</i> , 2014 , 2014, 23-8	1.1	4
138	Make the most of your samples: Bayes factor estimators for high-dimensional models of sequence evolution. <i>BMC Bioinformatics</i> , 2013 , 14, 85	3.6	80
137	The spread of type 2 Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in North America: a phylogeographic approach. <i>Virology</i> , 2013 , 447, 146-54	3.6	36
136	Distinguishable epidemics of multidrug-resistant Salmonella Typhimurium DT104 in different hosts. <i>Science</i> , 2013 , 341, 1514-7	33.3	237
135	The comparative genomics of human respiratory syncytial virus subgroups A and B: genetic variability and molecular evolutionary dynamics. <i>Journal of Virology</i> , 2013 , 87, 8213-26	6.6	66
134	The HIV-1 reservoir in eight patients on long-term suppressive antiretroviral therapy is stable with few genetic changes over time. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E4987-96	11.5	198
133	Bayesian evolutionary model testing in the phylogenomics era: matching model complexity with computational efficiency. <i>Bioinformatics</i> , 2013 , 29, 1970-9	7.2	65
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17	Sequence databases and database searching	33-67	1
16	Phylogenetic analysis using protein sequences	313-342	5
15	Introduction to recombination detection	493-518	9
14	Molecular clock analysis	362-380	5

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