Xiangfeng Wang

List of Publications by Year
in descending order

71 papers	6,384 citations	94433 37 h-index	82547 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. Plant Cell, 2010, 22, 17-33.	6.6	514
2	Genome-Wide and Organ-Specific Landscapes of Epigenetic Modifications and Their Relationships to mRNA and Small RNA Transcriptomes in Maize. Plant Cell, 2009, 21, 1053-1069.	6.6	291
3	High-Resolution Mapping of Epigenetic Modifications of the Rice Genome Uncovers Interplay between DNA Methylation, Histone Methylation, and Gene Expression. Plant Cell, 2008, 20, 259-276.	6.6	281
4	Global genome expression analysis of rice in response to drought and high-salinity stresses in shoot, flag leaf, and panicle. Plant Molecular Biology, 2007, 63, 591-608.	3.9	275
5	Genome‐wide mapping of the <i>HY5</i>‐mediated genenetworks in Arabidopsis that involve both transcriptional and post‐transcriptional regulation. Plant Journal, 2011, 65, 346-358.	5.7	274
6	Machine learning for Big Data analytics in plants. Trends in Plant Science, 2014, 19, 798-808.	8.8	220
7	RNA Sequencing of Laser-Capture Microdissected Compartments of the Maize Kernel Identifies Regulatory Modules Associated with Endosperm Cell Differentiation. Plant Cell, 2015, 27, 513-531.	6.6	206
8	The Reference Genome of the Halophytic Plant Eutrema salsugineum. Frontiers in Plant Science, 2013, 4, 46.	3.6	198
9	DatabaseÂResources of the National Genomics Data Center, China National Center for Bioinformation in 2021. Nucleic Acids Research, 2021, 49, D18-D28.	14.5	168
10	Genome-wide profiling of histone H3 lysine 9 acetylation and dimethylation in Arabidopsis reveals correlation between multiple histone marks and gene expression. Plant Molecular Biology, 2010, 72, 585-595.	3.9	167
11	Database Resources of the National Genomics Data Center in 2020. Nucleic Acids Research, 2020, 48, D24-D33.	14.5	165
12	Genome-wide transcription analyses in rice using tiling microarrays. Nature Genetics, 2006, 38, 124-129.	21.4	154
13	CGmapTools improves the precision of heterozygous SNV calls and supports allele-specific methylation detection and visualization in bisulfite-sequencing data. Bioinformatics, 2018, 34, 381-387.	4.1	152
14	Temporal patterns of gene expression in developing maize endosperm identified through transcriptome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7582-7587.	7.1	146
15	A microarray analysis of the rice transcriptome and its comparison to Arabidopsis. Genome Research, 2005, 15, 1274-1283.	5.5	112
16	Machine Learning‐Based Differential Network Analysis: A Study of Stress-Responsive Transcriptomes in <i>Arabidopsis</i>. Plant Cell, 2014, 26, 520-537.	6.6	104
17	Dynamic Expression of Imprinted Genes Associates with Maternally Controlled Nutrient Allocation during Maize Endosperm Development. Plant Cell, 2013, 25, 3212-3227.	6.6	97
18	Transcriptome Association Identifies Regulators of Wheat Spike Architecture. Plant Physiology, 2017, 175, 746-757.	4.8	94

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19	Transcriptome Comparison of Susceptible and Resistant Wheat in Response to Powdery Mildew Infection. Genomics, Proteomics and Bioinformatics, 2012, 10, 94-106.	6.9	90
20	BES1 hinders ABSCISIC ACID INSENSITIVE5 and promotes seed germination in *Arabidopsis*. New Phytologist, 2019, 221, 908-918.	7.3	86
21	Opaque-2 Regulates a Complex Gene Network Associated with Cell Differentiation and Storage Functions of Maize Endosperm. Plant Cell, 2018, 30, 2425-2446.	6.6	83
22	Global Identification and Characterization of Transcriptionally Active Regions in the Rice Genome. PLoS ONE, 2007, 2, e294.	2.5	82
23	LightGBM: accelerated genomically designed crop breeding through ensemble learning. Genome Biology, 2021, 22, 271.	8.8	76
24	The genetic mechanism of heterosis utilization in maize improvement. Genome Biology, 2021, 22, 148.	8.8	69
25	Application of the Gini Correlation Coefficient to Infer Regulatory Relationships in Transcriptome Analysis Â. Plant Physiology, 2012, 160, 192-203.	4.8	65
26	IbBBX24 Promotes the Jasmonic Acid Pathway and Enhances Fusarium Wilt Resistance in Sweet Potato. Plant Cell, 2020, 32, 1102-1123.	6.6	65
27	Transcript profile analysis reveals important roles of jasmonic acid signalling pathway in the response of sweet potato to salt stress. Scientific Reports, 2017, 7, 40819.	3.3	62
28	The roles of endomembrane trafficking in plant abiotic stress responses. Journal of Integrative Plant Biology, 2020, 62, 55-69.	8.5	57
29	A Tiling Microarray Expression Analysis of Rice Chromosome 4 Suggests a Chromosome-Level Regulation of Transcription. Plant Cell, 2005, 17, 1641-1657.	6.6	56
30	A dirigent family protein confers variation of Casparian strip thickness and salt tolerance in maize. Nature Communications, 2022, 13, 2222.	12.8	55
31	Systematic Curation of miRBase Annotation Using Integrated Small RNA High-Throughput Sequencing Data for C. elegans and Drosophila. Frontiers in Genetics, 2011, 2, 25.	2.3	52
32	Ethylene Signaling Modulates Cortical Microtubule Reassembly in Response to Salt Stress. Plant Physiology, 2018, 176, 2071-2081.	4.8	49
33	VAMP711 Is Required for Abscisic Acid-Mediated Inhibition of Plasma Membrane H^+-ATPase Activity. Plant Physiology, 2018, 178, 1332-1343.	4.8	47
34	Divergent selection and genetic introgression shape the genome landscape of heterosis in hybrid rice. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4623-4631.	7.1	46
35	Metabolomicsâ€driven gene mining and genetic improvement of tolerance to saltâ€induced osmotic stress in maize. New Phytologist, 2021, 230, 2355-2370.	7.3	46
36	Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle. Frontiers in Microbiology, 2018, 9, 3160.	3.5	45

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37	Understanding the functions and mechanisms of plant cytoskeleton in response to environmental signals. Current Opinion in Plant Biology, 2019, 52, 86-96.	7.1	42
38	Tiling microarray analysis of rice chromosome 10 to identify the transcriptome and relate its expression to chromosomal architecture. Genome Biology, 2005, 6, R52.	9.6	41
39	Organ Evolution in Angiosperms Driven by Correlated Divergences of Gene Sequences and Expression Patterns Â. Plant Cell, 2013, 25, 71-82.	6.6	39
40	Isoform Evolution in Primates through Independent Combination of Alternative RNA Processing Events. Molecular Biology and Evolution, 2017, 34, 2453-2468.	8.9	37
41	CrusView: A Java-Based Visualization Platform for Comparative Genomics Analyses in Brassicaceae Species. Plant Physiology, 2013, 163, 354-362.	4.8	33
42	Machine Learning Models for Genetic Risk Assessment of Infants with Non-syndromic Orofacial Cleft. Genomics, Proteomics and Bioinformatics, 2018, 16, 354-364.	6.9	31
43	NMPP: a user-customized NimbleGen microarray data processing pipeline. Bioinformatics, 2006, 22, 2955-2957.	4.1	29
44	The E3 ligase MREL57 modulates microtubule stability and stomatal closure in response to ABA. Nature Communications, 2021, 12, 2181.	12.8	27
45	Genome optimization for improvement of maize breeding. Theoretical and Applied Genetics, 2020, 133, 1491-1502.	3.6	26
46	Dynamic parent-of-origin effects on small interfering RNA expression in the developing maize endosperm. BMC Plant Biology, 2014, 14, 192.	3.6	21
47	Genome Size Evolution Mediated by Gypsy Retrotransposons in Brassicaceae. Genomics, Proteomics and Bioinformatics, 2020, 18, 321-332.	6.9	21
48	Resequencing 250 Soybean Accessions: New Insights into Genes Associated with Agronomic Traits and Genetic Networks. Genomics, Proteomics and Bioinformatics, 2022, 20, 29-41.	6.9	21
49	The genome of the warm-season turfgrass African bermudagrass (*Cynodon transvaalensis*). Horticulture Research, 2021, 8, 93.	6.3	19
50	A QTL atlas for grain yield and its component traits in maize (*Zea mays*). Plant Breeding, 2020, 139, 562-574.	1.9	18
51	SR4R: An Integrative SNP Resource for Genomic Breeding and Population Research in Rice. Genomics, Proteomics and Bioinformatics, 2020, 18, 173-185.	6.9	18
52	A Pilot Study of Transcription Unit Analysis in Rice Using Oligonucleotide Tiling-path Microarray. Plant Molecular Biology, 2005, 59, 137-149.	3.9	17
53	AP3M harbors actin filament binding activity that is crucial for vacuole morphology and stomatal closure in *Arabidopsis*. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18132-18141.	7.1	17
54	Forecasting rice latitude adaptation through a daylength-sensing-based environment adaptation simulator. Nature Food, 2021, 2, 348-362.	14.0	16

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55	Temporal small RNA transcriptome profiling unraveled partitioned miRNA expression in developing maize endosperms between reciprocal crosses. Frontiers in Plant Science, 2015, 6, 744.	3.6	14
56	Transcriptional analysis of highly syntenic regions between Medicago truncatula and Glycine max using tiling microarrays. Genome Biology, 2008, 9, R57.	9.6	13
57	RNA-Seq analysis of laser-capture microdissected cells of the developing central starchy endosperm of maize. Genomics Data, 2014, 2, 242-245.	1.3	13
58	The microtubule-associated protein WDL4 modulates auxin distribution to promote apical hook opening in Arabidopsis. Plant Cell, 2021, 33, 1927-1944.	6.6	13
59	KGBassembler: a karyotype-based genome assembler for Brassicaceae species. Bioinformatics, 2012, 28, 3141-3143.	4.1	12
60	Characterization of the genome expression trends in the heading-stage panicle of six rice lineages. Genomics, 2009, 93, 169-178.	2.9	11
61	Redox-Mediated Endocytosis of a Receptor-Like Kinase during Distal Stem Cell Differentiation Depends on Its Tumor Necrosis Factor Receptor Domain. Plant Physiology, 2019, 181, 1075-1095.	4.8	11
62	Genome-Wide Analysis of the HSP20 Gene Family and Expression Patterns of HSP20 Genes in Response to Abiotic Stresses in Cynodon transvaalensis. Frontiers in Genetics, 2021, 12, 732812.	2.3	11
63	Correlation of vacuole morphology with stomatal lineage development by whole-cell electron tomography. Plant Physiology, 2022, 188, 2085-2100.	4.8	11
64	A Computational Workflow to Identify Allele-specific Expression and Epigenetic Modification in Maize. Genomics, Proteomics and Bioinformatics, 2013, 11, 247-252.	6.9	10
65	The hybrid protein interactome contributes to rice heterosis as epistatic effects. Plant Journal, 2020, 102, 116-128.	5.7	10
66	Computational dissection of Arabidopsis smRNAome leads to discovery of novel microRNAs and short interfering RNAs associated with transcription start sites. Genomics, 2011, 97, 235-243.	2.9	8
67	Complete genome of Hainan papaya ringspot virus using small RNA deep sequencing. Virus Genes, 2014, 48, 502-508.	1.6	5
68	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. Genomics, 2010, 96, 308-315.	2.9	4
69	Transcriptionally active gene fragments derived from potentially fast-evolving donor genes in the rice genome. Bioinformatics, 2009, 25, 1215-1218.	4.1	3
70	Genome optimization via virtual simulation to accelerate maize hybrid breeding. Briefings in Bioinformatics, 2022, 23, .	6.5	3
71	Single-Molecule Sequencing Assists Genome Assembly Improvement and Structural Variation Inference. Molecular Plant, 2016, 9, 1085-1087.	8.3	2