

Claude W Depamphilis

List of Publications by Year in descending order

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88
papers

18,812
citations

30068

54
h-index

49904

87
g-index

94
all docs

94
docs citations

94
times ranked

15311
citing authors

#	ARTICLE	IF	CITATIONS
1	Ancestral polyploidy in seed plants and angiosperms. <i>Nature</i> , 2011, 473, 97-100.	27.8	1,862
2	GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. <i>Genome Biology</i> , 2020, 21, 241.	8.8	1,538
3	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.	7.1	1,123
4	Polyploidy and angiosperm diversification. <i>American Journal of Botany</i> , 2009, 96, 336-348.	1.7	1,031
5	Analysis of 81 genes from 64 plastid genomes resolves relationships in angiosperms and identifies genome-scale evolutionary patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19369-19374.	7.1	1,016
6	The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	27.8	964
7	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. <i>Science</i> , 2013, 342, 1241089.	12.6	743
8	Widespread genome duplications throughout the history of flowering plants. <i>Genome Research</i> , 2006, 16, 738-749.	5.5	664
9	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	6.4	582
10	The butterfly plant arms-race escalated by gene and genome duplications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8362-8366.	7.1	458
11	The evolution of parasitism in plants. <i>Trends in Plant Science</i> , 2010, 15, 227-235.	8.8	417
12	Methods for Obtaining and Analyzing Whole Chloroplast Genome Sequences. <i>Methods in Enzymology</i> , 2005, 395, 348-384.	1.0	410
13	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
14	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , 2012, 13, R3.	9.6	389
15	Patterns of gene duplication in the plant SKP1 gene family in angiosperms: evidence for multiple mechanisms of rapid gene birth. <i>Plant Journal</i> , 2007, 50, 873-885.	5.7	361
16	The Evolution of the SEPALLATA Subfamily of MADS-Box Genes Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY850178, AY850179, AY850180, AY850181, AY850182, AY850183, AY850184, AY850185, AY850186.. <i>Genetics</i> , 2005, 169, 2209-2223.	2.9	343
17	Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	9.6	329
18	Horizontal Transfer of Entire Genomes via Mitochondrial Fusion in the Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1468-1473.	12.6	322

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19	Identification of shared single copy nuclear genes in Arabidopsis, Populus, Vitis and Oryza and their phylogenetic utility across various taxonomic levels. BMC Evolutionary Biology, 2010, 10, 61.	3.2	304
20	MicroRNAs from the parasitic plant Cuscuta campestris target host messenger RNAs. Nature, 2018, 553, 82-85.	27.8	303
21	Expression Pattern Shifts Following Duplication Indicative of Subfunctionalization and Neofunctionalization in Regulatory Genes of Arabidopsis. Molecular Biology and Evolution, 2006, 23, 469-478.	8.9	273
22	Identifying the Basal Angiosperm Node in Chloroplast Genome Phylogenies: Sampling One's Way Out of the Felsenstein Zone. Molecular Biology and Evolution, 2005, 22, 1948-1963.	8.9	242
23	Genomic-scale exchange of mRNA between a parasitic plant and its hosts. Science, 2014, 345, 808-811.	12.6	234
24	Mitochondrial DNA suggests at least 11 origins of parasitism in angiosperms and reveals genomic chimerism in parasitic plants. BMC Evolutionary Biology, 2007, 7, 248.	3.2	205
25	The Evolution of Parasitism in Scrophulariaceae/Orobanchaceae: Plastid Gene Sequences Refute an Evolutionary Transition Series. Annals of the Missouri Botanical Garden, 1999, 86, 876.	1.3	187
26	Mechanistic model of evolutionary rate variation en route to a nonphotosynthetic lifestyle in plants. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9045-9050.	7.1	183
27	Monocot plastid phylogenomics, timeline, net rates of species diversification, the power of multi-gene analyses, and a functional model for the origin of monocots. American Journal of Botany, 2018, 105, 1888-1910.	1.7	161
28	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. American Journal of Botany, 2015, 102, 1089-1107.	1.7	157
29	Complete plastid genome sequences of Drimys, Liriodendron, and Piper: implications for the phylogenetic relationships of magnoliids. BMC Evolutionary Biology, 2006, 6, 77.	3.2	138
30	Comparative Transcriptome Analyses Reveal Core Parasitism Genes and Suggest Gene Duplication and Repurposing as Sources of Structural Novelty. Molecular Biology and Evolution, 2015, 32, 767-790.	8.9	137
31	Missing links: the genetic architecture of flower and floral diversification. Trends in Plant Science, 2002, 7, 22-31.	8.8	136
32	A phylogenomic assessment of ancient polyploidy and genome evolution across the Poales. Genome Biology and Evolution, 2016, 8, evw060.	2.5	117
33	De novo characterization of the gametophyte transcriptome in bracken fern, Pteridium aquilinum. BMC Genomics, 2011, 12, 99.	2.8	113
34	Genome Sequence of Striga asiatica Provides Insight into the Evolution of Plant Parasitism. Current Biology, 2019, 29, 3041-3052.e4.	3.9	109
35	The Parasitic Plant Genome Project: New Tools for Understanding the Biology of Orobanche and Striga. Weed Science, 2012, 60, 295-306.	1.5	106
36	The floral genome: an evolutionary history of gene duplication and shifting patterns of gene expression. Trends in Plant Science, 2007, 12, 358-367.	8.8	103

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37	Local Auxin Biosynthesis Mediated by a YUCCA Flavin Monooxygenase Regulates Haustorium Development in the Parasitic Plant <i>Phtheirospermum japonicum</i> . <i>Plant Cell</i> , 2016, 28, 1795-1814.	6.6	102
38	Floral gene resources from basal angiosperms for comparative genomics research. <i>BMC Plant Biology</i> , 2005, 5, 5.	3.6	100
39	ORIGIN AND BIOGEOGRAPHY OF <i>AESCULUS</i> L. (HIPPOCASTANACEAE): A MOLECULAR PHYLOGENETIC PERSPECTIVE. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 988-997.	2.3	97
40	Detecting and Characterizing the Highly Divergent Plastid Genome of the Nonphotosynthetic Parasitic Plant <i>Hydnora visseri</i> (Hydnoraceae). <i>Genome Biology and Evolution</i> , 2016, 8, 345-363.	2.5	97
41	Phylogenomic analysis of transcriptome data elucidates occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , 2012, 99, 397-406.	1.7	94
42	Plant Tribes: a gene and gene family resource for comparative genomics in plants. <i>Nucleic Acids Research</i> , 2007, 36, D970-D976.	14.5	93
43	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. <i>PLoS ONE</i> , 2016, 11, e0146062.	2.5	93
44	Assembly and Validation of the Genome of the Nonmodel Basal Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1516-1517.	12.6	89
45	ChloroplastDB: the Chloroplast Genome Database. <i>Nucleic Acids Research</i> , 2006, 34, D692-D696.	14.5	88
46	Evolution of Plant MADS Box Transcription Factors: Evidence for Shifts in Selection Associated with Early Angiosperm Diversification and Concerted Gene Duplications. <i>Molecular Biology and Evolution</i> , 2009, 26, 2229-2244.	8.9	88
47	Horizontal gene transfer is more frequent with increased heterotrophy and contributes to parasite adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7010-E7019.	7.1	85
48	Transcriptome Analysis Reveals the Same 17 <i>S-Locus F-Box</i> Genes in Two Haplotypes of the Self-Incompatibility Locus of <i>Petunia inflata</i> . <i>Plant Cell</i> , 2014, 26, 2873-2888.	6.6	84
49	Transcriptomes of the Parasitic Plant Family Orobanchaceae Reveal Surprising Conservation of Chlorophyll Synthesis. <i>Current Biology</i> , 2011, 21, 2098-2104.	3.9	82
50	Use of genomic history to improve phylogeny and understanding of births and deaths in a gene family. <i>Plant Journal</i> , 2005, 44, 409-419.	5.7	81
51	Single-Copy Nuclear Genes Place Haustorial Hydnoraceae within Piperales and Reveal a Cretaceous Origin of Multiple Parasitic Angiosperm Lineages. <i>PLoS ONE</i> , 2013, 8, e79204.	2.5	80
52	Convergent horizontal gene transfer and cross-talk of mobile nucleic acids in parasitic plants. <i>Nature Plants</i> , 2019, 5, 991-1001.	9.3	72
53	Highly Heterogeneous Rates of Evolution in the SKP1 Gene Family in Plants and Animals: Functional and Evolutionary Implications. <i>Molecular Biology and Evolution</i> , 2004, 21, 117-128.	8.9	69
54	Conservation and canalization of gene expression during angiosperm diversification accompany the origin and evolution of the flower. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22570-22575.	7.1	68

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55	Novel genetic code and record-setting AT-richness in the highly reduced plastid genome of the holoparasitic plant <i>Balanophora</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 934-943.	7.1	66
56	Phylogenetic analysis of pectin-related gene families in <i>Physcomitrella patens</i> and nine other plant species yields evolutionary insights into cell walls. BMC Plant Biology, 2014, 14, 79.	3.6	64
57	Functional genomics of a generalist parasitic plant: Laser microdissection of host-parasite interface reveals host-specific patterns of parasite gene expression. BMC Plant Biology, 2013, 13, 9.	3.6	61
58	Genomics of sorghum local adaptation to a parasitic plant. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4243-4251.	7.1	57
59	"Stealth dissemination" of macrophage-tumor cell fusions cultured from blood of patients with pancreatic ductal adenocarcinoma. PLoS ONE, 2017, 12, e0184451.	2.5	51
60	Insights into angiosperm evolution, floral development and chemical biosynthesis from the <i>Aristolochia fimbriata</i> genome. Nature Plants, 2021, 7, 1239-1253.	9.3	51
61	Genomic structural variants constrain and facilitate adaptation in natural populations of <i>Theobroma cacao</i> , the chocolate tree. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	50
62	Evolution of a horizontally acquired legume gene, albumin 1, in the parasitic plant <i>Phelipanche aegyptiaca</i> and related species. BMC Evolutionary Biology, 2013, 13, 48.	3.2	39
63	EST database for early flower development in California poppy (<i>Eschscholzia californica</i> Cham.) Tj ETQq1 1 0.784314 rgBT /Overlock 3.9 38	3.9	38
64	The Hemiparasitic Plant <i>Phtheirospermum</i> (Orobanchaceae) Is Polyphyletic and Contains Cryptic Species in the Hengduan Mountains of Southwest China. Frontiers in Plant Science, 2018, 9, 142.	3.6	38
65	Comparative transcriptomics among floral organs of the basal eudicot <i>Eschscholzia californica</i> as reference for floral evolutionary developmental studies. Genome Biology, 2010, 11, R101.	8.8	33
66	An EST database for <i>Liriodendron tulipifera</i> L. floral buds: the first EST resource for functional and comparative genomics in <i>Liriodendron</i> . Tree Genetics and Genomes, 2008, 4, 419-433.	1.6	31
67	The <i>TvPirin</i> Gene Is Necessary for Haustorium Development in the Parasitic Plant <i>Triphysaria versicolor</i> . Plant Physiology, 2012, 158, 1046-1053.	4.8	31
68	A physical map for the <i>Amborella trichopoda</i> genome sheds light on the evolution of angiosperm genome structure. Genome Biology, 2011, 12, R48.	9.6	28
69	Chasing the hare - Evaluating the phylogenetic utility of a nuclear single copy gene region at and below species level within the species rich group <i>Peperomia</i> (Piperaceae). BMC Evolutionary Biology, 2011, 11, 357.	3.2	27
70	Compensatory sequence variation between trans-species small RNAs and their target sites. ELife, 2019, 8, .	6.0	27
71	Genome-wide identification of MST, SUT and SWEET family sugar transporters in root parasitic angiosperms and analysis of their expression during host parasitism. BMC Plant Biology, 2019, 19, 196.	3.6	26
72	Development of a BAC library for yellow-poplar (<i>Liriodendron tulipifera</i>) and the identification of genes associated with flower development and lignin biosynthesis. Tree Genetics and Genomes, 2007, 3, 215-225.	1.6	25

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73	Characterization of the basal angiosperm <i>Aristolochia fimbriata</i> : a potential experimental system for genetic studies. <i>BMC Plant Biology</i> , 2013, 13, 13.	3.6	22
74	Gene Expression Modularity Reveals Footprints of Polygenic Adaptation in <i>Theobroma cacao</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 110-123.	8.9	22
75	Phylogenomic analysis of Ranunculales resolves branching events across the order. <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 157-166.	1.6	20
76	Transcriptomics of host-specific interactions in natural populations of the parasitic plant purple witchweed (<i>Striga hermonthica</i>). <i>Weed Science</i> , 2019, 67, 397-411.	1.5	16
77	Widely distributed variation in tolerance to <i>Phytophthora palmivora</i> in four genetic groups of cacao. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	15
78	Generation of a large-scale genomic resource for functional and comparative genomics in <i>Liriodendron tulipifera</i> L.. <i>Tree Genetics and Genomes</i> , 2011, 7, 941-954.	1.6	13
79	Regeneration and plantlet development from somatic tissues of <i>Aristolochia fimbriata</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2009, 98, 105-114.	2.3	10
80	Dissecting the contributions of dispersal and host properties to the local abundance of a tropical mistletoe. <i>Journal of Ecology</i> , 2017, 105, 1657-1667.	4.0	10
81	A derived ZW chromosome system in <i>Amborella trichopoda</i> , representing the sister lineage to all other extant flowering plants. <i>New Phytologist</i> , 2022, 233, 1636-1642.	7.3	10
82	Comparative Metabolomics of Early Development of the Parasitic Plants <i>Phelipanche aegyptiaca</i> and <i>Triphysaria versicolor</i> . <i>Metabolites</i> , 2019, 9, 114.	2.9	9
83	Transcriptomics of Differential Ripening in Anjou Pear (<i>Pyrus communis</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 609684.	3.6	7
84	The geography of parasite local adaptation to host communities. <i>Ecography</i> , 2021, 44, 1205-1217.	4.5	5
85	Risk versus reward: host dependent parasite mortality rates and phenotypes in the facultative generalist <i>Triphysaria versicolor</i> . <i>BMC Plant Biology</i> , 2019, 19, 334.	3.6	3
86	THE EFFECT OF MASSIVE GENE LOSS FOLLOWING WHOLE GENOME DUPLICATION ON THE ALGORITHMIC RECONSTRUCTION OF THE ANCESTRAL POPULUS DIPLOID. , 2008, , .		3
87	Utility of <i>Amborella trichopoda</i> and <i>Nuphar advena</i> expressed sequence tags for comparative sequence analysis. <i>Taxon</i> , 2008, 57, 1110.	0.7	2
88	In silico identification and structure function analysis of a putative coclaurine N-methyltransferase from <i>Aristolochia fimbriata</i> . <i>Computational Biology and Chemistry</i> , 2020, 85, 107201.	2.3	1