

# Bret Larget

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

23,692  
citations

430442

18  
h-index

676716

22  
g-index

26  
all docs

26  
docs citations

26  
times ranked

25896  
citing authors

#	ARTICLE	IF	CITATIONS
1	MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. <i>Systematic Biology</i> , 2012, 61, 539-542.	2.7	20,458
2	Potential Applications and Pitfalls of Bayesian Inference of Phylogeny. <i>Systematic Biology</i> , 2002, 51, 673-688.	2.7	721
3	Bayesian Phylogenetic Model Selection Using Reversible Jump Markov Chain Monte Carlo. <i>Molecular Biology and Evolution</i> , 2004, 21, 1123-1133.	3.5	502
4	Bayesian Phylogenetic Inference via Markov Chain Monte Carlo Methods. <i>Biometrics</i> , 1999, 55, 1-12.	0.8	460
5	Bayesian Estimation of Concordance among Gene Trees. <i>Molecular Biology and Evolution</i> , 2006, 24, 412-426.	3.5	420
6	A Compound Poisson Process for Relaxing the Molecular Clock. <i>Genetics</i> , 2000, 154, 1879-1892.	1.2	290
7	Ecosystem respiration: Drivers of daily variability and background respiration in lakes around the globe. <i>Limnology and Oceanography</i> , 2013, 58, 849-866.	1.6	195
8	Efficiency of Markov Chain Monte Carlo Tree Proposals in Bayesian Phylogenetics. <i>Systematic Biology</i> , 2008, 57, 86-103.	2.7	146
9	A BAYESIAN FRAMEWORK FOR THE ANALYSIS OF COSPECIATION. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 352-364.	1.1	111
10	A Bayesian Analysis of Metazoan Mitochondrial Genome Arrangements. <i>Molecular Biology and Evolution</i> , 2005, 22, 486-495.	3.5	78
11	Exploring Tree-Like and Non-Tree-Like Patterns Using Genome Sequences: An Example Using the Inbreeding Plant Species <i>Arabidopsis thaliana</i> (L.) Heynh. <i>Systematic Biology</i> , 2015, 64, 809-823.	2.7	57
12	Bayesian phylogenetic inference from animal mitochondrial genome arrangements. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002, 64, 681-693.	1.1	49
13	Hastings Ratio of the LOCAL Proposal Used in Bayesian Phylogenetics. <i>Systematic Biology</i> , 2005, 54, 961-965.	2.7	41
14	A Bayesian approach to the estimation of ancestral genome arrangements. <i>Molecular Phylogenetics and Evolution</i> , 2005, 36, 214-223.	1.2	37
15	The Estimation of Tree Posterior Probabilities Using Conditional Clade Probability Distributions. <i>Systematic Biology</i> , 2013, 62, 501-511.	2.7	35
16	Markov chain Monte Carlo for the Bayesian analysis of evolutionary trees from aligned molecular sequences. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 1999, 33, 143-162.	1.0	26
17	A Bayesian Model of AFLP Marker Evolution and Phylogenetic Inference. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2007, 6, Article11.	0.2	22
18	Comment on "Phylogenetic MCMC Algorithms Are Misleading on Mixtures of Trees". <i>Science</i> , 2006, 312, 367a-367a.	6.0	19

#	ARTICLE	IF	CITATIONS
19	Statistical evidence for common ancestry: Application to primates. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1354-1363.	1.1	8
20	Introduction to Markov Chain Monte Carlo Methods in Molecular Evolution. , 2005, , 45-62.		6
21	Phantom species: adjusting estimates of colonization and extinction for pseudoâ€turnover. <i>Oikos</i> , 2018, 127, 1605-1618.	1.2	6
22	BayesCAT: Bayesian Co-estimation of Alignment and Tree. <i>Biometrics</i> , 2018, 74, 270-279.	0.8	3
23	Phylogenetic Inference from Mitochondrial Genome Arrangement Data. <i>Lecture Notes in Computer Science</i> , 2001, , 1022-1028.	1.0	2
24	Statistical Analysis of DOE EML QAP Data from 1982 to 1998. <i>Journal of Chemical Information and Computer Sciences</i> , 2001, 41, 1099-1105.	2.8	0
25	Bayesian estimation of the phylogeography of African gorillas with genomeâ€differentiated population trees. <i>Biometrics</i> , 2014, 70, 683-694.	0.8	0