Carolyn Lawrence-Dill

List of Publications by Year
in descending order

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	Standardized genome-wide function prediction enables comparative functional genomics: a new application area for Gene Ontologies in plants. GigaScience, 2022, 11, .	6.4	2
2	Ten simple rules to ruin a collaborative environment. PLoS Computational Biology, 2022, 18, e1009957.	3.2	1
3	Gene Ontology Meta Annotator for Plants (GOMAP). Plant Methods, 2021, 17, 54.	4.3	21
4	Relative utility of agronomic, phenological, and morphological traits for assessing genotype‐by‐environment interaction in maize inbreds. Crop Science, 2020, 60, 62-81.	1.8	21
5	GenomeQC: a quality assessment tool for genome assemblies and gene structure annotations. BMC Genomics, 2020, 21, 193.	2.8	52
6	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. Frontiers in Genetics, 2020, 11, 592769.	2.3	44
7	Computing on Phenotypic Descriptions for Candidate Gene Discovery and Crop Improvement. Plant Phenomics, 2020, 2020, 1963251.	5.9	5
8	MaizeDIG: Maize Database of Images and Genomes. Frontiers in Plant Science, 2019, 10, 1050.	3.6	9
9	Assessing plant performance in the Enviratron. Plant Methods, 2019, 15, 117.	4.3	13
10	High-frequency random DNA insertions upon co-delivery of CRISPR-Cas9 ribonucleoprotein and selectable marker plasmid in rice. Scientific Reports, 2019, 9, 19902.	3.3	70
11	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. Genome Research, 2019, 29, 1962-1973.	5.5	35
12	Idea Factory: the Maize Genomes to Fields Initiative. Crop Science, 2019, 59, 1406-1410.	1.8	18
13	Automated Methods Enable Direct Computation on Phenotypic Descriptions for Novel Candidate Gene Prediction. Frontiers in Plant Science, 2019, 10, 1629.	3.6	10
14	Compare Expression Profiles for Pre-defined Gene Groups with C-REx. Journal of Open Source Software, 2019, 4, 1255.	4.6	0
15	Sowing the seeds of skepticism: Russian state news and anti-GMO sentiment. GM Crops and Food, 2018, 9, 53-58.	3.8	10
16	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. PLoS Computational Biology, 2018, 14, e1006337.	3.2	48
17	Response to Persistent ER Stress in Plants: A Multiphasic Process That Transitions Cells from Prosurvival Activities to Cell Death. Plant Cell, 2018, 30, 1220-1242.	6.6	67
18	Maize GO Annotation—Methods, Evaluation, and Review (maize‐GAMER). Plant Direct, 2018, 2, e00052.	1.9	97

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19	Transdisciplinary Graduate Training in Predictive Plant Phenomics. Agronomy, 2018, 8, 73.	3.0	3
20	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. BMC Research Notes, 2018, 11, 452.	1.4	25
21	The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.	12.8	105
22	A hypothesis-driven approach to assessing significance of differences in RNA expression levels among specific groups of genes. Current Plant Biology, 2017, 11-12, 46-51.	4.7	4
23	The quest for understanding phenotypic variation via integrated approaches in the field environment. Plant Physiology, 2016, 172, pp.00592.2016.	4.8	99
24	MaizeGDB update: new tools, data and interface for the maize model organism database. Nucleic Acids Research, 2016, 44, D1195-D1201.	14.5	170
25	MaizeGDB: The Maize Genetics and Genomics Database. Methods in Molecular Biology, 2016, 1374, 187-202.	0.9	37
26	A quick guide to CRISPR sgRNA design tools. GM Crops and Food, 2015, 6, 266-276.	3.8	80
27	Finding Our Way through Phenotypes. PLoS Biology, 2015, 13, e1002033.	5.6	178
28	An ontology approach to comparative phenomics in plants. Plant Methods, 2015, 11, 10.	4.3	53
29	Emerging semantics to link phenotype and environment. PeerJ, 2015, 3, e1470.	2.0	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 Â. Plant Physiology, 2014, 167, 25-39.	4.8	53
31	G-Quadruplex (G4) Motifs in the Maize (Zea mays L.) Genome Are Enriched at Specific Locations in Thousands of Genes Coupled to Energy Status, Hypoxia, Low Sugar, and Nutrient Deprivation. Journal of Genetics and Genomics, 2014, 41, 627-647.	3.9	49
32	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
33	Maize chromosomal knobs are located in gene-dense areas and suppress local recombination. Chromosoma, 2013, 122, 67-75.	2.2	33
34	Maize Metabolic Network Construction and Transcriptome Analysis. Plant Genome, 2013, 6, plantgenome2012.09.0025.	2.8	63
35	Plant Cytogenetics in Genome Databases. , 2012, , 311-322.		0
36	MaizeGDB: curation and outreach go hand-in-hand. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar022-bar022.	3.0	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.	3.0	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.	4.1	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.	3.0	31
42	MaizeGDB becomes 'sequence-centric'. Database: the Journal of Biological Databases and Curation, 2010, 2009, bap020-bap020.	3.0	44
43	BioExtract Serverâ€"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.	3.0	16
44	Highâ€throughput linkage analysis of <i>Mutator</i> insertion sites in maize. Plant Journal, 2009, 58, 883-892.	5.7	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.	6.6	57
48	Reply: Specific Reasons to Favor Maize in the U.S.. Plant Cell, 2007, 19, 2973-2973.	6.6	0
49	PlantGDB: a resource for comparative plant genomics. Nucleic Acids Research, 2007, 36, D959-D965.	14.5	246
50	MaizeGDB's new data types, resources and activities. Nucleic Acids Research, 2007, 35, D895-D900.	14.5	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.	2.9	26
53	Comparative Plant Genomics Resources at PlantGDB. Plant Physiology, 2005, 139, 610-618.	4.8	95
54	The Maize Genetics and Genomics Database. The Community Resource for Access to Diverse Maize Data. Plant Physiology, 2005, 138, 55-58.	4.8	59

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55	Plant Genome Research Outreach Portal. A Gateway to Plant Genome Research "Outreach" Programs and Activities. Plant Physiology, 2004, 134, 889-889.	4.8	4
56	LumberJack: a heuristic tool for sequence alignment exploration and phylogenetic inference. Bioinformatics, 2004, 20, 1977-1979.	4.1	5
57	MaizeGDB, the community database for maize genetics and genomics. Nucleic Acids Research, 2004, 32, 393D-397.	14.5	175
58	A standardized kinesin nomenclature. Journal of Cell Biology, 2004, 167, 19-22.	5.2	662
59	Maximum Likelihood Methods Reveal Conservation of Function Among Closely Related Kinesin Families. Journal of Molecular Evolution, 2002, 54, 42-53.	1.8	64
60	Dyneins Have Run Their Course in Plant Lineage. Traffic, 2001, 2, 362-363.	2.7	100
61	Effects of mild night chilling on respiration of expanding cotton leaves. Plant Science, 2000, 157, 233-244.	3.6	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