

Sherry A Flint-Garcia

List of Publications by Year in descending order

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64
papers

9,090
citations

172457

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123424

61
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72
all docs

72
docs citations

72
times ranked

7419
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of Linkage Disequilibrium in Plants. <i>Annual Review of Plant Biology</i> , 2003, 54, 357-374.	18.7	1,456
2	The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718.	12.6	1,284
3	Genome-wide association study of leaf architecture in the maize nested association mapping population. <i>Nature Genetics</i> , 2011, 43, 159-162.	21.4	987
4	Genetic Properties of the Maize Nested Association Mapping Population. <i>Science</i> , 2009, 325, 737-740.	12.6	959
5	Maize association population: a high-resolution platform for quantitative trait locus dissection. <i>Plant Journal</i> , 2005, 44, 1054-1064.	5.7	821
6	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , 2013, 14, R55.	8.8	458
7	The Genetic Architecture Of Maize Height. <i>Genetics</i> , 2014, 196, 1337-1356.	2.9	329
8	Genetic Architecture of Maize Kernel Composition in the Nested Association Mapping and Inbred Association Panels A. <i>Plant Physiology</i> , 2012, 158, 824-834.	4.8	307
9	<i>ZmCCT</i> 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.	7.1	290
10	Distinct Genetic Architectures for Male and Female Inflorescence Traits of Maize. <i>PLoS Genetics</i> , 2011, 7, e1002383.	3.5	231
11	Heterosis Is Prevalent for Multiple Traits in Diverse Maize Germplasm. <i>PLoS ONE</i> , 2009, 4, e7433.	2.5	173
12	Quantitative Trait Locus Analysis of Stalk Strength in Four Maize Populations. <i>Crop Science</i> , 2003, 43, 13.	1.8	132
13	The Genetic Architecture of Maize Stalk Strength. <i>PLoS ONE</i> , 2013, 8, e67066.	2.5	129
14	The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. <i>Heredity</i> , 2012, 108, 490-499.	2.6	128
15	Genetics and Consequences of Crop Domestication. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 8267-8276.	5.2	123
16	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, 1129-1142.	3.6	118
17	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	12.8	105
18	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, 1331-1336.	3.6	71

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19	Optimal Designs for Genomic Selection in Hybrid Crops. <i>Molecular Plant</i> , 2019, 12, 390-401.	8.3	63
20	Tissue-specific patterns of a maize Myb transcription factor are epigenetically regulated. <i>Plant Journal</i> , 2001, 27, 467-478.	5.7	56
21	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, .	1.8	52
22	Physiological and Genetic Characterization of End-of-Day Far-Red Light Response in Maize Seedlings. <i>Plant Physiology</i> , 2010, 154, 173-186.	4.8	47
23	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
24	Expanding Maize Genetic Resources with Predomestication Alleles: Maize-Teosinte Introgression Populations. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0053.	2.8	43
25	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	2.9	38
26	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.	1.4	38
27	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.	1.8	36
28	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , 2020, 215, 215-230.	2.9	35
29	Association Mapping of Flowering and Height Traits in Germplasm Enhancement of Maize Doubled Haploid (GEMDH) Lines. <i>Plant Genome</i> , 2018, 11, 170083.	2.8	33
30	Genetic Analysis of Kernel Traits in Maize-Teosinte Introgression Populations. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2523-2530.	1.8	32
31	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.	2.5	30
32	Hallauer's Tus3n: a decade of selection for tropical-to-temperate phenological adaptation in maize. <i>Heredity</i> , 2015, 114, 229-240.	2.6	30
33	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, 2162-2172.	5.2	28
34	Genetic Analysis of Teosinte Alleles for Kernel Composition Traits in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1157-1164.	1.8	27
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	Mining Natural Variation for Maize Improvement: Selection on Phenotypes and Genes. , 2014, , 615-649.		24

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37	Identification of Teosinte Alleles for Resistance to Southern Leaf Blight in Near Isogenic Maize Lines. <i>Crop Science</i> , 2017, 57, 1973-1983.	1.8	23
38	The Genomic Basis for Short-Term Evolution of Environmental Adaptation in Maize. <i>Genetics</i> , 2019, 213, 1479-1494.	2.9	23
39	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.	3.6	21
40	Relative utility of agronomic, phenological, and morphological traits for assessing genotype \times environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	1.8	21
41	Genetic Relationship of Stalk Strength and Ear Height in Maize. <i>Crop Science</i> , 2003, 43, 23.	1.8	20
42	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.	1.9	19
43	Registration of the Maize Germplasm CRW3(S1)C6 with Resistance to Western Corn Rootworm. <i>Journal of Plant Registrations</i> , 2007, 1, 151-152.	0.5	18
44	Integrating Genomic and Phenomic Approaches to Support Plant Genetic Resources Conservation and Use. <i>Plants</i> , 2021, 10, 2260.	3.5	15
45	Demonstration of local adaptation in maize landraces by reciprocal transplantation. <i>Evolutionary Applications</i> , 2022, 15, 817-837.	3.1	15
46	Stability Analysis of Kernel Quality Traits in Exotic-Derived Doubled Haploid Maize Lines. <i>Plant Genome</i> , 2019, 12, 170114.	2.8	12
47	DNAAlignEditor: DNA alignment editor tool. <i>BMC Bioinformatics</i> , 2008, 9, 154.	2.6	11
48	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, 1317-1324.	1.8	11
49	A B73 \times Palomero Toluque \pm o mapping population reveals local adaptation in Mexican highland maize. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	11
50	Compositional Variation in Trans-Ferulic, p-coumaric, and Diferulic Acids Levels Among Kernels of Modern and Traditional Maize (<i>Zea mays</i> L.) Hybrids. <i>Frontiers in Nutrition</i> , 2020, 7, 600747.	3.7	9
51	Multimiomics approach reveals a role of translational machinery in shaping maize kernel amino acid composition. <i>Plant Physiology</i> , 2022, 188, 111-133.	4.8	9
52	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.	1.8	8
53	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.	2.4	7
54	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.	2.9	7

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55	Genetic control of kernel compositional variation in a maize diversity panel. <i>Plant Genome</i> , 2021, 14, e20115.	2.8	7
56	Germplasm Resources for Mapping Quantitative Traits in Maize. <i>Compendium of Plant Genomes</i> , 2018, , 143-159.	0.5	6
57	View: introgression library visualization and query tool. <i>BMC Bioinformatics</i> , 2010, 11, S28.	2.6	4
58	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, 5282-5295.	5.2	4
59	The role of ear environment in postharvest susceptibility of maize to toxigenic <i>Aspergillus flavus</i> . <i>Plant Breeding</i> , 2019, 138, 38-50.	1.9	3
60	Predicting moisture content during maize nixtamalization using machine learning with NIR spectroscopy. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3743-3757.	3.6	3
61	Registration of tropical populations of maize selected in parallel for early flowering time across the United States. <i>Journal of Plant Registrations</i> , 2022, 16, 100-108.	0.5	3
62	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.	5.2	2
63	The potential to breed a low-protein maize for protein-restricted diets. <i>Crop Science</i> , 0, , .	1.8	0
64	Iron Bioavailability of Maize Is Improved by Degermination for Some but Not All Genotypes: Enhancing Maize Nutrition With Biofortification and Processing. <i>Current Developments in Nutrition</i> , 2022, 6, 1188.	0.3	0