

Lisa Pokorny

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

5,391
citations

270111

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41
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43
all docs

43
docs citations

43
times ranked

6410
citing authors

#	ARTICLE	IF	CITATIONS
1	A Comprehensive Phylogenomic Platform for Exploring the Angiosperm Tree of Life. <i>Systematic Biology</i> , 2022, 71, 301-319.	2.7	107
2	Taming the beast: a revised classification of Cortinariaceae based on genomic data. <i>Fungal Diversity</i> , 2022, 112, 89-170.	4.7	24
3	Erratic spatiotemporal vegetation growth anomalies drive population outbreaks in a trans-Saharan insect migrant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2121249119.	3.3	9
4	Resolving generic limits in Cyperaceae tribe Abildgaardieae using targeted sequencing. <i>Botanical Journal of the Linnean Society</i> , 2021, 196, 163-187.	0.8	10
5	Targeted sequencing supports morphology and embryo features in resolving the classification of Cyperaceae tribe Fuireneae s.l.. <i>Journal of Systematics and Evolution</i> , 2021, 59, 809-832.	1.6	10
6	Lineage-specific vs. universal: A comparison of the Compositae1061 and Angiosperms353 enrichment panels in the sunflower family. <i>Applications in Plant Sciences</i> , 2021, 9, .	0.8	19
7	A new classification of Cyperaceae (Poales) supported by phylogenomic data. <i>Journal of Systematics and Evolution</i> , 2021, 59, 852-895.	1.6	46
8	A comprehensive phylogenomic study of the monocot order Commelinales, with a new classification of Commelinaceae. <i>American Journal of Botany</i> , 2021, 108, 1066-1086.	0.8	16
9	Settling a family feud: a high-level phylogenomic framework for the Gentianales based on 353 nuclear genes and partial plastomes. <i>American Journal of Botany</i> , 2021, 108, 1143-1165.	0.8	34
10	A nuclear phylogenomic study of the angiosperm order Myrtales, exploring the potential and limitations of the universal Angiosperms353 probe set. <i>American Journal of Botany</i> , 2021, 108, 1087-1111.	0.8	53
11	Exploring Angiosperms353: Developing and applying a universal toolkit for flowering plant phylogenomics. <i>Applications in Plant Sciences</i> , 2021, 9, .	0.8	13
12	Exploring Angiosperms353: An open, community toolkit for collaborative phylogenomic research on flowering plants. <i>American Journal of Botany</i> , 2021, 108, 1059-1065.	0.8	36
13	Comprehending Cornales: phylogenetic reconstruction of the order using the Angiosperms353 probe set. <i>American Journal of Botany</i> , 2021, 108, 1112-1121.	0.8	23
14	Ecological and geological processes impacting speciation modes drive the formation of wide-range disjunctions within tribe Putorieae (Rubiaceae). <i>Journal of Systematics and Evolution</i> , 2021, 59, 915-934.	1.6	12
15	Organellomic data sets confirm a cryptic consensus on (unrooted) land-plant relationships and provide new insights into bryophyte molecular evolution. <i>American Journal of Botany</i> , 2020, 107, 91-115.	0.8	38
16	Editorial: Phylogenomic Approaches to Deal With Particularly Challenging Plant Lineages. <i>Frontiers in Plant Science</i> , 2020, 11, 591762.	1.7	10
17	Reconstructing the Complex Evolutionary History of the Papuasian Schefflera Radiation Through Herbariomics. <i>Frontiers in Plant Science</i> , 2020, 11, 258.	1.7	41
18	Strategies for reducing per-sample costs in target capture sequencing for phylogenomics and population genomics in plants. <i>Applications in Plant Sciences</i> , 2020, 8, e11337.	0.8	63

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19	A Target Capture-Based Method to Estimate Ploidy From Herbarium Specimens. <i>Frontiers in Plant Science</i> , 2019, 10, 937.	1.7	53
20	A customized nuclear target enrichment approach for developing a phylogenomic baseline for <i>Dioscorea</i> yams (Dioscoreaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e11254.	0.8	49
21	Hyb-Seq for Flowering Plant Systematics. <i>Trends in Plant Science</i> , 2019, 24, 887-891.	4.3	98
22	Factors Affecting Targeted Sequencing of 353 Nuclear Genes From Herbarium Specimens Spanning the Diversity of Angiosperms. <i>Frontiers in Plant Science</i> , 2019, 10, 1102.	1.7	124
23	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	13.7	1,162
24	A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-Medoids Clustering. <i>Systematic Biology</i> , 2019, 68, 594-606.	2.7	371
25	Tackling Rapid Radiations With Targeted Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1655.	1.7	106
26	A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , 2018, 105, 614-622.	0.8	38
27	Bridging the micro- and macroevolutionary levels in phylogenomics: Hyb-Seq solves relationships from populations to species and above. <i>New Phytologist</i> , 2018, 220, 636-650.	3.5	152
28	Geographic barriers and Pleistocene climate change shaped patterns of genetic variation in the Eastern African montane biodiversity hotspot. <i>Scientific Reports</i> , 2017, 7, 45749.	1.6	58
29	Living on the edge: timing of Rand Flora disjunctions congruent with ongoing aridification in Africa. <i>Frontiers in Genetics</i> , 2015, 6, 154.	1.1	90
30	Ancient vicariance and climate-driven extinction explain continental-wide disjunctions in Africa: the case of the Rand Flora genus <i>Canarina</i> (Campanulaceae). <i>Molecular Ecology</i> , 2015, 24, 1335-1354.	2.0	58
31	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <i>American Journal of Botany</i> , 2015, 102, 1089-1107.	0.8	157
32	Algal ancestor of land plants was preadapted for symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13390-13395.	3.3	292
33	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	3.3	582
34	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> , 2014, 111, E4859-68.	3.3	1,123
35	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6672-6677.	3.3	146
36	Disentangling knots of rapid evolution: origin and diversification of the moss order Hypnales. <i>Journal of Bryology</i> , 2012, 34, 187-211.	0.4	60

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37	Molecular evolution and diversification of the moss family Daltoniaceae (Hookeriales, Bryophyta) with emphasis on the unravelling of the phylogeny of Distichophyllum and its allies. Botanical Journal of the Linnean Society, 2012, 170, 157-175.	0.8	11
38	Phylogenetic analyses of morphological evolution in the gametophyte and sporophyte generations of the moss order Hookeriales (Bryopsida). Molecular Phylogenetics and Evolution, 2012, 63, 351-364.	1.2	11
39	Phylogeographic Patterns in Two Southern Hemisphere Species of Calypstrochaeta (Daltoniaceae, Tj ETQq1 1 0.784314 rgBT/Overloc 0.2 23	0.2	23
40	Genetic structure and genealogy in the Sphagnum subsecundum complex (Sphagnaceae: Bryophyta). Molecular Phylogenetics and Evolution, 2008, 49, 304-317.	1.2	32
41	A new Cheilolejeunea Marchantiopsida: Lejeuneaceae from montane forests in New Zealand. Journal of Bryology, 2003, 25, 169-174.	0.4	13