

Sherry A Flint-Garcia

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.

61
papers

6,725
citations

25
h-index

72
g-index

72
ext. papers

8,311
ext. citations

6.3
avg, IF

5.31
L-index

#	Paper	IF	Citations
61	Structure of linkage disequilibrium in plants. <i>Annual Review of Plant Biology</i> , 2003 , 54, 357-74	30.7	1125
60	The genetic architecture of maize flowering time. <i>Science</i> , 2009 , 325, 714-8	33.3	1043
59	Genetic properties of the maize nested association mapping population. <i>Science</i> , 2009 , 325, 737-40	33.3	775
58	Genome-wide association study of leaf architecture in the maize nested association mapping population. <i>Nature Genetics</i> , 2011 , 43, 159-62	36.3	746
57	Maize association population: a high-resolution platform for quantitative trait locus dissection. <i>Plant Journal</i> , 2005 , 44, 1054-64	6.9	633
56	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , 2013 , 14, R55	18.3	337
55	Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels. <i>Plant Physiology</i> , 2012 , 158, 824-34	6.6	242
54	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, E1913-215	11.5	226
53	The genetic architecture of maize height. <i>Genetics</i> , 2014 , 196, 1337-56	4	211
52	Distinct genetic architectures for male and female inflorescence traits of maize. <i>PLoS Genetics</i> , 2011 , 7, e1002383	6	175
51	Heterosis is prevalent for multiple traits in diverse maize germplasm. <i>PLoS ONE</i> , 2009 , 4, e7433	3.7	116
50	The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. <i>Heredity</i> , 2012 , 108, 490-9	3.6	96
49	Photoperiod-Insensitive Japanese Soybean Landraces Differ at Two Maturity Loci. <i>Crop Science</i> , 2003 , 43, 13	2.4	90
48	Genetics and consequences of crop domestication. <i>Journal of Agricultural and Food Chemistry</i> , 2013 , 61, 8267-76	5.7	83
47	The genetic architecture of maize stalk strength. <i>PLoS ONE</i> , 2013 , 8, e67066	3.7	81
46	Wide variability in kernel composition, seed characteristics, and zein profiles among diverse maize inbreds, landraces, and teosinte. <i>Theoretical and Applied Genetics</i> , 2009 , 119, 1129-42	6	73
45	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017 , 8, 1348	17.4	58

44	Phenotypic versus marker-assisted selection for stalk strength and second-generation European corn borer resistance in maize. <i>Theoretical and Applied Genetics</i> , 2003 , 107, 1331-6	6	57
43	Tissue-specific patterns of a maize Myb transcription factor are epigenetically regulated. <i>Plant Journal</i> , 2001 , 27, 467-78	6.9	47
42	Optimal Designs for Genomic Selection in Hybrid Crops. <i>Molecular Plant</i> , 2019 , 12, 390-401	14.4	41
41	Physiological and genetic characterization of end-of-day far-red light response in maize seedlings. <i>Plant Physiology</i> , 2010 , 154, 173-86	6.6	33
40	Expanding Maize Genetic Resources with Predomestication Alleles: Maize-Teosinte Introgression Populations. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.07.0053	4.4	30
39	Insights into the effects of long-term artificial selection on seed size in maize. <i>Genetics</i> , 2014 , 198, 409-21		25
38	Identification of Alleles Conferring Resistance to Gray Leaf Spot in Maize Derived from its Wild Progenitor Species Teosinte. <i>Crop Science</i> , 2016 , 56, 209-218	2.4	25
37	Genetic Analysis of Kernel Traits in Maize-Teosinte Introgression Populations. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 2523-30	3.2	25
36	Genetic analysis of central carbon metabolism unveils an amino acid substitution that alters maize NAD-dependent isocitrate dehydrogenase activity. <i>PLoS ONE</i> , 2010 , 5, e9991	3.7	24
35	Metabolomic Assessment of Key Maize Resources: GC-MS and NMR Profiling of Grain from B73 Hybrids of the Nested Association Mapping (NAM) Founders and of Geographically Diverse Landraces. <i>Journal of Agricultural and Food Chemistry</i> , 2016 , 64, 2162-72	5.7	23
34	Hallauer's Tussock: a decade of selection for tropical-to-temperate phenological adaptation in maize. <i>Heredity</i> , 2015 , 114, 229-40	3.6	19
33	Mining Natural Variation for Maize Improvement: Selection on Phenotypes and Genes 2014 , 615-649		17
32	Association Mapping of Flowering and Height Traits in Germplasm Enhancement of Maize Doubled Haploid (GEM-DH) Lines. <i>Plant Genome</i> , 2018 , 11, 170083	4.4	17
31	Maize genomes to fields (G2F): 2014-2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020 , 13, 71	2.3	16
30	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	2.3	16
29	Registration of LamontDat. <i>Crop Science</i> , 2003 , 43, 23	2.4	15
28	Single-plant GWAS coupled with bulk segregant analysis allows rapid identification and corroboration of plant-height candidate SNPs. <i>BMC Plant Biology</i> , 2019 , 19, 412	5.3	12
27	Development of Rigorous Fatty Acid Near-Infrared Spectroscopy Quantitation Methods in Support of Soybean Oil Improvement. <i>JAOCS, Journal of the American Oil Chemists Society</i> , 2017 , 94, 69-76	1.8	12

26	Identification of Teosinte Alleles for Resistance to Southern Leaf Blight in Near Isogenic Maize Lines. <i>Crop Science</i> , 2017 , 57, 1973-1983	2.4	12
25	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , 2020 , 215, 215-230	4	12
24	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	12
23	Registration of the Maize Germplasm CRW3(S1)C6 with Resistance to Western Corn Rootworm. <i>Journal of Plant Registrations</i> , 2007 , 1, 151-152	0.7	11
22	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	4.5	11
21	The Genomic Basis for Short-Term Evolution of Environmental Adaptation in Maize. <i>Genetics</i> , 2019 , 213, 1479-1494	4	11
20	Conventional screening overlooks resistance sources: rootworm damage of diverse inbred lines and their B73 hybrids is unrelated. <i>Journal of Economic Entomology</i> , 2009 , 102, 1317-24	2.2	10
19	Genetic Analysis of Teosinte Alleles for Kernel Composition Traits in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1157-1164	3.2	9
18	DNAAlignEditor: DNA alignment editor tool. <i>BMC Bioinformatics</i> , 2008 , 9, 154	3.6	9
17	Stability Analysis of Kernel Quality Traits in Exotic-Derived Doubled Haploid Maize Lines. <i>Plant Genome</i> , 2019 , 12, 170114	4.4	8
16	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , 2020 , 60, 62-81	2.4	7
15	Quantitative Trait Loci Mapping of Western Corn Rootworm (Coleoptera: Chrysomelidae) Host Plant Resistance in Two Populations of Doubled Haploid Lines in Maize (<i>Zea mays</i> L.). <i>Journal of Economic Entomology</i> , 2018 , 111, 435-444	2.2	6
14	Hybrid Decay: A Transgenerational Epigenetic Decline in Vigor and Viability Triggered in Backcross Populations of Teosinte with Maize. <i>Genetics</i> , 2019 , 213, 143-160	4	6
13	Germplasm Resources for Mapping Quantitative Traits in Maize. <i>Compendium of Plant Genomes</i> , 2018 , 143-159	0.8	5
12	Genetic variability of oxalate oxidase activity and elongation in water-stressed primary roots of diverse maize and rice lines. <i>Plant Signaling and Behavior</i> , 2013 , 8, e23454	2.5	4
11	Genetic Analysis of Lodging in Diverse Maize Hybrids		4
10	Compositional Variation in -Ferulic, -coumaric, and Diferulic Acids Levels Among Kernels of Modern and Traditional Maize (L.) Hybrids. <i>Frontiers in Nutrition</i> , 2020 , 7, 600747	6.2	4
9	Compositional assessments of key maize populations: B73 hybrids of the Nested Association Mapping founder lines and diverse landrace inbred lines. <i>Journal of Agricultural and Food Chemistry</i> , 2015 , 63, 5282-95	5.7	3

8	Assessment of Natural Variability of Maize Lipid Transfer Protein Using a Validated Sandwich ELISA. <i>Journal of Agricultural and Food Chemistry</i> , 2017 , 65, 1740-1749	5.7	2
7	The role of ear environment in postharvest susceptibility of maize to toxigenic <i>Aspergillus flavus</i> . <i>Plant Breeding</i> , 2019 , 138, 38-50	2.4	2
6	Genetic control of kernel compositional variation in a maize diversity panel. <i>Plant Genome</i> , 2021 , 14, e20115	4.4	2
5	IView: introgression library visualization and query tool. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 6, S28	3.6	1
4	A B73Palomero ToluqueB mapping population reveals local adaptation in Mexican highland maize.. <i>G3: Genes, Genomes, Genetics</i> , 2022 ,	3.2	1
3	Genetic Architecture of Kernel Compositional Variation in a Maize Diversity Panel		1
2	Predicting moisture content during maize nixtamalization using machine learning with NIR spectroscopy. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 3743-3757	6	1
1	Multimiomics approach reveals a role of translational machinery in shaping maize kernel amino acid composition. <i>Plant Physiology</i> , 2021 ,	6.6	1