Guy Baele

List of Publications by Citations

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	Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. *Systematic Biology*, **2018**, 67, 901-904	8.4	3267
125	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. *Virus Evolution*, **2018**, 4, vey016	3.7	1199
124	Improving the accuracy of demographic and molecular clock model comparison while accommodating phylogenetic uncertainty. *Molecular Biology and Evolution*, **2012**, 29, 2157-67	8.3	779
123	The genome of Tetranychus urticae reveals herbivorous pest adaptations. *Nature*, **2011**, 479, 487-92	50.4	684
122	Accurate model selection of relaxed molecular clocks in bayesian phylogenetics. *Molecular Biology and Evolution*, **2013**, 30, 239-43	8.3	416
121	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. *Science*, **2014**, 346, 56-61	33.3	370
120	Domestication and Divergence of Saccharomyces cerevisiae Beer Yeasts. *Cell*, **2016**, 166, 1397-1410.e16	56.2	332
119	Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous-Paleogene boundary. *Genome Research*, **2014**, 24, 1334-47	9.7	266
118	SpreaD3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. *Molecular Biology and Evolution*, **2016**, 33, 2167-9	8.3	241
117	Virus genomes reveal factors that spread and sustained the Ebola epidemic. *Nature*, **2017**, 544, 309-315	50.4	238
116	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. *PLoS Pathogens*, **2014**, 10, e1003932	7.6	230
115	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization.. *Nature*, **2021**,	50.4	230
114	Genomic and epidemiological monitoring of yellow fever virus transmission potential. *Science*, **2018**, 361, 894-899	33.3	184
113	Temporal signal and the phylodynamic threshold of SARS-CoV-2. *Virus Evolution*, **2020**, 6, veaa061	3.7	147
112	Make the most of your samples: Bayes factor estimators for high-dimensional models of sequence evolution. *BMC Bioinformatics*, **2013**, 14, 85	3.6	80
111	A63 Quantifying the dynamics of evolutionary rates through time. *Virus Evolution*, **2019**, 5,	3.7	78
110	Genealogical Working Distributions for Bayesian Model Testing with Phylogenetic Uncertainty. *Systematic Biology*, **2016**, 65, 250-64	8.4	72

109	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. *Systematic Biology*, **2019**, 68, 1052-1061	8.4	71
108	Air travel is associated with intracontinental spread of dengue virus serotypes 1-3 in Brazil. *PLoS Neglected Tropical Diseases*, **2014**, 8, e2769	4.8	67
107	The genealogical population dynamics of HIV-1 in a large transmission chain: bridging within and among host evolutionary rates. *PLoS Computational Biology*, **2014**, 10, e1003505	5	66
106	Bayesian evolutionary model testing in the phylogenomics era: matching model complexity with computational efficiency. *Bioinformatics*, **2013**, 29, 1970-9	7.2	65
105	Emerging Concepts of Data Integration in Pathogen Phylodynamics. *Systematic Biology*, **2017**, 66, e47-e65	8.4	55
104	Inferring heterogeneous evolutionary processes through time: from sequence substitution to phylogeography. *Systematic Biology*, **2014**, 63, 493-504	8.4	54
103	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. *Nature Communications*, **2020**, 11, 5110	17.4	49
102	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 12522-12523	11.5	46
101	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. *Cell*, **2019**, 178, 1057-1071.e11	56.2	45
100	Host ecology determines the dispersal patterns of a plant virus. *Virus Evolution*, **2015**, 1, vev016	3.7	43
99	A screening methodology based on Random Forests to improve the detection of gene-gene interactions. *European Journal of Human Genetics*, **2010**, 18, 1127-32	5.3	41
98	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. *Science*, **2021**, 373, 889-895	33.3	41
97	Interspecific hybridization facilitates niche adaptation in beer yeast. *Nature Ecology and Evolution*, **2019**, 3, 1562-1575	12.3	41
96	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. *Nature Communications*, **2018**, 9, 2222	17.4	39
95	Untangling introductions and persistence in COVID-19 resurgence in Europe. *Nature*, **2021**, 595, 713-717	50.4	37
94	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. *Molecular Biology and Evolution*, **2020**, 37, 2641-2654	8.3	36
93	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. *Molecular Biology and Evolution*, **2021**, 38, 1608-1613	8.3	36
92	Bayesian Inference Reveals Host-Specific Contributions to the Epidemic Expansion of Influenza A H5N1. *Molecular Biology and Evolution*, **2015**, 32, 3264-75	8.3	34

91	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. *Nature*,	50.4	34
90	Bayesian estimation of past population dynamics in BEAST 1.10 using the Skygrid coalescent model. *Molecular Biology and Evolution*, **2019**,	8.3	29
89	Recent advances in computational phylodynamics. *Current Opinion in Virology*, **2018**, 31, 24-32	7.5	29
88	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. *Molecular Biology and Evolution*, **2020**, 37, 3363-3379	8.3	27
87	Global disparities in SARS-CoV-2 genomic surveillance **2021**,		26
86	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. *PLoS Pathogens*, **2019**, 15, e1007976	7.6	25
85	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. *Molecular Biology and Evolution*, **2019**, 36, 1793-1803	8.3	24
84	A model-based approach to study nearest-neighbor influences reveals complex substitution patterns in non-coding sequences. *Systematic Biology*, **2008**, 57, 675-92	8.4	24
83	An improved statistical method for detecting heterotachy in nucleotide sequences. *Molecular Biology and Evolution*, **2006**, 23, 1397-405	8.3	24
82	Temporal signal and the phylodynamic threshold of SARS-CoV-2		24
81	Stability of selected chlorinated thiazide diuretics. *Journal of Pharmaceutical and Biomedical Analysis*, **2009**, 49, 519-24	3.5	23
80	Serum neutralization of SARS-CoV-2 Omicron sublineages BA.1 and BA.2 in patients receiving monoclonal antibodies.. *Nature Medicine*, **2022**,	50.5	22
79	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. *Bioinformatics*, **2017**, 33, 1798-1805	7.2	21
78	The epidemic dynamics of hepatitis C virus subtypes 4a and 4d in Saudi Arabia. *Scientific Reports*, **2017**, 7, 44947	4.9	19
77	BUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. *BMC Bioinformatics*, **2014**, 15, 133	3.6	18
76	Using phylogeographic approaches to analyse the dispersal history, velocity and direction of viral lineages Application to rabies virus spread in Iran. *Molecular Ecology*, **2019**, 28, 4335-4350	5.7	17
75	A Relaxed Directional Random Walk Model for Phylogenetic Trait Evolution. *Systematic Biology*, **2017**, 66, 299-319	8.4	16
74	A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages		16

73	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. *AIDS Research and Human Retroviruses*, **2016**, 32, 427-33	1.6	14
72	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. *Genome Biology and Evolution*, **2017**, 9, 3202-3213	3.9	14
71	Interpretation of urinary concentrations of pseudoephedrine and its metabolite cathine in relation to doping control. *Drug Testing and Analysis*, **2009**, 1, 209-13	3.5	14
70	Modelling the ancestral sequence distribution and model frequencies in context-dependent models for primate non-coding sequences. *BMC Evolutionary Biology*, **2010**, 10, 244	3	14
69	Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions. *Nature Communications*, **2021**, 12, 5769	17.4	14
68	PhyloGeoTool: interactively exploring large phylogenies in an epidemiological context. *Bioinformatics*, **2017**, 33, 3993-3995	7.2	13
67	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. *Aids*, **2015**, 29, 1549-56	3.5	13
66	Radiation of the coralline red algae (Corallinophycidae, Rhodophyta) crown group as inferred from a multilocus time-calibrated phylogeny. *Molecular Phylogenetics and Evolution*, **2020**, 150, 106845	4.1	12
65	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. *PLoS Computational Biology*, **2021**, 17, e1008561	5	12
64	Using non-reversible context-dependent evolutionary models to study substitution patterns in primate non-coding sequences. *Journal of Molecular Evolution*, **2010**, 71, 34-50	3.1	11
63	Travel-driven emergence and spread of SARS-CoV-2 lineage B.1.620 with multiple VOC-like mutations and deletions in Europe		11
62	Lying in wait: the resurgence of dengue virus after the Zika epidemic in Brazil. *Nature Communications*, **2021**, 12, 2619	17.4	11
61	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. *Viruses*, **2016**, 8,	6.2	11
60	Identifying the patterns and drivers of enzootic dynamics using reservoir sampling. *Virus Evolution*, **2019**, 5, vez009	3.7	10
59	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. *Molecular Biology and Evolution*, **2020**, 37, 1832-1842	8.3	9
58	Identifying predictors of time-inhomogeneous viral evolutionary processes. *Virus Evolution*, **2016**, 2, vew023	3.7	9
57	Open-ended on-board Evolutionary Robotics for robot swarms **2009**,		9
56	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations		9

55	Divergence dating using mixed effects clock modelling: An application to HIV-1. *Virus Evolution*, **2019**, 5, vez036	3.7	8
54	Efficient context-dependent model building based on clustering posterior distributions for non-coding sequences. *BMC Evolutionary Biology*, **2009**, 9, 87	3	8
53	Phylogenetic Factor Analysis. *Systematic Biology*, **2018**, 67, 384-399	8.4	8
52	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. *Frontiers in Public Health*, **2019**, 7, 208	6	7
51	Massive parallelization boosts big Bayesian multidimensional scaling. *Journal of Computational and Graphical Statistics*, **2021**, 30, 11-24	1.4	7
50	nosoi: A stochastic agent-based transmission chain simulation framework in r. *Methods in Ecology and Evolution*, **2020**, 11, 1002-1007	7.7	6
49	Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. *PLoS Neglected Tropical Diseases*, **2020**, 14, e0008117	4.8	6
48	In Search of Covariates of HIV-1 Subtype B Spread in the United States-A Cautionary Tale of Large-Scale Bayesian Phylogeography. *Viruses*, **2020**, 12,	6.2	6
47	Genomic Sequencing of SARS-CoV-2 in Rwanda: evolution and regional dynamics		6
46	Host relatedness and landscape connectivity shape pathogen spread in the puma, a large secretive carnivore. *Communications Biology*, **2021**, 4, 12	6.7	6
45	SARS-CoV-2 European resurgence foretold: interplay of introductions and persistence by leveraging genomic and mobility data **2021**,		6
44	Gradients Do Grow on Trees: A Linear-Time O(N)-Dimensional Gradient for Statistical Phylogenetics. *Molecular Biology and Evolution*, **2020**, 37, 3047-3060	8.3	5
43	Pliocene colonization of the Mediterranean by Great White Shark inferred from fossil records, historical jaws, phylogeographic and divergence time analyses. *Journal of Biogeography*, **2020**, 47, 1119-1129	4.1	5
42	On Adaptive Self-Organization in Artificial Robot Organisms **2009**,		5
41	Hamiltonian Monte Carlo sampling to estimate past population dynamics using the skygrid coalescent model in a Bayesian phylogenetics framework. *Wellcome Open Research*, **2020**, 5, 53	4.8	5
40	Accommodating individual travel history, global mobility, and unsampled diversity in phylogeography: a SARS-CoV-2 case study **2020**,		5
39	Bayesian Phylogeographic Analysis Incorporating Predictors and Individual Travel Histories in BEAST. *Current Protocols*, **2021**, 1, e98		5
38	Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City. *PLoS Pathogens*, **2021**, 17, e1009571	7.6	5

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37	Antibody escape and global spread of SARS-CoV-2 lineage A.27.. *Nature Communications*, **2022**, 13, 1152	17.4	5
36	Context-Dependent Evolutionary Models for Non-Coding Sequences: An Overview of Several Decades of Research and an Analysis of Laurasiatheria and Primate Evolution. *Evolutionary Biology*, **2012**, 39, 61-82	3	4
35	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference - Application to H5N1 spread in the Mekong region. *Bioinformatics*, **2020**, 36, 2098-2104	7.2	4
34	Mathematical modelling and phylodynamics for the study of dog rabies dynamics and control: A scoping review. *PLoS Neglected Tropical Diseases*, **2021**, 15, e0009449	4.8	4
33	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. *Methods in Molecular Biology*, **2019**, 1910, 691-722	1.4	3
32	Context-dependent codon partition models provide significant increases in model fit in atpB and rbcL protein-coding genes. *BMC Evolutionary Biology*, **2011**, 11, 145	3	3
31	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. **2021**,		3
30	Phylogeography reveals association between swine trade and the spread of porcine epidemic diarrhea virus in China and across the world.. *Molecular Biology and Evolution*, **2021**,	8.3	3
29	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. *Microbial Genomics*, **2016**, 2, e000057	4.4	3
28	Lying in wait: the resurgence of dengue virus after the Zika epidemic in Brazil		3
27	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. *Viruses*, **2021**, 13,	6.2	3
26	Intrahost speciations and host switches played an important role in the evolution of herpesviruses. *Virus Evolution*, **2021**, 7, veab025	3.7	3
25	Universal COVID-19 vaccine with updated spike antigen confers full protection against all SARS-CoV-2 variants of concern		2
24	Tracing foot-and-mouth disease virus phylogeographical patterns and transmission dynamics		2
23	Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic		2
22	The phylodynamics of SARS-CoV-2 during 2020 in Finland ⅼDisappearance and re-emergence of introduced strains.		2
21	Markov-Modulated Continuous-Time Markov Chains to Identify Site- and Branch-Specific Evolutionary Variation in BEAST. *Systematic Biology*, **2021**, 70, 181-189	8.4	2
20	Genomic sequencing of SARS-CoV-2 in Rwanda reveals the importance of incoming travelers on lineage diversity. *Nature Communications*, **2021**, 12, 5705	17.4	2

19	Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. *Scientific Reports*, **2021**, 11, 18580	4.9	2
18	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. **2021**,		2
17	A bio-inspired agent-based system for controlling robot behaviour **2011**,		1
16	Identification of the First SARS-CoV-2 Lineage B.1.1.529 Virus Detected in Europe.. *Microbiology Resource Announcements*, **2022**, e0116121	1.3	1
15	International travelers and genomics uncover a Ⓗidden Zika outbreak		1
14	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak		1
13	Quantifying rates of HIV-1 flow between risk groups and geographic locations in Kenya: A country-wide phylogenetic study.. *Virus Evolution*, **2022**, 8, veac016	3.7	1
12	Reconstruction of the Origin and Dispersal of the Worldwide Dominant Hepatitis B Virus Subgenotype D1. *Virus Evolution*,	3.7	1
11	YMrCA: Improving Y-chromosomal ancestor time estimation for DNA kinship research. *Human Mutation*, **2021**, 42, 1307-1320	4.7	0
10	Complex evolutionary history of felid anelloviruses. *Virology*, **2021**, 562, 176-189	3.6	0
9	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal.. *Virus Evolution*, **2022**, 8, veac029	3.7	0
8	Phycova - a tool for exploring covariates of pathogen spread.. *Virus Evolution*, **2022**, 8, veac015	3.7	0
7	Evolutionary history and introduction of SARS-CoV-2 Alpha VOC/B.1.1.7 in Pakistan through international travelers.. *Virus Evolution*, **2022**, 8, veac020	3.7	0
6	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. *Viruses*, **2022**, 14, 1198	6.2	0
5	Regional effect on the molecular clock rate of protein evolution in Eutherian and Metatherian genomes. *Bmc Ecology and Evolution*, **2021**, 21, 153	21	
4	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk **2021**, 17, e1008561		
3	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk **2021**, 17, e1008561		
2	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk **2021**, 17, e1008561		

LIST OF PUBLICATIONS

1. Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk **2021**
, 17, e1008561