

Shuxia Chen

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

410
citations

933447

10
h-index

940533

16
g-index

16
all docs

16
docs citations

16
times ranked

442
citing authors

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