

# Mingyue Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

1,333  
citations

759055

12  
h-index

794469

19  
g-index

19  
all docs

19  
docs citations

19  
times ranked

1357  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide comparison of the GRAS protein family in eight Rosaceae species and <i>GRAS</i> gene expression analysis in Chinese white pear ( <i>Pyrus bretschneideri</i> Rehder). <i>New Zealand Journal of Crop and Horticultural Science</i> , 2022, 50, 303-325.	0.7	5
2	Genome-wide genetic diversity and IBD analysis reveals historic dissemination routes of pear in China. <i>Tree Genetics and Genomes</i> , 2022, 18, 1.	0.6	3
3	Pear genetics: Recent advances, new prospects, and a roadmap for the future. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
4	The Variation of Stone Cell Content in 236 Germplasms of Sand Pear ( <i>Pyrus pyrifolia</i> ) and Identification of Related Candidate Genes. <i>Horticultural Plant Journal</i> , 2021, 7, 108-116.	2.3	25
5	A systems genetics approach reveals PbrNSC as a regulator of lignin and cellulose biosynthesis in stone cells of pear fruit. <i>Genome Biology</i> , 2021, 22, 313.	3.8	32
6	Contrasting genetic variation and positive selection followed the divergence of NBS-encoding genes in Asian and European pears. <i>BMC Genomics</i> , 2020, 21, 809.	1.2	7
7	Mining and evolution analysis of lateral organ boundaries domain (LBD) genes in Chinese white pear ( <i>Pyrus bretschneideri</i> ). <i>BMC Genomics</i> , 2020, 21, 644.	1.2	18
8	Overexpression of sugar transporter gene PbSWEET4 of pear causes sugar reduce and early senescence in leaves. <i>Gene</i> , 2020, 743, 144582.	1.0	27
9	Identification of key genes related to seedlessness by genome-wide detection of structural variation and transcriptome analysis in "Shijiwuhe" pear. <i>Gene</i> , 2020, 738, 144480.	1.0	2
10	Comparison of multiple algorithms to reliably detect structural variants in pears. <i>BMC Genomics</i> , 2020, 21, 61.	1.2	15
11	Development of an integrated 200K <i>SNP</i> genotyping array and application for genetic mapping, genome assembly improvement and genome wide association studies in pear ( <i>Pyrus</i> ). <i>Plant Biotechnology Journal</i> , 2019, 17, 1582-1594.	4.1	46
12	Genome-wide identification, expression and functional analysis of the phosphofructokinase gene family in Chinese white pear ( <i>Pyrus bretschneideri</i> ). <i>Gene</i> , 2019, 702, 133-142.	1.0	15
13	Comparative Transcriptomic Analysis Provides Insight into the Domestication and Improvement of Pear ( <i>P. pyrifolia</i> ) Fruit. <i>Plant Physiology</i> , 2019, 180, 435-452.	2.3	33
14	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	3.8	149
15	The southwestern origin and eastward dispersal of pear ( <i>Pyrus pyrifolia</i> ) in East Asia revealed by comprehensive genetic structure analysis with SSR markers. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	12
16	Genetic variation and population structure of "Zangli" pear landraces in Tibet revealed by SSR markers. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	7
17	Genetic diversity and population structure of pear ( <i>Pyrus</i> spp.) collections revealed by a set of core genome-wide SSR markers. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	45
18	Identifying genetic diversity and a preliminary core collection of <i>Pyrus pyrifolia</i> cultivars by a genome-wide set of SSR markers. <i>Scientia Horticulturae</i> , 2014, 167, 5-16.	1.7	48

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19	The genome of the pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832