

# Irina Makarevitch

## List of Publications by Year in descending order

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Version: 2024-02-01

22  
papers

1,727  
citations

516710

16  
h-index

677142

22  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2664  
citing authors

#	ARTICLE	IF	CITATIONS
1	QTL mapping of seedling tolerance to exposure to low temperature in the maize IBM RIL population. PLoS ONE, 2021, 16, e0254437.	2.5	17
2	Killing two birds with one stone: Model plant systems as a tool to teach the fundamental concepts of gene expression while analyzing biological data. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 166-173.	1.9	2
3	Natural variation for gene expression responses to abiotic stress in maize. Plant Journal, 2017, 89, 706-717.	5.7	145
4	Transposable Elements Contribute to Activation of Maize Genes in Response to Abiotic Stress. PLoS Genetics, 2015, 11, e1004915.	3.5	346
5	Authentic Research Experience and "Big Data" Analysis in the Classroom: Maize Response to Abiotic Stress. CBE Life Sciences Education, 2015, 14, ar27.	2.3	36
6	RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14728-14733.	7.1	179
7	Genomic Distribution of Maize Facultative Heterochromatin Marked by Trimethylation of H3K27. Plant Cell, 2013, 25, 780-793.	6.6	91
8	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. PLoS Genetics, 2012, 8, e1003127.	3.5	166
9	Brd1 Gene in Maize Encodes a Brassinosteroid C-6 Oxidase. PLoS ONE, 2012, 7, e30798.	2.5	116
10	Mapping maize genes: A series of research-based laboratory exercises. Biochemistry and Molecular Biology Education, 2011, 39, 367-375.	1.2	4
11	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. Plant Cell, 2011, 23, 4221-4233.	6.6	189
12	High-Throughput Genetic Mapping of Mutants via Quantitative Single Nucleotide Polymorphism Typing. Genetics, 2010, 184, 19-26.	2.9	66
13	Aneuploidy Causes Tissue-Specific Qualitative Changes in Global Gene Expression Patterns in Maize. Plant Physiology, 2010, 152, 927-938.	4.8	38
14	Profiling expression changes caused by a segmental aneuploid in maize. BMC Genomics, 2008, 9, 7.	2.8	38
15	Natural Variation for Alleles Under Epigenetic Control by the Maize Chromomethylase <i>Zmet2</i> . Genetics, 2007, 177, 749-760.	2.9	31
16	Association of Arabidopsis topoisomerase IIA cleavage sites with functional genomic elements and T-DNA loci. Plant Journal, 2006, 48, 697-709.	5.7	11
17	Purification and characterization of topoisomerase IIA from Arabidopsis thaliana. Plant Science, 2005, 168, 1023-1033.	3.6	8
18	Tissue specificity of the sugarcane bacilliform virus promoter in oat, barley and wheat. Molecular Breeding, 2004, 14, 331-338.	2.1	11

#	ARTICLE	IF	CITATIONS
19	Transgene integration in plants: poking or patching holes in promiscuous genomes?. <i>Current Opinion in Biotechnology</i> , 2004, 15, 126-131.	6.6	67
20	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
21	Complex transgene locus structures implicate multiple mechanisms for plant transgene rearrangement. <i>Plant Journal</i> , 2002, 32, 433-445.	5.7	71
22	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