

# Xiaozeng Yang

## List of Publications by Year in descending order

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27  
papers

1,179  
citations

623734

14  
h-index

526287

27  
g-index

29  
all docs

29  
docs citations

29  
times ranked

1728  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide mapping of the miR5-mediated gene networks in Arabidopsis that involve both transcriptional and post-transcriptional regulation. <i>Plant Journal</i> , 2011, 65, 346-358.	5.7	274
2	miRDeep-P: a computational tool for analyzing the microRNA transcriptome in plants. <i>Bioinformatics</i> , 2011, 27, 2614-2615.	4.1	257
3	PmiREN: a comprehensive encyclopedia of plant miRNAs. <i>Nucleic Acids Research</i> , 2020, 48, D1114-D1121.	14.5	120
4	miRDeep-P2: accurate and fast analysis of the microRNA transcriptome in plants. <i>Bioinformatics</i> , 2019, 35, 2521-2522.	4.1	101
5	Alternative mRNA processing increases the complexity of microRNA-based gene regulation in Arabidopsis. <i>Plant Journal</i> , 2012, 70, 421-431.	5.7	61
6	Asymmetric purine-pyrimidine distribution in cellular small RNA population of papaya. <i>BMC Genomics</i> , 2012, 13, 682.	2.8	41
7	Global analysis of gene-level microRNA expression in Arabidopsis using deep sequencing data. <i>Genomics</i> , 2011, 98, 40-46.	2.9	40
8	PmiREN2.0: from data annotation to functional exploration of plant microRNAs. <i>Nucleic Acids Research</i> , 2022, 50, D1475-D1482.	14.5	39
9	H2AK121ub in Arabidopsis associates with a less accessible chromatin state at transcriptional regulation hotspots. <i>Nature Communications</i> , 2021, 12, 315.	12.8	35
10	GC-rich coding sequences reduce transposon-like, small RNA-mediated transgene silencing. <i>Nature Plants</i> , 2017, 3, 875-884.	9.3	34
11	Quo vadis microRNAs?. <i>Trends in Genetics</i> , 2020, 36, 461-463.	6.7	24
12	Identification and characterization of a subset of microRNAs in wheat ( <i>Triticum aestivum</i> L.). <i>Genomics</i> , 2014, 103, 298-307.	2.9	22
13	Image-Based High-Throughput Detection and Phenotype Evaluation Method for Multiple Lettuce Varieties. <i>Frontiers in Plant Science</i> , 2020, 11, 563386.	3.6	20
14	Establishment of in vitro culture system for <i>Codonopsis pilosula</i> transgenic hairy roots. <i>3 Biotech</i> , 2020, 10, 137.	2.2	19
15	Greenhouse-based vegetable high-throughput phenotyping platform and trait evaluation for large-scale lettuces. <i>Computers and Electronics in Agriculture</i> , 2021, 186, 106193.	7.7	19
16	Analyzing the microRNA Transcriptome in Plants Using Deep Sequencing Data. <i>Biology</i> , 2012, 1, 297-310.	2.8	15
17	MicroRNA annotation in plants: current status and challenges. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	10
18	Quantitative phenotyping and evaluation for lettuce leaves of multiple semantic components. <i>Plant Methods</i> , 2022, 18, 54.	4.3	9

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19	Selection of suitable reference genes for qRT-PCR expression analysis of <i>Codonopsis pilosula</i> under different experimental conditions. <i>Molecular Biology Reports</i> , 2020, 47, 4169-4181.	2.3	8
20	Comprehensive Annotation and Functional Exploration of MicroRNAs in Lettuce. <i>Frontiers in Plant Science</i> , 2021, 12, 781836.	3.6	7
21	Expression of a novel bi-directional <i>Brassica napus</i> promoter in soybean. <i>Transgenic Research</i> , 2017, 26, 727-738.	2.4	6
22	Genome-Wide Characterization of SPL Gene Family in <i>Codonopsis pilosula</i> Reveals the Functions of CpSPL2 and CpSPL10 in Promoting the Accumulation of Secondary Metabolites and Growth of <i>C. pilosula</i> Hairy Root. <i>Genes</i> , 2021, 12, 1588.	2.4	5
23	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. <i>Genomics</i> , 2010, 96, 308-315.	2.9	4
24	Transcriptionally active gene fragments derived from potentially fast-evolving donor genes in the rice genome. <i>Bioinformatics</i> , 2009, 25, 1215-1218.	4.1	3
25	Elucidation of the MicroRNA Transcriptome in Western Corn Rootworm Reveals Its Dynamic and Evolutionary Complexity. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 800-814.	6.9	3
26	The Construction and Exploration of a Comprehensive MicroRNA Centered Regulatory Network in Foxtail Millet ( <i>Setaria italica</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	2
27	A Bioinformatics Pipeline to Accurately and Efficiently Analyze the MicroRNA Transcriptomes in Plants. <i>Journal of Visualized Experiments</i> , 2020, , .	0.3	1