

Joseph L Gage

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

699
citations

933447

10
h-index

1199594

12
g-index

17
all docs

17
docs citations

17
times ranked

1267
citing authors

#	ARTICLE	IF	CITATIONS
1	Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2112516119.	7.1	10
2	Images carried before the fire: The power, promise, and responsibility of latent phenotyping in plants. <i>The Plant Phenome Journal</i> , 2021, 4, e20023.	2.0	6
3	Ten Years of the Maize Nested Association Mapping Population: Impact, Limitations, and Future Directions. <i>Plant Cell</i> , 2020, 32, 2083-2093.	6.6	81
4	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
5	Multiple Maize Reference Genomes Impact the Identification of Variants by Genome-Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , 2019, 12, 180069.	2.8	37
6	Residual Heterozygosity and Epistatic Interactions Underlie the Complex Genetic Architecture of Yield in Diploid Potato. <i>Genetics</i> , 2019, 212, 317-332.	2.9	20
7	In-Field Whole-Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping. <i>The Plant Phenome Journal</i> , 2019, 2, 1-11.	2.0	23
8	Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. <i>Genetics</i> , 2018, 210, 1125-1138.	2.9	45
9	Comparing Genome-Wide Association Study Results from Different Measurements of an Underlying Phenotype. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3715-3722.	1.8	16
10	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	12.8	105
11	TIPS: a system for automated image-based phenotyping of maize tassels. <i>Plant Methods</i> , 2017, 13, 21.	4.3	62
12	Bridging the genotyping gap: using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2699-2716.	3.6	228