

# Norman J Wickett

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64  
papers

5,869  
citations

30  
h-index

68  
g-index

68  
ext. papers

7,997  
ext. citations

6.8  
avg, IF

6.42  
L-index

#	Paper	IF	Citations
64	Ancestral polyploidy in seed plants and angiosperms. <i>Nature</i> , <b>2011</b> , 473, 97-100	50.4	1362
63	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E4859-68	11.5	835
62	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , <b>2019</b> , 574, 679-685	50.4	529
61	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , <b>2014</b> , 3, 17	7.6	403
60	FLOWERING LOCUS T duplication coordinates reproductive and vegetative growth in perennial poplar. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 10756-61	11.5	306
59	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , <b>2012</b> , 13, R3	18.3	266
58	HybPiper: Extracting coding sequence and introns for phylogenetics from high-throughput sequencing reads using target enrichment. <i>Applications in Plant Sciences</i> , <b>2016</b> , 4, 1600016	2.3	204
57	Mechanisms of functional and physical genome reduction in photosynthetic and nonphotosynthetic parasitic plants of the broomrape family. <i>Plant Cell</i> , <b>2013</b> , 25, 3711-25	11.6	182
56	Moss diversity: A molecular phylogenetic analysis of genera. <i>Phytotaxa</i> , <b>2010</b> , 9, 175	0.7	141
55	A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-Medoids Clustering. <i>Systematic Biology</i> , <b>2019</b> , 68, 594-606	8.4	139
54	Functional gene losses occur with minimal size reduction in the plastid genome of the parasitic liverwort <i>Aneura mirabilis</i> . <i>Molecular Biology and Evolution</i> , <b>2008</b> , 25, 393-401	8.3	97
53	De novo characterization of the gametophyte transcriptome in bracken fern, <i>Pteridium aquilinum</i> . <i>BMC Genomics</i> , <b>2011</b> , 12, 99	4.5	96
52	Resolution of the ordinal phylogeny of mosses using targeted exons from organellar and nuclear genomes. <i>Nature Communications</i> , <b>2019</b> , 10, 1485	17.4	80
51	The Parasitic Plant Genome Project: New Tools for Understanding the Biology of Orobanche and Striga. <i>Weed Science</i> , <b>2012</b> , 60, 295-306	2	76
50	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. <i>PLoS ONE</i> , <b>2016</b> , 11, e0146062	3.7	76
49	Bridging the micro- and macroevolutionary levels in phylogenomics: Hyb-Seq solves relationships from populations to species and above. <i>New Phytologist</i> , <b>2018</b> , 220, 636-650	9.8	69
48	Phylogenomic analysis of transcriptome data elucidates co-occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , <b>2012</b> , 99, 397-406	2.7	68

47	Transcriptomes of the parasitic plant family Orobanchaceae reveal surprising conservation of chlorophyll synthesis. <i>Current Biology</i> , <b>2011</b> , 21, 2098-104	6.3	59
46	Taxonomy and Classification <b>2013</b> , 19-101		58
45	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). <i>GigaScience</i> , <b>2019</b> , 8,	7.6	52
44	Functional genomics of a generalist parasitic plant: laser microdissection of host-parasite interface reveals host-specific patterns of parasite gene expression. <i>BMC Plant Biology</i> , <b>2013</b> , 13, 9	5.3	46
43	Hyb-Seq for Flowering Plant Systematics. <i>Trends in Plant Science</i> , <b>2019</b> , 24, 887-891	13.1	39
42	Evolution of a horizontally acquired legume gene, albumin 1, in the parasitic plant <i>Phelipanche aegyptiaca</i> and related species. <i>BMC Evolutionary Biology</i> , <b>2013</b> , 13, 48	3	37
41	Allele phasing has minimal impact on phylogenetic reconstruction from targeted nuclear gene sequences in a case study of <i>Artocarpus</i> . <i>American Journal of Botany</i> , <b>2018</b> , 105, 404-416	2.7	36
40	Phylogenetic significance of the rpoA loss in the chloroplast genome of mosses. <i>Taxon</i> , <b>2005</b> , 54, 353-360.8		36
39	Phylogenomic delineation of <i>Physcomitrium</i> (Bryophyta: Funariaceae) based on targeted sequencing of nuclear exons and their flanking regions rejects the retention of <i>Physcomitrella</i> , <i>Physcomitridium</i> and <i>Aphanorrhagma</i> . <i>Journal of Systematics and Evolution</i> , <b>2019</b> , 57, 404-417	2.9	35
38	Signal, Uncertainty, and Conflict in Phylogenomic Data for a Diverse Lineage of Microbial Eukaryotes (Diatoms, Bacillariophyta). <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 80-93	8.3	33
37	Origin and relationships of the myco-heterotrophic liverwort <i>Cryptothallus mirabilis</i> Malmb. (Metzgeriales, Marchantiophyta). <i>Botanical Journal of the Linnean Society</i> , <b>2008</b> , 156, 1-12	2.2	32
36	Distribution and phylogenetic significance of the 71-kb inversion in the plastid genome in Funariidae (Bryophyta). <i>Annals of Botany</i> , <b>2007</b> , 99, 747-53	4.1	32
35	Deep sequencing of <i>Ptilidium</i> (Ptilidiaceae) suggests evolutionary stasis in liverwort plastid genome structure. <i>Plant Ecology and Evolution</i> , <b>2011</b> , 144, 29-43	1.6	30
34	Phylogenomics reveals an extensive history of genome duplication in diatoms (Bacillariophyta). <i>American Journal of Botany</i> , <b>2018</b> , 105, 330-347	2.7	27
33	Evolutionary dynamism in bryophytes: Phylogenomic inferences confirm rapid radiation in the moss family Funariaceae. <i>Molecular Phylogenetics and Evolution</i> , <b>2018</b> , 120, 240-247	4.1	26
32	A phylotranscriptomic analysis of gene family expansion and evolution in the largest order of pleurocarpous mosses (Hypnales, Bryophyta). <i>Molecular Phylogenetics and Evolution</i> , <b>2016</b> , 98, 29-40	4.1	24
31	Low-coverage, whole-genome sequencing of <i>Artocarpus camansi</i> (Moraceae) for phylogenetic marker development and gene discovery. <i>Applications in Plant Sciences</i> , <b>2016</b> , 4, 1600017	2.3	24
30	Application of qRT-PCR and RNA-Seq analysis for the identification of housekeeping genes useful for normalization of gene expression values during <i>Striga hermonthica</i> development. <i>Molecular Biology Reports</i> , <b>2013</b> , 40, 3395-407	2.8	22

29	Distribution and evolution of pseudogenes, gene losses, and a gene rearrangement in the plastid genome of the nonphotosynthetic liverwort, <i>Aneura mirabilis</i> (Metzgeriales, Jungermanniopsida). <i>Journal of Molecular Evolution</i> , <b>2008</b> , 67, 111-22	3.1	22
28	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. <i>Annual Review of Plant Biology</i> , <b>2020</b> , 71, 741-765	30.7	22
27	A Comprehensive Phylogenomic Platform for Exploring the Angiosperm Tree of Life. <i>Systematic Biology</i> , <b>2021</b> ,	8.4	21
26	New insights in the evolution of the liverwort family Aneuraceae (Metzgeriales, Marchantiophyta), with emphasis on the genus <i>Lobatiriccardia</i> . <i>Taxon</i> , <b>2010</b> , 59, 1424-1440	0.8	20
25	The TvPirin gene is necessary for haustorium development in the parasitic plant <i>Triphysaria versicolor</i> . <i>Plant Physiology</i> , <b>2012</b> , 158, 1046-53	6.6	19
24	Characterization of the basal angiosperm <i>Aristolochia fimbriata</i> : a potential experimental system for genetic studies. <i>BMC Plant Biology</i> , <b>2013</b> , 13, 13	5.3	17
23	The plastid genome of the hornwort <i>Nothoceros aenigmaticus</i> (Dendrocerotaceae): phylogenetic signal in inverted repeat expansion, pseudogenization, and intron gain. <i>American Journal of Botany</i> , <b>2013</b> , 100, 467-77	2.7	16
22	Recurrent Loss, Horizontal Transfer, and the Obscure Origins of Mitochondrial Introns in Diatoms (Bacillariophyta). <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 1504-1515	3.9	15
21	A molecular phylogeny of the Sematophyllaceae s.l. (Hypnales) based on plastid, mitochondrial and nuclear markers, and its taxonomic implications. <i>Taxon</i> , <b>2017</b> , 66, 811-831	0.8	15
20	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	15
19	Transcriptomic Insights into the Life History of Bolidophytes, the Sister Lineage to Diatoms. <i>Journal of Phycology</i> , <b>2014</b> , 50, 977-83	3	13
18	Frequent pseudogenization and loss of the plastid-encoded sulfate-transport gene <i>cysA</i> throughout the evolution of liverworts. <i>American Journal of Botany</i> , <b>2011</b> , 98, 1263-75	2.7	13
17	Generation of a large-scale genomic resource for functional and comparative genomics in <i>Liriodendron tulipifera</i> L.. <i>Tree Genetics and Genomes</i> , <b>2011</b> , 7, 941-954	2.1	10
16	Parasitic Plants & Striga and Phelipanche Dependent upon Exogenous Strigolactones for Germination Have Retained Genes for Strigolactone Biosynthesis. <i>American Journal of Plant Sciences</i> , <b>2015</b> , 06, 1151-1166	0.5	9
15	Paralogs and off-target sequences improve phylogenetic resolution in a densely-sampled study of the breadfruit genus ( <i>Artocarpus</i> , Moraceae). <i>Systematic Biology</i> , <b>2020</b> ,	8.4	9
14	Examining the efficacy of a genotyping-by-sequencing technique for population genetic analysis of the mushroom <i>Laccaria bicolor</i> and evaluating whether a reference genome is necessary to assess homology. <i>Mycologia</i> , <b>2015</b> , 107, 217-26	2.4	7
13	A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-medoids Clustering		7
12	A transcriptome screen for positive selection in domesticated breadfruit and its wild relatives ( <i>Artocarpus</i> spp.). <i>American Journal of Botany</i> , <b>2018</b> , 105, 915-926	2.7	6

11	A Comprehensive Phylogenomic Platform for Exploring the Angiosperm Tree of Life		6
10	The uncharacterized gene contributes to vessel element dimensions in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 5059-5066	11.5	5
9	The <i>Ceratodon purpureus</i> genome uncovers structurally complex, gene rich sex chromosomes		5
8	Phylogeny, host use, and diversification in the moth family Momphidae (Lepidoptera: Gelechioidea). <i>PLoS ONE</i> , <b>2019</b> , 14, e0207833	3.7	4
7	Molecular, morphological, and biogeographic perspectives on the classification of Acrobolboideae (Acrobolbaceae, Marchantiophyta). <i>Phytotaxa</i> , <b>2017</b> , 319, 56	0.7	4
6	Exploring Angiosperms353: An open, community toolkit for collaborative phylogenomic research on flowering plants. <i>American Journal of Botany</i> , <b>2021</b> , 108, 1059-1065	2.7	4
5	Elucidating the Evolutionary History of <i>Oenothera</i> Sect. <i>Pachylophus</i> (Onagraceae): A Phylogenomic Approach. <i>Systematic Botany</i> , <b>2021</b> , 46, 799-811	0.7	2
4	Exploring Angiosperms353: Developing and applying a universal toolkit for flowering plant phylogenomics. <i>Applications in Plant Sciences</i> , <b>2021</b> , 9,	2.3	2
3	Incomplete reproductive isolation and low genetic differentiation despite floral divergence across varying geographic scales in <i>Castilleja</i> . <i>American Journal of Botany</i> , <b>2021</b> , 108, 1270-1288	2.7	2
2	Methods for exploring the plant tree of life. <i>Applications in Plant Sciences</i> , <b>2018</b> , 6, e1039	2.3	1
1	Differential gene expression associated with a floral scent polymorphism in the evening primrose <i>Oenothera harringtonii</i> (Onagraceae).. <i>BMC Genomics</i> , <b>2022</b> , 23, 124	4.5	1