John F Doebley

List of Publications by Year
in descending order

92 papers	19,571 citations	29994 54 h-index	53109 85 g-index
97 all docs	97 docs citations	97 times ranked	12612 citing authors

#	Article	IF	Citations
1	The Molecular Genetics of Crop Domestication. Cell, 2006, 127, 1309-1321.	13.5	1,701
2	The evolution of apical dominance in maize. Nature, 1997, 386, 485-488.	13.7	1,404
3	A single domestication for maize shown by multilocus microsatellite genotyping. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6080-6084.	3.3	1,143
4	Dwarf8 polymorphisms associate with variation in flowering time. Nature Genetics, 2001, 28, 286-289.	9.4	960
5	Maize association population: a high-resolution platform for quantitative trait locus dissection. Plant Journal, 2005, 44, 1054-1064.	2.8	821
6	Comparative population genomics of maize domestication and improvement. Nature Genetics, 2012, 44, 808-811.	9.4	816
7	The Effects of Artificial Selection on the Maize Genome. Science, 2005, 308, 1310-1314.	6.0	742
8	The TCP domain: a motif found in proteins regulating plant growth and development. Plant Journal, 1999, 18, 215-222.	2.8	736
9	The limits of selection during maize domestication. Nature, 1999, 398, 236-239.	13.7	715
10	Identification of a functional transposon insertion in the maize domestication gene tb1. Nature Genetics, 2011, 43, 1160-1163.	9.4	639
11	The origin of the naked grains of maize. Nature, 2005, 436, 714-719.	13.7	561
12	The Genetics of Maize Evolution. Annual Review of Genetics, 2004, 38, 37-59.	3.2	529
13	Genetic Structure and Diversity Among Maize Inbred Lines as Inferred From DNA Microsatellites. Genetics, 2003, 165, 2117-2128.	1.2	447
14	Transcriptional Regulators and the Evolution of Plant Form. Plant Cell, 1998, 10, 1075-1082.	3.1	416
15	Parallel domestication of the Shattering1 genes in cereals. Nature Genetics, 2012, 44, 720-724.	9.4	401
16	A distant upstream enhancer at the maize domestication gene tb1 has pleiotropic effects on plant and inflorescent architecture. Nature Genetics, 2006, 38, 594-597.	9.4	389
17	Genetic signals of origin, spread, and introgression in a large sample of maize landraces. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1088-1092.	3.3	357
18	Pattern of diversity in the genomic region near the maize domestication gene tb1. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 700-707.	3.3	294

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19	<i>ZmCCT</i> and the genetic basis of day-length adaptation underlying the postdomestication spread of maize. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1913-21.	3.3	290
20	Early Allelic Selection in Maize as Revealed by Ancient DNA. Science, 2003, 302, 1206-1208.	6.0	287
21	Expression Patterns and Mutant Phenotype of <i>teosinte branched1</i> Correlate With Growth Suppression in Maize and Teosinte. Genetics, 2002, 162, 1927-1935.	1.2	263
22	Population structure and genetic diversity of New World maize races assessed by DNA microsatellites. American Journal of Botany, 2008, 95, 1240-1253.	0.8	251
23	Rate and Pattern of Mutation at Microsatellite Loci in Maize. Molecular Biology and Evolution, 2002, 19, 1251-1260.	3.5	248
24	A Large-Scale Screen for Artificial Selection in Maize Identifies Candidate Agronomic Loci for Domestication and Crop Improvement. Plant Cell, 2005, 17, 2859-2872.	3.1	234
25	Molecular Evidence and the Evolution of Maize. Economic Botany, 1990, 44, 6-27.	0.8	227
26	Duplicate FLORICAULA/LEAFY homologs zfl1 and zfl2 control inflorescence architecture and flower patterning in maize. Development (Cambridge), 2003, 130, 2385-2395.	1.2	222
27	<i>grassy tillers1</i> promotes apical dominance in maize and responds to shade signals in the grasses. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E506-12.	3.3	215
28	<i>ZmCCT9</i> enhances maize adaptation to higher latitudes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E334-E341.	3.3	210
29	Construction of the third-generation Zea mays haplotype map. GigaScience, 2018, 7, 1-12.	3.3	191
30	Meiotic Drive of Chromosomal Knobs Reshaped the Maize Genome. Genetics, 1999, 153, 415-426.	1.2	173
31	EVOLUTIONARY ANALYSIS OF THE LARGE SUBUNIT OF CARBOXYLASE (rbcL) NUCLEOTIDE SEQUENCE AMONG THE GRASSES (GRAMINEAE). Evolution; International Journal of Organic Evolution, 1990, 44, 1097-1108.	1.1	153
32	An Analysis of Genetic Diversity Across the Maize Genome Using Microsatellites. Genetics, 2005, 169, 1617-1630.	1.2	147
33	The Role of cis Regulatory Evolution in Maize Domestication. PLoS Genetics, 2014, 10, e1004745.	1.5	144
34	Evolution of Anthocyanin Biosynthesis in Maize Kernels: The Role of Regulatory and Enzymatic Loci. Genetics, 1996, 143, 1395-1407.	1.2	144
35	Epistatic and environmental interactions for quantitative trait loci involved in maize evolution. Genetical Research, 1999, 74, 291-302.	0.3	138
36	Unfallen Grains: How Ancient Farmers Turned Weeds into Crops. Science, 2006, 312, 1318-1319.	6.0	124

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37	Stepwise cis-Regulatory Changes in ZCN8 Contribute to Maize Flowering-Time Adaptation. Current Biology, 2018, 28, 3005-3015.e4.	1.8	116
38	Developmental analysis of Teosinte glume architecture1 : a key locus in the evolution of maize (Poaceae). American Journal of Botany, 1997, 84, 1313-1322.	0.8	115
39	From Many, One: Genetic Control of Prolificacy during Maize Domestication. PLoS Genetics, 2013, 9, e1003604.	1.5	111
40	Genetic Variation for Phenotypically Invariant Traits Detected in Teosinte: Implications for the Evolution of Novel Forms. Genetics, 2002, 160, 333-342.	1.2	98
41	Linkage Mapping of Domestication Loci in a Large Maizeâ€"Teosinte Backcross Resource. Genetics, 2007, 177, 1915-1928.	1.2	97
42	The origin of cornbelt maize: The isozyme evidence. Economic Botany, 1988, 42, 120-131.	0.8	95
43	Megabase-Scale Inversion Polymorphism in the Wild Ancestor of Maize. Genetics, 2012, 191, 883-894.	1.2	94
44	The Molecular Evolution of terminal ear1, a Regulatory Gene in the Genus Zea. Genetics, 1999, 153, 1455-1462.	1.2	91
45	Panzea: a database and resource for molecular and functional diversity in the maize genome. Nucleic Acids Research, 2006, 34, D752-D757.	6.5	89
46	Genome-wide Analysis of Transcriptional Variability in a Large Maize-Teosinte Population. Molecular Plant, 2018, 11, 443-459.	3.9	87
47	Evidence That the Origin of Naked Kernels During Maize Domestication Was Caused by a Single Amino Acid Substitution in<i>tga1</i>. Genetics, 2015, 200, 965-974.	1.2	86
48	Do Large Effect QTL Fractionate? A Case Study at the Maize Domestication QTL<i>teosinte branched1</i>. Genetics, 2011, 188, 673-681.	1.2	85
49	Estimating a Nucleotide Substitution Rate for Maize from Polymorphism at a Major Domestication Locus. Molecular Biology and Evolution, 2005, 22, 2304-2312.	3.5	82
50	Selection During Maize Domestication Targeted a Gene Network Controlling Plant and Inflorescence Architecture. Genetics, 2017, 207, 755-765.	1.2	75
51	ISOZYME VARIATION IN THE RACES OF MAIZE FROM MEXICO. American Journal of Botany, 1985, 72, 629-639.	0.8	74
52	MOLECULAR EVIDENCE FOR A MISSING WILD RELATIVE OF MAIZE AND THE INTROGRESSION OF ITS CHLOROPLAST GENOME INTO <i>ZEA PERENNIS</i>. Evolution; International Journal of Organic Evolution, 1989, 43, 1555-1559.	1.1	74
53	Chloroplast DNA diversity among wild and cultivated members of Cucurbita (Cucurbitaceae). Theoretical and Applied Genetics, 1992, 84-84, 859-865.	1.8	71
54	Major Regulatory Genes in Maize Contribute to Standing Variation in Teosinte (Zea mays ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	1.2	67

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55	ISOZYME VARIATION IN THE RACES OF MAIZE FROM MEXICO. , 1985, 72, 629.		61
56	The genetic architecture of teosinte catalyzed and constrained maize domestication. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5643-5652.	3.3	59
57	Genetics, development and plant evolution. Current Opinion in Genetics and Development, 1993, 3, 865-872.	1.5	57
58	Molecular Evolution of FLORICAULA/LEAFY Orthologs in the Andropogoneae (Poaceae). Molecular Biology and Evolution, 2005, 22, 1082-1094.	3.5	56
59	The Inheritance and Evolution of Leaf Pigmentation and Pubescence in Teosinte. Genetics, 2004, 167, 1949-1959.	1.2	55
60	CHLOROPLAST DNA VARIATION AND THE PHYLOGENY OF HORDEUM (POACEAE). American Journal of Botany, 1992, 79, 576-584.	0.8	54
61	MORPHOLOGICAL TRAITS DEFINING SPECIES DIFFERENCES IN WILD RELATIVES OF MAIZE ARE CONTROLLED BY MULTIPLE QUANTITATIVE TRAIT LOCI. Evolution; International Journal of Organic Evolution, 2002, 56, 273-283.	1.1	52
62	EXCEPTIONAL GENETIC DIVERGENCE OF NORTHERN FLINT CORN. , 1986, 73, 64.		50
63	EXCEPTIONAL GENETIC DIVERGENCE OF NORTHERN FLINT CORN. American Journal of Botany, 1986, 73, 64-69.	0.8	49
64	Maize Introgression Into Teosinte-A Reappraisal. Annals of the Missouri Botanical Garden, 1984, 71, 1100.	1.3	48
65	MADS-box genes of maize: frequent targets of selection during domestication. Genetical Research, 2011, 93, 65-75.	0.3	47
66	ALLOZYME VARIATION IN OLD WORLD RACES OF SORGHUM BICOLOR (POACEAE). American Journal of Botany, 1989, 76, 247-255.	0.8	43
67	The genome-wide dynamics of purging during selfing in maize. Nature Plants, 2019, 5, 980-990.	4.7	42
68	TeoNAM: A Nested Association Mapping Population for Domestication and Agronomic Trait Analysis in Maize. Genetics, 2019, 213, 1065-1078.	1.2	42
69	Genetic Evidence and the Origin of Maize. Latin American Antiquity, 2001, 12, 84-86.	0.3	39
70	TRIPSACUM ANDERSONII IS A NATURAL HYBRID INVOLVING ZEA AND TRIPSACUM: MOLECULAR EVIDENCE. American Journal of Botany, 1990, 77, 722-726.	0.8	37
71	Fine scale genetic structure in the wild ancestor of maize (<i>Zea mays</i>ssp.<i>parviglumis</i>). Molecular Ecology, 2010, 19, 1162-1173.	2.0	37
72	The role of <i>teosinte glume architecture</i> (<i>tga1</i>) in coordinated regulation and evolution of grass glumes and inflorescence axes. New Phytologist, 2012, 193, 204-215.	3.5	34

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73	Genetic Dissection of a Genomic Region with Pleiotropic Effects on Domestication Traits in Maize Reveals Multiple Linked QTL. Genetics, 2014, 198, 345-353.	1.2	34
74	CHLOROPLAST DNA VARIATION AND THE PHYLOGENY OF HORDEUM (POACEAE). , 1992, 79, 576.		32
75	Fine Mapping of a QTL Associated with Kernel Row Number on Chromosome 1 of Maize. PLoS ONE, 2016, 11, e0150276.	1.1	30
76	Wheat, rye, and barley on the cob?. Nature Biotechnology, 2002, 20, 337-338.	9.4	29
77	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. PLoS Genetics, 2020, 16, e1008791.	1.5	27
78	George Beadleâ€™s Other Hypothesis: One-Gene, One-Trait. Genetics, 2001, 158, 487-493.	1.2	26
79	Evidence for a Natural Allelic Series at the Maize Domestication Locus <i>teosinte branched1</i>. Genetics, 2012, 191, 951-958.	1.2	24
80	S uppressor of sessile spikelets 1 (S osl): a dominant mutant affecting inflorescence development in maize. American Journal of Botany, 1995, 82, 571-577.	0.8	20
81	Defining the Role of the MADS-Box Gene, Zea Agamous-like1, a Target of Selection During Maize Domestication. Journal of Heredity, 2018, 109, 333-338.	1.0	19
82	TRIPSACUM ANDERSONII IS A NATURAL HYBRID INVOLVING ZEA AND TRIPSACUM: MOLECULAR EVIDENCE. , 1990, 77, 722.		19
83	Defining the Role of prolamin-box binding factor1 Gene During Maize Domestication. Journal of Heredity, 2014, 105, 576-582.	1.0	17
84	ALLOZYME VARIATION IN OLD WORLD RACES OF SORGHUM BICOLOR (POACEAE). , 1989, 76, 247.		17
85	The Role of Regulatory Genes During Maize Domestication: Evidence From Nucleotide Polymorphism and Gene Expression. Genetics, 2008, 178, 2133-2143.	1.2	16
86	A Gene for Genetic Background in <i>Zea mays</i>: Fine-Mapping <i>enhancer of teosinte branched1.2</i> to a YABBY Class Transcription Factor. Genetics, 2016, 204, 1573-1585.	1.2	15
87	Using Association Mapping in Teosinte to Investigate the Function of Maize Selection-Candidate Genes. PLoS ONE, 2009, 4, e8227.	1.1	13
88	Hybrid Decay: A Transgenerational Epigenetic Decline in Vigor and Viability Triggered in Backcross Populations of Teosinte with Maize. Genetics, 2019, 213, 143-160.	1.2	7
89	Suppressor of sessile spikelets1 (Sosl): a dominant mutant affecting inflorescence development in maize. , 1995, 82, 571.		6
90	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. PLoS Genetics, 2021, 17, e1009797.	1.5	5

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91	Mapping Prolificacy QTL in Maize and Teosinte. Journal of Heredity, 2016, 107, 674-678.	1.0	2
92	A conserved genetic architecture among populations of the maize progenitor, teosinte, was radically altered by domestication. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	1