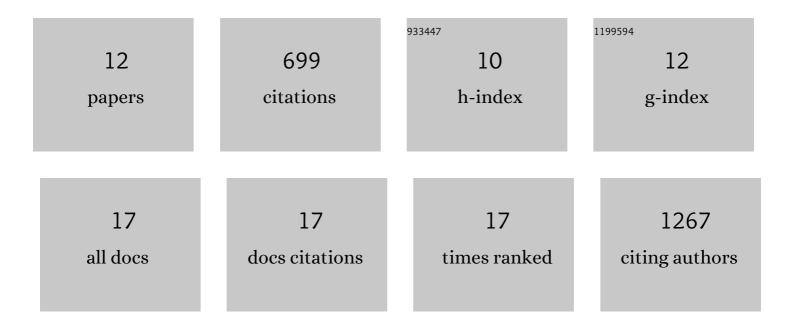
## Joseph L Gage

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/452842/publications.pdf Version: 2024-02-01



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| #  | Article  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance.<br>Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2112516119.                         | 7.1  | 10        |
| 2  | Images carried before the fire: The power, promise, and responsibility of latent phenotyping in plants.<br>The Plant Phenome Journal, 2021, 4, e20023.   | 2.0  | 6         |
| 3  | Ten Years of the Maize Nested Association Mapping Population: Impact, Limitations, and Future<br>Directions. Plant Cell, 2020, 32, 2083-2093.  | 6.6  | 81        |
| 4  | Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred<br>ear image datasets. BMC Research Notes, 2020, 13, 71.   | 1.4  | 38        |
| 5  | Multiple Maize Reference Genomes Impact the Identification of Variants by Genomeâ€Wide Association<br>Study in a Diverse Inbred Panel. Plant Genome, 2019, 12, 180069.   | 2.8  | 37        |
| 6  | Residual Heterozygosity and Epistatic Interactions Underlie the Complex Genetic Architecture of Yield in Diploid Potato. Genetics, 2019, 212, 317-332.   | 2.9  | 20        |
| 7  | Inâ€Field Wholeâ€Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space<br>Phenotyping. The Plant Phenome Journal, 2019, 2, 1-11.   | 2.0  | 23        |
| 8  | Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid<br>Maize Breeding. Genetics, 2018, 210, 1125-1138.   | 2.9  | 45        |
| 9  | Comparing Genome-Wide Association Study Results from Different Measurements of an Underlying Phenotype. G3: Genes, Genomes, Genetics, 2018, 8, 3715-3722.  | 1.8  | 16        |
| 10 | The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.  | 12.8 | 105       |
| 11 | TIPS: a system for automated image-based phenotyping of maize tassels. Plant Methods, 2017, 13, 21.  | 4.3  | 62        |
| 12 | Bridging the genotyping gap: using genotyping by sequencing (GBS) to add high-density SNP markers<br>and new value to traditional bi-parental mapping and breeding populations. Theoretical and Applied<br>Genetics, 2013, 126, 2699-2716. | 3.6  | 228       |