Cécile Ané

List of Publications by Year
in descending order

52 papers	6,118 citations	126907 33 h-index	175258 52 g-index
60 all docs	60 docs citations	60 times ranked	7581 citing authors

#	Article	IF	Citations
1	Evidence for hawkmoth pollination in the chiropterophilous African baobab (*Adansonia) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	5.6	2
2	KIMGENS: a novel method to estimate kinship in organisms with mixed haploid diploid genetic systems robust to population structure. Bioinformatics, 2022, 38, 3044-3050.	4.1	5
3	Assessing the fit of the multi-species network coalescent to multi-locus data. Bioinformatics, 2021, 37, 634-641.	4.1	14
4	A new carnivorous plant lineage (*Triantha*) with a unique sticky-inflorescence trap. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	26
5	Phylogenetic Trees and Networks Can Serve as Powerful and Complementary Approaches for Analysis of Genomic Data. Systematic Biology, 2020, 69, 593-601.	5.6	72
6	Reticulate Evolution Helps Explain Apparent Homoplasy in Floral Biology and Pollination in Baobabs (Adansonia; Bombacoideae; Malvaceae). Systematic Biology, 2020, 69, 462-478.	5.6	32
7	A Malvaceae mystery: A mallow maelstrom of genome multiplications and maybe misleading methods?. Journal of Integrative Plant Biology, 2019, 61, 12-31.	8.5	25
8	Phylogenetic Comparative Methods on Phylogenetic Networks with Reticulations. Systematic Biology, 2018, 67, 800-820.	5.6	88
9	Inference of Adaptive Shifts for Multivariate Correlated Traits. Systematic Biology, 2018, 67, 662-680.	5.6	78
10	Monocot plastid phylogenomics, timeline, net rates of species diversification, the power of multi‐gene analyses, and a functional model for the origin of monocots. American Journal of Botany, 2018, 105, 1888-1910.	1.7	161
11	Phase transition on the convergence rate of parameter estimation under an Ornstein–Uhlenbeck diffusion on a tree. Journal of Mathematical Biology, 2017, 74, 355-385.	1.9	13
12	Rphylopars: fast multivariate phylogenetic comparative methods for missing data and within‐species variation. Methods in Ecology and Evolution, 2017, 8, 22-27.	5.2	174
13	PhyloNetworks: A Package for Phylogenetic Networks. Molecular Biology and Evolution, 2017, 34, 3292-3298.	8.9	250
14	Inferring Phylogenetic Networks with Maximum Pseudolikelihood under Incomplete Lineage Sorting. PLoS Genetics, 2016, 12, e1005896.	3.5	348
15	Statistical evidence for common ancestry: Application to primates. Evolution; International Journal of Organic Evolution, 2016, 70, 1354-1363.	2.3	8
16	Fast and accurate detection of evolutionary shifts in Ornstein–Uhlenbeck models. Methods in Ecology and Evolution, 2016, 7, 811-824.	5.2	201
17	Inconsistency of Species Tree Methods under Gene Flow. Systematic Biology, 2016, 65, 843-851.	5.6	146
18	Evaluating and Characterizing Ancient Whole-Genome Duplications in Plants with Gene Count Data. Genome Biology and Evolution, 2016, 8, 1023-1037.	2.5	53

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19	Bayesian species delimitation combining multiple genes and traits in a unified framework. Evolution; International Journal of Organic Evolution, 2015, 69, 492-507.	2.3	152
20	Exploring Tree-Like and Non-Tree-Like Patterns Using Genome Sequences: An Example Using the Inbreeding Plant Species *Arabidopsis thaliana* (L.) Heynh. Systematic Biology, 2015, 64, 809-823.	5.6	57
21	Detecting and Locating Whole Genome Duplications on a Phylogeny: A Probabilistic Approach. Molecular Biology and Evolution, 2014, 31, 750-762.	8.9	73
22	A Linear-Time Algorithm for Gaussian and Non-Gaussian Trait Evolution Models. Systematic Biology, 2014, 63, 397-408.	5.6	782
23	Intrinsic inference difficulties for trait evolution with Ornstein–Uhlenbeck models. Methods in Ecology and Evolution, 2014, 5, 1133-1146.	5.2	154
24	Computing the Joint Distribution of Tree Shape and Tree Distance for Gene Tree Inference and Recombination Detection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1-1.	3.0	3
25	THE EVOLUTION OF HYBRID INCOMPATIBILITIES ALONG A PHYLOGENY. Evolution; International Journal of Organic Evolution, 2013, 67, n/a-n/a.	2.3	21
26	Asymptotic theory with hierarchical autocorrelation: Ornstein–Uhlenbeck tree models. Annals of Statistics, 2013, 41, .	2.6	45
27	Using HSV-1 Genome Phylogenetics to Track Past Human Migrations. PLoS ONE, 2013, 8, e76267.	2.5	76
28	Mapping Quantitative Trait Loci onto a Phylogenetic Tree. Genetics, 2012, 192, 267-279.	2.9	8
29	LOCATING EVOLUTIONARY PRECURSORS ON A PHYLOGENETIC TREE. Evolution; International Journal of Organic Evolution, 2012, 66, 3918-3930.	2.3	77
30	Single copy nuclear gene analysis of polyploidy in wild potatoes (Solanum section Petota). BMC Evolutionary Biology, 2012, 12, 70.	3.2	28
31	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in Plant Science, 2011, 2, 34.	3.6	396
32	Detecting Phylogenetic Breakpoints and Discordance from Genome-Wide Alignments for Species Tree Reconstruction. Genome Biology and Evolution, 2011, 3, 246-258.	2.5	28
33	Comparing Two Bayesian Methods for Gene Tree/Species Tree Reconstruction: Simulations with Incomplete Lineage Sorting and Horizontal Gene Transfer. Systematic Biology, 2011, 60, 261-275.	5.6	103
34	BUCKy: Gene tree/species tree reconciliation with Bayesian concordance analysis. Bioinformatics, 2010, 26, 2910-2911.	4.1	389
35	Fine-Scale Phylogenetic Discordance across the House Mouse Genome. PLoS Genetics, 2009, 5, e1000729.	3.5	104
36	Do potatoes and tomatoes have a single evolutionary history, and what proportion of the genome supports this history?. BMC Evolutionary Biology, 2009, 9, 191.	3.2	89

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37	Groves of Phylogenetic Trees. Annals of Combinatorics, 2009, 13, 139-167.	0.6	8
38	MACROEVOLUTIONARY TESTS OF POLLINATION SYNDROMES: A REPLY TO FENSTER ET AL.. Evolution; International Journal of Organic Evolution, 2009, 63, 2763-2767.	2.3	9
39	THE ROLE OF POLLINATOR SHIFTS IN THE FLORAL DIVERSIFICATION OF *IOCHROMA* (SOLANACEAE). Evolution; International Journal of Organic Evolution, 2008, 62, 793-806.	2.3	142
40	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. Advances in Applied Probability, 2008, 40, 229-249.	0.7	63
41	A Bayesian Perspective on a Non-parsimonious Parsimony Model. Systematic Biology, 2008, 57, 406-419.	5.6	28
42	Proteomic analysis of the winter-protected phenotype of hibernating ground squirrel intestine. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2008, 295, R316-R328.	1.8	45
43	Analysis of comparative data with hierarchical autocorrelation. Annals of Applied Statistics, 2008, 2, .	1.1	48
44	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. Advances in Applied Probability, 2008, 40, 229-249.	0.7	17
45	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. Evolution; International Journal of Organic Evolution, 2006, 60, 922.	2.3	183
46	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. Evolution; International Journal of Organic Evolution, 2006, 60, 922-933.	2.3	516
47	Bayesian Estimation of Concordance among Gene Trees. Molecular Biology and Evolution, 2006, 24, 412-426.	8.9	420
48	Covarion Structure in Plastid Genome Evolution: A New Statistical Test. Molecular Biology and Evolution, 2005, 22, 914-924.	8.9	66
49	Missing the Forest for the Trees: Phylogenetic Compression and Its Implications for Inferring Complex Evolutionary Histories. Systematic Biology, 2005, 54, 146-157.	5.6	47
50	Prospects for Building the Tree of Life from Large Sequence Databases. Science, 2004, 306, 1172-1174.	12.6	233
51	Population pharmacokinetics/pharmacodynamics relationships of an anticancer drug. Statistics in Medicine, 2003, 22, 833-846.	1.6	3
52	Dating with constraints. Peer Community in Evolutionary Biology, 0, , .	0.0	0