

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4646987/publications.pdf>

Version: 2024-02-01

52  
papers

6,118  
citations

145106

33  
h-index

198040

52  
g-index

60  
all docs

60  
docs citations

60  
times ranked

8587  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence for hawkmoth pollination in the chiropterophilous African baobab ( <i>Adansonia digitata</i> ). <i>Journal of Experimental Botany</i> , 2019, 60, 1073-1081.	0.8	10
2	KIMGENS: a novel method to estimate kinship in organisms with mixed haploid diploid genetic systems robust to population structure. <i>Bioinformatics</i> , 2022, 38, 3044-3050.	1.8	5
3	Assessing the fit of the multi-species network coalescent to multi-locus data. <i>Bioinformatics</i> , 2021, 37, 634-641.	1.8	14
4	A new carnivorous plant lineage ( <i>Triantha</i> ) with a unique sticky-inflorescence trap. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
5	Phylogenetic Trees and Networks Can Serve as Powerful and Complementary Approaches for Analysis of Genomic Data. <i>Systematic Biology</i> , 2020, 69, 593-601.	2.7	72
6	Reticulate Evolution Helps Explain Apparent Homoplasy in Floral Biology and Pollination in Baobabs ( <i>Adansonia</i> ; <i>Bombacoideae</i> ; <i>Malvaceae</i> ). <i>Systematic Biology</i> , 2020, 69, 462-478.	2.7	32
7	A Malvaceae mystery: A mallow maelstrom of genome duplications and maybe misleading methods?. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 12-31.	4.1	25
8	Phylogenetic Comparative Methods on Phylogenetic Networks with Reticulations. <i>Systematic Biology</i> , 2018, 67, 800-820.	2.7	88
9	Inference of Adaptive Shifts for Multivariate Correlated Traits. <i>Systematic Biology</i> , 2018, 67, 662-680.	2.7	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. <i>American Journal of Botany</i> , 2018, 105, 1888-1910.	0.8	161
11	Phase transition on the convergence rate of parameter estimation under an Ornstein-Uhlenbeck diffusion on a tree. <i>Journal of Mathematical Biology</i> , 2017, 74, 355-385.	0.8	13
12	Rphylopar: fast multivariate phylogenetic comparative methods for missing data and within-species variation. <i>Methods in Ecology and Evolution</i> , 2017, 8, 22-27.	2.2	174
13	PhyloNetworks: A Package for Phylogenetic Networks. <i>Molecular Biology and Evolution</i> , 2017, 34, 3292-3298.	3.5	250
14	Inferring Phylogenetic Networks with Maximum Pseudolikelihood under Incomplete Lineage Sorting. <i>PLoS Genetics</i> , 2016, 12, e1005896.	1.5	348
15	Statistical evidence for common ancestry: Application to primates. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1354-1363.	1.1	8
16	Fast and accurate detection of evolutionary shifts in Ornstein-Uhlenbeck models. <i>Methods in Ecology and Evolution</i> , 2016, 7, 811-824.	2.2	201
17	Inconsistency of Species Tree Methods under Gene Flow. <i>Systematic Biology</i> , 2016, 65, 843-851.	2.7	146
18	Evaluating and Characterizing Ancient Whole-Genome Duplications in Plants with Gene Count Data. <i>Genome Biology and Evolution</i> , 2016, 8, 1023-1037.	1.1	53

#	ARTICLE	IF	CITATIONS
19	Bayesian species delimitation combining multiple genes and traits in a unified framework. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 492-507.	1.1	152
20	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
21	Detecting and Locating Whole Genome Duplications on a Phylogeny: A Probabilistic Approach. <i>Molecular Biology and Evolution</i> , 2014, 31, 750-762.	3.5	73
22	A Linear-Time Algorithm for Gaussian and Non-Gaussian Trait Evolution Models. <i>Systematic Biology</i> , 2014, 63, 397-408.	2.7	782
23	Intrinsic inference difficulties for trait evolution with Ornstein-Uhlenbeck models. <i>Methods in Ecology and Evolution</i> , 2014, 5, 1133-1146.	2.2	154
24	Computing the Joint Distribution of Tree Shape and Tree Distance for Gene Tree Inference and Recombination Detection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1-1.	1.9	3
25	THE EVOLUTION OF HYBRID INCOMPATIBILITIES ALONG A PHYLOGENY. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, n/a-n/a.	1.1	21
26	Asymptotic theory with hierarchical autocorrelation: Ornstein-Uhlenbeck tree models. <i>Annals of Statistics</i> , 2013, 41, .	1.4	45
27	Using HSV-1 Genome Phylogenetics to Track Past Human Migrations. <i>PLoS ONE</i> , 2013, 8, e76267.	1.1	76
28	Mapping Quantitative Trait Loci onto a Phylogenetic Tree. <i>Genetics</i> , 2012, 192, 267-279.	1.2	8
29	LOCATING EVOLUTIONARY PRECURSORS ON A PHYLOGENETIC TREE. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3918-3930.	1.1	77
30	Single copy nuclear gene analysis of polyploidy in wild potatoes ( <i>Solanum</i> section <i>Petota</i> ). <i>BMC Evolutionary Biology</i> , 2012, 12, 70.	3.2	28
31	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	1.7	396
32	Detecting Phylogenetic Breakpoints and Discordance from Genome-Wide Alignments for Species Tree Reconstruction. <i>Genome Biology and Evolution</i> , 2011, 3, 246-258.	1.1	28
33	Comparing Two Bayesian Methods for Gene Tree/Species Tree Reconstruction: Simulations with Incomplete Lineage Sorting and Horizontal Gene Transfer. <i>Systematic Biology</i> , 2011, 60, 261-275.	2.7	103
34	BUCKy: Gene tree/species tree reconciliation with Bayesian concordance analysis. <i>Bioinformatics</i> , 2010, 26, 2910-2911.	1.8	389
35	Fine-Scale Phylogenetic Discordance across the House Mouse Genome. <i>PLoS Genetics</i> , 2009, 5, e1000729.	1.5	104
36	Do potatoes and tomatoes have a single evolutionary history, and what proportion of the genome supports this history?. <i>BMC Evolutionary Biology</i> , 2009, 9, 191.	3.2	89

#	ARTICLE	IF	CITATIONS
37	Groves of Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2009, 13, 139-167.	0.3	8
38	MACROEVOLUTIONARY TESTS OF POLLINATION SYNDROMES: A REPLY TO FENSTER ET AL.. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2763-2767.	1.1	9
39	THE ROLE OF POLLINATOR SHIFTS IN THE FLORAL DIVERSIFICATION OF <i>IOCHROMA</i> (SOLANACEAE). <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 793-806.	1.1	142
40	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. <i>Advances in Applied Probability</i> , 2008, 40, 229-249.	0.4	63
41	A Bayesian Perspective on a Non-parsimonious Parsimony Model. <i>Systematic Biology</i> , 2008, 57, 406-419.	2.7	28
42	Proteomic analysis of the winter-protected phenotype of hibernating ground squirrel intestine. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2008, 295, R316-R328.	0.9	45
43	Analysis of comparative data with hierarchical autocorrelation. <i>Annals of Applied Statistics</i> , 2008, 2, .	0.5	48
44	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. <i>Advances in Applied Probability</i> , 2008, 40, 229-249.	0.4	17
45	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 922.	1.1	183
46	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 922-933.	1.1	516
47	Bayesian Estimation of Concordance among Gene Trees. <i>Molecular Biology and Evolution</i> , 2006, 24, 412-426.	3.5	420
48	Covariation Structure in Plastid Genome Evolution: A New Statistical Test. <i>Molecular Biology and Evolution</i> , 2005, 22, 914-924.	3.5	66
49	Missing the Forest for the Trees: Phylogenetic Compression and Its Implications for Inferring Complex Evolutionary Histories. <i>Systematic Biology</i> , 2005, 54, 146-157.	2.7	47
50	Prospects for Building the Tree of Life from Large Sequence Databases. <i>Science</i> , 2004, 306, 1172-1174.	6.0	233
51	Population pharmacokinetics/pharmacodynamics relationships of an anticancer drug. <i>Statistics in Medicine</i> , 2003, 22, 833-846.	0.8	3
52	Dating with constraints. <i>Peer Community in Evolutionary Biology</i> , 0, , .	0.0	0