

Doreen H Ware

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

25,930
citations

41258

49
h-index

56606

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. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
2	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
3	The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718.	6.0	1,284
4	Development and Mapping of 2240 New SSR Markers for Rice (<i>Oryza sativa</i> L.). <i>DNA Research</i> , 2002, 9, 199-207.	1.5	1,203
5	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017, 546, 524-527.	13.7	1,113
6	Genetic Properties of the Maize Nested Association Mapping Population. <i>Science</i> , 2009, 325, 737-740.	6.0	959
7	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	9.4	955
8	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. <i>Science</i> , 2011, 333, 601-607.	6.0	838
9	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	9.4	816
10	A First-Generation Haplotype Map of Maize. <i>Science</i> , 2009, 326, 1115-1117.	6.0	747
11	Genetic structure and domestication history of the grape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3530-3535.	3.3	684
12	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015, 43, W589-W598.	6.5	682
13	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. <i>Genome Biology</i> , 2019, 20, 275.	3.8	579
14	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
15	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. <i>Nature Genetics</i> , 2011, 43, 163-168.	9.4	553
16	Ensembl Genomes 2016: more genomes, more complexity. <i>Nucleic Acids Research</i> , 2016, 44, D574-D580.	6.5	530
17	Unveiling the complexity of the maize transcriptome by single-molecule long-read sequencing. <i>Nature Communications</i> , 2016, 7, 11708.	5.8	510
18	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018, 46, D802-D808.	6.5	489

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19	Ensembl Genomes 2020“enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	6.5	416
20	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
21	MAKER-P: A Tool Kit for the Rapid Creation, Management, and Quality Control of Plant Genome Annotations. <i>Plant Physiology</i> , 2014, 164, 513-524.	2.3	412
22	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	1.7	396
23	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	9.4	335
24	A Genome-Wide Characterization of MicroRNA Genes in Maize. <i>PLoS Genetics</i> , 2009, 5, e1000716.	1.5	318
25	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. <i>Genome Research</i> , 2010, 20, 1689-1699.	2.4	309
26	The iPlant Collaborative: Cyberinfrastructure for Enabling Data to Discovery for the Life Sciences. <i>PLoS Biology</i> , 2016, 14, e1002342.	2.6	306
27	<i>ZmCCT</i> and the genetic basis of day-length adaptation underlying the postdomestication spread of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1913-21.	3.3	290
28	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	6.0	282
29	The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. <i>Genome Research</i> , 2013, 23, 1651-1662.	2.4	260
30	Ensembl Genomes 2013: scaling up access to genome-wide data. <i>Nucleic Acids Research</i> , 2014, 42, D546-D552.	6.5	205
31	Rapid Genomic Characterization of the Genus <i>Vitis</i> . <i>PLoS ONE</i> , 2010, 5, e8219.	1.1	203
32	The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , 2018, 50, 1282-1288.	9.4	183
33	Gramene database in 2010: updates and extensions. <i>Nucleic Acids Research</i> , 2011, 39, D1085-D1094.	6.5	182
34	Gramene 2013: comparative plant genomics resources. <i>Nucleic Acids Research</i> , 2014, 42, D1193-D1199.	6.5	163
35	Regulatory modules controlling maize inflorescence architecture. <i>Genome Research</i> , 2014, 24, 431-443.	2.4	160
36	Highly accurate long-read HiFi sequencing data for five complex genomes. <i>Scientific Data</i> , 2020, 7, 399.	2.4	155

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37	Gramene 2018: unifying comparative genomics and pathway resources for plant research. <i>Nucleic Acids Research</i> , 2018, 46, D1181-D1189.	6.5	147
38	Gramene 2016: comparative plant genomics and pathway resources. <i>Nucleic Acids Research</i> , 2016, 44, D1133-D1140.	6.5	138
39	A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses. <i>Plant Cell</i> , 2016, 28, tpc.00373.2016.	3.1	113
40	Reviving the Transcriptome Studies: An Insight Into the Emergence of Single-Molecule Transcriptome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 384.	1.1	112
41	A genome scale metabolic network for rice and accompanying analysis of tryptophan, auxin and serotonin biosynthesis regulation under biotic stress. <i>Rice</i> , 2013, 6, 15.	1.7	101
42	Gapless assembly of maize chromosomes using long-read technologies. <i>Genome Biology</i> , 2020, 21, 121.	3.8	101
43	Plant Reactome: a resource for plant pathways and comparative analysis. <i>Nucleic Acids Research</i> , 2017, 45, D1029-D1039.	6.5	95
44	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. <i>Nucleic Acids Research</i> , 2021, 49, D1452-D1463.	6.5	83
45	A comparative transcriptional landscape of maize and sorghum obtained by single-molecule sequencing. <i>Genome Research</i> , 2018, 28, 921-932.	2.4	76
46	Characterization of miRNAs in Response to Short-Term Waterlogging in Three Inbred Lines of Zea mays. <i>PLoS ONE</i> , 2012, 7, e39786.	1.1	74
47	High-throughput comparison, functional annotation, and metabolic modeling of plant genomes using the PlantSEED resource. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9645-9650.	3.3	69
48	Maize Metabolic Network Construction and Transcriptome Analysis. <i>Plant Genome</i> , 2013, 6, plantgenome2012.09.0025.	1.6	63
49	Revealing gene regulation and associations through biological networks. <i>Current Plant Biology</i> , 2015, 3-4, 30-39.	2.3	57
50	MSD1 regulates pedicellate spikelet fertility in sorghum through the jasmonic acid pathway. <i>Nature Communications</i> , 2018, 9, 822.	5.8	56
51	Identification of the First Nuclear Male Sterility Gene (<i>Ms1</i>) in Sorghum. <i>Plant Genome</i> , 2019, 12, 1-12.	1.6	56
52	An ultra-high-density map as a community resource for discerning the genetic basis of quantitative traits in maize. <i>BMC Genomics</i> , 2015, 16, 1078.	1.2	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. <i>Plant Physiology</i> , 2014, 167, 25-39.	2.3	53
54	Haplotyping the <i>Vitis</i> collinear core genome with rhAmpSeq improves marker transferability in a diverse genus. <i>Nature Communications</i> , 2020, 11, 413.	5.8	52

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55	Gramene database: Navigating plant comparative genomics resources. <i>Current Plant Biology</i> , 2016, 7-8, 10-15.	2.3	51
56	Genome-Wide Computational Prediction and Analysis of Core Promoter Elements across Plant Monocots and Dicots. <i>PLoS ONE</i> , 2013, 8, e79011.	1.1	45
57	Plant Reactome: a knowledgebase and resource for comparative pathway analysis. <i>Nucleic Acids Research</i> , 2020, 48, D1093-D1103.	6.5	44
58	Disentangling Methodological and Biological Sources of Gene Tree Discordance on <i>Oryza</i> (Poaceae) Chromosome 3. <i>Systematic Biology</i> , 2014, 63, 645-659.	2.7	43
59	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020, 11, 2288.	5.8	39
60	Efficient Identification of Causal Mutations through Sequencing of Bulk F2 from Two Allelic Bloomless Mutants of <i>Sorghum bicolor</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2267.	1.7	36
61	The <i>Oryza</i> BAC resource: a genus-wide and genome scale tool for exploring rice genome evolution and leveraging useful genetic diversity from wild relatives. <i>Breeding Science</i> , 2010, 60, 536-543.	0.9	34
62	Fertility of Pedicellate Spikelets in <i>Sorghum</i> Is Controlled by a Jasmonic Acid Regulatory Module. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4951.	1.8	31
63	Expanding and Vetting <i>Sorghum bicolor</i> Gene Annotations through Transcriptome and Methylome Sequencing. <i>Plant Genome</i> , 2014, 7, plantgenome2013.08.0025.	1.6	26
64	Amino Acid and Carbohydrate Metabolism Are Coordinated to Maintain Energetic Balance during Drought in Sugarcane. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9124.	1.8	25
65	<i>Sorghum</i> MSD3 Encodes an Δ^3 Fatty Acid Desaturase that Increases Grain Number by Reducing Jasmonic Acid Levels. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5359.	1.8	24
66	Gramene: A Resource for Comparative Analysis of Plants Genomes and Pathways. <i>Methods in Molecular Biology</i> , 2022, 2443, 101-131.	0.4	23
67	GrameneMart: the BioMart data portal for the Gramene project. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar056-bar056.	1.4	22
68	The Dominant and Poorly Penetrant Phenotypes of Maize <i>Unstable factor for orange1</i> Are Caused by DNA Methylation Changes at a Linked Transposon. <i>Plant Cell</i> , 2018, 30, 3006-3023.	3.1	21
69	SciApps: a cloud-based platform for reproducible bioinformatics workflows. <i>Bioinformatics</i> , 2018, 34, 3917-3920.	1.8	21
70	Variant phasing and haplotypic expression from long-read sequencing in maize. <i>Communications Biology</i> , 2020, 3, 78.	2.0	20
71	Gramene: A Resource for Comparative Analysis of Plants Genomes and Pathways. <i>Methods in Molecular Biology</i> , 2016, 1374, 141-163.	0.4	15
72	<i>Sorghum</i> Base: a web-based portal for sorghum genetic information and community advancement. <i>Planta</i> , 2022, 255, 35.	1.6	12

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73	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509.	2.3	11
74	BSAseq: an interactive and integrated web-based workflow for identification of causal mutations in bulked F2 populations. <i>Bioinformatics</i> , 2021, 37, 382-387.	1.8	11
75	Double triage to identify poorly annotated genes in maize: The missing link in community curation. <i>PLoS ONE</i> , 2019, 14, e0224086.	1.1	10
76	Gramene. , 2007, 406, 315-329.		8
77	Phylogenomic Analysis of BAC-end Sequence Libraries in <i>Oryza</i> (Poaceae). <i>Systematic Botany</i> , 2010, 35, 512-523.	0.2	8
78	Gene disruption by structural mutations drives selection in US rice breeding over the last century. <i>PLoS Genetics</i> , 2021, 17, e1009389.	1.5	6
79	A genome-wide association study platform built on iPlant cyberinfrastructure. <i>Concurrency Computation Practice and Experience</i> , 2015, 27, 420-432.	1.4	5
80	Sorghum root epigenetic landscape during limiting phosphorus conditions. <i>Plant Direct</i> , 2022, 6, .	0.8	5
81	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. <i>Frontiers in Plant Science</i> , 2020, 11, 289.	1.7	4
82	Ranked choice voting for representative transcripts with TRaCE. <i>Bioinformatics</i> , 2021, 38, 261-264.	1.8	4
83	A KBase case study on genome-wide transcriptomics and plant primary metabolism in response to drought stress in Sorghum.. <i>Current Plant Biology</i> , 2021, 28, 100229.	2.3	4
84	Pedigreed Mutant Library-A Unique Resource for Sorghum Improvement and Genomics. <i>Agronomy</i> , 0, , 73-96.	0.2	1
85	SciApps: An Automated Platform for Processing and Distribution of Plant Genomics Data. <i>Methods in Molecular Biology</i> , 2022, 2443, 197-209.	0.4	0