

Zhongping Xu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8406740/publications.pdf>

Version: 2024-02-01

14
papers

623
citations

759233

12
h-index

1058476

14
g-index

15
all docs

15
docs citations

15
times ranked

667
citing authors

#	ARTICLE	IF	CITATIONS
1	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. <i>Nature Communications</i> , 2019, 10, 4702.	12.8	115
2	Highly efficient and precise base editing of C to G to T to A in the allotetraploid cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 2020, 18, 45-56.	8.3	114
3	The chromosome-level wintersweet (<i>Chimonanthus praecox</i>) genome provides insights into floral scent biosynthesis and flowering in winter. <i>Genome Biology</i> , 2020, 21, 200.	8.8	69
4	The application of a heat-inducible CRISPR/Cas12b (C2c1) genome editing system in tetraploid cotton (<i>G. hirsutum</i>) plants. <i>Plant Biotechnology Journal</i> , 2020, 18, 2436-2443.	8.3	58
5	A transgenic strategy for controlling plant bugs (<i>Adelphocoris suturalis</i>) through expression of double-stranded RNA homologous to fatty acyl-coenzyme A reductase in cotton. <i>New Phytologist</i> , 2017, 215, 1173-1185.	7.3	53
6	The application of temperature sensitivity CRISPR/LbCpf1 (LbCas12a) mediated genome editing in allotetraploid cotton (<i>G. hirsutum</i>) and creation of nontransgenic, gossypol-free cotton. <i>Plant Biotechnology Journal</i> , 2021, 19, 221-223.	8.3	39
7	Development of an efficient and precise adenine base editor (ABE) with expanded target range in allotetraploid cotton (<i>Gossypium hirsutum</i>). <i>BMC Biology</i> , 2022, 20, 45.	3.8	33
8	Metabolic engineering of cottonseed oil biosynthesis pathway via RNA interference. <i>Scientific Reports</i> , 2016, 6, 33342.	3.3	31
9	Plant Single Cell Transcriptome Hub (PsctH): an integrated online tool to explore the plant single-cell transcriptome landscape. <i>Plant Biotechnology Journal</i> , 2022, 20, 10-12.	8.3	27
10	Genome sequencing reveals chromosome fusion and extensive expansion of genes related to secondary metabolism in <i>Artemisia argyi</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1902-1915.	8.3	25
11	Genome-Wide Identification of Papain-Like Cysteine Proteases in <i>Gossypium hirsutum</i> and Functional Characterization in Response to <i>Verticillium dahliae</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 134.	3.6	21
12	Transcriptome and metabolome analysis reveal that oral secretions from <i>Helicoverpa armigera</i> and <i>Spodoptera litura</i> influence wound-induced host response in cotton. <i>Crop Journal</i> , 2020, 8, 929-942.	5.2	16
13	Identification and Functional Analysis of lncRNA by CRISPR/Cas9 During the Cotton Response to Sap-Sucking Insect Infestation. <i>Frontiers in Plant Science</i> , 2022, 13, 784511.	3.6	12
14	Silencing of a LIM gene in cotton exhibits enhanced resistance against <i>Apolygus lucorum</i> . <i>Journal of Cellular Physiology</i> , 2021, 236, 5921-5936.	4.1	8