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List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

15,280
citations

94269

37
h-index

98622

67
g-index

75
all docs

75
docs citations

75
times ranked

24223
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>Clumpak</scp>: a program for identifying clustering modes and packaging population structure inferences across <i>K</i> . Molecular Ecology Resources, 2015, 15, 1179-1191.	2.2	2,411
2	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. Nucleic Acids Research, 2016, 44, W344-W350.	6.5	2,395
3	ConSurf 2005: the projection of evolutionary conservation scores of residues on protein structures. Nucleic Acids Research, 2005, 33, W299-W302.	6.5	1,255
4	The frequency of polyploid speciation in vascular plants. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13875-13879.	3.3	1,136
5	TRY plant trait database – enhanced coverage and open access. Global Change Biology, 2020, 26, 119-188.	4.2	1,038
6	Sex Determination: Why So Many Ways of Doing It?. PLoS Biology, 2014, 12, e1001899.	2.6	916
7	The Chromosome Counts Database (<scp>CCDB</scp>) – a community resource of plant chromosome numbers. New Phytologist, 2015, 206, 19-26.	3.5	561
8	Rate4Site: an algorithmic tool for the identification of functional regions in proteins by surface mapping of evolutionary determinants within their homologues. Bioinformatics, 2002, 18, S71-S77.	1.8	536
9	ConSurf: Using Evolutionary Data to Raise Testable Hypotheses about Protein Function. Israel Journal of Chemistry, 2013, 53, 199-206.	1.0	459
10	Recently Formed Polyploid Plants Diversify at Lower Rates. Science, 2011, 333, 1257-1257.	6.0	424
11	Comparison of Site-Specific Rate-Inference Methods for Protein Sequences: Empirical Bayesian Methods Are Superior. Molecular Biology and Evolution, 2004, 21, 1781-1791.	3.5	405
12	Model selection may not be a mandatory step for phylogeny reconstruction. Nature Communications, 2019, 10, 934.	5.8	266
13	The global biogeography of polyploid plants. Nature Ecology and Evolution, 2019, 3, 265-273.	3.4	208
14	Whole-genome duplication as a key factor in crop domestication. Nature Plants, 2016, 2, 16115.	4.7	207
15	Computational characterization of B-cell epitopes. Molecular Immunology, 2008, 45, 3477-3489.	1.0	194
16	Probabilistic Models of Chromosome Number Evolution and the Inference of Polyploidy. Systematic Biology, 2010, 59, 132-144.	2.7	190
17	Epitopia: a web-server for predicting B-cell epitopes. BMC Bioinformatics, 2009, 10, 287.	1.2	177
18	ChromEvol: Assessing the Pattern of Chromosome Number Evolution and the Inference of Polyploidy along a Phylogeny. Molecular Biology and Evolution, 2014, 31, 1914-1922.	3.5	154

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19	Body sizes and diversification rates of lizards, snakes, amphisbaenians and the tuatara. <i>Global Ecology and Biogeography</i> , 2016, 25, 187-197.	2.7	154
20	A machine learning approach for predicting CRISPR-Cas9 cleavage efficiencies and patterns underlying its mechanism of action. <i>PLoS Computational Biology</i> , 2017, 13, e1005807.	1.5	147
21	Selecton: a server for detecting evolutionary forces at a single amino-acid site. <i>Bioinformatics</i> , 2005, 21, 2101-2103.	1.8	129
22	A Gamma mixture model better accounts for among site rate heterogeneity. <i>Bioinformatics</i> , 2005, 21, ii151-ii158.	1.8	129
23	Pepitope: epitope mapping from affinity-selected peptides. <i>Bioinformatics</i> , 2007, 23, 3244-3246.	1.8	129
24	A machine-learning approach for predicting B-cell epitopes. <i>Molecular Immunology</i> , 2009, 46, 840-847.	1.0	108
25	Epitope mapping using combinatorial phage-display libraries: a graph-based algorithm. <i>Nucleic Acids Research</i> , 2007, 35, 69-78.	6.5	102
26	Stepwise prediction of conformational discontinuous B-cell epitopes using the Mapitope algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 294-304.	1.5	82
27	Methods for studying polyploid diversification and the dead end hypothesis: a reply to Soltis & Soltis (2014). <i>New Phytologist</i> , 2015, 206, 27-35.	3.5	82
28	Karyotypic Changes through Dysploidy Persist Longer over Evolutionary Time than Polyploid Changes. <i>PLoS ONE</i> , 2014, 9, e85266.	1.1	78
29	Broad phylogenetic analysis of cation/proton antiporters reveals transport determinants. <i>Nature Communications</i> , 2018, 9, 4205.	5.8	74
30	Increased growth in sunflower correlates with reduced defences and altered gene expression in response to biotic and abiotic stress. <i>Molecular Ecology</i> , 2011, 20, 4683-4694.	2.0	68
31	Macroevolutionary synthesis of flowering plant sexual systems. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 898-912.	1.1	68
32	Towards realistic codon models: among site variability and dependency of synonymous and non-synonymous rates. <i>Bioinformatics</i> , 2007, 23, i319-i327.	1.8	60
33	Macroevolutionary Patterns of Flowering Plant Speciation and Extinction. <i>Annual Review of Plant Biology</i> , 2018, 69, 685-706.	8.6	60
34	Interaction among ploidy, breeding system and lineage diversification. <i>New Phytologist</i> , 2019, 224, 1252-1265.	3.5	59
35	The DFNA15 Deafness Mutation Affects POU4F3 Protein Stability, Localization, and Transcriptional Activity. <i>Molecular and Cellular Biology</i> , 2003, 23, 7957-7964.	1.1	57
36	Evolutionary Models Accounting for Layers of Selection in Protein-Coding Genes and their Impact on the Inference of Positive Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 3297-3308.	3.5	54

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37	Sex determination, longevity, and the birth and death of reptilian species. <i>Ecology and Evolution</i> , 2016, 6, 5207-5220.	0.8	47
38	Multispeed genome diploidization and diversification after an ancient allopolyploidization. <i>Molecular Ecology</i> , 2017, 26, 6445-6462.	2.0	44
39	Phylogenetic evidence for cladogenetic polyploidization in land plants. <i>American Journal of Botany</i> , 2016, 103, 1252-1258.	0.8	39
40	Polyploidy and sexual system in angiosperms: Is there an association?. <i>American Journal of Botany</i> , 2016, 103, 1223-1235.	0.8	39
41	The Evolution of Chromosome Numbers: Mechanistic Models and Experimental Approaches. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	38
42	Diocy does not consistently accelerate or slow lineage diversification across multiple genera of angiosperms. <i>New Phytologist</i> , 2016, 209, 1290-1300.	3.5	37
43	An Evolutionary Analysis of Lateral Gene Transfer in Thymidylate Synthase Enzymes. <i>Systematic Biology</i> , 2010, 59, 212-225.	2.7	36
44	Site-Specific Evolutionary Rate Inference: Taking Phylogenetic Uncertainty into Account. <i>Journal of Molecular Evolution</i> , 2005, 60, 345-353.	0.8	34
45	A Likelihood Method for Detecting Trait-Dependent Shifts in the Rate of Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 759-770.	3.5	34
46	An Integrated Model of Phenotypic Trait Changes and Site-Specific Sequence Evolution. <i>Systematic Biology</i> , 2017, 66, 917-933.	2.7	34
47	Meiotic drive shapes rates of karyotype evolution in mammals. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 511-523.	1.1	32
48	Comparative analysis reveals that polyploidy does not decelerate diversification in fish. <i>Journal of Evolutionary Biology</i> , 2014, 27, 391-403.	0.8	31
49	<scp>COVID</scp> â€19 pandemicâ€™related lockdown: response time is more important than its strictness. <i>EMBO Molecular Medicine</i> , 2020, 12, e13171.	3.3	31
50	ModelTeller: Model Selection for Optimal Phylogenetic Reconstruction Using Machine Learning. <i>Molecular Biology and Evolution</i> , 2020, 37, 3338-3352.	3.5	30
51	OneTwoTree: An online tool for phylogeny reconstruction. <i>Molecular Ecology Resources</i> , 2018, 18, 1492-1499.	2.2	29
52	Synonymous site conservation in the HIV-1 genome. <i>BMC Evolutionary Biology</i> , 2013, 13, 164.	3.2	24
53	Harnessing machine learning to guide phylogenetic-tree search algorithms. <i>Nature Communications</i> , 2021, 12, 1983.	5.8	20
54	A Probabilistic Model for Indel Evolution: Differentiating Insertions from Deletions. <i>Molecular Biology and Evolution</i> , 2021, 38, 5769-5781.	3.5	19

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55	CRISPyS: Optimal sgRNA Design for Editing Multiple Members of a Gene Family Using the CRISPR System. <i>Journal of Molecular Biology</i> , 2018, 430, 2184-2195.	2.0	18
56	Regulation of alternative splicing at the single-cell level. <i>Molecular Systems Biology</i> , 2015, 11, 845.	3.2	17
57	Heterogeneity in the rate of molecular sequence evolution substantially impacts the accuracy of detecting shifts in diversification rates. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1620-1639.	1.1	12
58	Model adequacy tests for probabilistic models of chromosome number evolution. <i>New Phytologist</i> , 2021, 229, 3602-3613.	3.5	11
59	The Interplay between Scientific Overlap and Cooperation and the Resulting Gain in Co-Authorship Interactions. <i>PLoS ONE</i> , 2015, 10, e0137856.	1.1	10
60	Phenology and polyploidy in annual <i>Brachypodium</i> species (Poaceae) along the aridity gradient in Israel. <i>Journal of Systematics and Evolution</i> , 2020, 58, 189-199.	1.6	9
61	TraitRateProp: a web server for the detection of trait-dependent evolutionary rate shifts in sequence sites. <i>Nucleic Acids Research</i> , 2017, 45, W260-W264.	6.5	8
62	A Codon Model for Associating Phenotypic Traits with Altered Selective Patterns of Sequence Evolution. <i>Systematic Biology</i> , 2021, 70, 608-622.	2.7	5
63	Panoramic: A package for constructing eukaryotic pan-genomes. <i>Molecular Ecology Resources</i> , 2021, 21, 1393-1403.	2.2	4
64	Bee flowers drive macroevolutionary diversification in long-horned bees. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210533.	1.2	4
65	Mechanisms Underlying Host Range Variation in Flavivirus: From Empirical Knowledge to Predictive Models. <i>Journal of Molecular Evolution</i> , 2021, 89, 329-340.	0.8	3
66	A LASSO-based approach to sample sites for phylogenetic tree search. <i>Bioinformatics</i> , 2022, 38, i118-i124.	1.8	1
67	Using Phylogeny to Decipher Electrogenicity in Cation/Proton Antiporters. <i>Biophysical Journal</i> , 2019, 116, 554a.	0.2	0