

Carolyn Lawrence-Dill

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

3,858
citations

159358

30
h-index

155451

55
g-index

71
all docs

71
docs citations

71
times ranked

6314
citing authors

#	ARTICLE	IF	CITATIONS
1	Standardized genome-wide function prediction enables comparative functional genomics: a new application area for Gene Ontologies in plants. <i>GigaScience</i> , 2022, 11, .	3.3	2
2	Ten simple rules to ruin a collaborative environment. <i>PLoS Computational Biology</i> , 2022, 18, e1009957.	1.5	1
3	Gene Ontology Meta Annotator for Plants (GOMAP). <i>Plant Methods</i> , 2021, 17, 54.	1.9	21
4	Relative utility of agronomic, phenological, and morphological traits for assessing genotype×environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	0.8	21
5	GenomeQC: a quality assessment tool for genome assemblies and gene structure annotations. <i>BMC Genomics</i> , 2020, 21, 193.	1.2	52
6	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.	1.1	44
7	Computing on Phenotypic Descriptions for Candidate Gene Discovery and Crop Improvement. <i>Plant Phenomics</i> , 2020, 2020, 1963251.	2.5	5
8	MaizeDIG: Maize Database of Images and Genomes. <i>Frontiers in Plant Science</i> , 2019, 10, 1050.	1.7	9
9	Assessing plant performance in the Enviratron. <i>Plant Methods</i> , 2019, 15, 117.	1.9	13
10	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.	1.6	70
11	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , 2019, 29, 1962-1973.	2.4	35
12	Idea Factory: the Maize Genomes to Fields Initiative. <i>Crop Science</i> , 2019, 59, 1406-1410.	0.8	18
13	Automated Methods Enable Direct Computation on Phenotypic Descriptions for Novel Candidate Gene Prediction. <i>Frontiers in Plant Science</i> , 2019, 10, 1629.	1.7	10
14	Compare Expression Profiles for Pre-defined Gene Groups with C-REX. <i>Journal of Open Source Software</i> , 2019, 4, 1255.	2.0	0
15	Sowing the seeds of skepticism: Russian state news and anti-GMO sentiment. <i>GM Crops and Food</i> , 2018, 9, 53-58.	2.0	10
16	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. <i>PLoS Computational Biology</i> , 2018, 14, e1006337.	1.5	48
17	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.	3.1	67
18	Maize GO Annotation—Methods, Evaluation, and Review (maize—GAMER). <i>Plant Direct</i> , 2018, 2, e00052.	0.8	97

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19	Transdisciplinary Graduate Training in Predictive Plant Phenomics. <i>Agronomy</i> , 2018, 8, 73.	1.3	3
20	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.	0.6	25
21	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	5.8	105
22	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.	2.3	4
23	The quest for understanding phenotypic variation via integrated approaches in the field environment. <i>Plant Physiology</i> , 2016, 172, pp.00592.2016.	2.3	99
24	MaizeGDB update: new tools, data and interface for the maize model organism database. <i>Nucleic Acids Research</i> , 2016, 44, D1195-D1201.	6.5	170
25	MaizeGDB: The Maize Genetics and Genomics Database. <i>Methods in Molecular Biology</i> , 2016, 1374, 187-202.	0.4	37
26	A quick guide to CRISPR sgRNA design tools. <i>GM Crops and Food</i> , 2015, 6, 266-276.	2.0	80
27	Finding Our Way through Phenotypes. <i>PLoS Biology</i> , 2015, 13, e1002033.	2.6	178
28	An ontology approach to comparative phenomics in plants. <i>Plant Methods</i> , 2015, 11, 10.	1.9	53
29	Emerging semantics to link phenotype and environment. <i>PeerJ</i> , 2015, 3, e1470.	0.9	15
30	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
31	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.	1.7	49
32	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
33	Maize chromosomal knobs are located in gene-dense areas and suppress local recombination. <i>Chromosoma</i> , 2013, 122, 67-75.	1.0	33
34	Maize Metabolic Network Construction and Transcriptome Analysis. <i>Plant Genome</i> , 2013, 6, plantgenome2012.09.0025.	1.6	63
35	Plant Cytogenetics in Genome Databases. , 2012, , 311-322.		0
36	MaizeGDB: curation and outreach go hand-in-hand. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar022-bar022.	1.4	66

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37	POPcorn: An Online Resource Providing Access to Distributed and Diverse Maize Project Data. International Journal of Plant Genomics, 2011, 2011, 1-10.	2.2	20
38	Multi-source and ontology-based retrieval engine for maize mutant phenotypes. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar012-bar012.	1.4	6
39	MaizeGDB , maize genetics cooperation and the ~2500MB B73 genome generated tsunami. Nature Precedings, 2010, , .	0.1	0
40	The Locus Lookup tool at MaizeGDB: identification of genomic regions in maize by integrating sequence information with physical and genetic maps. Bioinformatics, 2010, 26, 434-436.	1.8	83
41	Choosing a genome browser for a Model Organism Database: surveying the Maize community. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq007.	1.4	31
42	MaizeGDB becomes 'sequence-centric'. Database: the Journal of Biological Databases and Curation, 2010, 2009, bap020-bap020.	1.4	44
43	BioExtract Server – An Integrated Workflow-Enabling System to Access and Analyze Heterogeneous, Distributed Biomolecular Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 12-24.	1.9	16
44	High-throughput linkage analysis of <i>Mutator</i> insertion sites in maize. Plant Journal, 2009, 58, 883-892.	2.8	16
45	Databases and Data Mining. , 2009, , 659-672.		0
46	MaizeGDB: The Maize Model Organism Database for Basic, Translational, and Applied Research. International Journal of Plant Genomics, 2008, 2008, 1-10.	2.2	95
47	Translational Genomics for Bioenergy Production from Fuelstock Grasses: Maize as the Model Species. Plant Cell, 2007, 19, 2091-2094.	3.1	57
48	Reply: Specific Reasons to Favor Maize in the U.S.. Plant Cell, 2007, 19, 2973-2973.	3.1	0
49	PlantGDB: a resource for comparative plant genomics. Nucleic Acids Research, 2007, 36, D959-D965.	6.5	246
50	MaizeGDB's new data types, resources and activities. Nucleic Acids Research, 2007, 35, D895-D900.	6.5	56
51	MaizeGDB. , 2007, 406, 331-345.		6
52	Predicting Chromosomal Locations of Genetically Mapped Loci in Maize Using the Morgan2McClintock Translator. Genetics, 2006, 172, 2007-2009.	1.2	26
53	Comparative Plant Genomics Resources at PlantGDB. Plant Physiology, 2005, 139, 610-618.	2.3	95
54	The Maize Genetics and Genomics Database. The Community Resource for Access to Diverse Maize Data. Plant Physiology, 2005, 138, 55-58.	2.3	59

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55	Plant Genome Research Outreach Portal. A Gateway to Plant Genome Research "Outreach" Programs and Activities. <i>Plant Physiology</i> , 2004, 134, 889-889.	2.3	4
56	LumberJack: a heuristic tool for sequence alignment exploration and phylogenetic inference. <i>Bioinformatics</i> , 2004, 20, 1977-1979.	1.8	5
57	MaizeGDB, the community database for maize genetics and genomics. <i>Nucleic Acids Research</i> , 2004, 32, 393D-397.	6.5	175
58	A standardized kinesin nomenclature. <i>Journal of Cell Biology</i> , 2004, 167, 19-22.	2.3	662
59	Maximum Likelihood Methods Reveal Conservation of Function Among Closely Related Kinesin Families. <i>Journal of Molecular Evolution</i> , 2002, 54, 42-53.	0.8	64
60	Dyneins Have Run Their Course in Plant Lineage. <i>Traffic</i> , 2001, 2, 362-363.	1.3	100
61	Effects of mild night chilling on respiration of expanding cotton leaves. <i>Plant Science</i> , 2000, 157, 233-244.	1.7	14
62	Board # 78 : Training Students with T-shaped Interdisciplinary Studies in Predictive Plant Phenomics. , 0, , .		0
63	An Interdisciplinary Graduate Course for Engineers, Plant Scientists, and Data Scientists in the Area of Predictive Plant Phenomics. , 0, , .		1