

Jianping Wang

List of Publications by Year in descending order

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68
papers

2,708
citations

201385

27
h-index

214527

47
g-index

71
all docs

71
docs citations

71
times ranked

2886
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic insights into the recent chromosome reduction of autopolyploid sugarcane <i>Saccharum spontaneum</i> . <i>Nature Genetics</i> , 2022, 54, 885-896.	9.4	33
2	Natural polymorphisms in a pair of NSP2 homoeologs can cause loss of nodulation in peanut. <i>Journal of Experimental Botany</i> , 2021, 72, 1104-1118.	2.4	15
3	Development and characterization of a Napier grass (<i>Cenchrus purpureus</i> Schumach) mapping population for flowering and biomass related traits reveal individuals with exceptional potential and hybrid vigor. <i>GCB Bioenergy</i> , 2021, 13, 1561-1575.	2.5	5
4	Advances in Genomics Approaches Shed Light on Crop Domestication. <i>Plants</i> , 2021, 10, 1571.	1.6	1
5	Characterization of a <i>Saccharum spontaneum</i> with a basic chromosome number of $x=10$ provides new insights on genome evolution in genus <i>Saccharum</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 187-199.	1.8	42
6	Genome assembly provides insights into the genome evolution and flowering regulation of orchardgrass. <i>Plant Biotechnology Journal</i> , 2020, 18, 373-388.	4.1	51
7	Over-expression of poplar NAC15 gene enhances wood formation in transgenic tobacco. <i>BMC Plant Biology</i> , 2020, 20, 12.	1.6	18
8	Deciphering the Role of Stay-Green Trait to Mitigate Terminal Heat Stress in Bread Wheat. <i>Agronomy</i> , 2020, 10, 1001.	1.3	10
9	Peanut FAD2 Genotype and Growing Location Interactions Significantly Affect the Level of Oleic Acid in Seeds. <i>JAOCs, Journal of the American Oil Chemists' Society</i> , 2020, 97, 1001-1010.	0.8	6
10	The application of CRISPR/Cas9 in hairy roots to explore the functions of AhNFR1 and AhNFR5 genes during peanut nodulation. <i>BMC Plant Biology</i> , 2020, 20, 417.	1.6	40
11	Identifying chromosomal introgressions from a wild species <i>Arachis diogeni</i> into interspecific peanut hybrids. <i>Plant Breeding</i> , 2020, 139, 969-976.	1.0	1
12	Isolation, Characterization, and Complete Genome Sequence of a Bradyrhizobium Strain Lb8 From Nodules of Peanut Utilizing Crack Entry Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 93.	1.5	13
13	Transcriptome analysis of salt-responsive and wood-associated NACs in <i>Populus simonii</i> and <i>Populus nigra</i> . <i>BMC Plant Biology</i> , 2020, 20, 317.	1.6	15
14	Molecular Basis of Root Nodule Symbiosis between Bradyrhizobium and Crack-Entry™ Legume Groundnut (<i>Arachis hypogaea</i> L.). <i>Plants</i> , 2020, 9, 276.	1.6	39
15	Mapping quantitative trait loci (QTLs) and estimating the epistasis controlling stem rot resistance in cultivated peanut (<i>Arachis hypogaea</i>). <i>Theoretical and Applied Genetics</i> , 2020, 133, 1201-1212.	1.8	24
16	Genome-wide association study of multiple yield traits in a diversity panel of polyploid sugarcane (<i>Saccharum</i> spp.). <i>Plant Genome</i> , 2020, 13, e20006.	1.6	27
17	Molecular detection of sugarcane striate virus and sugarcane white streak virus and their prevalence in the Miami World Collection of sugarcane and related grasses. <i>Plant Pathology</i> , 2020, 69, 1060-1069.	1.2	4
18	Comparison of SNP Calling Pipelines and NGS Platforms to Predict the Genomic Regions Harboring Candidate Genes for Nodulation in Cultivated Peanut. <i>Frontiers in Genetics</i> , 2020, 11, 222.	1.1	7

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19	Methods for Target Enrichment Sequencing via Probe Capture in Legumes. <i>Methods in Molecular Biology</i> , 2020, 2107, 199-231.	0.4	2
20	Target enrichment sequencing of 307 germplasm accessions identified ancestry of ancient and modern hybrids and signatures of adaptation and selection in sugarcane (<i>Saccharum</i> spp.), a "sweet" crop with "bitter" genomes. <i>Plant Biotechnology Journal</i> , 2019, 17, 488-498.	4.1	33
21	Development of an Axiom Sugarcane100K SNP array for genetic map construction and QTL identification. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2829-2845.	1.8	41
22	A novel effect of glycine on the growth and starch biosynthesis of storage root in sweetpotato (<i>Ipomoea batatas</i> Lam.). <i>Plant Physiology and Biochemistry</i> , 2019, 144, 395-403.	2.8	6
23	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
24	Whole chloroplast genome and gene locus phylogenies reveal the taxonomic placement and relationship of <i>Triplidium</i> (Panicoidae: Andropogoneae) to sugarcane. <i>BMC Evolutionary Biology</i> , 2019, 19, 33.	3.2	48
25	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019, 51, 865-876.	9.4	398
26	Evaluation of genomic selection and marker-assisted selection in <i>Miscanthus</i> and energycane. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	20
27	Identifying loci controlling fiber composition in polyploid sugarcane (<i>Saccharum</i> spp.) through genome-wide association study. <i>Industrial Crops and Products</i> , 2019, 130, 598-605.	2.5	16
28	Genome-Wide Association Studies Identified Resistance Loci to Orange Rust and Yellow Leaf Virus Diseases in Sugarcane (<i>Saccharum</i> spp.). <i>Phytopathology</i> , 2019, 109, 623-631.	1.1	34
29	Pedigree, marker recruitment, and genetic diversity of modern sugarcane cultivars in China and the United States. <i>Euphytica</i> , 2018, 214, 1.	0.6	5
30	Editorial: Molecular and Cellular Mechanisms of the Legume-Rhizobia Symbiosis. <i>Frontiers in Plant Science</i> , 2018, 9, 1839.	1.7	12
31	New insights into the evolution and functional divergence of the SWEET family in <i>Saccharum</i> based on comparative genomics. <i>BMC Plant Biology</i> , 2018, 18, 270.	1.6	42
32	Comprehensively Characterizing the Cytological Features of <i>Saccharum spontaneum</i> by the Development of a Complete Set of Chromosome-Specific Oligo Probes. <i>Frontiers in Plant Science</i> , 2018, 9, 1624.	1.7	42
33	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
34	Surveying the genome and constructing a high-density genetic map of napiergrass (<i>Cenchrus</i>) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 142	1.6	32
35	Developing and validating microsatellite markers in elephant grass (<i>Pennisetum purpureum</i> S.). <i>Euphytica</i> , 2018, 214, 1.	0.6	2
36	Integration of small RNAs and transcriptome sequencing uncovers a complex regulatory network during vernalization and heading stages of orchardgrass (<i>Dactylis glomerata</i> L.). <i>BMC Genomics</i> , 2018, 19, 727.	1.2	15

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37	Morphological and Genetic Characterization of Non-Nodulating Peanut Recombinant Inbred Lines. <i>Crop Science</i> , 2018, 58, 540-550.	0.8	11
38	Molecular dissection of sugar related traits and it's attributes in <i>Saccharum</i> spp. hybrids. <i>Euphytica</i> , 2018, 214, 1.	0.6	4
39	Heritability of spotted wilt resistance in a Florida-derived peanut (<i>Arachis hypogaea</i>) population. <i>Plant Breeding</i> , 2018, 137, 614-620.	1.0	0
40	Molecular characterization of genetic basis of <i>Sugarcane Yellow Leaf Virus</i> (<i>SCYLV</i>) resistance in <i>Saccharum</i> spp. hybrid. <i>Plant Breeding</i> , 2018, 137, 598-604.	1.0	21
41	Development and Applications of a High Throughput Genotyping Tool for Polyploid Crops: Single Nucleotide Polymorphism (SNP) Array. <i>Frontiers in Plant Science</i> , 2018, 9, 104.	1.7	89
42	Potentials, Challenges, and Genetic and Genomic Resources for Sugarcane Biomass Improvement. <i>Frontiers in Plant Science</i> , 2018, 9, 151.	1.7	28
43	Development and Applications of Chromosome-Specific Cytogenetic BAC-FISH Probes in <i>S. spontaneum</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 218.	1.7	23
44	Identifying Quantitative Trait Loci (QTLs) and Developing Diagnostic Markers Linked to Orange Rust Resistance in Sugarcane (<i>Saccharum</i> spp.). <i>Frontiers in Plant Science</i> , 2018, 9, 350.	1.7	47
45	Refining a major QTL controlling spotted wilt disease resistance in cultivated peanut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10. <i>Genetics</i> , 2018, 19, 17.	2.7	10
46	Integrated omics data of two annual ryegrass (<i>Lolium multiflorum</i> L.) genotypes reveals core metabolic processes under drought stress. <i>BMC Plant Biology</i> , 2018, 18, 26.	1.6	30
47	EST-SSR marker characterization based on RNA-sequencing of <i>Lolium multiflorum</i> and cross transferability to related species. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	15
48	Transcriptome profiles reveal gene regulation of peanut (<i>Arachis hypogaea</i> L.) nodulation. <i>Scientific Reports</i> , 2017, 7, 40066.	1.6	42
49	Target enrichment sequencing in cultivated peanut (<i>Arachis hypogaea</i> L.) using probes designed from transcript sequences. <i>Molecular Genetics and Genomics</i> , 2017, 292, 955-965.	1.0	17
50	Characterization of ERF76 promoter cloned from <i>Populus simonii</i> P. nigra. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	10
51	Constructing high-density genetic maps for polyploid sugarcane (<i>Saccharum</i> spp.) and identifying quantitative trait loci controlling brown rust resistance. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	34
52	Direct organogenesis from cotyledonary node explants suitable for <i>Agrobacterium</i> -mediated transformation in peanut (<i>Arachis hypogaea</i> L.). <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 128, 161-175.	1.2	15
53	Mining sequence variations in representative polyploid sugarcane germplasm accessions. <i>BMC Genomics</i> , 2017, 18, 594.	1.2	46
54	Enriching Genomic Resources and Marker Development from Transcript Sequences of <i>Jatropha curcas</i> for Microgravity Studies. <i>International Journal of Genomics</i> , 2017, 2017, 1-14.	0.8	7

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55	Comparative proteomic analyses reveal the proteome response to short-term drought in Italian ryegrass (<i>Lolium multiflorum</i>). PLoS ONE, 2017, 12, e0184289.	1.1	13
56	Comprehensive transcriptome analysis reveals distinct regulatory programs during vernalization and floral bud development of orchardgrass (<i>Dactylis glomerata</i> L.). BMC Plant Biology, 2017, 17, 216.	1.6	28
57	Transcriptional Profiles of Drought-Related Genes in Modulating Metabolic Processes and Antioxidant Defenses in <i>Lolium multiflorum</i> . Frontiers in Plant Science, 2016, 7, 519.	1.7	81
58	Natural Allelic Variations in Highly Polyploidy <i>Saccharum</i> Complex. Frontiers in Plant Science, 2016, 7, 804.	1.7	40
59	Comparative structural analysis of Bru1 region homeologs in <i>Saccharum spontaneum</i> and <i>S. officinarum</i> . BMC Genomics, 2016, 17, 446.	1.2	8
60	Construction of high-density genetic linkage map and identification of flowering-time QTLs in orchardgrass using SSRs and SLAF-seq. Scientific Reports, 2016, 6, 29345.	1.6	48
61	Identification of major QTLs underlying tomato spotted wilt virus resistance in peanut cultivar Florida-EPTM 113™. BMC Genetics, 2016, 17, 128.	2.7	31
62	Genome-Wide Analysis of NBS-LRR Genes in Sorghum Genome Revealed Several Events Contributing to NBS-LRR Gene Evolution in Grass Species. Evolutionary Bioinformatics, 2016, 12, EBO.S36433.	0.6	34
63	Molecular marker development from transcript sequences and germplasm evaluation for cultivated peanut (<i>Arachis hypogaea</i> L.). Molecular Genetics and Genomics, 2016, 291, 363-381.	1.0	21
64	Genetic linkage map of <i>Lolium multiflorum</i> Lam. constructed from a BC ₁ population derived from an interspecific hybridization, <i>Lolium multiflorum</i> × <i>Lolium temulentum</i> L. Grassland Science, 2014, 60, 142-149.	0.6	3
65	Identification of QTLs associated with oil content and mapping FAD2 genes and their relative contribution to oil quality in peanut (<i>Arachis hypogaea</i> L.). BMC Genetics, 2014, 15, 133.	2.7	117
66	Phenotypic characterization of the Miami World Collection of sugarcane (<i>Saccharum</i> spp.) and related grasses for selecting a representative core. Genetic Resources and Crop Evolution, 2014, 61, 1581-1596.	0.8	25
67	Promoting Utilization of <i>Saccharum</i> spp. Genetic Resources through Genetic Diversity Analysis and Core Collection Construction. PLoS ONE, 2014, 9, e110856.	1.1	51
68	Carbon partitioning in sugarcane (<i>Saccharum</i> species). Frontiers in Plant Science, 2013, 4, 201.	1.7	123