Huw A Ogilvie

List of Publications by Year
in descending order

21 papers	3,751 citations	759233 12 h-index	752698 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. PLoS Computational Biology, 2019, 15, e1006650.	3.2	2,484
2	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. Molecular Biology and Evolution, 2017, 34, 2101-2114.	8.9	371
3	The peptide-encoding CEP1 gene modulates lateral root and nodule numbers in Medicago truncatula. Journal of Experimental Botany, 2013, 64, 5395-5409.	4.8	182
4	Bayesian Inference of Species Networks from Multilocus Sequence Data. Molecular Biology and Evolution, 2018, 35, 504-517.	8.9	158
5	Computational Performance and Statistical Accuracy of *BEAST and Comparisons with Other Methods. Systematic Biology, 2016, 65, 381-396.	5.6	107
6	Fungal phytopathogens encode functional homologues of plant rapid alkalinization factor (RALF) peptides. Molecular Plant Pathology, 2017, 18, 811-824.	4.2	95
7	Diversification of the C-TERMINALLY ENCODED PEPTIDE (CEP) gene family in angiosperms, and evolution of plant-family specific CEP genes. BMC Genomics, 2014, 15, 870.	2.8	63
8	Advances in Computational Methods for Phylogenetic Networks in the Presence of Hybridization. Computational Biology, 2019, , 317-360.	0.2	55
9	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. Genome Research, 2021, 31, 635-644.	5.5	39
10	CEP–CEPR1 signalling inhibits the sucrose-dependent enhancement of lateral root growth. Journal of Experimental Botany, 2019, 70, 3955-3967.	4.8	37
11	microRNA profiling of root tissues and root forming explant cultures in Medicago truncatula. Planta, 2013, 238, 91-105.	3.2	30
12	A divide-and-conquer method for scalable phylogenetic network inference from multilocus data. Bioinformatics, 2019, 35, i370-i378.	4.1	16
13	Validation and description of two new north-western Australian Rainbow skinks with multispecies coalescent methods and morphology. PeerJ, 2017, 5, e3724.	2.0	11
14	Maximum Parsimony Inference of Phylogenetic Networks in the Presence of Polyploid Complexes. Systematic Biology, 2022, 71, 706-720.	5.6	9
15	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales. Systematic Biology, 2021, 71, 208-220.	5.6	9
16	Phylogenomic assessment of the role of hybridization and introgression in trait evolution. PLoS Genetics, 2021, 17, e1009701.	3.5	8
17	Practical Speedup of Bayesian Inference of Species Phylogenies by Restricting the Space of Gene Trees. Molecular Biology and Evolution, 2020, 37, 1809-1818.	8.9	4
18	Variational inference using approximate likelihood under the coalescent with recombination. Genome Research, 2021, 31, 2107-2119.	5.5	4

#	Article	IF	Citations
19	Phylovar: toward scalable phylogeny-aware inference of single-nucleotide variations from single-cell DNA sequencing data. Bioinformatics, 2022, 38, i195-i202.	4.1	4
20	Rosette core fungal resistance in Arabidopsis thaliana. Planta, 2019, 250, 1941-1953.	3.2	2
21	Annotation-free delineation of prokaryotic homology groups. PLoS Computational Biology, 2022, 18, e1010216.	3.2	0