

# Xiangfeng Wang

## List of Publications by Year in descending order

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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	Genome optimization via virtual simulation to accelerate maize hybrid breeding. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
2	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.	6.9	21
3	Correlation of vacuole morphology with stomatal lineage development by whole-cell electron tomography. <i>Plant Physiology</i> , 2022, 188, 2085-2100.	4.8	11
4	A dirigent family protein confers variation of Casparian strip thickness and salt tolerance in maize. <i>Nature Communications</i> , 2022, 13, 2222.	12.8	55
5	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	14.5	168
6	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.	6.6	13
7	Metabolomics-driven gene mining and genetic improvement of tolerance to salt-induced osmotic stress in maize. <i>New Phytologist</i> , 2021, 230, 2355-2370.	7.3	46
8	The E3 ligase MREL57 modulates microtubule stability and stomatal closure in response to ABA. <i>Nature Communications</i> , 2021, 12, 2181.	12.8	27
9	The genome of the warm-season turfgrass African bermudagrass ( <i>Cynodon transvaalensis</i> ). <i>Horticulture Research</i> , 2021, 8, 93.	6.3	19
10	Forecasting rice latitude adaptation through a daylength-sensing-based environment adaptation simulator. <i>Nature Food</i> , 2021, 2, 348-362.	14.0	16
11	The genetic mechanism of heterosis utilization in maize improvement. <i>Genome Biology</i> , 2021, 22, 148.	8.8	69
12	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.	2.3	11
13	LightGBM: accelerated genomically designed crop breeding through ensemble learning. <i>Genome Biology</i> , 2021, 22, 271.	8.8	76
14	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	14.5	165
15	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , 2020, 102, 116-128.	5.7	10
16	Genome optimization for improvement of maize breeding. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1491-1502.	3.6	26
17	The roles of endomembrane trafficking in plant abiotic stress responses. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 55-69.	8.5	57
18	Genome Size Evolution Mediated by Gypsy Retrotransposons in Brassicaceae. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 321-332.	6.9	21

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19	A QTL atlas for grain yield and its component traits in maize ( <i>Zea mays</i> ). <i>Plant Breeding</i> , 2020, 139, 562-574.	1.9	18
20	SR4R: An Integrative SNP Resource for Genomic Breeding and Population Research in Rice. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 173-185.	6.9	18
21	IbBBX24 Promotes the Jasmonic Acid Pathway and Enhances Fusarium Wilt Resistance in Sweet Potato. <i>Plant Cell</i> , 2020, 32, 1102-1123.	6.6	65
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	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.	7.1	17
24	Understanding the functions and mechanisms of plant cytoskeleton in response to environmental signals. <i>Current Opinion in Plant Biology</i> , 2019, 52, 86-96.	7.1	42
25	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.	4.8	11
26	BES1 hinders ABSCISIC ACID INSENSITIVE5 and promotes seed germination in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2019, 221, 908-918.	7.3	86
27	Ethylene Signaling Modulates Cortical Microtubule Reassembly in Response to Salt Stress. <i>Plant Physiology</i> , 2018, 176, 2071-2081.	4.8	49
28	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.	4.1	152
29	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.	3.5	45
30	Machine Learning Models for Genetic Risk Assessment of Infants with Non-syndromic Orofacial Cleft. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 354-364.	6.9	31
31	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.	6.6	83
32	VAMP711 Is Required for Abscisic Acid-Mediated Inhibition of Plasma Membrane H <sup>+</sup> -ATPase Activity. <i>Plant Physiology</i> , 2018, 178, 1332-1343.	4.8	47
33	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.	3.3	62
34	Isoform Evolution in Primates through Independent Combination of Alternative RNA Processing Events. <i>Molecular Biology and Evolution</i> , 2017, 34, 2453-2468.	8.9	37
35	Transcriptome Association Identifies Regulators of Wheat Spike Architecture. <i>Plant Physiology</i> , 2017, 175, 746-757.	4.8	94
36	Single-Molecule Sequencing Assists Genome Assembly Improvement and Structural Variation Inference. <i>Molecular Plant</i> , 2016, 9, 1085-1087.	8.3	2

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37	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.	3.6	14
38	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.	6.6	206
39	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.	7.1	146
40	Complete genome of Hainan papaya ringspot virus using small RNA deep sequencing. <i>Virus Genes</i> , 2014, 48, 502-508.	1.6	5
41	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
42	Machine Learning-Based Differential Network Analysis: A Study of Stress-Responsive Transcriptomes in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 520-537.	6.6	104
43	Machine learning for Big Data analytics in plants. <i>Trends in Plant Science</i> , 2014, 19, 798-808.	8.8	220
44	Dynamic parent-of-origin effects on small interfering RNA expression in the developing maize endosperm. <i>BMC Plant Biology</i> , 2014, 14, 192.	3.6	21
45	A Computational Workflow to Identify Allele-specific Expression and Epigenetic Modification in Maize. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 247-252.	6.9	10
46	Organ Evolution in Angiosperms Driven by Correlated Divergences of Gene Sequences and Expression Patterns. <i>Plant Cell</i> , 2013, 25, 71-82.	6.6	39
47	CrusView: A Java-Based Visualization Platform for Comparative Genomics Analyses in Brassicaceae Species. <i>Plant Physiology</i> , 2013, 163, 354-362.	4.8	33
48	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198
49	Dynamic Expression of Imprinted Genes Associates with Maternally Controlled Nutrient Allocation during Maize Endosperm Development. <i>Plant Cell</i> , 2013, 25, 3212-3227.	6.6	97
50	Application of the Gini Correlation Coefficient to Infer Regulatory Relationships in Transcriptome Analysis. <i>Plant Physiology</i> , 2012, 160, 192-203.	4.8	65
51	KGBassembler: a karyotype-based genome assembler for Brassicaceae species. <i>Bioinformatics</i> , 2012, 28, 3141-3143.	4.1	12
52	Transcriptome Comparison of Susceptible and Resistant Wheat in Response to Powdery Mildew Infection. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 94-106.	6.9	90
53	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.	2.9	8
54	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.	2.3	52

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55	Genome-wide mapping of the H3K9me3-mediated gene networks in Arabidopsis that involve both transcriptional and post-transcriptional regulation. <i>Plant Journal</i> , 2011, 65, 346-358.	5.7	274
56	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.	3.9	167
57	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. <i>Genomics</i> , 2010, 96, 308-315.	2.9	4
58	Global Epigenetic and Transcriptional Trends among Two Rice Subspecies and Their Reciprocal Hybrids. <i>Plant Cell</i> , 2010, 22, 17-33.	6.6	514
59	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.	6.6	291
60	Transcriptionally active gene fragments derived from potentially fast-evolving donor genes in the rice genome. <i>Bioinformatics</i> , 2009, 25, 1215-1218.	4.1	3
61	Characterization of the genome expression trends in the heading-stage panicle of six rice lineages. <i>Genomics</i> , 2009, 93, 169-178.	2.9	11
62	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.	9.6	13
63	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.	6.6	281
64	Global Identification and Characterization of Transcriptionally Active Regions in the Rice Genome. <i>PLoS ONE</i> , 2007, 2, e294.	2.5	82
65	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.	3.9	275
66	Genome-wide transcription analyses in rice using tiling microarrays. <i>Nature Genetics</i> , 2006, 38, 124-129.	21.4	154
67	NMPP: a user-customized NimbleGen microarray data processing pipeline. <i>Bioinformatics</i> , 2006, 22, 2955-2957.	4.1	29
68	A Pilot Study of Transcription Unit Analysis in Rice Using Oligonucleotide Tiling-path Microarray. <i>Plant Molecular Biology</i> , 2005, 59, 137-149.	3.9	17
69	A Tiling Microarray Expression Analysis of Rice Chromosome 4 Suggests a Chromosome-Level Regulation of Transcription. <i>Plant Cell</i> , 2005, 17, 1641-1657.	6.6	56
70	A microarray analysis of the rice transcriptome and its comparison to Arabidopsis. <i>Genome Research</i> , 2005, 15, 1274-1283.	5.5	112
71	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.	9.6	41