

Xiangfeng Wang

List of Publications by Year in descending order

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71
papers

6,384
citations

94381

37
h-index

82499

72
g-index

76
all docs

76
docs citations

76
times ranked

10392
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.	3.1	514
2	Genome-Wide and Organ-Specific Landscapes of Epigenetic Modifications and Their Relationships to mRNA and Small RNA Transcriptomes in Maize. <i>Plant Cell</i> , 2009, 21, 1053-1069.	3.1	291
3	High-Resolution Mapping of Epigenetic Modifications of the Rice Genome Uncovers Interplay between DNA Methylation, Histone Methylation, and Gene Expression. <i>Plant Cell</i> , 2008, 20, 259-276.	3.1	281
4	Global genome expression analysis of rice in response to drought and high-salinity stresses in shoot, flag leaf, and panicle. <i>Plant Molecular Biology</i> , 2007, 63, 591-608.	2.0	275
5	Genome-wide mapping of the <i>HY5</i> -mediated gene networks in Arabidopsis that involve both transcriptional and post-transcriptional regulation. <i>Plant Journal</i> , 2011, 65, 346-358.	2.8	274
6	Machine learning for Big Data analytics in plants. <i>Trends in Plant Science</i> , 2014, 19, 798-808.	4.3	220
7	RNA Sequencing of Laser-Capture Microdissected Compartments of the Maize Kernel Identifies Regulatory Modules Associated with Endosperm Cell Differentiation. <i>Plant Cell</i> , 2015, 27, 513-531.	3.1	206
8	The Reference Genome of the Halophytic Plant <i>Eutrema salsgineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	1.7	198
9	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	6.5	168
10	Genome-wide profiling of histone H3 lysine 9 acetylation and dimethylation in Arabidopsis reveals correlation between multiple histone marks and gene expression. <i>Plant Molecular Biology</i> , 2010, 72, 585-595.	2.0	167
11	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	6.5	165
12	Genome-wide transcription analyses in rice using tiling microarrays. <i>Nature Genetics</i> , 2006, 38, 124-129.	9.4	154
13	CGmapTools improves the precision of heterozygous SNV calls and supports allele-specific methylation detection and visualization in bisulfite-sequencing data. <i>Bioinformatics</i> , 2018, 34, 381-387.	1.8	152
14	Temporal patterns of gene expression in developing maize endosperm identified through transcriptome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7582-7587.	3.3	146
15	A microarray analysis of the rice transcriptome and its comparison to Arabidopsis. <i>Genome Research</i> , 2005, 15, 1274-1283.	2.4	112
16	Machine Learning-Based Differential Network Analysis: A Study of Stress-Responsive Transcriptomes in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 520-537.	3.1	104
17	Dynamic Expression of Imprinted Genes Associates with Maternally Controlled Nutrient Allocation during Maize Endosperm Development. <i>Plant Cell</i> , 2013, 25, 3212-3227.	3.1	97
18	Transcriptome Association Identifies Regulators of Wheat Spike Architecture. <i>Plant Physiology</i> , 2017, 175, 746-757.	2.3	94

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19	Transcriptome Comparison of Susceptible and Resistant Wheat in Response to Powdery Mildew Infection. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 94-106.	3.0	90
20	<scp>BES</scp>1 hinders <scp>ABSCISIC ACID INSENSITIVE</scp>5 and promotes seed germination in <i>Arabidopsis</i>. <i>New Phytologist</i> , 2019, 221, 908-918.	3.5	86
21	Opaque-2 Regulates a Complex Gene Network Associated with Cell Differentiation and Storage Functions of Maize Endosperm. <i>Plant Cell</i> , 2018, 30, 2425-2446.	3.1	83
22	Global Identification and Characterization of Transcriptionally Active Regions in the Rice Genome. <i>PLoS ONE</i> , 2007, 2, e294.	1.1	82
23	LightGBM: accelerated genomically designed crop breeding through ensemble learning. <i>Genome Biology</i> , 2021, 22, 271.	3.8	76
24	The genetic mechanism of heterosis utilization in maize improvement. <i>Genome Biology</i> , 2021, 22, 148.	3.8	69
25	Application of the Gini Correlation Coefficient to Infer Regulatory Relationships in Transcriptome Analysis. <i>Plant Physiology</i> , 2012, 160, 192-203.	2.3	65
26	IbBBX24 Promotes the Jasmonic Acid Pathway and Enhances Fusarium Wilt Resistance in Sweet Potato. <i>Plant Cell</i> , 2020, 32, 1102-1123.	3.1	65
27	Transcript profile analysis reveals important roles of jasmonic acid signalling pathway in the response of sweet potato to salt stress. <i>Scientific Reports</i> , 2017, 7, 40819.	1.6	62
28	The roles of endomembrane trafficking in plant abiotic stress responses. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 55-69.	4.1	57
29	A Tiling Microarray Expression Analysis of Rice Chromosome 4 Suggests a Chromosome-Level Regulation of Transcription. <i>Plant Cell</i> , 2005, 17, 1641-1657.	3.1	56
30	A dirigent family protein confers variation of Casparian strip thickness and salt tolerance in maize. <i>Nature Communications</i> , 2022, 13, 2222.	5.8	55
31	Systematic Curation of miRBase Annotation Using Integrated Small RNA High-Throughput Sequencing Data for <i>C. elegans</i> and <i>Drosophila</i> . <i>Frontiers in Genetics</i> , 2011, 2, 25.	1.1	52
32	Ethylene Signaling Modulates Cortical Microtubule Reassembly in Response to Salt Stress. <i>Plant Physiology</i> , 2018, 176, 2071-2081.	2.3	49
33	VAMP711 Is Required for Abscisic Acid-Mediated Inhibition of Plasma Membrane H ⁺ -ATPase Activity. <i>Plant Physiology</i> , 2018, 178, 1332-1343.	2.3	47
34	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.	3.3	46
35	Metabolomics-driven gene mining and genetic improvement of tolerance to salt-induced osmotic stress in maize. <i>New Phytologist</i> , 2021, 230, 2355-2370.	3.5	46
36	Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle. <i>Frontiers in Microbiology</i> , 2018, 9, 3160.	1.5	45

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37	Understanding the functions and mechanisms of plant cytoskeleton in response to environmental signals. <i>Current Opinion in Plant Biology</i> , 2019, 52, 86-96.	3.5	42
38	Tiling microarray analysis of rice chromosome 10 to identify the transcriptome and relate its expression to chromosomal architecture. <i>Genome Biology</i> , 2005, 6, R52.	13.9	41
39	Organ Evolution in Angiosperms Driven by Correlated Divergences of Gene Sequences and Expression Patterns. <i>Plant Cell</i> , 2013, 25, 71-82.	3.1	39
40	Isoform Evolution in Primates through Independent Combination of Alternative RNA Processing Events. <i>Molecular Biology and Evolution</i> , 2017, 34, 2453-2468.	3.5	37
41	CrusView: A Java-Based Visualization Platform for Comparative Genomics Analyses in Brassicaceae Species. <i>Plant Physiology</i> , 2013, 163, 354-362.	2.3	33
42	Machine Learning Models for Genetic Risk Assessment of Infants with Non-syndromic Orofacial Cleft. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 354-364.	3.0	31
43	NMPP: a user-customized NimbleGen microarray data processing pipeline. <i>Bioinformatics</i> , 2006, 22, 2955-2957.	1.8	29
44	The E3 ligase MREL57 modulates microtubule stability and stomatal closure in response to ABA. <i>Nature Communications</i> , 2021, 12, 2181.	5.8	27
45	Genome optimization for improvement of maize breeding. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1491-1502.	1.8	26
46	Dynamic parent-of-origin effects on small interfering RNA expression in the developing maize endosperm. <i>BMC Plant Biology</i> , 2014, 14, 192.	1.6	21
47	Genome Size Evolution Mediated by Gypsy Retrotransposons in Brassicaceae. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 321-332.	3.0	21
48	Resequencing 250 Soybean Accessions: New Insights into Genes Associated with Agronomic Traits and Genetic Networks. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 29-41.	3.0	21
49	The genome of the warm-season turfgrass African bermudagrass (<i>Cynodon transvaalensis</i>). <i>Horticulture Research</i> , 2021, 8, 93.	2.9	19
50	A QTL atlas for grain yield and its component traits in maize (<i>Zea mays</i>). <i>Plant Breeding</i> , 2020, 139, 562-574.	1.0	18
51	SR4R: An Integrative SNP Resource for Genomic Breeding and Population Research in Rice. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 173-185.	3.0	18
52	A Pilot Study of Transcription Unit Analysis in Rice Using Oligonucleotide Tiling-path Microarray. <i>Plant Molecular Biology</i> , 2005, 59, 137-149.	2.0	17
53	AP3M harbors actin filament binding activity that is crucial for vacuole morphology and stomatal closure in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18132-18141.	3.3	17
54	Forecasting rice latitude adaptation through a daylength-sensing-based environment adaptation simulator. <i>Nature Food</i> , 2021, 2, 348-362.	6.2	16

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55	Temporal small RNA transcriptome profiling unraveled partitioned miRNA expression in developing maize endosperms between reciprocal crosses. <i>Frontiers in Plant Science</i> , 2015, 6, 744.	1.7	14
56	Transcriptional analysis of highly syntenic regions between <i>Medicago truncatula</i> and <i>Glycine max</i> using tiling microarrays. <i>Genome Biology</i> , 2008, 9, R57.	13.9	13
57	RNA-Seq analysis of laser-capture microdissected cells of the developing central starchy endosperm of maize. <i>Genomics Data</i> , 2014, 2, 242-245.	1.3	13
58	The microtubule-associated protein WDL4 modulates auxin distribution to promote apical hook opening in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2021, 33, 1927-1944.	3.1	13
59	KGBAssembler: a karyotype-based genome assembler for Brassicaceae species. <i>Bioinformatics</i> , 2012, 28, 3141-3143.	1.8	12
60	Characterization of the genome expression trends in the heading-stage panicle of six rice lineages. <i>Genomics</i> , 2009, 93, 169-178.	1.3	11
61	Redox-Mediated Endocytosis of a Receptor-Like Kinase during Distal Stem Cell Differentiation Depends on Its Tumor Necrosis Factor Receptor Domain. <i>Plant Physiology</i> , 2019, 181, 1075-1095.	2.3	11
62	Genome-Wide Analysis of the HSP20 Gene Family and Expression Patterns of HSP20 Genes in Response to Abiotic Stresses in <i>Cynodon transvaalensis</i> . <i>Frontiers in Genetics</i> , 2021, 12, 732812.	1.1	11
63	Correlation of vacuole morphology with stomatal lineage development by whole-cell electron tomography. <i>Plant Physiology</i> , 2022, 188, 2085-2100.	2.3	11
64	A Computational Workflow to Identify Allele-specific Expression and Epigenetic Modification in Maize. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 247-252.	3.0	10
65	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , 2020, 102, 116-128.	2.8	10
66	Computational dissection of <i>Arabidopsis</i> smRNAome leads to discovery of novel microRNAs and short interfering RNAs associated with transcription start sites. <i>Genomics</i> , 2011, 97, 235-243.	1.3	8
67	Complete genome of Hainan papaya ringspot virus using small RNA deep sequencing. <i>Virus Genes</i> , 2014, 48, 502-508.	0.7	5
68	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. <i>Genomics</i> , 2010, 96, 308-315.	1.3	4
69	Transcriptionally active gene fragments derived from potentially fast-evolving donor genes in the rice genome. <i>Bioinformatics</i> , 2009, 25, 1215-1218.	1.8	3
70	Genome optimization via virtual simulation to accelerate maize hybrid breeding. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	3
71	Single-Molecule Sequencing Assists Genome Assembly Improvement and Structural Variation Inference. <i>Molecular Plant</i> , 2016, 9, 1085-1087.	3.9	2