

Zhang Zhongbao

List of Publications by Year in Descending Order

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

15
papers

4,199
citations

7
h-index

18
g-index

18
ext. papers

6,011
ext. citations

4
avg. IF

4.9
L-index

#	Paper	IF	Citations
15	Natural variation of ZmCGT1 is responsible for isoorientin accumulation in maize silk. <i>Plant Journal</i> , 2021 ,	6.9	1
14	Isoorientin Affects Markers of Alzheimer's Disease via Effects on the Oral and Gut Microbiota in APP/PS1 Mice. <i>Journal of Nutrition</i> , 2021 ,	4.1	3
13	Identifying key regulatory genes of maize root growth and development by RNA sequencing. <i>Genomics</i> , 2020 , 112, 5157-5169	4.3	3
12	Analyses of the Complete Genome Sequence of the Strain Bacillus pumilus ZB201701 Isolated from Rhizosphere Soil of Maize under Drought and Salt Stress. <i>Microbes and Environments</i> , 2019 , 34, 310-315	2.6	3
11	Pre-breeding: the role of antioxidant enzymes on maize in salt stress tolerance. <i>Acta Physiologiae Plantarum</i> , 2019 , 41, 1	2.6	1
10	Effects of potassium-solubilizing and photosynthetic bacteria on tolerance to salt stress in maize. <i>Journal of Applied Microbiology</i> , 2019 , 126, 1530-1540	4.7	14
9	Analysis of the complete genome sequence of Brevibacterium frigoritolerans ZB201705 isolated from drought- and salt-stressed rhizosphere soil of maize. <i>Annals of Microbiology</i> , 2019 , 69, 1489-1496	3.2	5
8	Complete genome sequence of Bacillus licheniformis BL-010. <i>Microbial Pathogenesis</i> , 2018 , 118, 199-201	3.8	7
7	The complete genome sequence of Bacillus halotolerans ZB201702 isolated from a drought- and salt-stressed rhizosphere soil. <i>Microbial Pathogenesis</i> , 2018 , 123, 246-249	3.8	2
6	Effective Biodegradation of Aflatoxin B1 Using the (BL010) Strain. <i>Toxins</i> , 2018 , 10,	4.9	16
5	Isolation, structural analysis, and expression characteristics of the maize nuclear factor Y gene families. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 478, 752-8	3.4	22
4	Isolation, structural analysis, and expression characteristics of the maize TIFY gene family. <i>Molecular Genetics and Genomics</i> , 2015 , 290, 1849-58	3.1	29
3	Isolation, structural analysis, and expression characteristics of the maize (Zea mays L.) hexokinase gene family. <i>Molecular Biology Reports</i> , 2014 , 41, 6157-66	2.8	23
2	Genome-wide analysis and identification of HAK potassium transporter gene family in maize (Zea mays L.). <i>Molecular Biology Reports</i> , 2012 , 39, 8465-73	2.8	57
1	TASSEL: software for association mapping of complex traits in diverse samples. <i>Bioinformatics</i> , 2007 , 23, 2633-5	7.2	4013