

Philippe Lemey

List of Publications by Citations

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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	RDP3: a flexible and fast computer program for analyzing recombination. <i>Bioinformatics</i> , 2010 , 26, 2462-3.2	7.2	1392
299	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018 , 4, vey016	3.7	1199
298	Bayesian phylogeography finds its roots. <i>PLoS Computational Biology</i> , 2009 , 5, e1000520	5	1101
297	Improving the accuracy of demographic and molecular clock model comparison while accommodating phylogenetic uncertainty. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2157-67	8.3	779
296	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021 , 372, 815-821.33.3	33.3	603
295	Phylogeography takes a relaxed random walk in continuous space and time. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1877-85	8.3	450
294	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
293	Accurate model selection of relaxed molecular clocks in bayesian phylogenetics. <i>Molecular Biology and Evolution</i> , 2013 , 30, 239-43	8.3	416
292	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014 , 346, 56-61	33.3	370
291	SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. <i>Bioinformatics</i> , 2011 , 27, 2910-27.2	7.2	369
290	Mapping the origins and expansion of the Indo-European language family. <i>Science</i> , 2012 , 337, 957-60	33.3	368
289	Complete genomic sequence of human coronavirus OC43: molecular clock analysis suggests a relatively recent zoonotic coronavirus transmission event. <i>Journal of Virology</i> , 2005 , 79, 1595-604	6.6	344
288	Improving Bayesian population dynamics inference: a coalescent-based model for multiple loci. <i>Molecular Biology and Evolution</i> , 2013 , 30, 713-24	8.3	312
287	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015 , 523, 217-20.4	30.4	302
286	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260	33.3	277
285	Tracing the origin and history of the HIV-2 epidemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 6588-92	11.5	254
284	Spread3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2167-9	8.3	241

283	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
282	Distinguishable epidemics of multidrug-resistant Salmonella Typhimurium DT104 in different hosts. <i>Science</i> , 2013 , 341, 1514-7	33.3	237
281	Assessing substitution saturation with DAMBE	615-630	237
280	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
279	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014 , 3, e01914	8.9	213
278	Phylogenetic analyses of rotavirus genotypes G9 and G12 underscore their potential for swift global spread. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2431-6	8.3	207
277	Ancient hybridization and an Irish origin for the modern polar bear matriline. <i>Current Biology</i> , 2011 , 21, 1251-8	6.3	203
276	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
275	The spread of tomato yellow leaf curl virus from the Middle East to the world. <i>PLoS Pathogens</i> , 2010 , 6, e1001164	7.6	197
274	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
273	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020 , 370, 564-570	33.3	183
272	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019 , 4, 10-19	26.6	179
271	Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox (<i>Ovibos moschatus</i>) population dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 5675-80	11.5	175
270	Genetic history of hepatitis C virus in East Asia. <i>Journal of Virology</i> , 2009 , 83, 1071-82	6.6	169
269	Evolutionary history of the closely related group 2 coronaviruses: porcine hemagglutinating encephalomyelitis virus, bovine coronavirus, and human coronavirus OC43. <i>Journal of Virology</i> , 2006 , 80, 7270-4	6.6	168
268	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
267	HIV evolutionary dynamics within and among hosts. <i>AIDS Reviews</i> , 2006 , 8, 125-40	1.5	160
266	Unifying the spatial epidemiology and molecular evolution of emerging epidemics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 15066-71	11.5	159

265	Evolutionary dynamics of human rotaviruses: balancing reassortment with preferred genome constellations. <i>PLoS Pathogens</i> , 2009 , 5, e1000634	7.6	153
264	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020 , 6, veaa061	3.7	147
263	Synonymous substitution rates predict HIV disease progression as a result of underlying replication dynamics. <i>PLoS Computational Biology</i> , 2007 , 3, e29	5	138
262	Metagenomic sequencing at the epicenter of the Nigeria 2018 Lassa fever outbreak. <i>Science</i> , 2019 , 363, 74-77	33.3	130
261	Ancient papillomavirus-host co-speciation in Felidae. <i>Genome Biology</i> , 2007 , 8, R57	18.3	124
260	Phylodynamic reconstruction reveals norovirus GII.4 epidemic expansions and their molecular determinants. <i>PLoS Pathogens</i> , 2010 , 6, e1000884	7.6	114
259	Genetic variability and molecular evolution of the human respiratory syncytial virus subgroup B attachment G protein. <i>Journal of Virology</i> , 2005 , 79, 9157-67	6.6	111
258	1970s and Patient 0 HIV-1 genomes illuminate early HIV/AIDS history in North America. <i>Nature</i> , 2016 , 539, 98-101	50.4	110
257	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
256	The mode and tempo of hepatitis C virus evolution within and among hosts. <i>BMC Evolutionary Biology</i> , 2011 , 11, 131	3	107
255	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016 , 5, e12217	8.9	106
254	Phylodynamics and human-mediated dispersal of a zoonotic virus. <i>PLoS Pathogens</i> , 2010 , 6, e1001166	7.6	102
253	Simultaneously reconstructing viral cross-species transmission history and identifying the underlying constraints. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120196	5.8	101
252	Spatial dynamics of human-origin H1 influenza A virus in North American swine. <i>PLoS Pathogens</i> , 2011 , 7, e1002077	7.6	101
251	Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000. <i>Journal of Medical Virology</i> , 2003 , 70, 420-9	19.7	100
250	U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains. <i>Journal of Virology</i> , 2003 , 77, 6359-66	6.6	100
249	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
248	Molecular evolution and circulation patterns of human respiratory syncytial virus subgroup a: positively selected sites in the attachment g glycoprotein. <i>Journal of Virology</i> , 2004 , 78, 4675-83	6.6	95

247	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015 , 6, 6696	17.4	91
246	The molecular population genetics of HIV-1 group O. <i>Genetics</i> , 2004 , 167, 1059-68	4	89
245	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
244	Analysing recombination in nucleotide sequences. <i>Molecular Ecology Resources</i> , 2011 , 11, 943-55	8.4	85
243	Single cell analysis of lymph node tissue from HIV-1 infected patients reveals that the majority of CD4+ T-cells contain one HIV-1 DNA molecule. <i>PLoS Pathogens</i> , 2013 , 9, e1003432	7.6	84
242	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
241	Phylogeography and population dynamics of dengue viruses in the Americas. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1533-43	8.3	81
240	Three roads diverged? Routes to phylogeographic inference. <i>Trends in Ecology and Evolution</i> , 2010 , 25, 626-32	10.9	81
239	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
238	A63 Quantifying the dynamics of evolutionary rates through time. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
237	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
236	Quantifying differences in the tempo of human immunodeficiency virus type 1 subtype evolution. <i>Journal of Virology</i> , 2009 , 83, 12917-24	6.6	77
235	Recombination confounds the early evolutionary history of human immunodeficiency virus type 1: subtype G is a circulating recombinant form. <i>Journal of Virology</i> , 2007 , 81, 8543-51	6.6	75
234	Reconstructing the initial global spread of a human influenza pandemic: a Bayesian spatial-temporal model for the global spread of H1N1pdm. <i>PLOS Currents</i> , 2009 , 1, RRN1031		74
233	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016 , 32, 3204-3206	7.2	73
232	Genealogical Working Distributions for Bayesian Model Testing with Phylogenetic Uncertainty. <i>Systematic Biology</i> , 2016 , 65, 250-64	8.4	72
231	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
230	Investigating the origin and spread of hepatitis C virus genotype 5a. <i>Journal of Virology</i> , 2006 , 80, 4220-6.6		71

229	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015 , 12, 18	3.6	67
228	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
227	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
226	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
225	Bayesian evolutionary model testing in the phylogenomics era: matching model complexity with computational efficiency. <i>Bioinformatics</i> , 2013 , 29, 1970-9	7.2	65
224	Molecular dating of human-to-bovid host jumps by <i>Staphylococcus aureus</i> reveals an association with the spread of domestication. <i>Biology Letters</i> , 2012 , 8, 829-32	3.6	63
223	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
222	Genetic variability among complete human respiratory syncytial virus subgroup A genomes: bridging molecular evolutionary dynamics and epidemiology. <i>PLoS ONE</i> , 2012 , 7, e51439	3.7	62
221	Rates of viral evolution are linked to host geography in bat rabies. <i>PLoS Pathogens</i> , 2012 , 8, e1002720	7.6	62
220	Circulation of genetically distinct contemporary human coronavirus OC43 strains. <i>Virology</i> , 2005 , 337, 85-92	3.6	61
219	Molecular footprint of drug-selective pressure in a human immunodeficiency virus transmission chain. <i>Journal of Virology</i> , 2005 , 79, 11981-9	6.6	61
218	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021 , 184, 5189-5200.e7	56.2	61
217	Phylogeography of dengue virus serotype 4, Brazil, 2010-2011. <i>Emerging Infectious Diseases</i> , 2012 , 18, 1858-64	10.2	60
216	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
215	Toward a quantitative understanding of viral phylogeography. <i>Current Opinion in Virology</i> , 2011 , 1, 423-9	7.5	56
214	Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017 , 66, e47-e65	6.4	55
213	Inferring heterogeneous evolutionary processes through time: from sequence substitution to phylogeography. <i>Systematic Biology</i> , 2014 , 63, 493-504	8.4	54
212	A counting renaissance: combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection. <i>Bioinformatics</i> , 2012 , 28, 3248-56	7.2	54

211	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic		54
210	Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 963-71	9.7	53
209	Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil 2021 ,		53
208	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
207	Reconstructing the history of maize streak virus strain a dispersal to reveal diversification hot spots and its origin in southern Africa. <i>Journal of Virology</i> , 2011 , 85, 9623-36	6.6	52
206	Genomic characterization of novel dolphin papillomaviruses provides indications for recombination within the Papillomaviridae. <i>Virology</i> , 2008 , 378, 151-61	3.6	51
205	Evolutionary trajectory of the VP1 gene of human enterovirus 71 genogroup B and C viruses. <i>Journal of General Virology</i> , 2010 , 91, 1949-1958	4.9	50
204	Are hepatitis B virus "subgenotypes" defined accurately?. <i>Journal of Clinical Virology</i> , 2010 , 47, 356-60	14.5	49
203	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
202	Yellow fever virus maintenance in Trinidad and its dispersal throughout the Americas. <i>Journal of Virology</i> , 2010 , 84, 9967-77	6.6	47
201	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
200	Phylogeographical footprint of colonial history in the global dispersal of human immunodeficiency virus type 2 group A. <i>Journal of General Virology</i> , 2012 , 93, 889-899	4.9	46
199	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
198	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
197	Phylogenetics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 453-60	4.5	45
196	Identifying recombinants in human and primate immunodeficiency virus sequence alignments using quartet scanning. <i>BMC Bioinformatics</i> , 2009 , 10, 126	3.6	45
195	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
194	Isolation and cloning of the raccoon (<i>Procyon lotor</i>) papillomavirus type 1 by using degenerate papillomavirus-specific primers. <i>Journal of General Virology</i> , 2005 , 86, 2029-2033	4.9	44

193	Mannan-binding lectin (MBL) gene polymorphisms in ulcerative colitis and Crohn's disease. <i>Genes and Immunity</i> , 2001 , 2, 323-8	4.4	44
192	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015 , 1, vev016	3.7	43
191	Complete genome sequence, taxonomic assignment, and comparative analysis of the untranslated regions of the Modoc virus, a flavivirus with no known vector. <i>Virology</i> , 2002 , 293, 125-40	3.6	43
190	Genomic analysis of hepatitis B virus reveals antigen state and genotype as sources of evolutionary rate variation. <i>Viruses</i> , 2011 , 3, 83-101	6.2	42
189	Measles virus and rinderpest virus divergence dated to the sixth century BCE. <i>Science</i> , 2020 , 368, 1367-1370	3.9	40
188	Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018 , 9, 2222	17.4	39
187	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
186	Molecular testing of multiple HIV-1 transmissions in a criminal case. <i>Aids</i> , 2005 , 19, 1649-58	3.5	39
185	High GUD incidence in the early 20 century created a particularly permissive time window for the origin and initial spread of epidemic HIV strains. <i>PLoS ONE</i> , 2010 , 5, e9936	3.7	39
184	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
183	Novel hepatitis B virus subgenotype A6 in African-Belgian patients. <i>Journal of Clinical Virology</i> , 2010 , 47, 93-6	14.5	38
182	Impact of CCR5delta32 host genetic background and disease progression on HIV-1 intrahost evolutionary processes: efficient hypothesis testing through hierarchical phylogenetic models. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1605-16	8.3	37
181	A genotypic resistance assay for the detection of drug resistance in the human immunodeficiency virus type 1 envelope gene. <i>Journal of Virological Methods</i> , 2005 , 123, 25-34	2.6	37
180	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021 , 595, 713-717	50.4	37
179	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2641-2654	8.3	36
178	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
177	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
176	A large Finnish echovirus 30 outbreak was preceded by silent circulation of the same genotype. <i>Virus Genes</i> , 2011 , 42, 28-36	2.3	35

175	The emergence of SARS-CoV-2 in Europe and the US 2020 ,		35
174	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
173	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
172	Complete genome sequence of Montana Myotis leukoencephalitis virus, phylogenetic analysis and comparative study of the 3' untranslated region of flaviviruses with no known vector. <i>Journal of General Virology</i> , 2002 , 83, 1875-1885	4.9	33
171	On the biogeography of Centipeda: a species-tree diffusion approach. <i>Systematic Biology</i> , 2014 , 63, 178-81	8.1	32
170	Limitations to contact tracing and phylogenetic analysis in establishing HIV type 1 transmission networks in Cuba. <i>AIDS Research and Human Retroviruses</i> , 2007 , 23, 347-56	1.6	32
169	HIV-1 compartmentalization in diverse leukocyte populations during antiretroviral therapy. <i>Journal of Leukocyte Biology</i> , 2004 , 76, 562-70	6.5	32
168	Understanding Past Population Dynamics: Bayesian Coalescent-Based Modeling with Covariates. <i>Systematic Biology</i> , 2016 , 65, 1041-1056	8.4	32
167	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
166	Phylogeography of Lassa Virus in Nigeria. <i>Journal of Virology</i> , 2019 , 93,	6.6	30
165	Molecular evolutionary analysis and mutational pattern of full-length genomes of hepatitis B virus isolated from Belgian patients with different clinical manifestations. <i>Journal of Medical Virology</i> , 2010 , 82, 379-89	19.7	30
164	A Bayesian statistical analysis of human T-cell lymphotropic virus evolutionary rates. <i>Infection, Genetics and Evolution</i> , 2005 , 5, 291-8	4.5	30
163	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
162	Characterization of a putative ancestor of coxsackievirus B5. <i>Journal of Virology</i> , 2010 , 84, 9695-708	6.6	29
161	Phylogenetic analysis of hepatitis B virus full-length genomes reveals evidence for a large nosocomial outbreak in Belgium. <i>Journal of Clinical Virology</i> , 2009 , 46, 61-8	14.5	29
160	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018 , 31, 24-32	7.5	29
159	Phylodynamics of H5N1 avian influenza virus in Indonesia. <i>Molecular Ecology</i> , 2012 , 21, 3062-77	5.7	28
158	Circulation of HRSV in Belgium: from multiple genotype circulation to prolonged circulation of predominant genotypes. <i>PLoS ONE</i> , 2013 , 8, e60416	3.7	28

157	Natural selection in the evolution of SARS-CoV-2 in bats, not humans, created a highly capable human pathogen 2020 ,		28
156	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
155	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3363-3379	8.3	27
154	Genetic analyses reveal structured HIV-1 populations in serially sampled T lymphocytes of patients receiving HAART. <i>Virology</i> , 2006 , 348, 35-46	3.6	26
153	Estimating the relative contribution of dNTP pool imbalance and APOBEC3G/3F editing to HIV evolution in vivo. <i>Journal of Computational Biology</i> , 2007 , 14, 1105-14	1.7	26
152	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
151	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
150	Full-genome analysis of a highly divergent simian T-cell lymphotropic virus type 1 strain in <i>Macaca arctoides</i> . <i>Journal of General Virology</i> , 2005 , 86, 1953-1959	4.9	25
149	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2016 , 12, e1005894	7.6	25
148	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
147	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1793-1803	8.3	24
146	Differential Infection Patterns and Recent Evolutionary Origins of Equine Hepaciviruses in Donkeys. <i>Journal of Virology</i> , 2017 , 91,	6.6	24
145	Emergence in Japan of an HIV-1 variant associated with transmission among men who have sex with men (MSM) in China: first indication of the International Dissemination of the Chinese MSM lineage. <i>Journal of Virology</i> , 2013 , 87, 5351-61	6.6	24
144	The phylogeography and spatiotemporal spread of south-central skunk rabies virus. <i>PLoS ONE</i> , 2013 , 8, e82348	3.7	24
143	Phylogenetic reconstruction of a known HIV-1 CRF04_cpx transmission network using maximum likelihood and Bayesian methods. <i>Journal of Molecular Evolution</i> , 2004 , 59, 709-17	3.1	24
142	Evolutionary dynamics of human retroviruses investigated through full-genome scanning. <i>Molecular Biology and Evolution</i> , 2005 , 22, 942-51	8.3	24
141	Temporal signal and the phylodynamic threshold of SARS-CoV-2		24
140	ASSESSING PHENOTYPIC CORRELATION THROUGH THE MULTIVARIATE PHYLOGENETIC LATENT LIABILITY MODEL. <i>Annals of Applied Statistics</i> , 2015 , 9, 969-991	2.1	23

139	Genesis of avian-origin H7N9 influenza A viruses. <i>Lancet, The</i> , 2013 , 381, 1883-5	4.0	23
138	Estimation of an in vivo fitness landscape experienced by HIV-1 under drug selective pressure useful for prediction of drug resistance evolution during treatment. <i>Bioinformatics</i> , 2008 , 24, 34-41	7.2	23
137	Analysis of the evolutionary relationships of HIV-1 and SIVcpz sequences using bayesian inference: implications for the origin of HIV-1. <i>Molecular Biology and Evolution</i> , 2003 , 20, 1986-96	8.3	23
136	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
135	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
134	Molecular characterization of hepatitis B virus strains circulating in Belgian patients co-infected with HIV and HBV: overt and occult infection. <i>Journal of Medical Virology</i> , 2011 , 83, 1876-84	19.7	22
133	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. <i>Bioinformatics</i> , 2017 , 33, 1798-1805	7.2	21
132	Plasma exchange-associated immunoglobulin m-negative hantavirus disease after a camping holiday in southern france. <i>Clinical Infectious Diseases</i> , 2004 , 38, 1350-6	11.6	21
131	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
130	Covering all bases in HIV research: unveiling a hidden world of viral evolution. <i>AIDS Reviews</i> , 2010 , 12, 89-102	1.5	21
129	HBV subgenotype misclassification expands quasi-subgenotype A3. <i>Clinical Microbiology and Infection</i> , 2011 , 17, 947-9	9.5	20
128	SlidingBayes: exploring recombination using a sliding window approach based on Bayesian phylogenetic inference. <i>Bioinformatics</i> , 2005 , 21, 1274-5	7.2	20
127	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
126	The epidemic dynamics of hepatitis C virus subtypes 4a and 4d in Saudi Arabia. <i>Scientific Reports</i> , 2017 , 7, 44947	4.9	19
125	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
124	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021 , 597, 539-543	50.4	19
123	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
122	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 ¹⁸	11.5	18

121	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018 , 4, vey033	3.3	18
120	BUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. <i>BMC Bioinformatics</i> , 2014 , 15, 133	3.6	18
119	Role of viral evolutionary rate in HIV-1 disease progression in a linked cohort. <i>Retrovirology</i> , 2005 , 2, 41	3.6	18
118	Genetic variability of human respiratory coronavirus OC43. <i>Journal of Virology</i> , 2005 , 79, 3223-4; author reply 3224-5	6.6	18
117	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018 , 14, e1007392	7.6	18
116	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
115	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
114	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
113	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
112	Proposal for a new subtype of the zoonotic genotype 3 Hepatitis E virus: HEV-3l. <i>Virus Research</i> , 2018 , 248, 1-4	6.4	16
111	A Relaxed Directional Random Walk Model for Phylogenetic Trait Evolution. <i>Systematic Biology</i> , 2017 , 66, 299-319	8.4	16
110	Enzootic transmission of yellow fever virus, Venezuela. <i>Emerging Infectious Diseases</i> , 2015 , 21, 99-102	10.2	16
109	Graph hierarchies for phylogeography. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120206	5.8	15
108	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
107	Dynamic features of the selective pressure on the human immunodeficiency virus type 1 (HIV-1) gp120 CD4-binding site in a group of long term non progressor (LTNP) subjects. <i>Retrovirology</i> , 2009 , 6, 4	3.6	15
106	Evidence for a complex mosaic genome pattern in a full-length hepatitis C virus sequence. <i>Evolutionary Bioinformatics</i> , 2008 , 4, 249-54	1.9	15
105	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
104	High inpatient HIV-1 evolutionary rate is associated with CCR5-to-CXCR4 coreceptor switch. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 369-77	4.5	14

103	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
102	The epidemic history of hepatitis C among injecting drug users in Flanders, Belgium. <i>Journal of Viral Hepatitis</i> , 2008 , 15, 399-408	3.4	14
101	Phylogenetic classification of TT virus groups based on the N22 region is unreliable. <i>Virus Research</i> , 2002 , 85, 47-59	6.4	14
100	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
99	The introduction of fox rabies into Italy (2008-2011) was due to two viral genetic groups with distinct phylogeographic patterns. <i>Infection, Genetics and Evolution</i> , 2013 , 17, 202-9	4.5	13
98	Time-measured phylogenies of gag, pol and env sequence data reveal the direction and time interval of HIV-1 transmission. <i>Aids</i> , 2011 , 25, 1035-9	3.5	13
97	Increasing importance of European lineages in seeding the hepatitis C virus subtype 1a epidemic in Spain. <i>Eurosurveillance</i> , 2019 , 24,	19.8	13
96	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
95	Genetic variation in mother-child acute seroconverter pairs from Zambia. <i>Aids</i> , 2008 , 22, 817-24	3.5	12
94	Cyclorraphan yolk proteins and lepidopteran minor yolk proteins originate from two unrelated lipase families. <i>Insect Molecular Biology</i> , 2004 , 13, 615-23	3.4	12
93	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
92	Complete nucleotide sequence and evolutionary analysis of a gorilla foamy virus. <i>Journal of General Virology</i> , 2011 , 92, 582-6	4.9	11
91	Exploring full-genome sequences for phylogenetic support of HIV-1 transmission events. <i>Aids</i> , 2005 , 19, 1551-2	3.5	11
90	Genomic Epidemiology of 2015-2016 Zika Virus Outbreak in Cape Verde. <i>Emerging Infectious Diseases</i> , 2020 , 26, 1084-1090	10.2	11
89	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016 , 8,	6.2	11
88	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
87	Virome characterization of game animals in China reveals a spectrum of emerging pathogens.. <i>Cell</i> , 2022 ,	56.2	11
86	Comparing patterns and scales of plant virus phylogeography: in Madagascar and in continental Africa. <i>Virus Evolution</i> , 2019 , 5, vez023	3.7	10

85	Identifying the patterns and drivers of enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019 , 5, vez009	3.7	10
84	The evolution of human immunodeficiency virus type-1 (HIV-1) envelope molecular properties and coreceptor use at all stages of infection in an HIV-1 donor-recipient pair. <i>Virology</i> , 2012 , 422, 70-80	3.6	10
83	Estimating the individualized HIV-1 genetic barrier to resistance using a nelfinavir fitness landscape. <i>BMC Bioinformatics</i> , 2010 , 11, 409	3.6	10
82	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
81	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
80	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
79	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1832-1842	8.3	9
78	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016 , 2, vew023	9.7	9
77	On hepatitis C virus evolution: the interaction between virus and host towards treatment outcome. <i>PLoS ONE</i> , 2013 , 8, e62393	3.7	9
76	Introduction to recombination detection493-518		9
75	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020 , 9,	8.9	9
74	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations		9
73	Phylogenetic analysis of two genotype 3 Hepatitis E viruses from wild boar, Italy. <i>Virus Genes</i> , 2018 , 54, 812-817	2.3	9
72	Divergence dating using mixed effects clock modelling: An application to HIV-1. <i>Virus Evolution</i> , 2019 , 5, vez036	3.7	8
71	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
70	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
69	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
68	Site stripping based on likelihood ratio reduction is a useful tool to evaluate the impact of non-clock-like behavior on viral phylogenetic reconstructions. <i>FEMS Immunology and Medical Microbiology</i> , 2003 , 39, 125-32		8

67	Towards a unified classification for human respiratory syncytial virus genotypes. <i>Virus Evolution</i> , 2020 , 6, veaa052	3.7	8
66	Phylogenetic Factor Analysis. <i>Systematic Biology</i> , 2018 , 67, 384-399	8.4	8
65	Iran's hepatitis elimination programme is under threat. <i>Lancet, The</i> , 2018 , 392, 1009	4.0	8
64	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019 , 7, 208	6	7
63	HIV-1 evolution in patients undergoing immunotherapy with Tat, Rev, and Nef expressing dendritic cells followed by treatment interruption. <i>Aids</i> , 2013 , 27, 2679-89	3.5	7
62	A comparative study of HIV-1 clade C env evolution in a Zambian infant with an infected rhesus macaque during disease progression. <i>Aids</i> , 2009 , 23, 1817-28	3.5	7
61	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020 , 11, 5620	17.4	7
60	Massive parallelization boosts big Bayesian multidimensional scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021 , 30, 11-24	1.4	7
59	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
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,	6.2	6
57	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
56	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
55	SARS-CoV-2 European resurgence foretold: interplay of introductions and persistence by leveraging genomic and mobility data 2021 ,		6
54	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
53	Emergence of primary NNRTI resistance mutations without antiretroviral selective pressure in a HAART-treated child. <i>PLoS ONE</i> , 2009 , 4, e4806	3.7	5
52	HCV genotype distribution in Flanders and Brussels (Belgium): unravelling the spread of an uncommon HCV genotype 5a cluster. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2010 , 29, 1427-34	5.3	5
51	Phylogenetic analysis using protein sequences313-342		5
50	Molecular clock analysis362-380		5

49	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
48	Accommodating individual travel history, global mobility, and unsampled diversity in phylogeography: a SARS-CoV-2 case study 2020 ,		5
47	Bayesian Phylogeographic Analysis Incorporating Predictors and Individual Travel Histories in BEAST. <i>Current Protocols</i> , 2021 , 1, e98		5
46	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
45	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
44	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
43	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
42	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
41	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
40	A21 HIV-1 sub-subtype F1 outbreak among MSM in Belgium. <i>Virus Evolution</i> , 2017 , 3,	3.7	3
39	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. <i>Methods in Molecular Biology</i> , 2019 , 1910, 691-722	1.4	3
38	High frequency of HIV-1 dual infections in Cameroon, West Central Africa. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2011 , 57, e25-7	3.1	3
37	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
36	Report 46: Factors driving extensive spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals 2021 ,		3
35	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. <i>Microbial Genomics</i> , 2016 , 2, e000057	4.4	3
34	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
33	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
32	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

31	Relaxed Random Walks at Scale. <i>Systematic Biology</i> , 2021 , 70, 258-267	8.4	3
30	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	6	3
29	Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. <i>Statistics in Medicine</i> , 2018 , 37, 195-206	2.3	2
28	Universal COVID-19 vaccine with updated spike antigen confers full protection against all SARS-CoV-2 variants of concern		2
27	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
26	The history of measles: from a 1912 genome to an antique origin		2
25	A near-full-length HIV-1 genome from 1966 recovered from formalin-fixed paraffin-embedded tissue		2
24	Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic		2
23	Air conditioning system usage and SARS-CoV-2 transmission dynamics in Iran. <i>Medical Hypotheses</i> , 2020 , 143, 110164	3.8	2
22	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
21	The phylodynamics of SARS-CoV-2 during 2020 in Finland [Disappearance and re-emergence of introduced strains.		2
20	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
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	8.4	2
18	Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , 2021 , 7, veab036	3.7	2
17	A systematic review on global RSV genetic data: Identification of knowledge gaps. <i>Reviews in Medical Virology</i> , 2021 , e2284	11.7	2
16	Global spatial dynamics and vaccine-induced fitness changes of .. <i>Science Translational Medicine</i> , 2022 , 14, eabn3253	17.5	2
15	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic.. <i>Nature Communications</i> , 2022 , 13, 2314	17.4	2
14	Determinants of dengue virus dispersal in the Americas. <i>Virus Evolution</i> , 2020 , 6, veaa074	3.7	1

13	High-throughput HIV sequencing: evolution in 2D. <i>Future Virology</i> , 2011 , 6, 417-420	2.4	1
12	Sequence databases and database searching33-67		1
11	Unravelling the evolutionary relationships of hepaciviruses within and across rodent hosts		1
10	Phyldynamic assessment of intervention strategies for the West African Ebola virus outbreak		1
9	Archival influenza virus genomes from Europe reveal genomic and phenotypic variability during the 1918 pandemic		1
8	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
7	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. <i>Viruses</i> , 2021 , 13,	6.2	1
6	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
5	Reconstruction of the Origin and Dispersal of the Worldwide Dominant Hepatitis B Virus Subgenotype D1. <i>Virus Evolution</i> ,	3.7	1
4	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
3	Phycova - a tool for exploring covariates of pathogen spread.. <i>Virus Evolution</i> , 2022 , 8, veac015	3.7	0
2	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
1	The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022 , 14, 973	6.2	0