

Doreen H Ware

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

91
papers

18,536
citations

44
h-index

98
g-index

98
ext. papers

23,330
ext. citations

13.8
avg, IF

5.6
L-index

#	Paper	IF	Citations
91	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , 2009 , 326, 1112-5	33.3	2949
90	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009 , 457, 551-6	50.4	2200
89	The genetic architecture of maize flowering time. <i>Science</i> , 2009 , 325, 714-8	33.3	1043
88	Development and mapping of 2240 new SSR markers for rice (<i>Oryza sativa</i> L.). <i>DNA Research</i> , 2002 , 9, 199-207	4.5	1009
87	Genetic properties of the maize nested association mapping population. <i>Science</i> , 2009 , 325, 737-40	33.3	775
86	Evidence for network evolution in an Arabidopsis interactome map. <i>Science</i> , 2011 , 333, 601-7	33.3	689
85	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017 , 546, 524-527	50.4	643
84	A first-generation haplotype map of maize. <i>Science</i> , 2009 , 326, 1115-7	33.3	613
83	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012 , 44, 808-11	36.3	600
82	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012 , 44, 803-7	36.3	470
81	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015 , 43, W589-98	20.1	468
80	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, 3530-5	11.5	468
79	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. <i>Nature Genetics</i> , 2011 , 43, 163-8	36.3	444
78	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018 , 36, 566-569	44.5	419
77	Ensembl Genomes 2016: more genomes, more complexity. <i>Nucleic Acids Research</i> , 2016 , 44, D574-80	20.1	408
76	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018 , 46, D802-D808	20.1	330
75	Unveiling the complexity of the maize transcriptome by single-molecule long-read sequencing. <i>Nature Communications</i> , 2016 , 7, 11708	17.4	322

74	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011 , 2, 34	6.2	306
73	A genome-wide characterization of microRNA genes in maize. <i>PLoS Genetics</i> , 2009 , 5, e1000716	6	265
72	MAKER-P: a tool kit for the rapid creation, management, and quality control of plant genome annotations. <i>Plant Physiology</i> , 2014 , 164, 513-24	6.6	260
71	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. <i>Genome Research</i> , 2010 , 20, 1689-99	9.7	236
70	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	36.3	229
69	ZmCCT 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 ^{11.5}	11.5	226
68	Ensembl Genomes 2020-enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020 , 48, D689-D695	20.1	214
67	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018 , 50, 1289-1295	36.3	201
66	The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. <i>Genome Research</i> , 2013 , 23, 1651-62	9.7	199
65	The iPlant Collaborative: Cyberinfrastructure for Enabling Data to Discovery for the Life Sciences. <i>PLoS Biology</i> , 2016 , 14, e1002342	9.7	191
64	Ensembl Genomes 2013: scaling up access to genome-wide data. <i>Nucleic Acids Research</i> , 2014 , 42, D546-52.1	20.1	179
63	Rapid genomic characterization of the genus <i>vitis</i> . <i>PLoS ONE</i> , 2010 , 5, e8219	3.7	166
62	Gramene database in 2010: updates and extensions. <i>Nucleic Acids Research</i> , 2011 , 39, D1085-94	20.1	145
61	Gramene 2013: comparative plant genomics resources. <i>Nucleic Acids Research</i> , 2014 , 42, D1193-9	20.1	143
60	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. <i>Genome Biology</i> , 2019 , 20, 275	18.3	128
59	The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , 2018 , 50, 1282-1288	36.3	114
58	Gramene 2018: unifying comparative genomics and pathway resources for plant research. <i>Nucleic Acids Research</i> , 2018 , 46, D1181-D1189	20.1	107
57	Gramene 2016: comparative plant genomics and pathway resources. <i>Nucleic Acids Research</i> , 2016 , 44, D1133-40	20.1	102

56	Regulatory modules controlling maize inflorescence architecture. <i>Genome Research</i> , 2014 , 24, 431-43	9.7	102
55	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	5.8	72
54	A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses. <i>Plant Cell</i> , 2016 , 28, 1551-62	11.6	68
53	Characterization of miRNAs in response to short-term waterlogging in three inbred lines of Zea mays. <i>PLoS ONE</i> , 2012 , 7, e39786	3.7	65
52	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, 9645-50	11.5	60
51	A comparative transcriptional landscape of maize and sorghum obtained by single-molecule sequencing. <i>Genome Research</i> , 2018 , 28, 921-932	9.7	54
50	Plant Reactome: a resource for plant pathways and comparative analysis. <i>Nucleic Acids Research</i> , 2017 , 45, D1029-D1039	20.1	52
49	Maize Metabolic Network Construction and Transcriptome Analysis. <i>Plant Genome</i> , 2013 , 6, plantgenome.2012.00025	12.99	50
48	Reviving the Transcriptome Studies: An Insight Into the Emergence of Single-Molecule Transcriptome Sequencing. <i>Frontiers in Genetics</i> , 2019 , 10, 384	4.5	48
47	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> , 2015 , 167, 25-39	6.6	43
46	Gapless assembly of maize chromosomes using long-read technologies. <i>Genome Biology</i> , 2020 , 21, 121	18.3	41
45	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021 , 373, 655-662	33.3	40
44	Highly accurate long-read HiFi sequencing data for five complex genomes. <i>Scientific Data</i> , 2020 , 7, 399	8.2	39
43	Disentangling methodological and biological sources of gene tree discordance on Oryza (Poaceae) chromosome 3. <i>Systematic Biology</i> , 2014 , 63, 645-59	8.4	37
42	MSD1 regulates pedicellate spikelet fertility in sorghum through the jasmonic acid pathway. <i>Nature Communications</i> , 2018 , 9, 822	17.4	36
41	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	4.5	35
40	Gramene Database: Navigating Plant Comparative Genomics Resources. <i>Current Plant Biology</i> , 2016 , 7-8, 10-15	3.3	35
39	Genome-wide computational prediction and analysis of core promoter elements across plant monocots and dicots. <i>PLoS ONE</i> , 2013 , 8, e79011	3.7	33

38	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. <i>Nucleic Acids Research</i> , 2021 , 49, D1452-D1463	20.1	29
37	The Oryza 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	2	26
36	Haplotyping the <i>Vitis</i> collinear core genome with rhAmpSeq improves marker transferability in a diverse genus. <i>Nature Communications</i> , 2020 , 11, 413	17.4	24
35	Plant Reactome: a knowledgebase and resource for comparative pathway analysis. <i>Nucleic Acids Research</i> , 2020 , 48, D1093-D1103	20.1	24
34	Expanding and Vetting Sorghum bicolor Gene Annotations through Transcriptome and Methylome Sequencing. <i>Plant Genome</i> , 2014 , 7, plantgenome2013.08.0025	4.4	22
33	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020 , 11, 2288	17.4	21
32	Revealing gene regulation and associations through biological networks. <i>Current Plant Biology</i> , 2015 , 3-4, 30-39	3.3	21
31	GrameneMart: the BioMart data portal for the Gramene project. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bar056	5	21
30	Efficient Identification of Causal Mutations through Sequencing of Bulkcd F from Two Allelic Bloomless Mutants of. <i>Frontiers in Plant Science</i> , 2017 , 8, 2267	6.2	20
29	Fertility of Pedicellate Spikelets in Sorghum Is Controlled by a Jasmonic Acid Regulatory Module. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	17
28	Gramene: A Resource for Comparative Analysis of Plants Genomes and Pathways. <i>Methods in Molecular Biology</i> , 2016 , 1374, 141-63	1.4	14
27	The Dominant and Poorly Penetrant Phenotypes of Maize Are Caused by DNA Methylation Changes at a Linked Transposon. <i>Plant Cell</i> , 2018 , 30, 3006-3023	11.6	13
26	Identification of the First Nuclear Male Sterility Gene (Male-sterile 9) in Sorghum. <i>Plant Genome</i> , 2019 , 12, 1-12	4.4	11
25	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017 , 175, 1499-1509	6.6	10
24	Sorghum Encodes an Δ^6 Fatty Acid Desaturase that Increases Grain Number by Reducing Jasmonic Acid Levels. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	9
23	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes		9
22	Variant phasing and haplotypic expression from long-read sequencing in maize. <i>Communications Biology</i> , 2020 , 3, 78	6.7	8
21	SciApps: a cloud-based platform for reproducible bioinformatics workflows. <i>Bioinformatics</i> , 2018 , 34, 3917-3920	7.2	8

20	Gramene. <i>Methods in Molecular Biology</i> , 2007 , 406, 315-29	1.4	8
19	Phylogenomic Analysis of BAC-end Sequence Libraries in <i>Oryza</i> (Poaceae). <i>Systematic Botany</i> , 2010 , 35, 512-523	0.7	6
18	Double triage to identify poorly annotated genes in maize: The missing link in community curation. <i>PLoS ONE</i> , 2019 , 14, e0224086	3.7	5
17	Effect of Sequence Depth and Length in Long-read Assembly of the Maize Inbred NC358		5
16	Gramene: A Resource for Comparative Analysis of Plants Genomes and Pathways.. <i>Methods in Molecular Biology</i> , 2022 , 2443, 101-131	1.4	4
15	A genome-wide association study platform built on iPlant cyber-infrastructure. <i>Concurrency Computation Practice and Experience</i> , 2015 , 27, 420-432	1.4	3
14	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. <i>Frontiers in Plant Science</i> , 2020 , 11, 289	6.2	3
13	Gapless assembly of maize chromosomes using long read technologies		3
12	BSAseq: an interactive and integrated web-based workflow for identification of causal mutations in bulked F2 populations. <i>Bioinformatics</i> , 2021 , 37, 382-387	7.2	3
11	Pan-genome Analysis in Sorghum Highlights the Extent of Genomic Variation and Sugarcane Aphid Resistance Genes		3
10	Highly accurate long-read HiFi sequencing data for five complex genomes		2
9	Ranked Choice Voting for Representative Transcripts with TRaCE		2
8	Amino Acid and Carbohydrate Metabolism Are Coordinated to Maintain Energetic Balance during Drought in Sugarcane. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
7	Ranked Choice Voting for Representative Transcripts with TRaCE. <i>Bioinformatics</i> , 2021 ,	7.2	2
6	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	3.3	1
5	Pedigreed Mutant Library-A Unique Resource for Sorghum Improvement and Genomics. <i>Agronomy</i> , 2021 , 11, 73-96.8		1
4	Sorghum Root Epigenetic Landscape During Limiting Phosphorus Conditions		1
3	SorghumBase: a web-based portal for sorghum genetic information and community advancement.. <i>Planta</i> , 2022 , 255, 35	4.7	0

- 2 Gene disruption by structural mutations drives selection in US rice breeding over the last century. *PLoS Genetics*, **2021**, 17, e1009389 6 o
- 1 SciApps: An Automated Platform for Processing and Distribution of Plant Genomics Data.. *Methods in Molecular Biology*, **2022**, 2443, 197-209 1.4