

Huw A Ogilvie

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

3,751
citations

758635

12
h-index

752256

20
g-index

30
all docs

30
docs citations

30
times ranked

6524
citing authors

#	ARTICLE	IF	CITATIONS
1	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	1.5	2,484
2	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2101-2114.	3.5	371
3	The peptide-encoding CEP1 gene modulates lateral root and nodule numbers in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2013, 64, 5395-5409.	2.4	182
4	Bayesian Inference of Species Networks from Multilocus Sequence Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 504-517.	3.5	158
5	Computational Performance and Statistical Accuracy of *BEAST and Comparisons with Other Methods. <i>Systematic Biology</i> , 2016, 65, 381-396.	2.7	107
6	Fungal phytopathogens encode functional homologues of plant rapid alkalization factor (RALF) peptides. <i>Molecular Plant Pathology</i> , 2017, 18, 811-824.	2.0	95
7	Diversification of the C-TERMINALLY ENCODED PEPTIDE (CEP) gene family in angiosperms, and evolution of plant-family specific CEP genes. <i>BMC Genomics</i> , 2014, 15, 870.	1.2	63
8	Advances in Computational Methods for Phylogenetic Networks in the Presence of Hybridization. <i>Computational Biology</i> , 2019, , 317-360.	0.1	55
9	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021, 31, 635-644.	2.4	39
10	CEPâ€“CEPR1 signalling inhibits the sucrose-dependent enhancement of lateral root growth. <i>Journal of Experimental Botany</i> , 2019, 70, 3955-3967.	2.4	37
11	microRNA profiling of root tissues and root forming explant cultures in <i>Medicago truncatula</i> . <i>Planta</i> , 2013, 238, 91-105.	1.6	30
12	A divide-and-conquer method for scalable phylogenetic network inference from multilocus data. <i>Bioinformatics</i> , 2019, 35, i370-i378.	1.8	16
13	Validation and description of two new north-western Australian Rainbow skinks with multispecies coalescent methods and morphology. <i>PeerJ</i> , 2017, 5, e3724.	0.9	11
14	Maximum Parsimony Inference of Phylogenetic Networks in the Presence of Polyploid Complexes. <i>Systematic Biology</i> , 2022, 71, 706-720.	2.7	9
15	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales. <i>Systematic Biology</i> , 2021, 71, 208-220.	2.7	9
16	Phylogenomic assessment of the role of hybridization and introgression in trait evolution. <i>PLoS Genetics</i> , 2021, 17, e1009701.	1.5	8
17	Practical Speedup of Bayesian Inference of Species Phylogenies by Restricting the Space of Gene Trees. <i>Molecular Biology and Evolution</i> , 2020, 37, 1809-1818.	3.5	4
18	Variational inference using approximate likelihood under the coalescent with recombination. <i>Genome Research</i> , 2021, 31, 2107-2119.	2.4	4

#	ARTICLE	IF	CITATIONS
19	Phylovar: toward scalable phylogeny-aware inference of single-nucleotide variations from single-cell DNA sequencing data. <i>Bioinformatics</i> , 2022, 38, i195-i202.	1.8	4
20	Rosette core fungal resistance in <i>Arabidopsis thaliana</i> . <i>Planta</i> , 2019, 250, 1941-1953.	1.6	2
21	Annotation-free delineation of prokaryotic homology groups. <i>PLoS Computational Biology</i> , 2022, 18, e1010216.	1.5	0