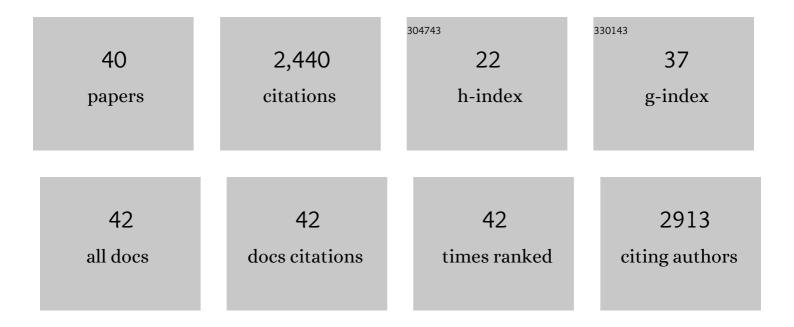
## **Patrick A Reeves**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2390170/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Disintegration of the Scrophulariaceae. American Journal of Botany, 2001, 88, 348-361.	1.7	523
2	Microstructural Changes in Noncoding Chloroplast DNA: Interpretation, Evolution, and Utility of Indels and Inversions in Basal Angiosperm Phylogenetic Inference. International Journal of Plant Sciences, 2000, 161, S83-S96.	1.3	225
3	Rapid speciation and the evolution of hummingbird pollination in neotropical <i>Costus</i> subgenus <i>Costus</i> (Costaceae): evidence from nrDNA ITS and ETS sequences. American Journal of Botany, 2005, 92, 1899-1910.	1.7	204
4	Evolutionary Conservation of the FLOWERING LOCUS C-Mediated Vernalization Response: Evidence From the Sugar Beet (Beta vulgaris). Genetics, 2007, 176, 295-307.	2.9	142
5	Phylogeny inLabiatae s. l., inferred from cpDNA sequences. Plant Systematics and Evolution, 1998, 209, 265-274.	0.9	128
6	Genetic diversity and population structure in Malus sieversii, a wild progenitor species of domesticated apple. Tree Genetics and Genomes, 2009, 5, 339-347.	1.6	117
7	Inference of higher-order conifer relationships from a multi-locus plastid data setThis paper is one of a selection of papers published in the Special Issue on Systematics Research Botany, 2008, 86, 658-669.	1.0	116
8	Germins: A diverse protein family important for crop improvement. Plant Science, 2009, 177, 499-510.	3.6	115
9	H igherâ€level systematics of A canthaceae determined by chloroplast DNA sequences. American Journal of Botany, 1995, 82, 266-275.	1.7	82
10	Inference of higher-order relationships in the cycads from a large chloroplast data set. Molecular Phylogenetics and Evolution, 2003, 29, 350-359.	2.7	77
11	Species Delimitation under the General Lineage Concept: An Empirical Example Using Wild North American Hops (Cannabaceae: Humulus lupulus). Systematic Biology, 2011, 60, 45-59.	5.6	76
12	Evolution of novel morphological and reproductive traits in a clade containing Antirrhinum majus (Scrophulariaceae). American Journal of Botany, 1998, 85, 1047-1056.	1.7	66
13	Implications ofrbcL sequence data for higher order relationships of theLoasaceae and the anomalous aquatic plantHydrostachys (Hydrostachyaceae). Plant Systematics and Evolution, 1995, 194, 25-37.	0.9	54
14	Accurate Inference of Subtle Population Structure (and Other Genetic Discontinuities) Using Principal Coordinates. PLoS ONE, 2009, 4, e4269.	2.5	54
15	Evolution of the TCP Gene Family in Asteridae: Cladistic and Network Approaches to Understanding Regulatory Gene Family Diversification and Its Impact on Morphological Evolution. Molecular Biology and Evolution, 2003, 20, 1997-2009.	8.9	51
16	Retention of agronomically important variation in germplasm core collections: implications for allele mining. Theoretical and Applied Genetics, 2012, 124, 1155-1171.	3.6	48
17	Exploring the fate of mRNA in aging seeds: protection, destruction, or slow decay?. Journal of Experimental Botany, 2018, 69, 4309-4321.	4.8	43
18	Molecular Evidence for Two Domestication Events in the Pea Crop. Genes, 2018, 9, 535.	2.4	42

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19	Genetic Diversity and Disease Resistance of Wild Malus orientalis from Turkey and Southern Russia. Journal of the American Society for Horticultural Science, 2008, 133, 383-389.	1.0	35
20	The utility of aged seeds in DNA banks. Seed Science Research, 2006, 16, 169-178.	1.7	31
21	Distinguishing Terminal Monophyletic Groups from Reticulate Taxa: Performance of Phenetic, Tree-Based, and Network Procedures. Systematic Biology, 2007, 56, 302-320.	5.6	30
22	Higher-Level Systematics of Acanthaceae Determined by Chloroplast DNA Sequences. American Journal of Botany, 1995, 82, 266.	1.7	24
23	Diversity Captured in the USDA-ARS National Plant Germplasm System Apple Core Collection. Journal of the American Society for Horticultural Science, 2013, 138, 375-381.	1.0	21
24	Genetic diversity and biogeographic determinants of population structure in Araucaria angustifolia (Bert.) O. Ktze. Conservation Genetics, 2020, 21, 217-229.	1.5	16
25	Integrating Genomic and Phenomic Approaches to Support Plant Genetic Resources Conservation and Use. Plants, 2021, 10, 2260.	3.5	15
26	Germination Syndromes and Their Relevance to Rangeland Seeding Strategies in the Intermountain Western United States. Rangeland Ecology and Management, 2020, 73, 334-341.	2.3	13
27	Geography of Genetic Structure in Barley Wild Relative Hordeum vulgare subsp. spontaneum in Jordan. PLoS ONE, 2016, 11, e0160745.	2.5	13
28	Slope and Aspect Effects on Seedbed Microclimate and Germination Timing of Fall-Planted Seeds. Rangeland Ecology and Management, 2021, 75, 58-67.	2.3	11
29	Hydrothermal Germination Models: Assessment of the Wetâ€Thermal Approximation of Potential Field Response. Crop Science, 2018, 58, 2042-2049.	1.8	10
30	Phylogeography of the wild and cultivated stimulant plant qat ( Catha edulis , Celastraceae) in areas of historical cultivation. American Journal of Botany, 2017, 104, 538-549.	1.7	9
31	Genetic structure and gene flow in Beta vulgaris subspecies maritima along the Atlantic coast of France. Genetic Resources and Crop Evolution, 2014, 61, 651-662.	1.6	8
32	Capturing haplotypes in germplasm core collections using bioinformatics. Genetic Resources and Crop Evolution, 2017, 64, 1821-1828.	1.6	8
33	Effect of a Geographic Barrier on Adaptation in the Dwarf Sunflower ( <i>Helianthus) Tj ETQq1 1 0.784314 rgBT</i>	/Overlock	10 <sub>6</sub> 7f 50 182
34	Biases induced by using geography and environment to guide ex situ conservation. Conservation Genetics, 2018, 19, 1281-1293.	1.5	6
35	Bioinformatic Extraction of Functional Genetic Diversity from Heterogeneous Germplasm Collections for Crop Improvement. Agronomy, 2020, 10, 593.	3.0	6
36	Genetic diversity in the USDA Limnanthes germplasm collection assessed by simple sequence repeats. Plant Genetic Resources: Characterisation and Utilisation, 2009, 7, 33-41.	0.8	4

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#	Article	IF	CITATIONS
37	wolfPAC. Applied Bioinformatics, 2005, 4, 61-64.	1.6	3
38	Clonal Diversity, Cultivar Traits, Geographic Dispersal, and the Ethnotaxonomy of Cultivated Qat (Catha edulis, Celastraceae). Economic Botany, 2020, 74, 273-291.	1.7	0
39	A pan-genome data structure induced by pooled sequencing facilitates variant mining in heterogeneous germplasm. Molecular Breeding, 2022, 42, .	2.1	Ο
40	Postplanting Microclimate, Germination, and Emergence of Perennial Grasses in Wyoming Big Sagebrush Steppe. Rangeland Ecology and Management, 2022, 84, 63-74.	2.3	0