

Victor A Albert

List of Publications by Year in descending order

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52
papers

8,146
citations

87888

38
h-index

175258

52
g-index

56
all docs

56
docs citations

56
times ranked

7765
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetics of Seed Plants: An Analysis of Nucleotide Sequences from the Plastid Gene <i>rbcl</i> . <i>Annals of the Missouri Botanical Garden</i> , 1993, 80, 528.	1.3	1,708
2	Polyploidy and angiosperm diversification. <i>American Journal of Botany</i> , 2009, 96, 336-348.	1.7	1,081
3	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. <i>Science</i> , 2013, 342, 1241089.	12.6	743
4	Widespread genome duplications throughout the history of flowering plants. <i>Genome Research</i> , 2006, 16, 738-749.	5.5	664
5	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	12.6	520
6	Architecture and evolution of a minute plant genome. <i>Nature</i> , 2013, 498, 94-98.	27.8	293
7	A TCP domain transcription factor controls flower type specification along the radial axis of the <i>Gerbera</i> (<i>Asteraceae</i>) inflorescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9117-9122.	7.1	229
8	Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch. <i>Nature Genetics</i> , 2017, 49, 904-912.	21.4	221
9	Organ identity genes and modified patterns of flower development in <i>Gerbera hybrida</i> (<i>Asteraceae</i>). <i>Plant Journal</i> , 1999, 17, 51-62.	5.7	220
10	Phylogeny and diversification of <i>MADS</i> -box genes in angiosperms: evolutionary and functional implications of a 260-million-year-old duplication. <i>American Journal of Botany</i> , 2004, 91, 2102-2118.	1.7	185
11	Activation of Anthocyanin Biosynthesis in <i>Gerbera hybrida</i> (<i>Asteraceae</i>) Suggests Conserved Protein-Protein and Protein-Promoter Interactions between the Anciently Diverged Monocots and Eudicots. <i>Plant Physiology</i> , 2003, 133, 1831-1842.	4.8	137
12	The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17081-17089.	7.1	134
13	Evolution and Diversification of the <i>CYC/TB1</i> Gene Family in <i>Asteraceae</i> —A Comparative Study in <i>Gerbera</i> (<i>Mutisieae</i>) and <i>Sunflower</i> (<i>Heliantheae</i>). <i>Molecular Biology and Evolution</i> , 2012, 29, 1155-1166.	8.9	127
14	Integration of reproductive meristem fates by a <i>SEPALLATA</i> -like <i>MADS</i> -box gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15817-15822.	7.1	113
15	Floral gene resources from basal angiosperms for comparative genomics research. <i>BMC Plant Biology</i> , 2005, 5, 5.	3.6	100
16	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59.	7.8	99
17	Functional diversification of duplicated <i>CYC</i> clade genes in regulation of inflorescence development in <i>Gerbera hybrida</i> (<i>Asteraceae</i>). <i>Plant Journal</i> , 2014, 79, 783-796.	5.7	98
18	Long-read sequencing uncovers the adaptive topography of a carnivorous plant genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4435-E4441.	7.1	95

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19	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. <i>Nature Genetics</i> , 2022, 54, 73-83.	21.4	88
20	GRCD1, an AGL2-like MADS Box Gene, Participates in the C Function during Stamen Development in <i>Gerbera hybrida</i> . <i>Plant Cell</i> , 2000, 12, 1893-1902.	6.6	82
21	Ontogenetic Systematics, Molecular Developmental Genetics, and the Angiosperm Petal. , 1998, , 349-374.		82
22	Molecular Rates Parallel Diversification Contrasts between Carnivorous Plant Sister Lineages1. <i>Cladistics</i> , 2002, 18, 127-136.	3.3	74
23	Deep sequencing of the Mexican avocado transcriptome, an ancient angiosperm with a high content of fatty acids. <i>BMC Genomics</i> , 2015, 16, 599.	2.8	69
24	Molecular phylogenetics of an aquatic plant lineage, Potamogetonaceae. <i>Cladistics</i> , 2006, 22, 568-588.	3.3	61
25	Genotyping-by-sequencing provides the first well-resolved phylogeny for coffee (<i>Coffea</i>) and insights into the evolution of caffeine content in its species. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 351-361.	2.7	59
26	Functional characterization of B class MADS-box transcription factors in <i>Gerbera hybrida</i> . <i>Journal of Experimental Botany</i> , 2010, 61, 75-85.	4.8	58
27	Phylogenetic diversification of glycogen synthase kinase 3/SHAGGY-like kinase genes in plants. <i>BMC Plant Biology</i> , 2006, 6, 3.	3.6	55
28	Adaptive evolution of cytochrome c oxidase: Infrastructure for a carnivorous plant radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 18064-18068.	7.1	54
29	High Gene Family Turnover Rates and Gene Space Adaptation in the Compact Genome of the Carnivorous Plant <i>Utricularia gibba</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 1284-1295.	8.9	53
30	Patterns of MADS-box gene expression mark flower-type development in <i>Gerbera hybrida</i> (Asteraceae). <i>BMC Plant Biology</i> , 2006, 6, 11.	3.6	51
31	The carnivorous bladderwort (<i>Utricularia</i> , Lentibulariaceae): a system inflates. <i>Journal of Experimental Botany</i> , 2010, 61, 5-9.	4.8	51
32	Cladogenesis and reticulation in the Hawaiian endemic mints (Lamiaceae). <i>Cladistics</i> , 2003, 19, 480-495.	3.3	50
33	Transcriptomics and molecular evolutionary rate analysis of the bladderwort (<i>Utricularia</i>), a carnivorous plant with a minimal genome. <i>BMC Plant Biology</i> , 2011, 11, 101.	3.6	50
34	Co-opting floral meristem identity genes for patterning of the flower-like Asteraceae inflorescence. <i>Plant Physiology</i> , 2016, 172, pp.00779.2016.	4.8	49
35	<i>Persea americana</i> (avocado): bringing ancient flowers to fruit in the genomics era. <i>BioEssays</i> , 2008, 30, 386-396.	2.5	46
36	Dissecting functions of <i>SEPALLATA</i> -like MADS box genes in patterning of the pseudanthial inflorescence of <i>Gerbera hybrida</i> . <i>New Phytologist</i> , 2017, 216, 939-954.	7.3	46

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37	Pleiotropy, redundancy and the evolution of flowers. <i>Trends in Plant Science</i> , 2002, 7, 297-301.	8.8	44
38	Characterization of SQUAMOSA-like genes in <i>Gerbera hybrida</i> , including one involved in reproductive transition. <i>BMC Plant Biology</i> , 2010, 10, 128.	3.6	44
39	Large scale interaction analysis predicts that the <i>Gerbera hybrida</i> floral E function is provided both by general and specialized proteins. <i>BMC Plant Biology</i> , 2010, 10, 129.	3.6	44
40	Genome-Wide Analysis of Adaptive Molecular Evolution in the Carnivorous Plant <i>Utricularia gibba</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 444-456.	2.5	33
41	TCP and MADS-Box Transcription Factor Networks Regulate Heteromorphic Flower Type Identity in <i>Gerbera hybrida</i> . <i>Plant Physiology</i> , 2020, 184, 1455-1468.	4.8	33
42	<i>Buxus</i> and <i>Tetracentron</i> genomes help resolve eudicot genome history. <i>Nature Communications</i> , 2022, 13, 643.	12.8	24
43	The digestive systems of carnivorous plants. <i>Plant Physiology</i> , 2022, 190, 44-59.	4.8	20
44	Molecular phylogenetics of tribe Synandreae, a North American lineage of lamioid mints (Lamiaceae). <i>Cladistics</i> , 2008, 24, 299-314.	3.3	18
45	De novo sequencing and analysis of <i>Lophophora williamsii</i> transcriptome, and searching for putative genes involved in mescaline biosynthesis. <i>BMC Genomics</i> , 2015, 16, 657.	2.8	17
46	The double-corolla phenotype in the Hawaiian lobelioid genus <i>Clermontia</i> involves ectopic expression of PISTILLATA B-function MADS box gene homologs. <i>EvoDevo</i> , 2012, 3, 26.	3.2	15
47	Is GC bias in the nuclear genome of the carnivorous plant <i>Utricularia</i> driven by ROS-based mutation and biased gene conversion?. <i>Plant Signaling and Behavior</i> , 2011, 6, 1631-1634.	2.4	13
48	Insights into bear evolution from a Pleistocene polar bear genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
49	Evolution of RLSB, a nuclear-encoded S1 domain RNA binding protein associated with post-transcriptional regulation of plastid-encoded <i>rbcl</i> mRNA in vascular plants. <i>BMC Evolutionary Biology</i> , 2016, 16, 141.	3.2	9
50	Aquatic angiosperm ambiguities answered. <i>Nature Plants</i> , 2020, 6, 181-183.	9.3	9
51	Atypical DNA methylation, sRNA-size distribution, and female gametogenesis in <i>Utricularia gibba</i> . <i>Scientific Reports</i> , 2021, 11, 15725.	3.3	5
52	Syntenic block overlap multiplicities with a panel of reference genomes provide a signature of ancient polyploidization events. <i>BMC Genomics</i> , 2015, 16, S8.	2.8	4