

Lyza Maron

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

2,705
citations

471477

17
h-index

677123

22
g-index

25
all docs

25
docs citations

25
times ranked

3191
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic architecture of root and shoot ionomes in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2613-2637.	3.6	9
2	Low Additive Genetic Variation in a Trait Under Selection in Domesticated Rice. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2435-2443.	1.8	9
3	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	2.8	51
4	<i>ALUMINUM RESISTANCE TRANSCRIPTION FACTOR 1</i> (<i>ART1</i>) contributes to natural variation in aluminum resistance in diverse genetic backgrounds of rice (<i>O. Tj ETQq0 0 0 rBT /Overlock 10 TF</i>)		
5	Open access resources for genome-wide association mapping in rice. <i>Nature Communications</i> , 2016, 7, 10532.	12.8	371
6	Redefining "stress resistance genes"™, and why it matters. <i>Journal of Experimental Botany</i> , 2016, 67, 5588-5591.	4.8	7
7	Development and GBS-genotyping of introgression lines (ILs) using two wild species of rice, <i>O. meridionalis</i> and <i>O. rufipogon</i> , in a common recurrent parent, <i>O. sativa</i> cv. Curinga. <i>Molecular Breeding</i> , 2015, 35, 81.	2.1	77
8	Genetic dissection of Al tolerance QTLs in the maize genome by high density SNP scan. <i>BMC Genomics</i> , 2014, 15, 153.	2.8	35
9	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. <i>Genome Biology</i> , 2014, 15, 506.	8.8	228
10	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. <i>Genome Biology</i> , 2014, 15, 506.	9.6	123
11	Incomplete transfer of accessory loci influencing <i>SbMATE</i> expression underlies genetic background effects for aluminum tolerance in sorghum. <i>Plant Journal</i> , 2013, 73, 276-288.	5.7	31
12	Aluminum tolerance in maize is associated with higher <i>MATE1</i> gene copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5241-5246.	7.1	265
13	Maize <i>ZmALMT2</i> is a root anion transporter that mediates constitutive root malate efflux. <i>Plant, Cell and Environment</i> , 2012, 35, 1185-1200.	5.7	74
14	Two functionally distinct members of the MATE (multi-drug and toxic compound extrusion) family of transporters potentially underlie two major aluminum tolerance QTLs in maize. <i>Plant Journal</i> , 2010, 61, 728-740.	5.7	266
15	Not all ALMT1-type transporters mediate aluminum-activated organic acid responses: the case of <i>ZmALMT1</i> an anion-selective transporter. <i>Plant Journal</i> , 2008, 53, 352-367.	5.7	97
16	Transcriptional profiling of aluminum toxicity and tolerance responses in maize roots. <i>New Phytologist</i> , 2008, 179, 116-128.	7.3	129
17	Characterization of <i>AtALMT1</i> Expression in Aluminum-Inducible Malate Release and Its Role for Rhizotoxic Stress Tolerance in Arabidopsis. <i>Plant Physiology</i> , 2007, 145, 843-852.	4.8	184
18	<i>AtALMT1</i> , which encodes a malate transporter, is identified as one of several genes critical for aluminum tolerance in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9738-9743.	7.1	509

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19	Glutathione S-transferase and aluminum toxicity in maize. <i>Functional Plant Biology</i> , 2005, 32, 1045.	2.1	30
20	Molecular characterization and mapping of <i>ALMT1</i> , the aluminium-tolerance gene of bread wheat (<i>Triticum aestivum</i> L.). <i>Genome</i> , 2005, 48, 781-791.	2.0	149
21	Making Colony PCR Easier by Adding Gel-Loading Buffer to the Amplification Reaction. <i>BioTechniques</i> , 2000, 28, 424-426.	1.8	11