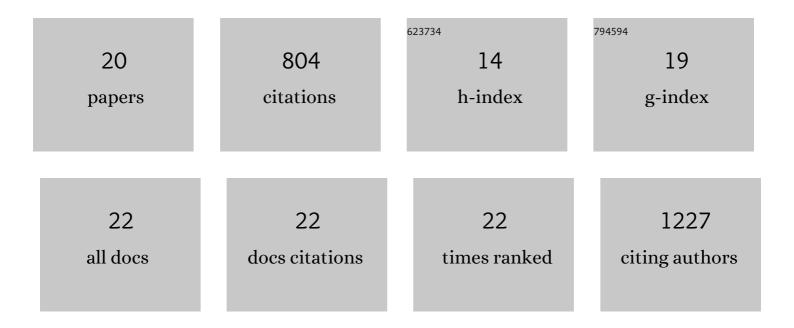
## Yanqiang Li

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	XA23 Is an Executor R Protein and Confers Broad-Spectrum Disease Resistance in Rice. Molecular Plant, 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 (Cucumis sativus L.). Scientific Reports, 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. Plant Cell, 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. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4248-56.	7.1	79
5	The chromatin remodeler DDM1 promotes hybrid vigor by regulating salicylic acid metabolism. Cell Discovery, 2016, 2, 16027.	6.7	55
6	A PRC2-independent function for EZH2 in regulating rRNA 2′-O methylation and IRES-dependent translation. Nature Cell Biology, 2021, 23, 341-354.	10.3	54
7	Comparative expression profiling reveals gene functions in female meiosis and gametophyte development in Arabidopsis. Plant Journal, 2014, 80, 615-628.	5.7	40
8	Efficient Generation of diRNAs Requires Components in the Posttranscriptional Gene Silencing Pathway. Scientific Reports, 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.). Plant and Cell Physiology, 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. Journal of Experimental Botany, 2015, 66, 6149-6166.	4.8	26
11	Machine learning uncovers cell identity regulator by histone code. Nature Communications, 2020, 11, 2696.	12.8	25
12	Integration of Hormonal and Nutritional Cues Orchestrates Progressive Corolla Opening Â. Plant Physiology, 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. Toxicology and Applied Pharmacology, 2018, 357, 70-79.	2.8	17
14	Deep Sequencing Uncovers Rice Long siRNAs and Its Involvement in Immunity Against <i>Rhizoctonia solani</i> . Phytopathology, 2018, 108, 60-69.	2.2	15
15	The conserved DNMT1-dependent methylation regions in human cells are vulnerable to neurotoxicant rotenone exposure. Epigenetics and Chromatin, 2020, 13, 17.	3.9	12
16	TADsplimer reveals splits and mergers of topologically associating domains for epigenetic regulation of transcription. Genome Biology, 2020, 21, 84.	8.8	6
17	Methylation-dependent and -independent roles of EZH2 synergize in CDCA8 activation in prostate cancer. Oncogene, 2022, 41, 1610-1621.	5.9	6
18	HrcQ is necessary for Xanthomonas oryzae pv. oryzae HR-induction in non-host tobacco and pathogenicity in host rice. Crop Journal, 2013, 1, 143-150.	5.2	5

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