

# Matthew B Hufford

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

5,749  
citations

186265

28  
h-index

155660

55  
g-index

82  
all docs

82  
docs citations

82  
times ranked

7071  
citing authors

#	ARTICLE	IF	CITATIONS
1	A B73—Palomero Toluque mapping population reveals local adaptation in Mexican highland maize. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	11
2	Demonstration of local adaptation in maize landraces by reciprocal transplantation. <i>Evolutionary Applications</i> , 2022, 15, 817-837.	3.1	15
3	An adaptive teosinte <i>mexicana</i> introgression modulates phosphatidylcholine levels and is associated with maize flowering time. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	21
4	A Tutorial of EDTA: Extensive De Novo TE Annotator. <i>Methods in Molecular Biology</i> , 2021, 2250, 55-67.	0.9	22
5	How the pan-genome is changing crop genomics and improvement. <i>Genome Biology</i> , 2021, 22, 3.	8.8	142
6	Major locus for spontaneous haploid genome doubling detected by a case-control GWAS in exotic maize germplasm. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1423-1434.	3.6	9
7	Molecular Parallelism Underlies Convergent Highland Adaptation of Maize Landraces. <i>Molecular Biology and Evolution</i> , 2021, 38, 3567-3580.	8.9	35
8	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , 2021, 31, 1245-1257.	5.5	29
9	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	2.8	14
10	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	12.6	282
11	The <i>Streptochaeta</i> Genome and the Evolution of the Grasses. <i>Frontiers in Plant Science</i> , 2021, 12, 710383.	3.6	8
12	Haplotype structure in commercial maize breeding programs in relation to key founder lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 547-561.	3.6	23
13	SequelTools: a suite of tools for working with PacBio Sequel raw sequence data. <i>BMC Bioinformatics</i> , 2020, 21, 429.	2.6	19
14	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020, 11, 2288.	12.8	39
15	GenomeQC: a quality assessment tool for genome assemblies and gene structure annotations. <i>BMC Genomics</i> , 2020, 21, 193.	2.8	52
16	Genome-wide selection and genetic improvement during modern maize breeding. <i>Nature Genetics</i> , 2020, 52, 565-571.	21.4	146
17	Gapless assembly of maize chromosomes using long-read technologies. <i>Genome Biology</i> , 2020, 21, 121.	8.8	101
18	Parallelism and convergence in post-domestication adaptation in cereal grasses. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180245.	4.0	16

#	ARTICLE	IF	CITATIONS
19	Crop Biodiversity: An Unfinished Magnum Opus of Nature. Annual Review of Plant Biology, 2019, 70, 727-751.	18.7	74
20	Technological advances in maize breeding: past, present and future. Theoretical and Applied Genetics, 2019, 132, 817-849.	3.6	97
21	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. Genome Biology, 2019, 20, 275.	8.8	579
22	The extent of adaptive wild introgression in crops. New Phytologist, 2019, 221, 1279-1288.	7.3	75
23	Characterization of introgression from the teosinte <i>Zea mays</i> ssp. <i>mexicana</i> to Mexican highland maize. PeerJ, 2019, 7, e6815.	2.0	24
24	Evolution and Adaptation in the Maize Genome. Compendium of Plant Genomes, 2018, , 319-332.	0.5	6
25	Domestication Genomics: Untangling the Complex History of African Rice. Current Biology, 2018, 28, R786-R788.	3.9	3
26	Evidence for a Unique DNA-Dependent RNA Polymerase in Cereal Crops. Molecular Biology and Evolution, 2018, 35, 2454-2462.	8.9	21
27	The interplay of demography and selection during maize domestication and expansion. Genome Biology, 2017, 18, 215.	8.8	172
28	Genomic abundance is not predictive of tandem repeat localization in grass genomes. PLoS ONE, 2017, 12, e0177896.	2.5	5
29	The potential role of genetic assimilation during maize domestication. PLoS ONE, 2017, 12, e0184202.	2.5	17
30	Comparative genomics provides insight into maize adaptation in temperate regions. Genome Biology, 2016, 17, 155.	8.8	1
31	Crop Domestication: A Sneak-Peek into the Midpoint of Maize Evolution. Current Biology, 2016, 26, R1240-R1242.	3.9	8
32	Recent demography drives changes in linked selection across the maize genome. Nature Plants, 2016, 2, 16084.	9.3	111
33	Climate structures genetic variation across a species' elevation range: a test of range limits hypotheses. Molecular Ecology, 2016, 25, 911-928.	3.9	41
34	The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003.	9.3	138
35	Independent Molecular Basis of Convergent Highland Adaptation in Maize. Genetics, 2015, 200, 1297-1312.	2.9	67
36	Natural variation in teosinte at the domestication locus <i>teosinte branched1</i> ( <i>tb1</i> ). PeerJ, 2015, 3, e900.	2.0	13

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37	Diversity and abundance of the abnormal chromosome 10 meiotic drive complex in <i>Zea mays</i> . <i>Heredity</i> , 2013, 110, 570-577.	2.6	22
38	The Genomic Signature of Crop-Wild Introgression in Maize. <i>PLoS Genetics</i> , 2013, 9, e1003477.	3.5	291
39	Complex Patterns of Local Adaptation in Teosinte. <i>Genome Biology and Evolution</i> , 2013, 5, 1594-1609.	2.5	139
40	Historical genomics of North American maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12420-12425.	7.1	151
41	Reshaping of the maize transcriptome by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11878-11883.	7.1	154
42	Teosinte as a model system for population and ecological genomics. <i>Trends in Genetics</i> , 2012, 28, 606-615.	6.7	65
43	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
44	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	21.4	816
45	Inferences from the Historical Distribution of Wild and Domesticated Maize Provide Ecological and Evolutionary Insight. <i>PLoS ONE</i> , 2012, 7, e47659.	2.5	79
46	Genome Size and Transposable Element Content as Determined by High-Throughput Sequencing in Maize and <i>Zea luxurians</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 219-229.	2.5	167
47	Influence of cryptic population structure on observed mating patterns in the wild progenitor of maize ( <i>Zea mays</i> ssp. <i>parviglumis</i> ). <i>Molecular Ecology</i> , 2011, 20, 46-55.	3.9	16
48	Controlling invasive species in complex social landscapes. <i>Frontiers in Ecology and the Environment</i> , 2010, 8, 210-216.	4.0	184
49	Transgenes in Mexican maize: molecular evidence and methodological considerations for GMO detection in landrace populations. <i>Molecular Ecology</i> , 2009, 18, 750-761.	3.9	113
50	Resolution of the Mexican transgene detection controversy: error sources and scientific practice in commercial and ecological contexts. <i>Molecular Ecology</i> , 2009, 18, 4145-4150.	3.9	14
51	Practical Challenges in Private Stewardship of Rangeland Ecosystems: Yellow Starthistle Control in Sierra Nevada Foothills. <i>Rangeland Ecology and Management</i> , 2009, 62, 28-37.	2.3	29
52	Long-distance pollen flow assessment through evaluation of pollinator foraging range suggests transgene escape distances. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13456-13461.	7.1	174
53	PLAB, a novel placental bone morphogenetic protein. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1997, 1354, 40-44.	2.4	190