

# Lyza Maron

## List of Publications by Year in descending order

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21  
papers

2,705  
citations

471509

17  
h-index

677142

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.). Theoretical and Applied Genetics, 2021, 134, 2613-2637.	3.6	9
2	Low Additive Genetic Variation in a Trait Under Selection in Domesticated Rice. G3: Genes, Genomes, Genetics, 2020, 10, 2435-2443.	1.8	9
3	Hybrid assembly with long and short reads improves discovery of gene family expansions. BMC Genomics, 2017, 18, 541.	2.8	51
4	<i>OsALU1</i> , a member of the <i>OsALU</i> gene family, contributes to natural variation in aluminum resistance in diverse genetic backgrounds of rice ( <i>O. sativa</i> ). Theoretical and Applied Genetics, 2021, 134, 2613-2637.	3.6	9
5	Open access resources for genome-wide association mapping in rice. Nature Communications, 2016, 7, 10532.	12.8	371
6	Redefining "stress resistance genes", and why it matters. Journal of Experimental Botany, 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. Molecular Breeding, 2015, 35, 81.	2.1	77
8	Genetic dissection of Al tolerance QTLs in the maize genome by high density SNP scan. BMC Genomics, 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. Genome Biology, 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. Genome Biology, 2014, 15, 506.	9.6	123
11	Incomplete transfer of accessory loci influencing <i>SbMATE1</i> expression underlies genetic background effects for aluminum tolerance in sorghum. Plant Journal, 2013, 73, 276-288.	5.7	31
12	Aluminum tolerance in maize is associated with higher <i>MATE1</i> gene copy number. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5241-5246.	7.1	265
13	Maize <i>ZmALMT2</i> is a root anion transporter that mediates constitutive root malate efflux. Plant, Cell and Environment, 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. Plant Journal, 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. Plant Journal, 2008, 53, 352-367.	5.7	97
16	Transcriptional profiling of aluminum toxicity and tolerance responses in maize roots. New Phytologist, 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. Plant Physiology, 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. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9738-9743.	7.1	509

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19	Glutathione S-transferase and aluminum toxicity in maize. Functional Plant Biology, 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.). Genome, 2005, 48, 781-791.	2.0	149
21	Making Colony PCR Easier by Adding Gel-Loading Buffer to the Amplification Reaction. BioTechniques, 2000, 28, 424-426.	1.8	11