

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 | Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811. | 21.4 | 816 |
| 2 | Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. <i>Genome Biology</i> , 2019, 20, 275. | 8.8 | 579 |
| 3 | Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807. | 21.4 | 577 |
| 4 | The Genomic Signature of Crop-Wild Introgression in Maize. <i>PLoS Genetics</i> , 2013, 9, e1003477. | 3.5 | 291 |
| 5 | De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662. | 12.6 | 282 |
| 6 | PLAB, a novel placental bone morphogenetic protein. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1997, 1354, 40-44. | 2.4 | 190 |
| 7 | Controlling invasive species in complex social landscapes. <i>Frontiers in Ecology and the Environment</i> , 2010, 8, 210-216. | 4.0 | 184 |
| 8 | 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 |
| 9 | The interplay of demography and selection during maize domestication and expansion. <i>Genome Biology</i> , 2017, 18, 215. | 8.8 | 172 |
| 10 | 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 |
| 11 | 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 |
| 12 | 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 |
| 13 | Genome-wide selection and genetic improvement during modern maize breeding. <i>Nature Genetics</i> , 2020, 52, 565-571. | 21.4 | 146 |
| 14 | How the pan-genome is changing crop genomics and improvement. <i>Genome Biology</i> , 2021, 22, 3. | 8.8 | 142 |
| 15 | Complex Patterns of Local Adaptation in Teosinte. <i>Genome Biology and Evolution</i> , 2013, 5, 1594-1609. | 2.5 | 139 |
| 16 | The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015, 1, 14003. | 9.3 | 138 |
| 17 | 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 |
| 18 | Recent demography drives changes in linked selection across the maize genome. <i>Nature Plants</i> , 2016, 2, 16084. | 9.3 | 111 |

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|----|---|------|-----------|
| 19 | Gapless assembly of maize chromosomes using long-read technologies. <i>Genome Biology</i> , 2020, 21, 121. | 8.8 | 101 |
| 20 | Technological advances in maize breeding: past, present and future. <i>Theoretical and Applied Genetics</i> , 2019, 132, 817-849. | 3.6 | 97 |
| 21 | 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 |
| 22 | The extent of adaptive wild introgression in crops. <i>New Phytologist</i> , 2019, 221, 1279-1288. | 7.3 | 75 |
| 23 | Crop Biodiversity: An Unfinished Magnum Opus of Nature. <i>Annual Review of Plant Biology</i> , 2019, 70, 727-751. | 18.7 | 74 |
| 24 | Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , 2015, 200, 1297-1312. | 2.9 | 67 |
| 25 | Teosinte as a model system for population and ecological genomics. <i>Trends in Genetics</i> , 2012, 28, 606-615. | 6.7 | 65 |
| 26 | GenomeQC: a quality assessment tool for genome assemblies and gene structure annotations. <i>BMC Genomics</i> , 2020, 21, 193. | 2.8 | 52 |
| 27 | Climate structures genetic variation across a species' elevation range: a test of range limits hypotheses. <i>Molecular Ecology</i> , 2016, 25, 911-928. | 3.9 | 41 |
| 28 | 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 |
| 29 | Molecular Parallelism Underlies Convergent Highland Adaptation of Maize Landraces. <i>Molecular Biology and Evolution</i> , 2021, 38, 3567-3580. | 8.9 | 35 |
| 30 | Practical Challenges in Private Stewardship of Rangeland Ecosystems: Yellow Starthistle Control in Sierra Nevadan Foothills. <i>Rangeland Ecology and Management</i> , 2009, 62, 28-37. | 2.3 | 29 |
| 31 | 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 |
| 32 | Characterization of introgression from the teosinte <i>Zea mays</i> ssp. <i>mexicana</i> to Mexican highland maize. <i>PeerJ</i> , 2019, 7, e6815. | 2.0 | 24 |
| 33 | 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 |
| 34 | 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 |
| 35 | A Tutorial of EDTA: Extensive De Novo TE Annotator. <i>Methods in Molecular Biology</i> , 2021, 2250, 55-67. | 0.9 | 22 |
| 36 | Evidence for a Unique DNA-Dependent RNA Polymerase in Cereal Crops. <i>Molecular Biology and Evolution</i> , 2018, 35, 2454-2462. | 8.9 | 21 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | 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 |
| 38 | SequelTools: a suite of tools for working with PacBio Sequel raw sequence data. <i>BMC Bioinformatics</i> , 2020, 21, 429. | 2.6 | 19 |
| 39 | The potential role of genetic assimilation during maize domestication. <i>PLoS ONE</i> , 2017, 12, e0184202. | 2.5 | 17 |
| 40 | Influence of cryptic population structure on observed mating patterns in the wild progenitor of maize (<i>Zea mays ssp. parviglumis</i>). <i>Molecular Ecology</i> , 2011, 20, 46-55. | 3.9 | 16 |
| 41 | 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 |
| 42 | Demonstration of local adaptation in maize landraces by reciprocal transplantation. <i>Evolutionary Applications</i> , 2022, 15, 817-837. | 3.1 | 15 |
| 43 | 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 |
| 44 | Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114. | 2.8 | 14 |
| 45 | Natural variation in teosinte at the domestication locus <i>teosinte branched1</i> . <i>PeerJ</i> , 2015, 3, e900. | 2.0 | 13 |
| 46 | A B73-Palomero Toluque mapping population reveals local adaptation in Mexican highland maize. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, . | 1.8 | 11 |
| 47 | 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 |
| 48 | Crop Domestication: A Sneak-Peek into the Midpoint of Maize Evolution. <i>Current Biology</i> , 2016, 26, R1240-R1242. | 3.9 | 8 |
| 49 | The <i>Streptochaeta</i> Genome and the Evolution of the Grasses. <i>Frontiers in Plant Science</i> , 2021, 12, 710383. | 3.6 | 8 |
| 50 | Evolution and Adaptation in the Maize Genome. <i>Compendium of Plant Genomes</i> , 2018, , 319-332. | 0.5 | 6 |
| 51 | Genomic abundance is not predictive of tandem repeat localization in grass genomes. <i>PLoS ONE</i> , 2017, 12, e0177896. | 2.5 | 5 |
| 52 | Domestication Genomics: Untangling the Complex History of African Rice. <i>Current Biology</i> , 2018, 28, R786-R788. | 3.9 | 3 |
| 53 | Comparative genomics provides insight into maize adaptation in temperate regions. <i>Genome Biology</i> , 2016, 17, 155. | 8.8 | 1 |