

# Meixia Zhao

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

6,209  
citations

394421

19  
h-index

552781

26  
g-index

28  
all docs

28  
docs citations

28  
times ranked

5311  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
2	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
3	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
4	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. <i>Genome Biology</i> , 2013, 14, r53.	8.8	225
5	<i>Dt2</i> Is a Gain-of-Function MADS-Domain Factor Gene That Specifies Semideterminacy in Soybean. <i>Plant Cell</i> , 2014, 26, 2831-2842.	6.6	136
6	Bolbase: a comprehensive genomics database for <i>Brassica oleracea</i> . <i>BMC Genomics</i> , 2013, 14, 664.	2.8	99
7	Evolutionary Patterns and Coevolutionary Consequences of <i>MIRNA</i> Genes and MicroRNA Targets Triggered by Multiple Mechanisms of Genomic Duplications in Soybean. <i>Plant Cell</i> , 2015, 27, 546-562.	6.6	89
8	Patterns and Consequences of Subgenome Differentiation Provide Insights into the Nature of Paleopolyploidy in Plants. <i>Plant Cell</i> , 2017, 29, 2974-2994.	6.6	88
9	<i>GmHs1-1</i> , encoding a calcineurin-like protein, controls hard-seededness in soybean. <i>Nature Genetics</i> , 2015, 47, 939-943.	21.4	85
10	Molecular mapping of two genes conferring resistance to <i>Phytophthora sojae</i> in a soybean landrace PI 567139B. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2177-2185.	3.6	84
11	Pericentromeric Effects Shape the Patterns of Divergence, Retention, and Expression of Duplicated Genes in the Paleopolyploid Soybean. <i>Plant Cell</i> , 2012, 24, 21-32.	6.6	79
12	Molecular response to the pathogen <i>Phytophthora sojae</i> among ten soybean near isogenic lines revealed by comparative transcriptomics. <i>BMC Genomics</i> , 2014, 15, 18.	2.8	67
13	Fine mapping and candidate gene analysis of two loci conferring resistance to <i>Phytophthora sojae</i> in soybean. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2379-2386.	3.6	54
14	Genome-Wide Characterization of Nonreference Transposons Reveals Evolutionary Propensities of Transposons in Soybean. <i>Plant Cell</i> , 2012, 24, 4422-4436.	6.6	51
15	Plasticity and innovation of regulatory mechanisms underlying seed oil content mediated by duplicated genes in the palaeopolyploid soybean. <i>Plant Journal</i> , 2017, 90, 1120-1133.	5.7	51
16	Co-evolution of plant LTR-retrotransposons and their host genomes. <i>Protein and Cell</i> , 2013, 4, 493-501.	11.0	42
17	Shifts in the evolutionary rate and intensity of purifying selection between two <i>Brassica</i> genomes revealed by analyses of orthologous transposons and relics of a whole genome triplication. <i>Plant Journal</i> , 2013, 76, 211-222.	5.7	38
18	Coordination of MicroRNAs, PhasiRNAs, and NB-CLRR Genes in Response to a Plant Pathogen: Insights from Analyses of a Set of Soybean Rps Gene Near-Isogenic Lines. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.09.0044.	2.8	31

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19	Transposable elements employ distinct integration strategies with respect to transcriptional landscapes in eukaryotic genomes. <i>Nucleic Acids Research</i> , 2020, 48, 6685-6698.	14.5	30
20	Silencing of <i>Mutator</i> Elements in Maize Involves Distinct Populations of Small RNAs and Distinct Patterns of DNA Methylation. <i>Genetics</i> , 2020, 215, 379-391.	2.9	19
21	The <i>mop1</i> mutation affects the recombination landscape in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	17
22	Small RNA-Mediated <i>De Novo</i> Silencing of <i>Ac/Ds</i> Transposons Is Initiated by Alternative Transposition in Maize. <i>Genetics</i> , 2020, 215, 393-406.	2.9	11
23	Analysis of CACTA transposase genes unveils the mechanism of intron loss and distinct small RNA silencing pathways underlying divergent evolution of <i>Brassica</i> genomes. <i>Plant Journal</i> , 2021, 105, 34-48.	5.7	5
24	Genome-wide Estimation of Evolutionary Distance and Phylogenetic Analysis of Homologous Genes. <i>Bio-protocol</i> , 2018, 8, e3097.	0.4	3
25	Cost-Effective Profiling of <i>Mutator</i> Transposon Insertions in Maize by Next-Generation Sequencing. <i>Methods in Molecular Biology</i> , 2020, 2072, 39-50.	0.9	2
26	Transposable Elements. <i>Compendium of Plant Genomes</i> , 2017, , 171-181.	0.5	0
27	Asymmetric Evolution of Transposable Elements in <i>Brassica oleracea</i> . <i>Compendium of Plant Genomes</i> , 2021, , 77-90.	0.5	0