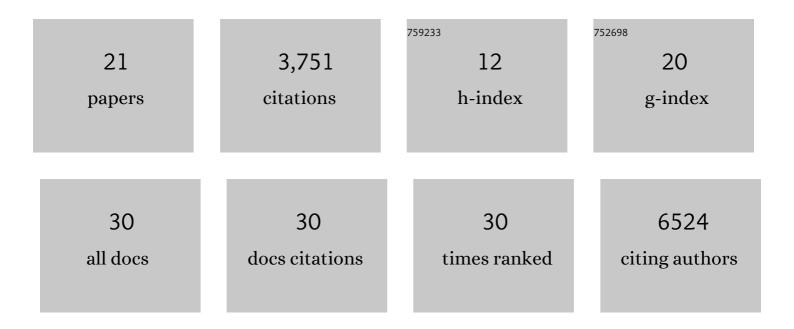
Huw A Ogilvie

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7942160/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Maximum Parsimony Inference of Phylogenetic Networks in the Presence of Polyploid Complexes. Systematic Biology, 2022, 71, 706-720.	5.6	9
2	Phylovar: toward scalable phylogeny-aware inference of single-nucleotide variations from single-cell DNA sequencing data. Bioinformatics, 2022, 38, i195-i202.	4.1	4
3	Annotation-free delineation of prokaryotic homology groups. PLoS Computational Biology, 2022, 18, e1010216.	3.2	Ο
4	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. Genome Research, 2021, 31, 635-644.	5.5	39
5	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales. Systematic Biology, 2021, 71, 208-220.	5.6	9
6	Phylogenomic assessment of the role of hybridization and introgression in trait evolution. PLoS Genetics, 2021, 17, e1009701.	3.5	8
7	Variational inference using approximate likelihood under the coalescent with recombination. Genome Research, 2021, 31, 2107-2119.	5.5	4
8	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
9	A divide-and-conquer method for scalable phylogenetic network inference from multilocus data. Bioinformatics, 2019, 35, i370-i378.	4.1	16
10	Rosette core fungal resistance in Arabidopsis thaliana. Planta, 2019, 250, 1941-1953.	3.2	2
11	CEP–CEPR1 signalling inhibits the sucrose-dependent enhancement of lateral root growth. Journal of Experimental Botany, 2019, 70, 3955-3967.	4.8	37
12	Advances in Computational Methods for Phylogenetic Networks in the Presence of Hybridization. Computational Biology, 2019, , 317-360.	0.2	55
13	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. PLoS Computational Biology, 2019, 15, e1006650.	3.2	2,484
14	Bayesian Inference of Species Networks from Multilocus Sequence Data. Molecular Biology and Evolution, 2018, 35, 504-517.	8.9	158
15	Fungal phytopathogens encode functional homologues of plant rapid alkalinization factor (RALF) peptides. Molecular Plant Pathology, 2017, 18, 811-824.	4.2	95
16	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. Molecular Biology and Evolution, 2017, 34, 2101-2114.	8.9	371
17	Validation and description of two new north-western Australian Rainbow skinks with multispecies coalescent methods and morphology. PeerJ, 2017, 5, e3724.	2.0	11
18	Computational Performance and Statistical Accuracy of *BEAST and Comparisons with Other Methods. Systematic Biology, 2016, 65, 381-396.	5.6	107

Huw A Ogilvie

#	Article	IF	CITATIONS
19	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
20	microRNA profiling of root tissues and root forming explant cultures in Medicago truncatula. Planta, 2013, 238, 91-105.	3.2	30
21	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