

Jerry W Jenkins

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

16,207
citations

41344

49
h-index

48315

88
g-index

105
all docs

105
docs citations

105
times ranked

17814
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiplex knockout of trichome-regulating MYB duplicates in hybrid poplar using a single gRNA. <i>Plant Physiology</i> , 2022, 189, 516-526.	4.8	18
2	Representing sex chromosomes in genome assemblies. <i>Cell Genomics</i> , 2022, 2, 100132.	6.5	13
3	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
4	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180
5	Improved chromosome-level genome assembly and annotation of the seagrass, <i>Zostera marina</i> (eelgrass). <i>F1000Research</i> , 2021, 10, 289.	1.6	26
6	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	12.8	43
7	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21
8	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
9	Genomic variation within the maize stiffâ€stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e201114.	2.8	14
10	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	12.8	49
11	A draft genome provides hypotheses on drought tolerance in a keystone plant species in Western North America threatened by climate change. <i>Ecology and Evolution</i> , 2021, 11, 15417-15429.	1.9	6
12	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	8.8	68
13	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. <i>Nature Biotechnology</i> , 2020, 38, 1203-1210.	17.5	103
14	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020, 50, 101990.	4.6	18
15	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
16	Genome-wide quantitative trait loci detection for biofuel traits in switchgrass (<i>Panicum</i>) Tj ETQq0 0 0 rgBT /Overlock 10, Tf 50 142	5.6	3
17	Sequencing and Analysis of the Sex Determination Region of <i>Populus trichocarpa</i> . <i>Genes</i> , 2020, 11, 843.	2.4	19
18	Gradual polyploid genome evolution revealed by pan-genomic analysis of <i>Brachypodium hybridum</i> and its diploid progenitors. <i>Nature Communications</i> , 2020, 11, 3670.	12.8	67

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19	Chloroplast genome sequences of <i>Carya illinoensis</i> from two distinct geographic populations. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	9
20	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	8.8	74
21	Optimizing genomic selection for blight resistance in American chestnut backcross populations: A trade-off with American chestnut ancestry implies resistance is polygenic. <i>Evolutionary Applications</i> , 2020, 13, 31-47.	3.1	48
22	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 820-830.	7.8	250
23	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	21.4	249
24	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
25	High-density linkage map reveals QTL underlying growth traits in AP13-VS16 biparental population of switchgrass. <i>GCB Bioenergy</i> , 2019, 11, 672-690.	5.6	13
26	Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass (<i>Thinopyrum intermedium</i>). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2325-2351.	3.6	30
27	A new reference genome for <i>Sorghum bicolor</i> reveals high levels of sequence similarity between sweet and grain genotypes: implications for the genetics of sugar metabolism. <i>BMC Genomics</i> , 2019, 20, 420.	2.8	73
28	QTL-environment interactions underlie adaptive divergence in switchgrass across a large latitudinal gradient. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12933-12941.	7.1	75
29	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
30	The Genetic Architecture of Shoot and Root Trait Divergence Between Mesic and Xeric Ecotypes of a Perennial Grass. <i>Frontiers in Plant Science</i> , 2019, 10, 366.	3.6	22
31	A chromosome-scale genome assembly and dense genetic map for <i>Xenopus tropicalis</i> . <i>Developmental Biology</i> , 2019, 452, 8-20.	2.0	43
32	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	2.8	59
33	Quantitative trait loci for cell wall composition traits measured using near-infrared spectroscopy in the model C4 perennial grass <i>Panicum hallii</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 25.	6.2	8
34	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	5.7	406
35	The <i>Sorghum bicolor</i> reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. <i>Plant Journal</i> , 2018, 93, 338-354.	5.7	431
36	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018, 9, 5213.	12.8	101

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37	Population genomics and climate adaptation of a C4 perennial grass, <i>Panicum hallii</i> (Poaceae). <i>BMC Genomics</i> , 2018, 19, 792.	2.8	9
38	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	2.8	35
39	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	12.8	299
40	Characterization of a large sex determination region in <i>Salix purpurea</i> L. (Salicaceae). <i>Molecular Genetics and Genomics</i> , 2018, 293, 1437-1452.	2.1	61
41	The <i>Aquilegia</i> genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>ELife</i> , 2018, 7, .	6.0	120
42	Sparse panicle1 is required for inflorescence development in <i>Setaria viridis</i> and maize. <i>Nature Plants</i> , 2017, 3, 17054.	9.3	63
43	Draft Nuclear Genome Sequence of the Liquid Hydrocarbon-accumulating Green Microalga <i>Botryococcus braunii</i> Race B (Showa). <i>Genome Announcements</i> , 2017, 5, .	0.8	21
44	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	7.8	94
45	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. <i>BMC Genomics</i> , 2017, 18, 225.	2.8	342
46	Draft Nuclear Genome Sequence of the Halophilic and Beta-Carotene-Accumulating Green Alga <i>Dunaliella salina</i> Strain CCAP19/18. <i>Genome Announcements</i> , 2017, 5, .	0.8	83
47	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	28.9	973
48	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6361-E6370.	7.1	233
49	The <i>Kalanchoe</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	12.8	159
50	Identification, characterization, and gene expression analysis of nucleotide binding site (NB)-type resistance gene homologues in switchgrass. <i>BMC Genomics</i> , 2016, 17, 892.	2.8	14
51	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	27.8	849
52	Genetic analysis of <i>Physcomitrella patens</i> identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. <i>Plant Cell</i> , 2016, 28, tpc.00091.2016.	6.6	98
53	Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. <i>BMC Genomics</i> , 2016, 17, 33.	2.8	137
54	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	27.8	460

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55	Drought responsive gene expression regulatory divergence between upland and lowland ecotypes of a perennial C ₄ grass. <i>Genome Research</i> , 2016, 26, 510-518.	5.5	52
56	Targeted Switchgrass BAC Library Screening and Sequence Analysis Identifies Predicted Biomass and Stress Response-Related Genes. <i>Bioenergy Research</i> , 2016, 9, 109-122.	3.9	10
57	Genome Analysis of Planctomycetes Inhabiting Blades of the Red Alga <i>Porphyra umbilicalis</i> . <i>PLoS ONE</i> , 2016, 11, e0151883.	2.5	39
58	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815.	5.7	47
59	A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	7.3	211
60	High-Density Single Nucleotide Polymorphism Linkage Maps of Lowland Switchgrass using Genotyping-by-Sequencing. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0065.	2.8	8
61	Updating algal evolutionary relationships through plastid genome sequencing: did alveolate plastids emerge through endosymbiosis of an ochrophyte?. <i>Scientific Reports</i> , 2015, 5, 10134.	3.3	102
62	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	8.8	256
63	SNP Assay Development for Linkage Map Construction, Anchoring Whole-Genome Sequence, and Other Genetic and Genomic Applications in Common Bean. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2285-2290.	1.8	147
64	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015, 527, 459-465.	27.8	217
65	High-resolution genetic maps of <i>Eucalyptus</i> improve <i>Eucalyptus grandis</i> genome assembly. <i>New Phytologist</i> , 2015, 206, 1283-1296.	7.3	90
66	The science and policy of critical loads of pollutant deposition to protect ecosystems in New York. <i>Annals of the New York Academy of Sciences</i> , 2014, 1313, 57-68.	3.8	6
67	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014, 32, 656-662.	17.5	572
68	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
69	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	21.4	1,159
70	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	21.4	1,031
71	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	21.4	374
72	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198

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73	Fine-scale variation in meiotic recombination in <i>Mimulus</i> inferred from population shotgun sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19478-19482.	7.1	190
74	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. Genome Biology, 2013, 14, r53.	8.8	225
75	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . Molecular Plant-Microbe Interactions, 2012, 25, 1350-1360.	2.6	264
76	Identical Genomic Organization of Two Hemichordate Hox Clusters. Current Biology, 2012, 22, 2053-2058.	3.9	43
77	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
78	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. PLoS ONE, 2012, 7, e33892.	2.5	50
79	Reference genome sequence of the model plant <i>Setaria</i> . Nature Biotechnology, 2012, 30, 555-561.	17.5	864
80	Mefloquine neurotoxicity is mediated by non-receptor tyrosine kinase. NeuroToxicology, 2011, 32, 578-585.	3.0	24
81	Automated refinement and inference of analytical models for metabolic networks. Physical Biology, 2011, 8, 055011.	1.8	108
82	Mefloquine induces oxidative stress and neurodegeneration in primary rat cortical neurons. NeuroToxicology, 2010, 31, 518-523.	3.0	42
83	Extracting kinetic rate constants from surface plasmon resonance array systems. Analytical Biochemistry, 2008, 373, 112-120.	2.4	71
84	Submonolayer measurements of adsorbed proteins in microfluidic channels. , 2006, , 257-274.		0
85	Chemo-sensitivity and reliability of flagellar rotary motor in a MEMS microfluidic actuation system. Sensors and Actuators B: Chemical, 2006, 114, 229-238.	7.8	10
86	A 2-D Microcantilever Array for Multiplexed Biomolecular Analysis. Journal of Microelectromechanical Systems, 2004, 13, 290-299.	2.5	138
87	Simulation of intermediate order in polymeric glasses. Macromolecular Symposia, 1999, 146, 235-241.	0.7	6