

David Bryant

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.

31
papers

10,834
citations

14
h-index

34
g-index

34
ext. papers

13,467
ext. citations

7.8
avg, IF

7.02
L-index

#	Paper	IF	Citations
31	Discrete coalescent trees. <i>Journal of Mathematical Biology</i> , 2021 , 83, 60	2	1
30	V-Spline: An Adaptive Smoothing Spline for Trajectory Reconstruction. <i>Sensors</i> , 2021 , 21,	3.8	1
29	Bayesian Inference of Species Trees using Diffusion Models. <i>Systematic Biology</i> , 2021 , 70, 145-161	8.4	4
28	Negative-Type Diversities, a Multi-dimensional Analogue of Negative-Type Metrics. <i>Journal of Geometric Analysis</i> , 2021 , 31, 1703-1720	0.9	0
27	An $O(n \log n)$ Time Algorithm for Computing the Path-Length Distance Between Trees. <i>Algorithmica</i> , 2019 , 81, 3692-3706	0.9	1
26	Failure to Recover Major Events of Gene Flux in Real Biological Data Due to Method Misapplication. <i>Genome Biology and Evolution</i> , 2018 , 10, 1198-1209	3.9	4
25	How disturbance and dispersal influence intraspecific structure. <i>Journal of Ecology</i> , 2018 , 106, 1298-1306		18
24	The dimensionality of niche space allows bounded and unbounded processes to jointly influence diversification. <i>Nature Communications</i> , 2018 , 9, 4258	17.4	11
23	Can We "Future-Proof" Consensus Trees?. <i>Systematic Biology</i> , 2017 , 66, 611-619	8.4	24
22	Efficient Recycled Algorithms for Quantitative Trait Models on Phylogenies. <i>Genome Biology and Evolution</i> , 2016 , 8, 1338-50	3.9	7
21	Constant Distortion Embeddings of Symmetric Diversities. <i>Analysis and Geometry in Metric Spaces</i> , 2016 , 4,	0.6	3
20	The probability of monophyly of a sample of gene lineages on a species tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 8002-9	11.5	12
19	Flexible methods for estimating genetic distances from single nucleotide polymorphisms. <i>Methods in Ecology and Evolution</i> , 2015 , 6, 938-948	7.7	26
18	Monte Carlo Strategies for Selecting Parameter Values in Simulation Experiments. <i>Systematic Biology</i> , 2015 , 64, 741-51	8.4	10
17	Endosymbiotic origin and differential loss of eukaryotic genes. <i>Nature</i> , 2015 , 524, 427-32	50.4	190
16	Origins of major archaeal clades correspond to gene acquisitions from bacteria. <i>Nature</i> , 2015 , 517, 77-80	50.4	169
15	popart: full-feature software for haplotype network construction. <i>Methods in Ecology and Evolution</i> , 2015 , 6, 1110-1116	7.7	2356

14	Statistical flaws undermine pre-Columbian chicken debate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E3584	11.5	4
13	Forty Years of Model-Based Phylogeography. <i>Computational Biology</i> , 2013 , 17-28	0.7	
12	The link between segregation and phylogenetic diversity. <i>Journal of Mathematical Biology</i> , 2012 , 64, 149-62	2	2
11	Inferring species trees directly from biallelic genetic markers: bypassing gene trees in a full coalescent analysis. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1917-32	8.3	553
10	Hyperconvexity and tight-span theory for diversities. <i>Advances in Mathematics</i> , 2012 , 231, 3172-3198	1.3	15
9	Investigating the global dispersal of chickens in prehistory using ancient mitochondrial DNA signatures. <i>PLoS ONE</i> , 2012 , 7, e39171	3.7	84
8	Bureaucratic set systems, and their role in phylogenetics. <i>Applied Mathematics Letters</i> , 2012 , 25, 1148-1153	1.5	3
7	Species delimitation and phylogeny of a New Zealand plant species radiation. <i>BMC Evolutionary Biology</i> , 2009 , 9, 111	3	46
6	Continuous and tractable models for the variation of evolutionary rates. <i>Mathematical Biosciences</i> , 2006 , 199, 216-33	3.9	30
5	Application of phylogenetic networks in evolutionary studies. <i>Molecular Biology and Evolution</i> , 2006 , 23, 254-67	8.3	5807
4	Neighbor-net: an agglomerative method for the construction of phylogenetic networks. <i>Molecular Biology and Evolution</i> , 2004 , 21, 255-65	8.3	1318
3	A classification of consensus methods for phylogenetics. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 2003 , 163-183		120
2	Hunting for trees in binary character sets: efficient algorithms for extraction, enumeration, and optimization. <i>Journal of Computational Biology</i> , 1996 , 3, 275-88	1.7	12
1	FRASLIMITS FOR RELATIONAL METRIC STRUCTURES. <i>Journal of Symbolic Logic</i> , 1-22	0.4	0