

Guy Baele

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.

126
papers

10,482
citations

34
h-index

102
g-index

142
ext. papers

16,161
ext. citations

10.4
avg, IF

6.81
L-index

#	Paper	IF	Citations
126	Identification of the First SARS-CoV-2 Lineage B.1.1.529 Virus Detected in Europe.. <i>Microbiology Resource Announcements</i> , 2022 , e0116121	1.3	1
125	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal.. <i>Virus Evolution</i> , 2022 , 8, veac029	3.7	0
124	Phycova - a tool for exploring covariates of pathogen spread.. <i>Virus Evolution</i> , 2022 , 8, veac015	3.7	0
123	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
122	Antibody escape and global spread of SARS-CoV-2 lineage A.27.. <i>Nature Communications</i> , 2022 , 13, 115217.4	17.4	5
121	Evolutionary history and introduction of SARS-CoV-2 Alpha VOC/B.1.1.7 in Pakistan through international travelers.. <i>Virus Evolution</i> , 2022 , 8, veac020	3.7	0
120	Serum neutralization of SARS-CoV-2 Omicron sublineages BA.1 and BA.2 in patients receiving monoclonal antibodies.. <i>Nature Medicine</i> , 2022 ,	50.5	22
119	Two Separate Clusters of SARS-CoV-2 Delta Variant Infections in A Group of 41 Students Travelling from India: An Illustration of the Need for Rigorous Testing and Quarantine. <i>Viruses</i> , 2022 , 14, 1198	6.2	0
118	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		3
117	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization.. <i>Nature</i> , 2021 ,	50.4	230
116	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
115	Bayesian Phylogeographic Analysis Incorporating Predictors and Individual Travel Histories in BEAST. <i>Current Protocols</i> , 2021 , 1, e98		5
114	Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City. <i>PLoS Pathogens</i> , 2021 , 17, e1009571	7.6	5
113	Mathematical modelling and phylodynamics for the study of dog rabies dynamics and control: A scoping review. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009449	4.8	4
112	Lying in wait: the resurgence of dengue virus after the Zika epidemic in Brazil. <i>Nature Communications</i> , 2021 , 12, 2619	17.4	11
111	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021 , 595, 713-717	50.4	37
110	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. <i>Viruses</i> , 2021 , 13,	6.2	3

109	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021 , 373, 889-895	33.3	41
108	YMrCA: Improving Y-chromosomal ancestor time estimation for DNA kinship research. <i>Human Mutation</i> , 2021 , 42, 1307-1320	4.7	0
107	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
106	Massive parallelization boosts big Bayesian multidimensional scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021 , 30, 11-24	1.4	7
105	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1608-1613	8.3	36
104	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. <i>PLoS Computational Biology</i> , 2021 , 17, e1008561	5	12
103	Host relatedness and landscape connectivity shape pathogen spread in the puma, a large secretive carnivore. <i>Communications Biology</i> , 2021 , 4, 12	6.7	6
102	Intrahost speciations and host switches played an important role in the evolution of herpesviruses. <i>Virus Evolution</i> , 2021 , 7, veab025	3.7	3
101	SARS-CoV-2 European resurgence foretold: interplay of introductions and persistence by leveraging genomic and mobility data 2021 ,		6
100	Regional effect on the molecular clock rate of protein evolution in Eutherian and Metatherian genomes. <i>Bmc Ecology and Evolution</i> , 2021 , 21, 153	21	
99	Global disparities in SARS-CoV-2 genomic surveillance 2021 ,		26
98	Genomic sequencing of SARS-CoV-2 in Rwanda reveals the importance of incoming travelers on lineage diversity. <i>Nature Communications</i> , 2021 , 12, 5705	17.4	2
97	Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. <i>Scientific Reports</i> , 2021 , 11, 18580	4.9	2
96	Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions. <i>Nature Communications</i> , 2021 , 12, 5769	17.4	14
95	Complex evolutionary history of felid anelloviruses. <i>Virology</i> , 2021 , 562, 176-189	3.6	0
94	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		2
93	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk 2021 , 17, e1008561		
92	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk 2021 , 17, e1008561		

91	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk 2021 , 17, e1008561		
90	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk 2021 , 17, e1008561		
89	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
88	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2641-2654	8.3	36
87	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
86	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
85	Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008117	4.8	6
84	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
83	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1832-1842	8.3	9
82	Pliocene colonization of the Mediterranean by Great White Shark inferred from fossil records, historical jaws, phylogeographic and divergence time analyses. <i>Journal of Biogeography</i> , 2020 , 47, 1119-1129	4.1	5
81	Radiation of the coralline red algae (Corallinophycidae, Rhodophyta) crown group as inferred from a multilocus time-calibrated phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2020 , 150, 106845	4.1	12
80	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
79	Accommodating individual travel history, global mobility, and unsampled diversity in phylogeography: a SARS-CoV-2 case study 2020 ,		5
78	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
77	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020 , 6, veaa061	3.7	147
76	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3363-3379	8.3	27
75	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
74	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019 , 178, 1057-1071.e11	56.2	45

73	Divergence dating using mixed effects clock modelling: An application to HIV-1. <i>Virus Evolution</i> , 2019 , 5, vez036	3.7	8
72	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1793-1803	8.3	24
71	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
70	Bayesian estimation of past population dynamics in BEAST 1.10 using the Skygrid coalescent model. <i>Molecular Biology and Evolution</i> , 2019 ,	8.3	29
69	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019 , 7, 208	6	7
68	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. <i>Methods in Molecular Biology</i> , 2019 , 1910, 691-722	1.4	3
67	A63 Quantifying the dynamics of evolutionary rates through time. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
66	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
65	Identifying the patterns and drivers of enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019 , 5, vez009	3.7	10
64	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
63	Interspecific hybridization facilitates niche adaptation in beer yeast. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1562-1575	12.3	41
62	Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. <i>Systematic Biology</i> , 2018 , 67, 901-904	8.4	3267
61	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
60	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018 , 4, vey016	3.7	1199
59	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018 , 9, 2222	17.4	39
58	Phylogenetic Factor Analysis. <i>Systematic Biology</i> , 2018 , 67, 384-399	8.4	8
57	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018 , 31, 24-32	7.5	29
56	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238

55	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. <i>Bioinformatics</i> , 2017 , 33, 1798-1805	7.2	21
54	A Relaxed Directional Random Walk Model for Phylogenetic Trait Evolution. <i>Systematic Biology</i> , 2017 , 66, 299-319	8.4	16
53	Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017 , 66, e47-e65	8.4	55
52	The epidemic dynamics of hepatitis C virus subtypes 4a and 4d in Saudi Arabia. <i>Scientific Reports</i> , 2017 , 7, 44947	4.9	19
51	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
50	PhyGeoTool: interactively exploring large phylogenies in an epidemiological context. <i>Bioinformatics</i> , 2017 , 33, 3993-3995	7.2	13
49	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016 , 2, vev023	9.7	9
48	Genealogical Working Distributions for Bayesian Model Testing with Phylogenetic Uncertainty. <i>Systematic Biology</i> , 2016 , 65, 250-64	8.4	72
47	Sub-Epidemics Explain Localized High Prevalence of Reduced Susceptibility to Rilpivirine in Treatment-Naive HIV-1-Infected Patients: Subtype and Geographic Compartmentalization of Baseline Resistance Mutations. <i>AIDS Research and Human Retroviruses</i> , 2016 , 32, 427-33	1.6	14
46	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. <i>Microbial Genomics</i> , 2016 , 2, e000057	4.4	3
45	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016 , 8,	6.2	11
44	Spread3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2167-9	8.3	241
43	Domestication and Divergence of <i>Saccharomyces cerevisiae</i> Beer Yeasts. <i>Cell</i> , 2016 , 166, 1397-1410.e1656.2	56.2	332
42	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
41	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
40	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015 , 1, vev016	3.7	43
39	Inferring heterogeneous evolutionary processes through time: from sequence substitution to phylogeography. <i>Systematic Biology</i> , 2014 , 63, 493-504	8.4	54
38	Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous-Paleogene boundary. <i>Genome Research</i> , 2014 , 24, 1334-47	9.7	266

37	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014 , 346, 56-61	33.3	370
36	BUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. <i>BMC Bioinformatics</i> , 2014 , 15, 133	3.6	18
35	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
34	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
33	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
32	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
31	Bayesian evolutionary model testing in the phylogenomics era: matching model complexity with computational efficiency. <i>Bioinformatics</i> , 2013 , 29, 1970-9	7.2	65
30	Accurate model selection of relaxed molecular clocks in bayesian phylogenetics. <i>Molecular Biology and Evolution</i> , 2013 , 30, 239-43	8.3	416
29	Context-Dependent Evolutionary Models for Non-Coding Sequences: An Overview of Several Decades of Research and an Analysis of Laurasiatheria and Primate Evolution. <i>Evolutionary Biology</i> , 2012 , 39, 61-82	3	4
28	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
27	Context-dependent codon partition models provide significant increases in model fit in atpB and rbcL protein-coding genes. <i>BMC Evolutionary Biology</i> , 2011 , 11, 145	3	3
26	The genome of <i>Tetranychus urticae</i> reveals herbivorous pest adaptations. <i>Nature</i> , 2011 , 479, 487-92	50.4	684
25	A bio-inspired agent-based system for controlling robot behaviour 2011 ,		1
24	A screening methodology based on Random Forests to improve the detection of gene-gene interactions. <i>European Journal of Human Genetics</i> , 2010 , 18, 1127-32	5.3	41
23	Using non-reversible context-dependent evolutionary models to study substitution patterns in primate non-coding sequences. <i>Journal of Molecular Evolution</i> , 2010 , 71, 34-50	3.1	11
22	Modelling the ancestral sequence distribution and model frequencies in context-dependent models for primate non-coding sequences. <i>BMC Evolutionary Biology</i> , 2010 , 10, 244	3	14
21	On Adaptive Self-Organization in Artificial Robot Organisms 2009 ,		5
20	Open-ended on-board Evolutionary Robotics for robot swarms 2009 ,		9

19	Efficient context-dependent model building based on clustering posterior distributions for non-coding sequences. <i>BMC Evolutionary Biology</i> , 2009 , 9, 87	3	8
18	Stability of selected chlorinated thiazide diuretics. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2009 , 49, 519-24	3.5	23
17	Interpretation of urinary concentrations of pseudoephedrine and its metabolite cathine in relation to doping control. <i>Drug Testing and Analysis</i> , 2009 , 1, 209-13	3.5	14
16	A model-based approach to study nearest-neighbor influences reveals complex substitution patterns in non-coding sequences. <i>Systematic Biology</i> , 2008 , 57, 675-92	8.4	24
15	An improved statistical method for detecting heterotachy in nucleotide sequences. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1397-405	8.3	24
14	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. <i>Nature</i> ,	50.4	34
13	Universal COVID-19 vaccine with updated spike antigen confers full protection against all SARS-CoV-2 variants of concern		2
12	Temporal signal and the phylodynamic threshold of SARS-CoV-2		24
11	A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages		16
10	Lying in wait: the resurgence of dengue virus after the Zika epidemic in Brazil		3
9	International travelers and genomics uncover a hidden Zika outbreak		1
8	Tracing foot-and-mouth disease virus phylogeographical patterns and transmission dynamics		2
7	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations		9
6	Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic		2
5	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak		1
4	Genomic Sequencing of SARS-CoV-2 in Rwanda: evolution and regional dynamics		6
3	Travel-driven emergence and spread of SARS-CoV-2 lineage B.1.620 with multiple VOC-like mutations and deletions in Europe		11
2	The phylodynamics of SARS-CoV-2 during 2020 in Finland [Disappearance and re-emergence of introduced strains.		2

1	Reconstruction of the Origin and Dispersal of the Worldwide Dominant Hepatitis B Virus Subgenotype D1. <i>Virus Evolution</i> ,	3-7	1
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