

Irina Makarevitch

List of Publications by Year in descending order

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22
papers

1,727
citations

516710

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677142

22
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docs citations

22
times ranked

2664
citing authors

#	ARTICLE	IF	CITATIONS
1	Transposable Elements Contribute to Activation of Maize Genes in Response to Abiotic Stress. <i>PLoS Genetics</i> , 2015, 11, e1004915.	3.5	346
2	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. <i>Plant Cell</i> , 2011, 23, 4221-4233.	6.6	189
3	RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14728-14733.	7.1	179
4	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. <i>PLoS Genetics</i> , 2012, 8, e1003127.	3.5	166
5	Natural variation for gene expression responses to abiotic stress in maize. <i>Plant Journal</i> , 2017, 89, 706-717.	5.7	145
6	Brd1 Gene in Maize Encodes a Brassinosteroid C-6 Oxidase. <i>PLoS ONE</i> , 2012, 7, e30798.	2.5	116
7	Genomic Distribution of Maize Facultative Heterochromatin Marked by Trimethylation of H3K27. <i>Plant Cell</i> , 2013, 25, 780-793.	6.6	91
8	Complex transgene locus structures implicate multiple mechanisms for plant transgene rearrangement. <i>Plant Journal</i> , 2002, 32, 433-445.	5.7	71
9	Phylogeny of the Genus <i>Chironomus</i> (Diptera) Inferred from DNA Sequences of Mitochondrial Cytochrome b and Cytochrome oxidase I. <i>Molecular Phylogenetics and Evolution</i> , 2001, 19, 9-21.	2.7	67
10	Transgene integration in plants: poking or patching holes in promiscuous genomes?. <i>Current Opinion in Biotechnology</i> , 2004, 15, 126-131.	6.6	67
11	High-Throughput Genetic Mapping of Mutants via Quantitative Single Nucleotide Polymorphism Typing. <i>Genetics</i> , 2010, 184, 19-26.	2.9	66
12	Profiling expression changes caused by a segmental aneuploid in maize. <i>BMC Genomics</i> , 2008, 9, 7.	2.8	38
13	Aneuploidy Causes Tissue-Specific Qualitative Changes in Global Gene Expression Patterns in Maize. <i>Plant Physiology</i> , 2010, 152, 927-938.	4.8	38
14	Authentic Research Experience and "Big Data" Analysis in the Classroom: Maize Response to Abiotic Stress. <i>CBE Life Sciences Education</i> , 2015, 14, ar27.	2.3	36
15	Natural Variation for Alleles Under Epigenetic Control by the Maize Chromomethylase <i>Zmet2</i> . <i>Genetics</i> , 2007, 177, 749-760.	2.9	31
16	Phylogenetic Relationships of the Siberian Iris Species Inferred from Noncoding Chloroplast DNA Sequences. <i>International Journal of Plant Sciences</i> , 2003, 164, 229-237.	1.3	28
17	QTL mapping of seedling tolerance to exposure to low temperature in the maize IBM RIL population. <i>PLoS ONE</i> , 2021, 16, e0254437.	2.5	17
18	Tissue specificity of the sugarcane bacilliform virus promoter in oat, barley and wheat. <i>Molecular Breeding</i> , 2004, 14, 331-338.	2.1	11

#	ARTICLE	IF	CITATIONS
19	Association of Arabidopsis topoisomerase IIA cleavage sites with functional genomic elements and T-DNA loci. <i>Plant Journal</i> , 2006, 48, 697-709.	5.7	11
20	Purification and characterization of topoisomerase IIA from <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2005, 168, 1023-1033.	3.6	8
21	Mapping maize genes: A series of research-based laboratory exercises. <i>Biochemistry and Molecular Biology Education</i> , 2011, 39, 367-375.	1.2	4
22	Killing two birds with one stone: Model plant systems as a tool to teach the fundamental concepts of gene expression while analyzing biological data. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 166-173.	1.9	2