

Yanqiang Li

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

804
citations

623734

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22
all docs

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docs citations

22
times ranked

1227
citing authors

#	ARTICLE	IF	CITATIONS
1	XA23 Is an Executor R Protein and Confers Broad-Spectrum Disease Resistance in Rice. <i>Molecular Plant</i> , 2015, 8, 290-302.	8.3	202
2	Transcriptomic analysis reveals the roles of microtubule-related genes and transcription factors in fruit length regulation in cucumber (<i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2015, 5, 8031.	3.3	89
3	A Functional Allele of <i>CsFUL1</i> Regulates Fruit Length through Repressing <i>CsSUP</i> and Inhibiting Auxin Transport in Cucumber. <i>Plant Cell</i> , 2019, 31, 1289-1307.	6.6	84
4	Methylation interactions in <i>Arabidopsis</i> hybrids require RNA-directed DNA methylation and are influenced by genetic variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4248-56.	7.1	79
5	The chromatin remodeler DDM1 promotes hybrid vigor by regulating salicylic acid metabolism. <i>Cell Discovery</i> , 2016, 2, 16027.	6.7	55
6	A PRC2-independent function for EZH2 in regulating rRNA 2â€²-O methylation and IRES-dependent translation. <i>Nature Cell Biology</i> , 2021, 23, 341-354.	10.3	54
7	Comparative expression profiling reveals gene functions in female meiosis and gametophyte development in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2014, 80, 615-628.	5.7	40
8	Efficient Generation of diRNAs Requires Components in the Posttranscriptional Gene Silencing Pathway. <i>Scientific Reports</i> , 2017, 7, 301.	3.3	34
9	Phloem transcriptome signatures underpin the physiological differentiation of the pedicel, stalk and fruit of cucumber (<i>Cucumis sativus</i> L.). <i>Plant and Cell Physiology</i> , 2016, 57, 19-34.	3.1	27
10	Asymmetric transcriptomic signatures between the cob and florets in the maize ear under optimal- and low-nitrogen conditions at silking, and functional characterization of amino acid transporters ZmAAP4 and ZmVAAT3. <i>Journal of Experimental Botany</i> , 2015, 66, 6149-6166.	4.8	26
11	Machine learning uncovers cell identity regulator by histone code. <i>Nature Communications</i> , 2020, 11, 2696.	12.8	25
12	Integration of Hormonal and Nutritional Cues Orchestrates Progressive Corolla Opening. <i>Plant Physiology</i> , 2016, 171, 1209-1229.	4.8	24
13	Sodium arsenite exposure inhibits histone acetyltransferase p300 for attenuating H3K27ac at enhancers in mouse embryonic fibroblast cells. <i>Toxicology and Applied Pharmacology</i> , 2018, 357, 70-79.	2.8	17
14	Deep Sequencing Uncovers Rice Long siRNAs and Its Involvement in Immunity Against <i>Rhizoctonia solani</i> . <i>Phytopathology</i> , 2018, 108, 60-69.	2.2	15
15	The conserved DNMT1-dependent methylation regions in human cells are vulnerable to neurotoxicant rotenone exposure. <i>Epigenetics and Chromatin</i> , 2020, 13, 17.	3.9	12
16	TADsplimer reveals splits and mergers of topologically associating domains for epigenetic regulation of transcription. <i>Genome Biology</i> , 2020, 21, 84.	8.8	6
17	Methylation-dependent and -independent roles of EZH2 synergize in CDCA8 activation in prostate cancer. <i>Oncogene</i> , 2022, 41, 1610-1621.	5.9	6
18	HrcQ is necessary for <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> HR-induction in non-host tobacco and pathogenicity in host rice. <i>Crop Journal</i> , 2013, 1, 143-150.	5.2	5

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19	MACMIC Reveals A Dual Role of CTCF in Epigenetic Regulation of Cell Identity Genes. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 140-153.	6.9	4
20	Editorial: Environmental Genomics and Epigenomics: Response, Development and Disease. <i>Frontiers in Genetics</i> , 2021, 12, 694288.	2.3	0