

# Shuxia Chen

## List of Publications by Year in descending order

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16  
papers

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citations

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#	ARTICLE	IF	CITATIONS
1	Substance metabolism, IAA and CTK signaling pathways regulating the origin of embryogenic callus during dedifferentiation and redifferentiation of cucumber cotyledon nodes. <i>Scientia Horticulturae</i> , 2022, 293, 110680.	3.6	7
2	Quantitative trait locus mapping of fruit aroma compounds in cucumber ( <i>Cucumis sativus</i> L.) based on a recombinant inbred line population. <i>Horticulture Research</i> , 2022, 9, .	6.3	2
3	Transcriptomic and Histological Analysis of the Response of Susceptible and Resistant Cucumber to <i>Meloidogyne incognita</i> Infection Revealing Complex Resistance via Multiple Signaling Pathways. <i>Frontiers in Plant Science</i> , 2021, 12, 675429.	3.6	5
4	Identification and expression analyzes of CC-type glutaredoxin in cucumber ( <i>Cucumis sativus</i> L.) under abiotic stress. <i>Scientia Horticulturae</i> , 2021, 289, 110417.	3.6	6
5	Relationship between CsLOX gene expression and C6 and C9 aldehydes during cucumber fruit storage. <i>Postharvest Biology and Technology</i> , 2020, 161, 111085.	6.0	4
6	Redox Status, JA and ET Signaling Pathway Regulating Responses to <i>Botrytis cinerea</i> Infection Between the Resistant Cucumber Genotype and Its Susceptible Mutant. <i>Frontiers in Plant Science</i> , 2020, 11, 559070.	3.6	16
7	Relationship between key environmental factors and profiling of volatile compounds during cucumber fruit development under protected cultivation. <i>Food Chemistry</i> , 2019, 290, 308-315.	8.2	28
8	Genetic analysis and QTL mapping of fruit length and diameter in a cucumber ( <i>Cucumis sativus</i> L.) recombinant inbred line (RIL) population. <i>Scientia Horticulturae</i> , 2019, 250, 214-222.	3.6	13
9	Morphological variability in leaves of Chinese wild <i>Vitis</i> species. <i>Scientia Horticulturae</i> , 2018, 238, 138-146.	3.6	8
10	Identification and functional characterization of APRR2 controlling green immature fruit color in cucumber ( <i>Cucumis sativus</i> L.). <i>Plant Growth Regulation</i> , 2017, 83, 233-243.	3.4	23
11	Map-based cloning, identification and characterization of the w gene controlling white immature fruit color in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2016, 129, 1247-1256.	3.6	87
12	Fine genetic mapping of the white immature fruit color gene w to a 33.0-kb region in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2015, 128, 2375-2385.	3.6	32
13	Profiling of Volatile Compounds and Associated Gene Expression and Enzyme Activity during Fruit Development in Two Cucumber Cultivars. <i>PLoS ONE</i> , 2015, 10, e0119444.	2.5	21
14	Analysis of the genetic diversity of garlic ( <i>Allium sativum</i> L.) by simple sequence repeat and inter simple sequence repeat analysis and agro-morphological traits. <i>Biochemical Systematics and Ecology</i> , 2014, 55, 260-267.	1.3	29
15	Analysis of the genetic diversity of garlic ( <i>Allium sativum</i> L.) germplasm by SRAP. <i>Biochemical Systematics and Ecology</i> , 2013, 50, 139-146.	1.3	28
16	Evaluation of Garlic Cultivars for Polyphenolic Content and Antioxidant Properties. <i>PLoS ONE</i> , 2013, 8, e79730.	2.5	101