

# Hang He

## List of Publications by Year in descending order

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54  
papers

3,488  
citations

186265  
28  
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161849  
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56  
all docs

56  
docs citations

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times ranked

4895  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Epigenetic and Transcriptional Trends among Two Rice Subspecies and Their Reciprocal Hybrids. <i>Plant Cell</i> , 2010, 22, 17-33.	6.6	514
2	Genome-Wide Analysis of DNA Methylation and Gene Expression Changes in Two <i>Arabidopsis</i> Ecotypes and Their Reciprocal Hybrids. <i>Plant Cell</i> , 2012, 24, 875-892.	6.6	297
3	A High-Density SNP Genotyping Array for Rice Biology and Molecular Breeding. <i>Molecular Plant</i> , 2014, 7, 541-553.	8.3	251
4	A high-quality genome assembly highlights rye genomic characteristics and agronomically important genes. <i>Nature Genetics</i> , 2021, 53, 574-584.	21.4	164
5	MYB20, MYB42, MYB43, and MYB85 Regulate Phenylalanine and Lignin Biosynthesis during Secondary Cell Wall Formation. <i>Plant Physiology</i> , 2020, 182, 1272-1283.	4.8	154
6	Genome-wide selection and genetic improvement during modern maize breeding. <i>Nature Genetics</i> , 2020, 52, 565-571.	21.4	146
7	SKIP Confers Osmotic Tolerance during Salt Stress by Controlling Alternative Gene Splicing in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2015, 8, 1038-1052.	8.3	140
8	<i>Arabidopsis</i> SAURs are critical for differential light regulation of the development of various organs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6071-6076.	7.1	127
9	<i>Arabidopsis</i> DE-ETIOLATED1 Represses Photomorphogenesis by Positively Regulating Phytochrome-Interacting Factors in the Dark. <i>Plant Cell</i> , 2014, 26, 3630-3645.	6.6	116
10	The DTH8-Hd1 Module Mediates Day-Length-Dependent Regulation of Rice Flowering. <i>Molecular Plant</i> , 2017, 10, 948-961.	8.3	107
11	Heat stress-induced transposon activation correlates with 3D chromatin organization rearrangement in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2020, 11, 1886.	12.8	102
12	Basic leucine zipper transcription factor OsbZIP16 positively regulates drought resistance in rice. <i>Plant Science</i> , 2012, 193-194, 8-17.	3.6	98
13	Development and application of a set of breeder-friendly SNP markers for genetic analyses and molecular breeding of rice ( <i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 869-879.	3.6	93
14	Origin and Evolution of Core Components Responsible for Monitoring Light Environment Changes during Plant Terrestrialization. <i>Molecular Plant</i> , 2019, 12, 847-862.	8.3	85
15	Poaceae-specific <i>MS1</i> encodes a phospholipid-binding protein for male fertility in bread wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12614-12619.	7.1	83
16	The Transcription Factors TCP4 and PIF3 Antagonistically Regulate Organ-Specific Light Induction of <i>SAUR</i> Genes to Modulate Cotyledon Opening during De-Etiolation in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2019, 31, 1155-1170.	6.6	74
17	A telomere-to-telomere gap-free reference genome of watermelon and its mutation library provide important resources for gene discovery and breeding. <i>Molecular Plant</i> , 2022, 15, 1268-1284.	8.3	74
18	Genome-wide regulation of light-controlled seedling morphogenesis by three families of transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6482-6487.	7.1	68

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19	Genome Variation Map: a data repository of genome variations in BIG Data Center. <i>Nucleic Acids Research</i> , 2018, 46, D944-D949.	14.5	53
20	Two-signal requirement for growth-promoting function of Yap in hepatocytes. <i>ELife</i> , 2015, 4, .	6.0	51
21	Development of genomics-based genotyping platforms and their applications in rice breeding. <i>Current Opinion in Plant Biology</i> , 2013, 16, 247-254.	7.1	46
22	Divergent selection and genetic introgression shape the genome landscape of heterosis in hybrid rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4623-4631.	7.1	46
23	The HuangZaoSi Maize Genome Provides Insights into Genomic Variation and Improvement History of Maize. <i>Molecular Plant</i> , 2019, 12, 402-409.	8.3	41
24	Characterization and fine-mapping of a novel premature leaf senescence mutant yellow leaf and dwarf 1 in rice. <i>Plant Physiology and Biochemistry</i> , 2017, 111, 50-58.	5.8	40
25	Simultaneous Identification of Multiple Causal Mutations in Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 2055.	3.6	40
26	Pedigree-based analysis of derivation of genome segments of an elite rice reveals key regions during its breeding. <i>Plant Biotechnology Journal</i> , 2016, 14, 638-648.	8.3	38
27	The Asymmetric Expression of SALUR Genes Mediated by ARF7/19 Promotes the Gravitropism and Phototropism of Plant Hypocotyls. <i>Cell Reports</i> , 2020, 31, 107529.	6.4	35
28	RNA-Seq Analysis Reveals MAPKKK Family Members Related to Drought Tolerance in Maize. <i>PLoS ONE</i> , 2015, 10, e0143128.	2.5	34
29	SKIP regulates environmental fitness and floral transition by forming two distinct complexes in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2019, 224, 321-335.	7.3	33
30	Improved de novo genome assembly and analysis of the Chinese cucurbit <i>Siraitia grosvenorii</i> , also known as monk fruit or luo-han-guo. <i>GigaScience</i> , 2018, 7, .	6.4	32
31	The telomere-free genome of four rice parents reveals SV and PAV patterns in hybrid rice breeding. <i>Plant Biotechnology Journal</i> , 2022, 20, 1642-1644.	8.3	31
32	<i>Arabidopsis</i> DET1 Represses Photomorphogenesis in Part by Negatively Regulating DELLA Protein Abundance in Darkness. <i>Molecular Plant</i> , 2015, 8, 622-630.	8.3	26
33	Chromatin remodeling complexes regulate genome architecture in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2022, 34, 2638-2651.	6.6	24
34	TCP transcription factors suppress cotyledon trichomes by impeding a cell differentiation-regulating complex. <i>Plant Physiology</i> , 2021, 186, 434-451.	4.8	20
35	Genome-wide dissection of heterosis for yield traits in two-line hybrid rice populations. <i>Scientific Reports</i> , 2017, 7, 7635.	3.3	18
36	Active DNA demethylation regulates tracheary element differentiation in <i>Arabidopsis</i> . <i>Science Advances</i> , 2020, 6, eaaz2963.	10.3	16

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37	Forecasting rice latitude adaptation through a daylength-sensing-based environment adaptation simulator. <i>Nature Food</i> , 2021, 2, 348-362.	14.0	16
38	MicroRNAs Are Involved in Maize Immunity Against <i>Fusarium verticillioides</i> Ear Rot. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 241-255.	6.9	14
39	Genome-Wide Association Study of the Genetic Basis of Effective Tiller Number in Rice. <i>Rice</i> , 2021, 14, 56.	4.0	14
40	Highly efficient genotyping of rice biparental populations by GoldenGate assays based on parental resequencing. <i>Theoretical and Applied Genetics</i> , 2014, 127, 297-307.	3.6	13
41	Genome-wide study of an elite rice pedigree reveals a complex history of genetic architecture for breeding improvement. <i>Scientific Reports</i> , 2017, 7, 45685.	3.3	13
42	New resources for genetic studies in maize ( <i>Zea mays</i> L.): a genome-wide Maize60K single nucleotide polymorphism array and its application. <i>Plant Journal</i> , 2021, 105, 1113-1122.	5.7	13
43	De novo assembly and comparative analysis of root transcriptomes from different varieties of <i>Panax ginseng</i> C. A. Meyer grown in different environments. <i>Science China Life Sciences</i> , 2015, 58, 1099-1110.	4.9	12
44	CHD3 chromatin-remodeling factor PICKLE regulates floral transition partially via modulating LEAFY expression at the chromatin level in <i>Arabidopsis</i> . <i>Science China Life Sciences</i> , 2016, 59, 516-528.	4.9	10
45	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , 2020, 102, 116-128.	5.7	10
46	Structural and Functional Analyses of Hub MicroRNAs in An Integrated Gene Regulatory Network of <i>Arabidopsis</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 747-764.	6.9	10
47	Time Series RNA-seq in Pigeonpea Revealed the Core Genes in Metabolic Pathways under Aluminum Stress. <i>Genes</i> , 2020, 11, 380.	2.4	9
48	Genomic insights on the contribution of introgressions from Xian/Indica to the genetic improvement of Geng/Japonica rice cultivars. <i>Plant Communications</i> , 2022, 3, 100325.	7.7	8
49	Allele-specific DNA methylation analyses associated with siRNAs in <i>Arabidopsis</i> hybrids. <i>Science China Life Sciences</i> , 2014, 57, 519-525.	4.9	7
50	A single nucleotide substitution at 5'UTR of GSN1 represses its translation and leads to an increase of grain length in rice. <i>Journal of Genetics and Genomics</i> , 2019, 46, 105-108.	3.9	6
51	A minus-end directed kinesin motor directs gravitropism in <i>Physcomitrella patens</i> . <i>Nature Communications</i> , 2021, 12, 4470.	12.8	4
52	Whole genome sequencing of <i>Enterobacter mori</i> , an emerging pathogen of kiwifruit and the potential genetic adaptation to pathogenic lifestyle. <i>AMB Express</i> , 2021, 11, 129.	3.0	4
53	Single-Molecule Sequencing Assists Genome Assembly Improvement and Structural Variation Inference. <i>Molecular Plant</i> , 2016, 9, 1085-1087.	8.3	2
54	Exploring the genetic characteristics of 93-11 and Nipponbare recombination inbred lines based on the GoldenGate SNP assay. <i>Science China Life Sciences</i> , 2016, 59, 700-708.	4.9	0