

Jeremy M Brown

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,298
citations

448610

19
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388640

36
g-index

41
all docs

41
docs citations

41
times ranked

3682
citing authors

#	ARTICLE	IF	CITATIONS
1	On the Need for New Measures of Phylogenomic Support. <i>Systematic Biology</i> , 2022, 71, 917-920.	2.7	9
2	Comparing Likelihood Ratios to Understand Genome-Wide Variation in Phylogenetic Support. <i>Systematic Biology</i> , 2022, 71, 973-985.	2.7	4
3	Phylogenomics Reveals Ancient Gene Tree Discordance in the Amphibian Tree of Life. <i>Systematic Biology</i> , 2021, 70, 49-66.	2.7	124
4	Identification and Visualization of Functionally Important Domains and Residues in Herpes Simplex Virus Glycoprotein K(gK) Using a Combination of Phylogenetics and Protein Modeling. <i>Scientific Reports</i> , 2019, 9, 14625.	1.6	9
5	Hinge Region in DNA Packaging Terminase pUL15 of Herpes Simplex Virus: A Potential Allosteric Target for Antiviral Drugs. <i>Biomolecules</i> , 2019, 9, 603.	1.8	5
6	The Behavior of Metropolis-Coupled Markov Chains When Sampling Rugged Phylogenetic Distributions. <i>Systematic Biology</i> , 2018, 67, 729-734.	2.7	6
7	P3: Phylogenetic Posterior Prediction in RevBayes. <i>Molecular Biology and Evolution</i> , 2018, 35, 1028-1034.	3.5	28
8	Variation Across Mitochondrial Gene Trees Provides Evidence for Systematic Error: How Much Gene Tree Variation Is Biological?. <i>Systematic Biology</i> , 2018, 67, 847-860.	2.7	51
9	Impact of Model Violations on the Inference of Species Boundaries Under the Multispecies Coalescent. <i>Systematic Biology</i> , 2018, 67, 269-284.	2.7	76
10	Evaluating Model Performance in Evolutionary Biology. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 95-114.	3.8	39
11	Bayes factors unmask highly variable information content, bias, and extreme influence in phylogenomic analyses. <i>Systematic Biology</i> , 2017, 66, syw101.	2.7	97
12	Short Communication: Lack of Support for Socially Connected HIV-1 Transmission Among Young Adult Black Men Who Have Sex with Men. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 935-940.	0.5	5
13	EmpPrior: using outside empirical data to inform branch-length priors for Bayesian phylogenetics. <i>BMC Bioinformatics</i> , 2016, 17, 253.	1.2	0
14	TreeScaper: Visualizing and Extracting Phylogenetic Signal from Sets of Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 3314-3316.	3.5	20
15	Quantifying the spatiotemporal dynamics in a chorus frog (<i>Pseudacris</i>) hybrid zone over 30 years. <i>Ecology and Evolution</i> , 2016, 6, 5013-5031.	0.8	16
16	Deflating Trees: Improving Bayesian Branch-Length Estimates using Informed Priors. <i>Systematic Biology</i> , 2015, 64, 441-447.	2.7	9
17	Can We Identify Genes with Increased Phylogenetic Reliability?. <i>Systematic Biology</i> , 2015, 64, 824-837.	2.7	80
18	Human adipose tissue as a reservoir for memory CD4+ T cells and HIV. <i>Aids</i> , 2015, 29, 667-674.	1.0	112

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19	Predictive Approaches to Assessing the Fit of Evolutionary Models. <i>Systematic Biology</i> , 2014, 63, 289-292.	2.7	47
20	Untangling the influences of unmodeled evolutionary processes on phylogenetic signal in a forensically important HIV-1 transmission cluster. <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 126-137.	1.2	5
21	Detection of Implausible Phylogenetic Inferences Using Posterior Predictive Assessment of Model Fit. <i>Systematic Biology</i> , 2014, 63, 334-348.	2.7	68
22	Poor Fit to the Multispecies Coalescent is Widely Detectable in Empirical Data. <i>Systematic Biology</i> , 2014, 63, 322-333.	2.7	78
23	A Phylogenomic Approach to Vertebrate Phylogeny Supports a Turtle-Archosaur Affinity and a Possible Paraphyletic Lissamphibia. <i>PLoS ONE</i> , 2012, 7, e48990.	1.1	61
24	DIM SUM: demography and individual migration simulated using a Markov chain. <i>Molecular Ecology Resources</i> , 2011, 11, 358-363.	2.2	1
25	NONADAPTIVE EVOLUTION OF MITOCHONDRIAL GENOME SIZE. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 2706-2711.	1.1	20
26	Guidelines for HIV in court cases. <i>Nature</i> , 2011, 473, 284-284.	13.7	5
27	Source identification in two criminal cases using phylogenetic analysis of HIV-1 DNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21242-21247.	3.3	80
28	When Trees Grow Too Long: Investigating the Causes of Highly Inaccurate Bayesian Branch-Length Estimates. <i>Systematic Biology</i> , 2010, 59, 145-161.	2.7	220
29	The Effect of Ambiguous Data on Phylogenetic Estimates Obtained by Maximum Likelihood and Bayesian Inference. <i>Systematic Biology</i> , 2009, 58, 130-145.	2.7	387
30	PuMA: Bayesian analysis of p -partitioned (and u - n -partitioned) m -model a -adequacy. <i>Bioinformatics</i> , 2009, 25, 537-538.	1.8	29
31	Newly discovered sister lineage sheds light on early ant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14913-14917.	3.3	105
32	The Importance of Data Partitioning and the Utility of Bayes Factors in Bayesian Phylogenetics. <i>Systematic Biology</i> , 2007, 56, 643-655.	2.7	310
33	INCREASED RATES OF MOLECULAR EVOLUTION IN AN EQUATORIAL PLANT CLADE: AN EFFECT OF ENVIRONMENT OR PHYLOGENETIC NONINDEPENDENCE?. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 238-242.	1.1	10
34	Increased rates of molecular evolution in an equatorial plant clade: an effect of environment or phylogenetic nonindependence?. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 238-42.	1.1	2
35	On the social structure of offspring rearing in the burrower bug, <i>Sehirus cinctus</i> (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	11
36	An Analysis of Single Clutch Paternity in the Burrower Bug <i>Sehirus cinctus</i> Using Microsatellites. <i>Journal of Insect Behavior</i> , 2003, 16, 731-745.	0.4	3

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37	Parent-Offspring Coadaptation and the Dual Genetic Control of Maternal Care. Science, 2001, 292, 1710-1712.	6.0	164