

# Jerry W Jenkins

## List of Publications by Year in descending order

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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	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	27.8	1,204
2	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
3	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
4	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	28.9	973
5	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	17.5	864
6	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	27.8	849
7	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
8	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
9	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
10	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
11	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
12	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
13	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
14	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
15	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
16	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	12.8	299
17	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	2.6	264
18	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	8.8	256

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19	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 820-830.	7.8	250
20	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
21	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangioophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6361-E6370.	7.1	233
22	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. <i>Genome Biology</i> , 2013, 14, r53.	8.8	225
23	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015, 527, 459-465.	27.8	217
24	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
25	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198
26	Fine-scale variation in meiotic recombination in <i>Mimulus</i> inferred from population shotgun sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19478-19482.	7.1	190
27	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180
28	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	12.8	159
29	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
30	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
31	A 2-D Microcantilever Array for Multiplexed Biomolecular Analysis. <i>Journal of Microelectromechanical Systems</i> , 2004, 13, 290-299.	2.5	138
32	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
33	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
34	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
35	Automated refinement and inference of analytical models for metabolic networks. <i>Physical Biology</i> , 2011, 8, 055011.	1.8	108
36	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

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37	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
38	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
39	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
40	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	7.8	94
41	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
42	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
43	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
44	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	8.8	74
45	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
46	Extracting kinetic rate constants from surface plasmon resonance array systems. <i>Analytical Biochemistry</i> , 2008, 373, 112-120.	2.4	71
47	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
48	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
49	Sparse panicle1 is required for inflorescence development in <i>Setaria viridis</i> and maize. <i>Nature Plants</i> , 2017, 3, 17054.	9.3	63
50	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
51	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	2.8	59
52	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
53	Drought responsive gene expression regulatory divergence between upland and lowland ecotypes of a perennial C <sub>4</sub> grass. <i>Genome Research</i> , 2016, 26, 510-518.	5.5	52
54	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. <i>PLoS ONE</i> , 2012, 7, e33892.	2.5	50

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55	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	12.8	49
56	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
57	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815.	5.7	47
58	Identical Genomic Organization of Two Hemichordate Hox Clusters. <i>Current Biology</i> , 2012, 22, 2053-2058.	3.9	43
59	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
60	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	12.8	43
61	Mefloquine induces oxidative stress and neurodegeneration in primary rat cortical neurons. <i>NeuroToxicology</i> , 2010, 31, 518-523.	3.0	42
62	Genome Analysis of Planctomycetes Inhabiting Blades of the Red Alga <i>Porphyra umbilicalis</i> . <i>PLoS ONE</i> , 2016, 11, e0151883.	2.5	39
63	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	2.8	35
64	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
65	Improved chromosome-level genome assembly and annotation of the seagrass, <i>Zostera marina</i> (eelgrass). <i>F1000Research</i> , 2021, 10, 289.	1.6	26
66	Mefloquine neurotoxicity is mediated by non-receptor tyrosine kinase. <i>NeuroToxicology</i> , 2011, 32, 578-585.	3.0	24
67	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
68	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
69	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21
70	Sequencing and Analysis of the Sex Determination Region of <i>Populus trichocarpa</i> . <i>Genes</i> , 2020, 11, 843.	2.4	19
71	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
72	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

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73	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
74	Genomic variation within the maize stiffâ€stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	2.8	14
75	Highâ€density linkage map reveals QTL underlying growth traits in AP13Ã—VS16 biparental population of switchgrass. <i>GCB Bioenergy</i> , 2019, 11, 672-690.	5.6	13
76	Representing sex chromosomes in genome assemblies. <i>Cell Genomics</i> , 2022, 2, 100132.	6.5	13
77	Chemo-sensitivity and reliability of flagellar rotary motor in a MEMS microfluidic actuation system. <i>Sensors and Actuators B: Chemical</i> , 2006, 114, 229-238.	7.8	10
78	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
79	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
80	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
81	Highâ€Density Single Nucleotide Polymorphism Linkage Maps of Lowland Switchgrass using Genotypingâ€byâ€Sequencing. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0065.	2.8	8
82	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
83	Simulation of intermediate order in polymeric glasses. <i>Macromolecular Symposia</i> , 1999, 146, 235-241.	0.7	6
84	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
85	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
86	Genomeâ€wide quantitative trait loci detection for biofuel traits in switchgrass ( <i>Panicum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	3.6	3
87	Submonolayer measurements of adsorbed proteins in microfluidic channels. , 2006, , 257-274.		0