

Maria Magallanes-Lundback

List of Publications by Year in descending order

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13
papers

1,506
citations

840776

11
h-index

1125743

13
g-index

15
all docs

15
docs citations

15
times ranked

2153
citing authors

#	ARTICLE	IF	CITATIONS
1	Vitamin E Is Essential for Seed Longevity and for Preventing Lipid Peroxidation during Germination. <i>Plant Cell</i> , 2004, 16, 1419-1432.	6.6	552
2	The Arabidopsis LUT1 locus encodes a member of the cytochrome P450 family that is required for carotenoid Å-ring hydroxylation activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 402-407.	7.1	209
3	<i>CAROTENOID CLEAVAGE DIOXYGENASE4</i> Is a Negative Regulator of Î²-Carotene Content in <i>Arabidopsis</i> Seeds. <i>Plant Cell</i> , 2014, 25, 4812-4826.	6.6	180
4	A Foundation for Provitamin A Biofortification of Maize: Genome-Wide Association and Genomic Prediction Models of Carotenoid Levels. <i>Genetics</i> , 2014, 198, 1699-1716.	2.9	180
5	Metabolite Diversity in Alkaloid Biosynthesis: A Multilane (Diastereomer) Highway for Camptothecin Synthesis in <i>Camptotheca acuminata</i>. <i>Plant Cell</i> , 2016, 28, 1926-1944.	6.6	95
6	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , 2017, 29, 2374-2392.	6.6	93
7	<i>ZEAXANTHIN EPOXIDASE</i> Activity Potentiates Carotenoid Degradation in Maturing Seed. <i>Plant Physiology</i> , 2016, 171, 1837-1851.	4.8	44
8	Genome-Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. <i>Plant Genome</i> , 2019, 12, 180038.	2.8	37
9	Natural variation for carotenoids in fresh kernels is controlled by uncommon variants in sweet corn. <i>Plant Genome</i> , 2020, 13, e20008.	2.8	34
10	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021, 33, 882-900.	6.6	31
11	Maize Å <i>w3</i> Ådisrupts <i>homogentisate solanesyl transferase</i> Å(<i>ZmHst</i>) and reveals a plastoquinone-independent path for phytoene desaturation and tocopherol accumulation in kernels. <i>Plant Journal</i>, 2018, 93, 799-813.</i>	5.7	24
12	Combining GWAS and TWAS to identify candidate causal genes for tocochromanol levels in maize grain. <i>Genetics</i> , 2022, 221, .	2.9	15
13	Genome-wide association identifies a missing hydrolase for tocopherol synthesis in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11