

Kenong Xu

List of Publications by Year in descending order

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16
papers

1,222
citations

759233

12
h-index

940533

16
g-index

16
all docs

16
docs citations

16
times ranked

1364
citing authors

#	ARTICLE	IF	CITATIONS
1	Classifying Cider Apple Germplasm Using Genetic Markers for Fruit Acidity. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 267-275.	1.0	4
2	Integrative Morphological, Physiological, Proteomics Analyses of Jujube Fruit Development Provide Insights Into Fruit Quality Domestication From Wild Jujube to Cultivated Jujube. <i>Frontiers in Plant Science</i> , 2021, 12, 773825.	3.6	12
3	Apple ALMT9 Requires a Conserved C-Terminal Domain for Malate Transport Underlying Fruit Acidity. <i>Plant Physiology</i> , 2020, 182, 992-1006.	4.8	41
4	Identification of two QTLs associated with high fruit acidity in apple using pooled genome sequencing analysis. <i>Horticulture Research</i> , 2020, 7, 171.	6.3	15
5	Phased diploid genome assemblies and pan-genomes provide insights into the genetic history of apple domestication. <i>Nature Genetics</i> , 2020, 52, 1423-1432.	21.4	168
6	<i>ERF4</i> affects fruit firmness through TPL4 by reducing ethylene production. <i>Plant Journal</i> , 2020, 103, 937-950.	5.7	51
7	Exploring DNA Variant Segregation Types Enables Mapping Loci for Recessive Phenotypic Suppression of Columnar Growth in Apple. <i>Frontiers in Plant Science</i> , 2020, 11, 692.	3.6	5
8	Exploring DNA variant segregation types in pooled genome sequencing enables effective mapping of weeping trait in <i>Malus</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 1499-1516.	4.8	33
9	Genome re-sequencing reveals the history of apple and supports a two-stage model for fruit enlargement. <i>Nature Communications</i> , 2017, 8, 249.	12.8	286
10	Assessing the allelotypic effect of two aminocyclopropane carboxylic acid synthase-encoding genes <i>MdACS1</i> and <i>MdACS3a</i> on fruit ethylene production and softening in <i>Malus</i> . <i>Horticulture Research</i> , 2016, 3, 16024.	6.3	19
11	Suppressing Sorbitol Synthesis Substantially Alters the Global Expression Profile of Stress Response Genes in Apple (<i>Malus domestica</i>) Leaves. <i>Plant and Cell Physiology</i> , 2015, 56, 1748-1761.	3.1	29
12	Transcriptome analysis of an apple (<i>Malus domestica</i>) yellow fruit somatic mutation identifies a gene network module highly associated with anthocyanin and epigenetic regulation. <i>Journal of Experimental Botany</i> , 2015, 66, 7359-7376.	4.8	253
13	Uncovering co-expression gene network modules regulating fruit acidity in diverse apples. <i>BMC Genomics</i> , 2015, 16, 612.	2.8	68
14	Genetic characterization of the Ma locus with pH and titratable acidity in apple. <i>Molecular Breeding</i> , 2012, 30, 899-912.	2.1	83
15	A natural mutation-led truncation in one of the two aluminum-activated malate transporter-like genes at the Ma locus is associated with low fruit acidity in apple. <i>Molecular Genetics and Genomics</i> , 2012, 287, 663-678.	2.1	124
16	EST contig-based SSR linkage maps for <i>Malus domestica</i> cv Royal Gala and an apple scab resistant accession of <i>M. sieversii</i> , the progenitor species of domestic apple. <i>Molecular Breeding</i> , 2012, 29, 379-397.	2.1	31