Keith E Woeste

List of Publications by Year
in descending order

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		159585	175258
93	3,130	30	52
papers	citations	h-index	g-index
97	97	97	2272
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	A Strong Loss-of-Function Mutation in RAN1 Results in Constitutive Activation of the Ethylene Response Pathway as Well as a Rosette-Lethal Phenotype. Plant Cell, 2000, 12, 443-455.	6.6	215
2	Two Arabidopsis Mutants That Overproduce Ethylene Are Affected in the Posttranscriptional Regulation of 1-Aminocyclopropane-1-Carboxylic Acid Synthase1. Plant Physiology, 1999, 119, 521-530.	4.8	210
3	Rethinking the history of common walnut (Juglans regia L.) in Europe: Its origins and human interactions. PLoS ONE, 2017, 12, e0172541.	2.5	124
4	Characterization of 14 Microsatellite Markers for Genetic Analysis and Cultivar Identification of Walnut. Journal of the American Society for Horticultural Science, 2005, 130, 348-354.	1.0	124
5	Isolation and Characterization of Arabidopsis Mutants Defective in the Induction of Ethylene Biosynthesis by Cytokinin. Genetics, 1998, 149, 417-427.	2.9	114
6	Completion of the Chloroplast Genomes of Five Chinese Juglans and Their Contribution to Chloroplast Phylogeny. Frontiers in Plant Science, 2016, 7, 1955.	3.6	110
7	Genetic homogeneity in <i>Juglans nigra</i> (Juglandaceae) at nuclear microsatellites. American Journal of Botany, 2006, 93, 118-126.	1.7	101
8	Demographically idiosyncratic responses to climate change and rapid Pleistocene diversification of the walnut genus <i>Juglans</i> (Juglandaceae) revealed by wholeâ€genome sequences. New Phytologist, 2018, 217, 1726-1736.	7.3	98
9	Landscape genetics of Persian walnut (Juglans regia L.) across its Asian range. Tree Genetics and Genomes, 2014, 10, 1027-1043.	1.6	81
10	Phylogenomics Reveals an Ancient Hybrid Origin of the Persian Walnut. Molecular Biology and Evolution, 2019, 36, 2451-2461.	8.9	79
11	Population genetics, phylogenomics and hybrid speciation of Juglans in China determined from whole chloroplast genomes, transcriptomes, and genotyping-by-sequencing (GBS). Molecular Phylogenetics and Evolution, 2018, 126, 250-265.	2.7	78
12	Ancient Humans Influenced the Current Spatial Genetic Structure of Common Walnut Populations in Asia. PLoS ONE, 2015, 10, e0135980.	2.5	74
13	Factors regulating ethylene biosynthesis in etiolatedArabidopsis thalianaseedlings. Physiologia Plantarum, 1999, 105, 478-484.	5.2	73
14	Genomic Variation Among and Within Six<i>Juglans</i>Species. G3: Genes, Genomes, Genetics, 2018, 8, 2153-2165.	1.8	73
15	Long-term human impacts on genetic structure of Italian walnut inferred by SSR markers. Tree Genetics and Genomes, 2011, 7, 707-723.	1.6	68
16	DNA markers identify hybrids between butternut (Juglans cinerea L.) and Japanese walnut (Juglans) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	66
17	Retrospective identification of hybridogenic walnut plants by SSR fingerprinting and parentage analysis. Molecular Breeding, 2009, 24, 321-335.	2.1	65
18	Susceptibility of Walnut and Hickory Species to <i>Geosmithia morbida</i>. Plant Disease, 2013, 97, 601-607.	1.4	65

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19	De novo assembly and characterization of the leaf, bud, and fruit transcriptome from the vulnerable tree Juglans mandshurica for the development of 20 new microsatellite markers using Illumina sequencing. Molecular Genetics and Genomics, 2016, 291, 849-862.	2.1	65
20	Pyrosequencing of the northern red oak (Quercus rubra L.) chloroplast genome reveals high quality polymorphisms for population management. Tree Genetics and Genomes, 2014, 10, 803-812.	1.6	52
21	De Novo Assembly and Characterization of Bud, Leaf and Flowers Transcriptome from Juglans Regia L. for the Identification and Characterization of New EST-SSRs. Forests, 2016, 7, 247.	2.1	52
22	Genetic diversity and population structure of common walnut (Juglans regia) in China based on EST-SSRs and the nuclear gene phenylalanine ammonia-lyase (PAL). Tree Genetics and Genomes, 2016, 12, 1.	1.6	47
23	Genetic diversity and gene flow of some Persian walnut populations in southeast of Iran revealed by SSR markers. Plant Systematics and Evolution, 2015, 301, 691-699.	0.9	45
24	Genetic diversity and genetic structure of Persian walnut (Juglans regia) accessions from 14 European, African, and Asian countries using SSR markers. Tree Genetics and Genomes, 2016, 12, 1.	1.6	45
25	De novo assembly and characterization of transcriptome using Illumina sequencing and development of twenty five microsatellite markers for an endemic tree Juglans hopeiensis Hu in China. Biochemical Systematics and Ecology, 2015, 63, 201-211.	1.3	41
26	The Phytogeographic History of Common Walnut in China. Frontiers in Plant Science, 2018, 9, 1399.	3.6	39
27	A robust set of black walnut microsatellites for parentage and clonal identification. New Forests, 2006, 32, 179-196.	1.7	38
28	Population Structure of Geosmithia morbida, the Causal Agent of Thousand Cankers Disease of Walnut Trees in the United States. PLoS ONE, 2014, 9, e112847.	2.5	38
29	Improving disease resistance of butternut (Juglans cinerea), a threatened fine hardwood: a case for single-tree selection through genetic improvement and deployment. Tree Physiology, 2006, 26, 121-128.	3.1	35
30	Morphological and molecular methods to identify butternut (Juglans cinerea) and butternut hybrids: relevance to butternut conservation. Tree Physiology, 2008, 28, 1127-1133.	3.1	34
31	Genetic diversity of Persian walnut (Juglans regia) in the cold-temperate zone of the United States and Europe. Scientia Horticulturae, 2017, 220, 36-41.	3.6	33
32	Molecular Characterization of Persian Walnut Populations in Iran with Microsatellite Markers. Hortscience: A Publication of the American Society for Hortcultural Science, 2010, 45, 1403-1406.	1.0	32
33	Vegetative and Adaptive Traits Predict Different Outcomes for Restoration Using Hybrids. Frontiers in Plant Science, 2016, 7, 1741.	3.6	28
34	Genetic diversity and population structure in the narrow endemic Chinese walnut Juglans hopeiensis Hu: implications for conservation. Tree Genetics and Genomes, 2017, 13, 1.	1.6	28
35	Barriers to interspecific hybridization between Juglans nigra L. and J. regia L species. Tree Genetics and Genomes, 2013, 9, 291-305.	1.6	24
36	YeATS - a tool suite for analyzing RNA-seq derived transcriptome identifies a highly transcribed putative extensin in heartwood/sapwood transition zone in black walnut. F1000Research, 2015, 4, 155.	1.6	23

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37	Microsatellite markers for Juglans cinerea L. and their utility in other Juglandaceae species. Conservation Genetics, 2008, 9, 465-469.	1.5	22
38	Variation in needle and cone traits in natural populations of Pinus yunnanensis. Journal of Forestry Research, 2016, 27, 41-49.	3.6	21
39	Improved de novo chromosomeâ€level genome assembly of the vulnerable walnut tree <i>Juglans mandshurica</i> reveals gene family evolution and possible genome basis of resistance to lesion nematode. Molecular Ecology Resources, 2021, 21, 2063-2076.	4.8	20
40	Randomly Amplified Polymorphic DNA Loci from a Walnut Backcross [(Juglans hindsii Ã— J. regia) Ã— J. regia]. Journal of the American Society for Horticultural Science, 1996, 121, 358-361.	1.0	20
41	Variation among Persian Walnuts in Response to Inoculation with Xanthomonas campestris pv. juglandis. Journal of the American Society for Horticultural Science, 1992, 117, 527-531.	1.0	19
42	The identification and characterization of a genetic marker linked to hypersensitivity to the cherry leafroll virus in walnut. Molecular Breeding, 1996, 2, 261-266.	2.1	18
43	Genetic diversity of butternut (<i>Juglans cinerea</i>) and implications for conservation. Canadian Journal of Forest Research, 2008, 38, 899-907.	1.7	18
44	A KNAT3-like homeobox gene from Juglans nigra L., JnKNAT3-like, highly expressed during heartwood formation. Plant Cell Reports, 2009, 28, 1717-1724.	5.6	18
45	Comparative Genomics of Pathogenic and Nonpathogenic Beetle-Vectored Fungi in the Genus Geosmithia. Genome Biology and Evolution, 2017, 9, 3312-3327.	2.5	18
46	Signatures of Selection in the Genomes of Chinese Chestnut (Castanea mollissima Blume): The Roots of Nut Tree Domestication. Frontiers in Plant Science, 2018, 9, 810.	3.6	18
47	A Forest Manager's Guide to Butternut. Northern Journal of Applied Forestry, 2009, 26, 9-14.	0.5	16
48	Exploration of a rare population of Chinese chestnut in North America: stand dynamics, health and genetic relationships. AoB PLANTS, 2014, 6, .	2.3	16
49	Genetic Diversity and Population Structure of Pinus yunnanensis by Simple Sequence Repeat Markers. Forest Science, 2016, 62, 38-47.	1.0	15
50	Germination and early seedling growth of Pinus densata Mast. provenances. Journal of Forestry Research, 2016, 27, 283-294.	3.6	15
51	A Cross-species Transcriptional Profile Analysis of Heartwood Formation in Black Walnut. Plant Molecular Biology Reporter, 2010, 28, 222-230.	1.8	13
52	Genotypic data changes family rank for growth and quality traits in a black walnut (Juglans nigra L.) progeny test. New Forests, 2013, 44, 357-368.	1.7	13
53	Conservation Status of a Threatened Tree Species: Establishing a Baseline for Restoration of<i>Juglans cinerea</i>L. in the Southern Appalachian Mountains, USA. Natural Areas Journal, 2013, 33, 413-426.	0.5	13
54	Estimating heritability of disease resistance and factors that contribute to long-term survival in butternut (Juglans cinerea L.). Tree Genetics and Genomes, 2015, 11, 1.	1.6	13

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55	Population structure and genotypic variation of Crataegus pontica inferred by molecular markers. Gene, 2015, 572, 123-129.	2.2	13
56	Juglans. , 2011, , 77-88.		13
57	Morph-specific mating patterns in a low-density population of a heterodichogamous tree, Juglans ailantifolia. Plant Ecology, 2012, 213, 1477-1487.	1.6	12
58	The complete chloroplast genome of common walnut (<i>Juglans regia</i>). Mitochondrial DNA Part B: Resources, 2016, 1, 189-190.	0.4	12
59	Resources for studies of iron walnut (Juglans sigillata) gene expression, genetic diversity, and evolution. Tree Genetics and Genomes, 2018, 14, 1.	1.6	12
60	Pollen gene flow, male reproductive success, and genetic correlations among offspring in a northern red oak (Quercus rubra L.) seed orchard. PLoS ONE, 2017, 12, e0171598.	2.5	12
61	Whole genome based insights into the phylogeny and evolution of the Juglandaceae. Bmc Ecology and Evolution, 2021, 21, 191.	1.6	11
62	Half-sib seed source and nursery sowing density affect black walnut (Juglans nigra) growth after 5Âyears. New Forests, 2011, 41, 235-245.	1.7	10
63	Figured grain in aspen is heritable and not affected by graft-transmissible signals. Trees - Structure and Function, 2013, 27, 973-983.	1.9	10
64	Discrimination and assessment of black walnut (<i>Juglans nigra</i> L.) cultivars using phenology and microsatellite markers (SSRs). Canadian Journal of Plant Science, 2018, 98, 616-627.	0.9	10
65	Pollen flow and paternity in an isolated and non-isolated black walnut (Juglans nigra L.) timber seed orchard. PLoS ONE, 2018, 13, e0207861.	2.5	10
66	Population genetic structure and adaptive differentiation of iron walnut <i>Juglans regia</i> subsp. <i>sigillata</i> in southwestern China. Ecology and Evolution, 2019, 9, 14154-14166.	1.9	10
67	YeATS - a tool suite for analyzing RNA-seq derived transcriptome identifies a highly transcribed putative extensin in heartwood/sapwood transition zone in black walnut. F1000Research, 2015, 4, 155.	1.6	10
68	Evaluation of four herbicides and tillage for weed control on third year growth of tree seedlings. Weed Science, 2005, 53, 331-336.	1.5	9
69	Biotic and abiotic factors affecting the genetic structure and diversity of butternut in the southern Appalachian Mountains, USA. Tree Genetics and Genomes, 2014, 10, 541-554.	1.6	9
70	Soil pretreatment and fast cell lysis for direct polymerase chain reaction from forest soils for terminal restriction fragment length polymorphism analysis of fungal communities. Brazilian Journal of Microbiology, 2016, 47, 817-827.	2.0	9
71	Microsatellite Borders and Micro-sequence Conservation in Juglans. Scientific Reports, 2019, 9, 3748.	3.3	9
72	<i>De novo</i>genome assembly of<i>Geosmithia morbida</i>, the causal agent of thousand cankers disease. PeerJ, 2016, 4, e1952.	2.0	9

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73	Comparative Analysis of the Complete Chloroplast Genomes of Four Chestnut Species (Castanea). Forests, 2021, 12, 861.	2.1	8
74	Save Our Species: A Blueprint for Restoring Butternut (<i>Juglans cinerea</i>) across Eastern North America. Journal of Forestry, 2021, 119, 196-206.	1.0	8
75	Evaluation of Four Herbicides and Tillage for Weed Control on 1-0 Planted Tree Seedlings. Northern Journal of Applied Forestry, 2002, 19, 101-105.	0.5	7
76	Genetic consequences of harvest in a mature second-growth stand of black walnut (Juglans nigra L.). Annals of Forest Science, 2010, 67, 702-702.	2.0	7
77	Roles of JnRAP2.6-like from the Transition Zone of Black Walnut in Hormone Signaling. PLoS ONE, 2013, 8, e75857.	2.5	6
78	Genetic diversity and differentiation of yellowwood [Cladrastis kentukea (Dum.Cours.) Rudd] growing in the wild and in planted populations outside the natural range. New Forests, 2017, 48, 263-274.	1.7	6
79	Characterization of the complete chloroplast genome of wheel wingnut (Cyclocarya paliurus), an endemic in China. Conservation Genetics Resources, 2017, 9, 273-275.	0.8	6
80	Rapid Tree Diameter Computation with Terrestrial Stereoscopic Photogrammetry. Journal of Forestry, 2020, 118, 355-361.	1.0	6
81	Gene flow among wild and cultivated common walnut (Juglans regia) trees in the Qinling Mountains revealed by microsatellite markers. Journal of Forestry Research, 2021, 32, 2189-2201.	3.6	6
82	Low Correlation Between Genomic and Morphological Introgression Estimates in a Walnut Backcross. Journal of the American Society for Horticultural Science, 1998, 123, 258-263.	1.0	6
83	Plant Breeding and Rural Development in the United States. Crop Science, 2010, 50, 1625-1632.	1.8	5
84	RAPD derived markers for separating Manchurian walnut (<scp><i>J</i></scp><i>uglans) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Td (Journal of Systematics and Evolution, 2014, 52, 101-111.	3.1	5
85	White Oak Growth after 23 Years in a Three-Site Provenance/Progeny Trial on a Latitudinal Gradient in Indiana. Forest Science, 2016, 62, 99-106.	1.0	5
86	Effects of gibberellin A4/7, 6-benzylaminopurine and chlormequat chloride on the number of male and female strobili and immature cones in Chinese pine (Pinus tabuliformis) with foliar sprays. Journal of Forestry Research, 2011, 22, 353-359.	3.6	4
87	Characterization of the complete chloroplast genome of the endangered species Carya sinensis (Juglandaceae). Conservation Genetics Resources, 2016, 8, 467-470.	0.8	4
88	The complete plastid genome of the endangered species midget crabapple (Malus micromalus). Conservation Genetics Resources, 2018, 10, 531-533.	0.8	4
89	Characterization of stem volume and form tradeoffs in a northern red oak (Quercus rubra) breeding population in early stages of selection. Annals of Forest Science, 2021, 78, 1.	2.0	4
90	The de novo genome assembly of Tapiscia sinensis and the transcriptomic and developmental bases of androdioecy. Horticulture Research, 2020, 7, 191.	6.3	3

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91	The complete chloroplast genome sequence of American elm (Ulmus americana) and comparative genomics of related species. Tree Genetics and Genomes, 2021, 17, 1.	1.6	3
92	Comparative phylogeography of Juglans regia and J. mandshurica combining organellar and nuclear DNA markers to assess genetic diversity and introgression in regions of sympatry. Trees - Structure and Function, 0, , 1.	1.9	3
93	Characterization of the complete chloroplast genome of Platycarya strobilacea (Juglandaceae). Conservation Genetics Resources, 2017, 9, 79-81.	0.8	2