

John E Carlson

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

3,146
citations

218677

26
h-index

161849

54
g-index

62
all docs

62
docs citations

62
times ranked

4554
citing authors

#	ARTICLE	IF	CITATIONS
1	Widespread genome duplications throughout the history of flowering plants. <i>Genome Research</i> , 2006, 16, 738-749.	5.5	664
2	Lignin degradation in wood-feeding insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12932-12937.	7.1	279
3	Comparison of the transcriptomes of American chestnut (<i>Castanea dentata</i>) and Chinese chestnut (<i>Castanea mollissima</i>) in response to the chestnut blight infection. <i>BMC Plant Biology</i> , 2009, 9, 51.	3.6	197
4	Comparison of next generation sequencing technologies for transcriptome characterization. <i>BMC Genomics</i> , 2009, 10, 347.	2.8	168
5	Complete plastid genome sequences of <i>Drimys</i> , <i>Liriodendron</i> , and <i>Piper</i> : implications for the phylogenetic relationships of magnoliids. <i>BMC Evolutionary Biology</i> , 2006, 6, 77.	3.2	138
6	Single Tree Genetic Linkage Mapping in Conifers Using Haploid DNA from Megagametophytes. <i>Nature Biotechnology</i> , 1992, 10, 686-690.	17.5	132
7	Metagenomic Profiling Reveals Lignocellulose Degrading System in a Microbial Community Associated with a Wood-Feeding Beetle. <i>PLoS ONE</i> , 2013, 8, e73827.	2.5	125
8	Genomics of Fagaceae. <i>Tree Genetics and Genomes</i> , 2012, 8, 583-610.	1.6	109
9	Floral gene resources from basal angiosperms for comparative genomics research. <i>BMC Plant Biology</i> , 2005, 5, 5.	3.6	100
10	Functional genomics and microbiome profiling of the Asian longhorned beetle (<i>Anoplophora</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 beetles. <i>BMC Genomics</i> , 2014, 15, 1096.	2.8	93
11	Large-scale identification of microRNAs from a basal eudicot (<i>Eschscholzia californica</i>) and conservation in flowering plants. <i>Plant Journal</i> , 2007, 51, 991-1003.	5.7	77
12	Chestnut resistance to the blight disease: insights from transcriptome analysis. <i>BMC Plant Biology</i> , 2012, 12, 38.	3.6	68
13	Midgut transcriptome profiling of <i>Anoplophora glabripennis</i> , a lignocellulose degrading cerambycid beetle. <i>BMC Genomics</i> , 2013, 14, 850.	2.8	65
14	Effect of Host Tree Species on Cellulase Activity and Bacterial Community Composition in the Gut of Larval Asian Longhorned Beetle. <i>Environmental Entomology</i> , 2009, 38, 686-699.	1.4	64
15	Developmentally regulated patterns of expression directed by poplar PAL promoters in transgenic tobacco and poplar. <i>Plant Molecular Biology</i> , 1999, 39, 657-669.	3.9	51
16	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	3.6	50
17	cDNA cloning and heterologous expression of coniferin beta-glucosidase. <i>Plant Molecular Biology</i> , 1999, 40, 365-372.	3.9	43
18	Microbial Community Profiling to Investigate Transmission of Bacteria Between Life Stages of the Wood-Boring Beetle, <i>Anoplophora glabripennis</i> . <i>Microbial Ecology</i> , 2009, 58, 199-211.	2.8	42

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19	EST database for early flower development in California poppy (<i>Eschscholzia californica</i> Cham.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.9	38
20	A physical map of the Chinese chestnut (<i>Castanea mollissima</i>) genome and its integration with the genetic map. <i>Tree Genetics and Genomes</i> , 2013, 9, 525-537.	1.6	36
21	Improved Sugar Release from Lignocellulosic Material by Introducing a Tyrosine-rich Cell Wall Peptide Gene in Poplar. <i>Clean - Soil, Air, Water</i> , 2008, 36, 662-668.	1.1	34
22	Proteomic Analysis of <i>Fusarium solani</i> Isolated from the Asian Longhorned Beetle, <i>Anoplophora glabripennis</i> . <i>PLoS ONE</i> , 2012, 7, e32990.	2.5	33
23	Substantial genome synteny preservation among woody angiosperm species: comparative genomics of Chinese chestnut (<i>Castanea mollissima</i>) and plant reference genomes. <i>BMC Genomics</i> , 2015, 16, 744.	2.8	33
24	The green ash transcriptome and identification of genes responding to abiotic and biotic stresses. <i>BMC Genomics</i> , 2016, 17, 702.	2.8	32
25	An EST database for <i>Liriodendron tulipifera</i> L. floral buds: the first EST resource for functional and comparative genomics in <i>Liriodendron</i> . <i>Tree Genetics and Genomes</i> , 2008, 4, 419-433.	1.6	31
26	High-quality genetic mapping with ddRADseq in the non-model tree <i>Quercus rubra</i> . <i>BMC Genomics</i> , 2017, 18, 417.	2.8	29
27	Preliminary Genomic Characterization of Ten Hardwood Tree Species from Multiplexed Low Coverage Whole Genome Sequencing. <i>PLoS ONE</i> , 2015, 10, e0145031.	2.5	28
28	Development of a BAC library for yellow-poplar (<i>Liriodendron tulipifera</i>) and the identification of genes associated with flower development and lignin biosynthesis. <i>Tree Genetics and Genomes</i> , 2007, 3, 215-225.	1.6	25
29	Host-plant induced changes in microbial community structure and midgut gene expression in an invasive polyphage (<i>Anoplophora glabripennis</i>). <i>Scientific Reports</i> , 2018, 8, 9620.	3.3	22
30	Fagaceae Trees. , 2007, , 161-187.		20
31	Phylogenetic Analysis of <i>Fusarium solani</i> Associated with the Asian Longhorned Beetle, <i>Anoplophora glabripennis</i> . <i>Insects</i> , 2012, 3, 141-160.	2.2	20
32	The Camelina aquaporin CsPIP2;1 is regulated by phosphorylation at Ser273, but not at Ser277, of the C-terminus and is involved in salt- and drought-stress responses. <i>Journal of Plant Physiology</i> , 2014, 171, 1401-1412.	3.5	20
33	Use of Genomic Resources to Assess Adaptive Divergence and Introgression in Oaks. <i>Forests</i> , 2021, 12, 690.	2.1	17
34	Polyamine biosynthesis during somatic embryogenesis in interior spruce (<i>Picea glauca</i> x <i>Picea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142	5.6	16
35	Genome-wide association study identifies a major gene for beech bark disease resistance in American beech (<i>Fagus grandifolia</i> Ehrh.). <i>BMC Genomics</i> , 2017, 18, 547.	2.8	15
36	A petiole-galling insect herbivore decelerates leaf lamina litter decomposition rates. <i>Functional Ecology</i> , 2012, 26, 628-636.	3.6	14

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37	âœA reference genome assembly and adaptive trait analysis of <i>Castanea mollissima</i> âœVanuxem,âœ™ a source of resistance to chestnut blight in restoration breedingâœ. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	14
38	Host genomic influence on bacterial composition in the switchgrass rhizosphere. <i>Molecular Ecology</i> , 2022, 31, 3934-3950.	3.9	13
39	Factoring Ecological, Societal, and Economic Considerations into Inoculant Development. <i>Trends in Biotechnology</i> , 2019, 37, 572-573.	9.3	12
40	A highâœquality reference genome for <i>Fraxinus pennsylvanica</i> for ash species restoration and research. <i>Molecular Ecology Resources</i> , 2022, 22, 1284-1302.	4.8	12
41	Effect of environmental and cultural conditions on medium pH and explant growth performance of Douglas-fir (<i>Pseudotsuga menziesii</i>) shoot cultures. <i>F1000Research</i> , 2014, 3, 298.	1.6	11
42	Genome Sequence of <i>Fusarium</i> Isolate MYA-4552 from the Midgut of <i>Anoplophora glabripennis</i> , an Invasive, Wood-Boring Beetle. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
43	Transcriptome profiles of <i>Quercus rubra</i> responding to increased O3 stress. <i>BMC Genomics</i> , 2020, 21, 160.	2.8	11
44	Development of genomic microsatellites in <i>Gleditsia triacanthos</i> (Fabaceae) using Illumina sequencing. <i>Applications in Plant Sciences</i> , 2013, 1, 1300050.	2.1	10
45	NaCl-induced CsRC12E and CsRC12F interact with aquaporin CsPIP2;1 to reduce water transport in <i>Camelina sativa</i> L.. <i>Biochemical and Biophysical Research Communications</i> , 2019, 513, 213-218.	2.1	10
46	Development of novel genic microsatellite markers from transcriptome sequencing in sugar maple (<i>Acer saccharum</i> Marsh.). <i>BMC Research Notes</i> , 2017, 10, 369.	1.4	9
47	Neutral Genetic and Phenotypic Variation within and among Isolated Headwater Populations of Brook Trout. <i>Transactions of the American Fisheries Society</i> , 2019, 148, 58-72.	1.4	9
48	The first genetic linkage map for <i>Fraxinus pennsylvanica</i> and syntenic relationships with four related species. <i>Plant Molecular Biology</i> , 2019, 99, 251-264.	3.9	9
49	Characterization of the Transcriptome of the Xerophyte <i>Ammopiptanthus mongolicus</i> Leaves under Drought Stress by 454 Pyrosequencing. <i>PLoS ONE</i> , 2015, 10, e0136495.	2.5	8
50	Construction of a Framework Genetic Linkage Map in <i>Gleditsia triacanthos</i> L.. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 177-187.	1.8	7
51	Comparison of gene order of GIGANTEA loci in yellow-poplar, monocots, and eudicots. <i>Genome</i> , 2010, 53, 533-544.	2.0	6
52	Microsatellite DNA loci for Western Hemlock [<i>Tsuga heterophylla</i> (Raf.) Sarg]. <i>Molecular Ecology Notes</i> , 2002, 2, 236-238.	1.7	4
53	Organization of the chromosome region harboring a FLORICAULA/LEAFY gene in <i>Liriodendron</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 373-384.	1.6	4
54	Transcriptome analysis of contrasting resistance to herbivory by <i>Empoasca fabae</i> in two shrub willow species and their hybrid progeny. <i>PLoS ONE</i> , 2020, 15, e0236586.	2.5	4

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55	Polyamine biosynthesis during somatic embryogenesis in interior spruce (<i>Picea glauca</i> Mill. / <i>Picea</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	5.6	4
56	Oak Population Genomics. Population Genomics, 2021, , .	0.5	3
57	Utility of <i>Amborella trichopoda</i> and <i>Nuphar advena</i> expressed sequence tags for comparative sequence analysis. Taxon, 2008, 57, 1110.	0.7	2
58	Deciphering the genome structure and paleohistory of <i>Theobroma cacao</i> . Nature Precedings, 2010, , .	0.1	1
59	Progress and Prospects of Population Genomics of North American Hardwoods. Population Genomics, 2021, , 1.	0.5	1
60	Genetic Variation and Conservation Implications in Pennsylvania for the Rare and Imperiled Buffalo Nut (<i>Cervantesiaceae</i> ; <i>Pyralaria pubera</i> Michaux). Annals of Carnegie Museum, 2022, 87, .	0.5	0