

# Kunkun Zhao

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/966552/publications.pdf>

Version: 2024-02-01

9  
papers

236  
citations

1163117

8  
h-index

1474206

9  
g-index

10  
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10  
docs citations

10  
times ranked

307  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome of an allotetraploid wild peanut <i>Arachis monticola</i> : a de novo assembly. <i>GigaScience</i> , 2018, 7, .	6.4	75
2	Comparison of <i>Arachis monticola</i> with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. <i>Advanced Science</i> , 2020, 7, 1901672.	11.2	43
3	Genome-wide identification and analysis of long noncoding RNAs (lncRNAs) during seed development in peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 192.	3.6	28
4	Small RNA and Degradome Deep Sequencing Reveals the Roles of microRNAs in Seed Expansion in Peanut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 349.	3.6	27
5	Genome-Wide Analysis of the Growth-Regulating Factor Family in Peanut ( <i>Arachis hypogaea</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 4120.	4.1	19
6	Genome-wide identification of circular RNAs in peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2019, 20, 653.	2.8	15
7	Comprehensive Transcriptome Analyses Reveal Candidate Genes for Variation in Seed Size/Weight During Peanut ( <i>Arachis hypogaea</i> L.) Domestication. <i>Frontiers in Plant Science</i> , 2021, 12, 666483.	3.6	13
8	Chromatin spatial organization of wild type and mutant peanuts reveals high-resolution genomic architecture and interaction alterations. <i>Genome Biology</i> , 2021, 22, 315.	8.8	13
9	Genome-wide identification and expression analysis of <i>auxin response factors</i> in peanut ( <i>Arachis hypogaea</i> L.). <i>PeerJ</i> , 2021, 9, e12319.	2.0	3