

# Suoyi Han

## List of Publications by Year in descending order

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Version: 2024-02-01

18  
papers

517  
citations

933447

10  
h-index

839539

18  
g-index

23  
all docs

23  
docs citations

23  
times ranked

512  
citing authors

#	ARTICLE	IF	CITATIONS
1	Smash-ridging cultivation improves crop production. <i>Outlook on Agriculture</i> , 2022, 51, 173-177.	3.4	2
2	<scp><i>AhNPR3</i></scp> regulates the expression of <scp>WRKY</scp> and <scp><i>PR</i></scp> genes, and mediates the immune response of the peanut (<i>Arachis hypogaea</i> L.). <i>Plant Journal</i> , 2022, 110, 735-747.	5.7	6
3	Transcriptome analysis of pod mutant reveals plant hormones are important regulators in controlling pod size in peanut (<i>Arachis hypogaea</i> L.). <i>PeerJ</i> , 2022, 10, e12965.	2.0	8
4	Physical mapping of repetitive oligonucleotides facilitates the establishment of a genome map-based karyotype to identify chromosomal variations in peanut. <i>BMC Plant Biology</i> , 2021, 21, 107.	3.6	6
5	Genome-wide identification of mlo genes in the cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2021, 217, 1.	1.2	4
6	Genome-Wide Identification and Expression Analysis of AP2/ERF Transcription Factor Related to Drought Stress in Cultivated Peanut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 750761.	2.3	21
7	Transcriptomic analyses reveal the expression and regulation of genes associated with resistance to early leaf spot in peanut. <i>BMC Research Notes</i> , 2020, 13, 381.	1.4	15
8	QTL mapping of web blotch resistance in peanut by high-throughput genome-wide sequencing. <i>BMC Plant Biology</i> , 2020, 20, 249.	3.6	9
9	Development of an oligonucleotide dye solution facilitates high throughput and cost-efficient chromosome identification in peanut. <i>Plant Methods</i> , 2019, 15, 69.	4.3	7
10	Mutagenesis of FAD2 genes in peanut with CRISPR/Cas9 based gene editing. <i>BMC Biotechnology</i> , 2019, 19, 24.	3.3	83
11	Genetic Diversity, Population Structure, and Botanical Variety of 320 Global Peanut Accessions Revealed Through Tunable Genotyping-by-Sequencing. <i>Scientific Reports</i> , 2018, 8, 14500.	3.3	33
12	High-resolution chromosome painting with repetitive and single-copy oligonucleotides in <i>Arachis</i> species identifies structural rearrangements and genome differentiation. <i>BMC Plant Biology</i> , 2018, 18, 240.	3.6	10
13	Salinity Inhibits Rice Seed Germination by Reducing $\hat{\pm}$ -Amylase Activity via Decreased Bioactive Gibberellin Content. <i>Frontiers in Plant Science</i> , 2018, 9, 275.	3.6	102
14	A SNP-Based Linkage Map Revealed QTLs for Resistance to Early and Late Leaf Spot Diseases in Peanut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1012.	3.6	63
15	Physiological and Proteomics Analyses Reveal Low-Phosphorus Stress Affected the Regulation of Photosynthesis in Soybean. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1688.	4.1	32
16	Comparative analysis of NBS-LRR genes and their response to <i>Aspergillus flavus</i> in <i>Arachis</i> . <i>PLoS ONE</i> , 2017, 12, e0171181.	2.5	50
17	Differential gene expression in leaf tissues between mutant and wild-type genotypes response to late leaf spot in peanut ( <i>Arachis hypogaea</i> L.). <i>PLoS ONE</i> , 2017, 12, e0183428.	2.5	14
18	Identification of lipoxygenase (LOX) genes from legumes and their responses in wild type and cultivated peanut upon <i>Aspergillus flavus</i> infection. <i>Scientific Reports</i> , 2016, 6, 35245.	3.3	52