

# Zhang Zhongbao

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/236642/publications.pdf>

Version: 2024-02-01

17  
papers

6,800  
citations

933410

10  
h-index

940516

16  
g-index

18  
all docs

18  
docs citations

18  
times ranked

7873  
citing authors

#	ARTICLE	IF	CITATIONS
1	TASSEL: software for association mapping of complex traits in diverse samples. <i>Bioinformatics</i> , 2007, 23, 2633-2635.	4.1	6,407
2	Genome-wide analysis and identification of HAK potassium transporter gene family in maize ( <i>Zea mays</i> ) Tj ETQq0 0.0.rgBT /Overlock 10	2.3	88
3	Isolation, structural analysis, and expression characteristics of the maize TIFY gene family. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1849-1858.	2.1	46
4	Isolation, structural analysis, and expression characteristics of the maize nuclear factor Y gene families. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 752-758.	2.1	42
5	Isolation, structural analysis, and expression characteristics of the maize ( <i>Zea mays</i> L.) hexokinase gene family. <i>Molecular Biology Reports</i> , 2014, 41, 6157-6166.	2.3	39
6	Efficient and genotype independent maize transformation using pollen transfected by DNA-coated magnetic nanoparticles. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1145-1156.	8.5	36
7	Effective Biodegradation of Aflatoxin B1 Using the <i>Bacillus licheniformis</i> (BL010) Strain. <i>Toxins</i> , 2018, 10, 497.	3.4	32
8	Effects of potassium-solubilizing and photosynthetic bacteria on tolerance to salt stress in maize. <i>Journal of Applied Microbiology</i> , 2019, 126, 1530-1540.	3.1	25
9	Analysis of the complete genome sequence of <i>Brevibacterium frigoritolerans</i> ZB201705 isolated from drought- and salt-stressed rhizosphere soil of maize. <i>Annals of Microbiology</i> , 2019, 69, 1489-1496.	2.6	19
10	Identifying key regulatory genes of maize root growth and development by RNA sequencing. <i>Genomics</i> , 2020, 112, 5157-5169.	2.9	13
11	Natural variation of <i>ZmCGT1</i> is responsible for isoorientin accumulation in maize silk. <i>Plant Journal</i> , 2022, 109, 64-76.	5.7	13
12	The complete genome sequence of <i>Bacillus halotolerans</i> ZB201702 isolated from a drought- and salt-stressed rhizosphere soil. <i>Microbial Pathogenesis</i> , 2018, 123, 246-249.	2.9	11
13	Complete genome sequence of <i>Bacillus licheniformis</i> BL-010. <i>Microbial Pathogenesis</i> , 2018, 118, 199-201.	2.9	10
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> , 2022, 152, 140-152.	2.9	10
15	Analyses of the Complete Genome Sequence of the Strain <i>Bacillus pumilus</i> ZB201701 Isolated from Rhizosphere Soil of Maize under Drought and Salt Stress. <i>Microbes and Environments</i> , 2019, 34, 310-315.	1.6	5
16	Pre-breeding: the role of antioxidant enzymes on maize in salt stress tolerance. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	2.1	4
17	Heterologous expression of ZmNF-YA12 confers tolerance to drought and salt stress in <i>Arabidopsis</i> . <i>Plant Biotechnology Reports</i> , 0, , .	1.5	0