

Carolyn Lawrence-Dill

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

3,858
citations

159585

30
h-index

155660

55
g-index

71
all docs

71
docs citations

71
times ranked

6314
citing authors

#	ARTICLE	IF	CITATIONS
1	A standardized kinesin nomenclature. <i>Journal of Cell Biology</i> , 2004, 167, 19-22.	5.2	662
2	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.	4.8	412
3	PlantGDB: a resource for comparative plant genomics. <i>Nucleic Acids Research</i> , 2007, 36, D959-D965.	14.5	246
4	Finding Our Way through Phenotypes. <i>PLoS Biology</i> , 2015, 13, e1002033.	5.6	178
5	MaizeGDB, the community database for maize genetics and genomics. <i>Nucleic Acids Research</i> , 2004, 32, 393D-397.	14.5	175
6	MaizeGDB update: new tools, data and interface for the maize model organism database. <i>Nucleic Acids Research</i> , 2016, 44, D1195-D1201.	14.5	170
7	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	12.8	105
8	Dyneins Have Run Their Course in Plant Lineage. <i>Traffic</i> , 2001, 2, 362-363.	2.7	100
9	The quest for understanding phenotypic variation via integrated approaches in the field environment. <i>Plant Physiology</i> , 2016, 172, pp.00592.2016.	4.8	99
10	Maize GO Annotation Methods, Evaluation, and Review (maizeGAMER). <i>Plant Direct</i> , 2018, 2, e00052.	1.9	97
11	Comparative Plant Genomics Resources at PlantGDB. <i>Plant Physiology</i> , 2005, 139, 610-618.	4.8	95
12	MaizeGDB: The Maize Model Organism Database for Basic, Translational, and Applied Research. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-10.	2.2	95
13	The Locus Lookup tool at MaizeGDB: identification of genomic regions in maize by integrating sequence information with physical and genetic maps. <i>Bioinformatics</i> , 2010, 26, 434-436.	4.1	83
14	A quick guide to CRISPR sgRNA design tools. <i>GM Crops and Food</i> , 2015, 6, 266-276.	3.8	80
15	High-frequency random DNA insertions upon co-delivery of CRISPR-Cas9 ribonucleoprotein and selectable marker plasmid in rice. <i>Scientific Reports</i> , 2019, 9, 19902.	3.3	70
16	Response to Persistent ER Stress in Plants: A Multiphasic Process That Transitions Cells from Prosurvival Activities to Cell Death. <i>Plant Cell</i> , 2018, 30, 1220-1242.	6.6	67
17	MaizeGDB: curation and outreach go hand-in-hand. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar022-bar022.	3.0	66
18	Maximum Likelihood Methods Reveal Conservation of Function Among Closely Related Kinesin Families. <i>Journal of Molecular Evolution</i> , 2002, 54, 42-53.	1.8	64

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19	Maize Metabolic Network Construction and Transcriptome Analysis. <i>Plant Genome</i> , 2013, 6, plantgenome2012.09.0025.	2.8	63
20	The Maize Genetics and Genomics Database. The Community Resource for Access to Diverse Maize Data. <i>Plant Physiology</i> , 2005, 138, 55-58.	4.8	59
21	Translational Genomics for Bioenergy Production from Fuelstock Grasses: Maize as the Model Species. <i>Plant Cell</i> , 2007, 19, 2091-2094.	6.6	57
22	MaizeGDB's new data types, resources and activities. <i>Nucleic Acids Research</i> , 2007, 35, D895-D900.	14.5	56
23	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.	4.8	53
24	An ontology approach to comparative phenomics in plants. <i>Plant Methods</i> , 2015, 11, 10.	4.3	53
25	GenomeQC: a quality assessment tool for genome assemblies and gene structure annotations. <i>BMC Genomics</i> , 2020, 21, 193.	2.8	52
26	G-Quadruplex (G4) Motifs in the Maize (<i>Zea mays</i> L.) Genome Are Enriched at Specific Locations in Thousands of Genes Coupled to Energy Status, Hypoxia, Low Sugar, and Nutrient Deprivation. <i>Journal of Genetics and Genomics</i> , 2014, 41, 627-647.	3.9	49
27	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. <i>PLoS Computational Biology</i> , 2018, 14, e1006337.	3.2	48
28	MaizeGDB becomes 'sequence-centric'. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2009, bap020-bap020.	3.0	44
29	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. <i>Frontiers in Genetics</i> , 2020, 11, 592769.	2.3	44
30	MaizeGDB: The Maize Genetics and Genomics Database. <i>Methods in Molecular Biology</i> , 2016, 1374, 187-202.	0.9	37
31	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , 2019, 29, 1962-1973.	5.5	35
32	Maize chromosomal knobs are located in gene-dense areas and suppress local recombination. <i>Chromosoma</i> , 2013, 122, 67-75.	2.2	33
33	Choosing a genome browser for a Model Organism Database: surveying the Maize community. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq007.	3.0	31
34	Predicting Chromosomal Locations of Genetically Mapped Loci in Maize Using the Morgan2McClintock Translator. <i>Genetics</i> , 2006, 172, 2007-2009.	2.9	26
35	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , 2018, 11, 452.	1.4	25
36	Relative utility of agronomic, phenological, and morphological traits for assessing genotype × environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	1.8	21

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37	Gene Ontology Meta Annotator for Plants (GOMAP). <i>Plant Methods</i> , 2021, 17, 54.	4.3	21
38	POPCorn: An Online Resource Providing Access to Distributed and Diverse Maize Project Data. <i>International Journal of Plant Genomics</i> , 2011, 2011, 1-10.	2.2	20
39	Idea Factory: the Maize Genomes to Fields Initiative. <i>Crop Science</i> , 2019, 59, 1406-1410.	1.8	18
40	High-throughput linkage analysis of <i> Mutator </i> insertion sites in maize. <i>Plant Journal</i> , 2009, 58, 883-892.	5.7	16
41	BioExtract Server: An Integrated Workflow-Enabling System to Access and Analyze Heterogeneous, Distributed Biomolecular Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 12-24.	3.0	16
42	Emerging semantics to link phenotype and environment. <i>PeerJ</i> , 2015, 3, e1470.	2.0	15
43	Effects of mild night chilling on respiration of expanding cotton leaves. <i>Plant Science</i> , 2000, 157, 233-244.	3.6	14
44	Assessing plant performance in the Enviratron. <i>Plant Methods</i> , 2019, 15, 117.	4.3	13
45	Sowing the seeds of skepticism: Russian state news and anti-GMO sentiment. <i>GM Crops and Food</i> , 2018, 9, 53-58.	3.8	10
46	Automated Methods Enable Direct Computation on Phenotypic Descriptions for Novel Candidate Gene Prediction. <i>Frontiers in Plant Science</i> , 2019, 10, 1629.	3.6	10
47	MaizeDIG: Maize Database of Images and Genomes. <i>Frontiers in Plant Science</i> , 2019, 10, 1050.	3.6	9
48	MaizeGDB. , 2007, 406, 331-345.		6
49	Multi-source and ontology-based retrieval engine for maize mutant phenotypes. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar012-bar012.	3.0	6
50	LumberJack: a heuristic tool for sequence alignment exploration and phylogenetic inference. <i>Bioinformatics</i> , 2004, 20, 1977-1979.	4.1	5
51	Computing on Phenotypic Descriptions for Candidate Gene Discovery and Crop Improvement. <i>Plant Phenomics</i> , 2020, 2020, 1963251.	5.9	5
52	Plant Genome Research Outreach Portal. A Gateway to Plant Genome Research "Outreach" Programs and Activities. <i>Plant Physiology</i> , 2004, 134, 889-889.	4.8	4
53	A hypothesis-driven approach to assessing significance of differences in RNA expression levels among specific groups of genes. <i>Current Plant Biology</i> , 2017, 11-12, 46-51.	4.7	4
54	Transdisciplinary Graduate Training in Predictive Plant Phenomics. <i>Agronomy</i> , 2018, 8, 73.	3.0	3

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55	Standardized genome-wide function prediction enables comparative functional genomics: a new application area for Gene Ontologies in plants. <i>GigaScience</i> , 2022, 11, .	6.4	2
56	An Interdisciplinary Graduate Course for Engineers, Plant Scientists, and Data Scientists in the Area of Predictive Plant Phenomics. , 0, , .		1
57	Ten simple rules to ruin a collaborative environment. <i>PLoS Computational Biology</i> , 2022, 18, e1009957.	3.2	1
58	Reply: Specific Reasons to Favor Maize in the U.S.. <i>Plant Cell</i> , 2007, 19, 2973-2973.	6.6	0
59	Databases and Data Mining. , 2009, , 659-672.		0
60	MaizeGDB , maize genetics cooperation and the ~2500MB B73 genome generated tsunami. <i>Nature Precedings</i> , 2010, , .	0.1	0
61	Plant Cytogenetics in Genome Databases. , 2012, , 311-322.		0
62	Compare Expression Profiles for Pre-defined Gene Groups with C-REx. <i>Journal of Open Source Software</i> , 2019, 4, 1255.	4.6	0
63	Board # 78 : Training Students with T-shaped Interdisciplinary Studies in Predictive Plant Phenomics. , 0, , .		0