Doreen H Ware

List of Publications by Year
in descending order

85 papers	25,930 citations	41344 49 h-index	56724 83 g-index
98 all docs	98 docs citations	98 times ranked	26776 citing authors

#	Article	IF	Citations
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	12.6	3,612
2	The Sorghum bicolor genome and the diversification of grasses. Nature, 2009, 457, 551-556.	27.8	2,642
3	The Genetic Architecture of Maize Flowering Time. Science, 2009, 325, 714-718.	12.6	1,284
4	Development and Mapping of 2240 New SSR Markers for Rice (Oryza sativa L.). DNA Research, 2002, 9, 199-207.	3.4	1,203
5	Improved maize reference genome with single-molecule technologies. Nature, 2017, 546, 524-527.	27.8	1,113
6	Genetic Properties of the Maize Nested Association Mapping Population. Science, 2009, 325, 737-740.	12.6	959
7	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	17.5	955
8	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. Science, 2011, 333, 601-607.	12.6	838
9	Comparative population genomics of maize domestication and improvement. Nature Genetics, 2012, 44, 808-811.	21.4	816
10	A First-Generation Haplotype Map of Maize. Science, 2009, 326, 1115-1117.	12.6	747
11	Genetic structure and domestication history of the grape. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3530-3535.	7.1	684
12	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	14.5	682
13	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. Genome Biology, 2019, 20, 275.	8.8	579
14	Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012, 44, 803-807.	21.4	577
15	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. Nature Genetics, 2011, 43, 163-168.	21.4	553
16	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	14.5	530
17	Unveiling the complexity of the maize transcriptome by single-molecule long-read sequencing. Nature Communications, 2016, 7, 11708.	12.8	510
18	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. Nucleic Acids Research, 2018, 46, D802-D808.	14.5	489

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19	Ensembl Genomes 2020â€"enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	14.5	416
20	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. Nature Genetics, 2018, 50, 285-296.	21.4	413
21	MAKER-P: A Tool Kit for the Rapid Creation, Management, and Quality Control of Plant Genome Annotations Â Â. Plant Physiology, 2014, 164, 513-524.	4.8	412
22	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in Plant Science, 2011, 2, 34.	3.6	396
23	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. Nature Genetics, 2018, 50, 1289-1295.	21.4	335
24	A Genome-Wide Characterization of MicroRNA Genes in Maize. PLoS Genetics, 2009, 5, e1000716.	3.5	318
25	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. Genome Research, 2010, 20, 1689-1699.	5.5	309
26	The iPlant Collaborative: Cyberinfrastructure for Enabling Data to Discovery for the Life Sciences. PLoS Biology, 2016, 14, e1002342.	5.6	306
27	<i>ZmCCT</i> and the genetic basis of day-length adaptation underlying the postdomestication spread of maize. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1913-21.	7.1	290
28	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. Science, 2021, 373, 655-662.	12.6	282
29	The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. Genome Research, 2013, 23, 1651-1662.	5.5	260
30	Ensembl Genomes 2013: scaling up access to genome-wide data. Nucleic Acids Research, 2014, 42, D546-D552.	14.5	205
31	Rapid Genomic Characterization of the Genus Vitis. PLoS ONE, 2010, 5, e8219.	2.5	203
32	The maize W22 genome provides a foundation for functional genomics and transposon biology. Nature Genetics, 2018, 50, 1282-1288.	21.4	183
33	Gramene database in 2010: updates and extensions. Nucleic Acids Research, 2011, 39, D1085-D1094.	14.5	182
34	Gramene 2013: comparative plant genomics resources. Nucleic Acids Research, 2014, 42, D1193-D1199.	14.5	163
35	Regulatory modules controlling maize inflorescence architecture. Genome Research, 2014, 24, 431-443.	5.5	160
36	Highly accurate long-read HiFi sequencing data for five complex genomes. Scientific Data, 2020, 7, 399.	5.3	155

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37	Gramene 2018: unifying comparative genomics and pathway resources for plant research. Nucleic Acids Research, 2018, 46, D1181-D1189.	14.5	147
38	Gramene 2016: comparative plant genomics and pathway resources. Nucleic Acids Research, 2016, 44, D1133-D1140.	14.5	138
39	A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses. Plant Cell, 2016, 28, tpc.00373.2016.	6.6	113
40	Reviving the Transcriptome Studies: An Insight Into the Emergence of Single-Molecule Transcriptome Sequencing. Frontiers in Genetics, 2019, 10, 384.	2.3	112
41	A genome scale metabolic network for rice and accompanying analysis of tryptophan, auxin and serotonin biosynthesis regulation under biotic stress. Rice, 2013, 6, 15.	4.0	101
42	Gapless assembly of maize chromosomes using long-read technologies. Genome Biology, 2020, 21, 121.	8.8	101
43	Plant Reactome: a resource for plant pathways and comparative analysis. Nucleic Acids Research, 2017, 45, D1029-D1039.	14.5	95
44	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. Nucleic Acids Research, 2021, 49, D1452-D1463.	14.5	83
45	A comparative transcriptional landscape of maize and sorghum obtained by single-molecule sequencing. Genome Research, 2018, 28, 921-932.	5.5	76
46	Characterization of miRNAs in Response to Short-Term Waterlogging in Three Inbred Lines of Zea mays. PLoS ONE, 2012, 7, e39786.	2.5	74
47	High-throughput comparison, functional annotation, and metabolic modeling of plant genomes using the PlantSEED resource. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9645-9650.	7.1	69
48	Maize Metabolic Network Construction and Transcriptome Analysis. Plant Genome, 2013, 6, plantgenome2012.09.0025.	2.8	63
49	Revealing gene regulation and associations through biological networks. Current Plant Biology, 2015, 3-4, 30-39.	4.7	57
50	MSD1 regulates pedicellate spikelet fertility in sorghum through the jasmonic acid pathway. Nature Communications, 2018, 9, 822.	12.8	56
51	Identification of the First Nuclear Male Sterility Gene (<i>Male‑sterile 9</i>) in Sorghum. Plant Genome, 2019, 12, 1-12.	2.8	56
52	An ultra-high-density map as a community resource for discerning the genetic basis of quantitative traits in maize. BMC Genomics, 2015, 16, 1078.	2.8	55
53	Automated Update, Revision, and Quality Control of the Maize Genome Annotations Using MAKER-P Improves the B73 RefGen_v3 Gene Models and Identifies New Genes Â. Plant Physiology, 2014, 167, 25-39.	4.8	53
54	Haplotyping the Vitis collinear core genome with rhAmpSeq improves marker transferability in a diverse genus. Nature Communications, 2020, 11, 413.	12.8	52

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55	Gramene database: Navigating plant comparative genomics resources. Current Plant Biology, 2016, 7-8, 10-15.	4.7	51
56	Genome-Wide Computational Prediction and Analysis of Core Promoter Elements across Plant Monocots and Dicots. PLoS ONE, 2013, 8, e79011.	2.5	45
57	Plant Reactome: a knowledgebase and resource for comparative pathway analysis. Nucleic Acids Research, 2020, 48, D1093-D1103.	14.5	44
58	Disentangling Methodological and Biological Sources of Gene Tree Discordance on Oryza (Poaceae) Chromosome 3. Systematic Biology, 2014, 63, 645-659.	5.6	43
59	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. Nature Communications, 2020, 11, 2288.	12.8	39
60	Efficient Identification of Causal Mutations through Sequencing of Bulked F2 from Two Allelic Bloomless Mutants of Sorghum bicolor. Frontiers in Plant Science, 2017, 8, 2267.	3.6	36
61	The Oryza BAC resource: a genus-wide and genome scale tool for exploring rice genome evolution and leveraging useful genetic diversity from wild relatives. Breeding Science, 2010, 60, 536-543.	1.9	34
62	Fertility of Pedicellate Spikelets in Sorghum Is Controlled by a Jasmonic Acid Regulatory Module. International Journal of Molecular Sciences, 2019, 20, 4951.	4.1	31
63	Expanding and Vetting *Sorghum bicolor* Gene Annotations through Transcriptome and Methylome Sequencing. Plant Genome, 2014, 7, plantgenome2013.08.0025.	2.8	26
64	Amino Acid and Carbohydrate Metabolism Are Coordinated to Maintain Energetic Balance during Drought in Sugarcane. International Journal of Molecular Sciences, 2020, 21, 9124.	4.1	25
65	Sorghum MSD3 Encodes an Ï‰-3 Fatty Acid Desaturase that Increases Grain Number by Reducing Jasmonic Acid Levels. International Journal of Molecular Sciences, 2019, 20, 5359.	4.1	24
66	Gramene: A Resource for Comparative Analysis of Plants Genomes and Pathways. Methods in Molecular Biology, 2022, 2443, 101-131.	0.9	23
67	GrameneMart: the BioMart data portal for the Gramene project. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar056-bar056.	3.0	22
68	The Dominant and Poorly Penetrant Phenotypes of Maize *Unstable factor for orange1* Are Caused by DNA Methylation Changes at a Linked Transposon. Plant Cell, 2018, 30, 3006-3023.	6.6	21
69	SciApps: a cloud-based platform for reproducible bioinformatics workflows. Bioinformatics, 2018, 34, 3917-3920.	4.1	21
70	Variant phasing and haplotypic expression from long-read sequencing in maize. Communications Biology, 2020, 3, 78.	4.4	20
71	Gramene: A Resource for Comparative Analysis of Plants Genomes and Pathways. Methods in Molecular Biology, 2016, 1374, 141-163.	0.9	15
72	SorghumBase: a web-based portal for sorghum genetic information and community advancement. Planta, 2022, 255, 35.	3.2	12

#	ARTICLE	IF	CITATIONS
73	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. Plant Physiology, 2017, 175, 1499-1509.	4.8	11
74	BSAseq: an interactive and integrated web-based workflow for identification of causal mutations in bulked F2 populations. Bioinformatics, 2021, 37, 382-387.	4.1	11
75	Double triage to identify poorly annotated genes in maize: The missing link in community curation. PLoS ONE, 2019, 14, e0224086.	2.5	10
76	Gramene. , 2007, 406, 315-329.		8
77	Phylogenomic Analysis of BAC-end Sequence Libraries in <I>Oryza</I> (Poaceae). Systematic Botany, 2010, 35, 512-523.	0.5	8
78	Gene disruption by structural mutations drives selection in US rice breeding over the last century. PLoS Genetics, 2021, 17, e1009389.	3.5	6
79	A genome‐wide association study platform built on iPlant cyber‐infrastructure. Concurrency Computation Practice and Experience, 2015, 27, 420-432.	2.2	5
80	Sorghum root epigenetic landscape during limiting phosphorus conditions. Plant Direct, 2022, 6, .	1.9	5
81	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. Frontiers in Plant Science, 2020, 11, 289.	3.6	4
82	Ranked choice voting for representative transcripts with TRaCE. Bioinformatics, 2021, 38, 261-264.	4.1	4
83	A KBase case study on genome-wide transcriptomics and plant primary metabolism in response to drought stress in Sorghum.. Current Plant Biology, 2021, 28, 100229.	4.7	4
84	Pedigreed Mutant Library-A Unique Resource for Sorghum Improvement and Genomics. Agronomy, 0, , 73-96.	0.2	1
85	SciApps: An Automated Platform for Processing and Distribution of Plant Genomics Data. Methods in Molecular Biology, 2022, 2443, 197-209.	0.9	0