

# Shiqiang Liu

## List of Publications by Year in descending order

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35  
papers

2,035  
citations

623699

14  
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377849

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35  
all docs

35  
docs citations

35  
times ranked

2557  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and expression analysis of E2 ubiquitin-conjugating enzymes in cucumber. Canadian Journal of Plant Science, 2022, 102, 147-159.	0.9	0
2	Comprehensive identification of the VQ family genes in cucumber and their roles in response to abiotic and biotic stresses. Scientia Horticulturae, 2022, 295, 110874.	3.6	4
3	Genome-Wide Survey and Expression Analysis of B-Box Family Genes in Cucumber Reveal Their Potential Roles in Response to Diverse Abiotic and Biotic Stresses. Agriculture (Switzerland), 2022, 12, 827.	3.1	5
4	Molecular Cloning, Characterization, and Expression Analysis of SIMILAR TO RCD-ONE (SRO) Family Genes Responding to Abiotic and Biotic Stress in Cucumber. Horticulturae, 2022, 8, 634.	2.8	1
5	Identification and Transcriptional Analysis of Zinc Finger-Homeodomain (ZF-HD) Family Genes in Cucumber. Biochemical Genetics, 2021, 59, 884-901.	1.7	21
6	Comprehensive analysis of 14-3-3 family genes and their responses to cold and drought stress in cucumber. Functional Plant Biology, 2021, 48, 1264-1276.	2.1	4
7	Characterization of Germin-like Proteins (GLPs) and Their Expression in Response to Abiotic and Biotic Stresses in Cucumber. Horticulturae, 2021, 7, 412.	2.8	19
8	Comprehensive genomic analysis and expression profiling of the BTB and TAZ (BT) genes in cucumber ( <i>Cucumis sativus</i> L.). Czech Journal of Genetics and Plant Breeding, 2020, 56, 15-23.	0.8	11
9	In silico identification and expression analysis of Rare Cold Inducible 2 (RCI2) gene family in cucumber. Journal of Plant Biochemistry and Biotechnology, 2020, 29, 56-66.	1.7	7
10	In Silico Identification and Expression Analysis of Nuclear Factor Y (Nf-Y) Transcription Factors in Cucumber. Agronomy, 2020, 10, 236.	3.0	15
11	Identification and Characterization of Tonoplast Sugar Transporter (TST) Gene Family in Cucumber. Horticultural Plant Journal, 2020, 6, 145-157.	5.0	16
12	Identification and Expression Analysis of Stress-Associated Proteins (SAPs) Containing A20/AN1 Zinc Finger in Cucumber. Plants, 2020, 9, 400.	3.5	25
13	Isolation and characterization of a <i>MADS-box</i> gene in cucumber ( <i>Cucumis sativus</i> L.) that affects flowering time and leaf morphology in transgenic <i>Arabidopsis</i> . Biotechnology and Biotechnological Equipment, 2019, 33, 54-63.	1.3	13
14	Identification of the metallothionein gene family from cucumber and functional characterization of CsMT4 in <i>Escherichia coli</i> under salinity and osmotic stress. 3 Biotech, 2019, 9, 394.	2.2	11
15	Molecular cloning and functional analysis of a sugar transporter gene ( <i>CsTST2</i> ) from cucumber ( <i>Cucumis sativus</i> L.). Biotechnology and Biotechnological Equipment, 2019, 33, 118-127.	1.3	21
16	Overexpression of an APETALA1-like gene from cucumber ( <i>Cucumis sativus</i> L.) induces earlier flowering and abnormal leaf development in transgenic <i>Arabidopsis</i> . Canadian Journal of Plant Science, 2019, 99, 210-220.	0.9	3
17	Identification and Characterization of a SEPALLATA-like MADS-box Gene from Cucumber ( <i>Cucumis</i> ) Tj ETQq1 1 0.784314 rgBJ /Overlo	1.1	2
18	Ectopic expression of CsMADS24, an AGAMOUS ortholog from cucumber, causes homeotic conversion of sepals into carpels in transgenic <i>Arabidopsis</i> plants. Archives of Biological Sciences, 2019, 71, 13-20.	0.5	2

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19	Genome-wide identification, characterization, and transcriptional analysis of the metacaspase gene family in cucumber ( <i>Cucumis sativus</i> ). <i>Genome</i> , 2018, 61, 187-194.	2.0	12
20	Genome-wide identification of glutathione peroxidase (GPX) gene family and their response to abiotic stress in cucumber. <i>3 Biotech</i> , 2018, 8, 159.	2.2	36
21	Genome-wide identification and expression analysis of YTH domain-containing RNA-binding protein family in cucumber ( <i>Cucumis sativus</i> ). <i>Genes and Genomics</i> , 2018, 40, 579-589.	1.4	14
22	Isolation and Functional Characterization of an AGAMOUS-LIKE 18 (AGL18) MADS-box Gene from Cucumber ( <i>Cucumis sativus</i> L.). <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2018, 47, 300-307.	1.1	1
23	A Cucumber AGAMOUS-LIKE 15 (AGL15) MADS-Box Gene Mediates Abnormal Leaf Morphology in <i>Arabidopsis</i> . <i>Agronomy</i> , 2018, 8, 265.	3.0	1
24	Molecular cloning and functional characterization of a Cu/Zn superoxide dismutase gene (CsCSD1) from <i>Cucumis sativus</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2018, 135, 309-319.	2.3	4
25	Identification and transcriptional analysis of dehydrin gene family in cucumber ( <i>Cucumis sativus</i> ). <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	2.1	8
26	Genome-wide identification and characterization of cysteine-rich polycomb-like protein (CPP) family genes in cucumber ( <i>Cucumis sativus</i> ) and their roles in stress responses. <i>Biologia (Poland)</i> , 2018, 73, 425-435.	1.5	16
27	Molecular cloning and characterization of an ASR gene from <i>Cucumis sativus</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 130, 553-565.	2.3	10
28	Genome-wide identification and phylogenetic analysis of the chalcone synthase gene family in rice. <i>Journal of Plant Research</i> , 2017, 130, 95-105.	2.4	20
29	Genome-Wide Identification and Transcriptional Expression Analysis of Cucumber Superoxide Dismutase (SOD) Family in Response to Various Abiotic Stresses. <i>International Journal of Genomics</i> , 2017, 2017, 1-14.	1.6	68
30	Overexpression of CsLEA11, a Y3SK2-type dehydrin gene from cucumber ( <i>Cucumis sativus</i> ), enhances tolerance to heat and cold in <i>Escherichia coli</i> . <i>AMB Express</i> , 2017, 7, 182.	3.0	27
31	<i>CsCAT3</i> , a catalase gene from <i>Cucumis sativus</i> , confers resistance to a variety of stresses to <i>Escherichia coli</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2017, 31, 886-896.	1.3	22
32	The catalase gene family in cucumber: genome-wide identification and organization. <i>Genetics and Molecular Biology</i> , 2016, 39, 408-415.	1.3	44
33	Genome-wide analysis of the MADS-box gene family in cucumber. <i>Genome</i> , 2012, 55, 245-256.	2.0	94
34	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. <i>BMC Genomics</i> , 2010, 11, 384.	2.8	161
35	The genome of the cucumber, <i>Cucumis sativus</i> L.. <i>Nature Genetics</i> , 2009, 41, 1275-1281.	21.4	1,317