

Jihong Hu

List of Publications by Year in descending order

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34
papers

1,073
citations

394421

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times ranked

1321
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis of long non-coding RNAs unveils the regulatory roles in the heat tolerance of Chinese cabbage (<i>Brassica rapa</i> ssp.chinensis). <i>Scientific Reports</i> , 2019, 9, 5002.	3.3	95
2	Genome-wide analysis of the rice PPR gene family and their expression profiles under different stress treatments. <i>BMC Genomics</i> , 2018, 19, 720.	2.8	76
3	Identification and Expression Analysis of microRNAs at the Grain Filling Stage in Rice(<i>Oryza sativa</i>) Tj ETQq1 1 0.784314 rgBT /Overlo	2.5	75
4	A Genome-Wide Association Study Reveals New Loci for Resistance to Clubroot Disease in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1483.	3.6	74
5	Genome-Wide Association Mapping Reveals the Genetic Control Underlying Branch Angle in Rapeseed (<i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1054.	3.6	68
6	Comparative analysis of genetic diversity in sacred lotus (<i>Nelumbo nucifera</i> Gaertn.) using AFLP and SSR markers. <i>Molecular Biology Reports</i> , 2012, 39, 3637-3647.	2.3	55
7	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	21.4	55
8	Biased gene retention during diploidization in <i>Brassica</i> linked to three-dimensional genome organization. <i>Nature Plants</i> , 2019, 5, 822-832.	9.3	52
9	Comparative Transcriptome Analysis Reveals Heat-Responsive Genes in Chinese Cabbage (<i>Brassica rapa</i>) Tj ETQq1 1 0.784314 rgBT /O	3.6	46
10	Genome-wide analysis of DNA methylation in photoperiod- and thermo-sensitive male sterile rice Peiai 64S. <i>BMC Genomics</i> , 2015, 16, 102.	2.8	40
11	Soil microbial mechanisms promoting ultrahigh rice yield. <i>Soil Biology and Biochemistry</i> , 2020, 143, 107741.	8.8	38
12	An Integration of Genome-Wide Association Study and Gene Co-expression Network Analysis Identifies Candidate Genes of Stem Lodging-Related Traits in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 796.	3.6	36
13	DNA methylation changes in photoperiod-thermo-sensitive male sterile rice PA64S under two different conditions. <i>Gene</i> , 2014, 537, 143-148.	2.2	32
14	Unravelling miRNA regulation in yield of rice (<i>Oryza sativa</i>) based on differential network model. <i>Scientific Reports</i> , 2018, 8, 8498.	3.3	28
15	Small RNA and degradome profiling reveals miRNA regulation in the seed germination of ancient eudicot <i>Nelumbo nucifera</i> . <i>BMC Genomics</i> , 2016, 17, 684.	2.8	26
16	Association mapping of cadmium-tolerant QTLs in <i>Brassica napus</i> L. and insight into their contributions to phytoremediation. <i>Environmental and Experimental Botany</i> , 2018, 155, 420-428.	4.2	26
17	Small RNA Profiles of the Rice PTGMS Line Wuxiang S Reveal miRNAs Involved in Fertility Transition. <i>Frontiers in Plant Science</i> , 2016, 7, 514.	3.6	24
18	The Elite Alleles of OsSPL4 Regulate Grain Size and Increase Grain Yield in Rice. <i>Rice</i> , 2021, 14, 90.	4.0	23

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19	Genome-Wide Identification of SSR and SNP Markers Based on Whole-Genome Re-Sequencing of a Thailand Wild Sacred Lotus (<i>Nelumbo nucifera</i>). <i>PLoS ONE</i> , 2015, 10, e0143765.	2.5	21
20	Comparative transcript profiling of alloplasmic male-sterile lines revealed altered gene expression related to pollen development in rice (<i>Oryza sativa</i> L.). <i>BMC Plant Biology</i> , 2016, 16, 175.	3.6	19
21	Genetic diversity and differentiation of lotus (<i>Nelumbo nucifera</i>) accessions assessed by simple sequence repeats. <i>Annals of Applied Biology</i> , 2011, 159, 428-441.	2.5	18
22	Nucleo-cytoplasmic interactions affect RNA editing of <i>cox2</i> , <i>atp6</i> and <i>atp9</i> in alloplasmic male-sterile rice (<i>Oryza sativa</i> L.) lines. <i>Mitochondrion</i> , 2013, 13, 87-95.	3.4	18
23	Identification of conserved microRNAs and their targets in the model legume <i>Lotus japonicus</i> . <i>Journal of Biotechnology</i> , 2013, 164, 520-524.	3.8	16
24	Characterization of conserved microRNAs from five different cucurbit species using computational and experimental analysis. <i>Biochimie</i> , 2014, 102, 137-144.	2.6	14
25	Genome-wide association study (GWAS) reveals genetic loci of lead (Pb) tolerance during seedling establishment in rapeseed (<i>Brassica napus</i> L.). <i>BMC Genomics</i> , 2020, 21, 139.	2.8	14
26	Transcriptome analysis reveals genes expression pattern of seed response to heat stress in <i>Brassica napus</i> L.. <i>Oil Crop Science</i> , 2021, 6, 87-96.	2.0	14
27	Development and Characterization of Polymorphic MicroRNA-Based Microsatellite Markers in <i>Nelumbo nucifera</i> (Nelumbonaceae). <i>Applications in Plant Sciences</i> , 2016, 4, 1500091.	2.1	13
28	Identification of conserved microRNAs and their targets in chickpea (<i>Cicer arietinum</i> L.). <i>Plant Signaling and Behavior</i> , 2013, 8, e23604.	2.4	12
29	Bioinformatic Identification and Expression Analysis of <i>Nelumbo nucifera</i> MicroRNA and Their Targets. <i>Applications in Plant Sciences</i> , 2015, 3, 1500046.	2.1	9
30	Identification of Key Genes for the Ultrahigh Yield of Rice Using Dynamic Cross-tissue Network Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 256-270.	6.9	9
31	Development and characterization of microsatellite markers for <i>Sagittaria trifolia</i> var. <i>sinensis</i> (Alismataceae). <i>American Journal of Botany</i> , 2011, 98, e36-8.	1.7	8
32	Transcriptome analysis of non-heading Chinese cabbage under heat stress by RNA-seq and marker identification. <i>Euphytica</i> , 2017, 213, 1.	1.2	6
33	Auxin-related genes associated with leaf petiole angle at the seedling stage are involved in adaptation to low temperature in <i>Brassica napus</i> . <i>Environmental and Experimental Botany</i> , 2021, 182, 104308.	4.2	6
34	Robust ordered mRNA differential display: an improved method for global gene expression profiling. <i>BioTechniques</i> , 2011, 51, 271-275.	1.8	5