Hairong Wei

List of Publications by Year
in descending order

82 papers	4,732 citations	185998 28 h-index	102304 66 g-index
91 all docs	91 docs citations	91 times ranked	6886 citing authors

#	Article	IF	Citations
1	PtrHAT22, as a higher hierarchy regulator, coordinately regulates secondary cell wall component biosynthesis in Populus trichocarpa. Plant Science, 2022, 316, 111170.	1.7	7
2	The Chinese pine genome and methylome unveil key features of conifer evolution. Cell, 2022, 185, 204-217.e14.	13.5	151
3	Breeding polyploid <i>Populus</i>: progress and perspective. Forestry Research, 2022, 2, 0-0.	0.5	7
4	Single-Cell Transcriptome and Network Analyses Unveil Key Transcription Factors Regulating Mesophyll Cell Development in Maize. Genes, 2022, 13, 374.	1.0	13
5	Two high hierarchical regulators, PuMYB40 and PuWRKY75, control the low phosphorus driven adventitious root formation in <i>Populus ussuriensis</i>. Plant Biotechnology Journal, 2022, 20, 1561-1577.	4.1	14
6	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. Nature Plants, 2022, 8, 500-512.	4.7	42
7	MicroRNA319-mediated gene regulatory network impacts leaf development and morphogenesis in poplar. Forestry Research, 2021, 1, 1-10.	0.5	4
8	A systems biology approach identifies a regulator, <i>BplERF1</i>, of cold tolerance in <i>Betula platyphylla</i>. Forestry Research, 2021, 1, 1-10.	0.5	3
9	Genome sequence and evolution of <i>Betula platyphylla</i>. Horticulture Research, 2021, 8, 37.	2.9	53
10	Growthâ€regulating factor 5 (GRF5)â€mediated gene regulatory network promotes leaf growth and expansion in poplar. New Phytologist, 2021, 230, 612-628.	3.5	36
11	Characterization of a High Hierarchical Regulator, PtrGATA12, Functioning in Differentially Regulating Secondary Wall Component Biosynthesis in Populus trichocarpa. Frontiers in Plant Science, 2021, 12, 657787.	1.7	12
12	Comparative proteomic analysis provides insight into the molecular mechanism of vegetative growth advantage in allotriploid Populus. Genomics, 2021, 113, 1180-1192.	1.3	3
13	The diverse roles of cytokinins in regulating leaf development. Horticulture Research, 2021, 8, 118.	2.9	68
14	BEL1-like Homeodomain Protein BLH6a Is a Negative Regulator of CAld5H2 in Sinapyl Alcohol Monolignol Biosynthesis in Poplar. Frontiers in Plant Science, 2021, 12, 695223.	1.7	5
15	Toward an understanding of the detection and function of R-loops in plants. Journal of Experimental Botany, 2021, 72, 6110-6122.	2.4	5
16	Identification of biological pathway and process regulators using sparse partial least squares and triple-gene mutual interaction. Scientific Reports, 2021, 11, 13174.	1.6	2
17	Transcriptome-wide identification and characterization of microRNAs in diverse phases of wood formation in <i>Populus trichocarpa</i>. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	9
18	Chromosome-level genome assembly of a regenerable maize inbred line A188. Genome Biology, 2021, 22, 175.	3.8	32

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19	Transcriptome comparison of different ploidy reveals the mechanism of photosynthetic efficiency superiority of triploid poplar. Genomics, 2021, 113, 2211-2220.	1.3	14
20	HB-PLS: A statistical method for identifying biological process or pathway regulators by integrating Huber loss and Berhu penalty with partial least squares regression. Forestry Research, 2021, 1, 0-0.	0.5	1
21	LORSEN: Fast and Efficient eQTL Mapping With Low Rank Penalized Regression. Frontiers in Genetics, 2021, 12, 690926.	1.1	0
22	A R2R3-MYB Transcription Factor Gene, BpMYB123, Regulates BpLEA14 to Improve Drought Tolerance in Betula platyphylla. Frontiers in Plant Science, 2021, 12, 791390.	1.7	8
23	Overexpression of an AP2/ERF family gene, BpERF13, in birch enhances cold tolerance through upregulating CBF genes and mitigating reactive oxygen species. Plant Science, 2020, 292, 110375.	1.7	62
24	Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. NAR Genomics and Bioinformatics, 2020, 2, lqaa075.	1.5	8
25	High-quality de novo assembly of the Eucommia ulmoides haploid genome provides new insights into evolution and rubber biosynthesis. Horticulture Research, 2020, 7, 183.	2.9	28
26	DNA methylation and its effects on gene expression during primary to secondary growth in poplar stems. BMC Genomics, 2020, 21, 498.	1.2	23
27	Chromosome-scale genome assembly of sweet cherry (Prunus avium L.) cv. Tieton obtained using long-read and Hi-C sequencing. Horticulture Research, 2020, 7, 122.	2.9	44
28	Comparative Proteomic Analysis of Leaves at Different Ages in Allotriploid Populus. Forests, 2020, 11, 1154.	0.9	3
29	Overexpression of BplERD15 Enhances Drought Tolerance in Betula platyphylla Suk.. Forests, 2020, 11, 978.	0.9	7
30	PuHox52â€mediated hierarchical multilayered gene regulatory network promotes adventitious root formation in <i>Populus ussuriensis</i>. New Phytologist, 2020, 228, 1369-1385.	3.5	33
31	Coâ€expression analysis aids in the identification of genes in the cuticular wax pathway in maize. Plant Journal, 2019, 97, 530-542.	2.8	34
32	Characterization of functional relationships of R-loops with gene transcription and epigenetic modifications in rice. Genome Research, 2019, 29, 1287-1297.	2.4	38
33	R-Loop Identification and Profiling in Plants. Trends in Plant Science, 2019, 24, 971-972.	4.3	5
34	Genome Size Variation within Species of Chinese Jujube (Ziziphus jujuba Mill.) and Its Wild Ancestor Sour Jujube (Z. acidojujuba Cheng et Liu). Forests, 2019, 10, 460.	0.9	14
35	Morphological, cytological and nutritional changes of autotetraploid compared to its diploid counterpart in Chinese jujube (Ziziphus jujuba Mill.). Scientia Horticulturae, 2019, 249, 263-270.	1.7	22
36	Construction of a hierarchical gene regulatory network centered around a transcription factor. Briefings in Bioinformatics, 2019, 20, 1021-1031.	3.2	21

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37	JRmGRN: joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions. Bioinformatics, 2018, 34, 3470-3478.	1.8	19
38	TGMI: an efficient algorithm for identifying pathway regulators through evaluation of triple-gene mutual interaction. Nucleic Acids Research, 2018, 46, e67-e67.	6.5	16
39	Gene network analysis of poplar root transcriptome in response to drought stress identifies a PtaJAZ3PtaRAP2.6-centered hierarchical network. PLoS ONE, 2018, 13, e0208560.	1.1	13
40	A Resource for Inactivation of MicroRNAs Using Short Tandem Target Mimic Technology in Model and Crop Plants. Molecular Plant, 2018, 11, 1400-1417.	3.9	52
41	The Effect of Poplar PsnGS1.2 Overexpression on Growth, Secondary Cell Wall, and Fiber Characteristics in Tobacco. Frontiers in Plant Science, 2018, 9, 9.	1.7	33
42	Growth performance, organ-level ionic relations and organic osmoregulation of Elaeagnus angustifolia in response to salt stress. PLoS ONE, 2018, 13, e0191552.	1.1	22
43	SSGA and MSGA: two seed-growing algorithms for constructing collaborative subnetworks. Scientific Reports, 2017, 7, 1446.	1.6	2
44	Functional Characterization of Populus PsnSHN2 in Coordinated Regulation of Secondary Wall Components in Tobacco. Scientific Reports, 2017, 7, 42.	1.6	52
45	Recursive random forest algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways. PLoS ONE, 2017, 12, e0171532.	1.1	38
46	α-amanitin resistance in Drosophila melanogaster: A genome-wide association approach. PLoS ONE, 2017, 12, e0173162.	1.1	8
47	Identification of microRNAs Involved in Regeneration of the Secondary Vascular System in Populus tomentosa Carr. Frontiers in Plant Science, 2016, 7, 724.	1.7	29
48	Identification of Mitochondrial Genome-Encoded Small RNAs Related to Egg Deterioration Caused by Postovulatory Aging in Rainbow Trout. Marine Biotechnology, 2016, 18, 584-597.	1.1	14
49	A network of genes associated with poplar root development in response to low nitrogen. Plant Signaling and Behavior, 2016, 11, e1214792.	1.2	5
50	Bottom-up GGM algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways or processes. BMC Bioinformatics, 2016, 17, 132.	1.2	19
51	ExactSearch: a web-based plant motif search tool. Plant Methods, 2016, 12, 26.	1.9	6
52	A systems biology approach identifies new regulators of poplar root development under low nitrogen. Plant Journal, 2015, 84, 335-346.	2.8	36
53	Overexpression of Poplar Xylem Sucrose Synthase in Tobacco Leads to a Thickened Cell Wall and Increased Height. PLoS ONE, 2015, 10, e0120669.	1.1	40
54	Designing Microarray and RNA-Seq Experiments for Greater Systems Biology Discovery in Modern Plant Genomics. Molecular Plant, 2015, 8, 196-206.	3.9	24

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55	MicroRNA expression profiles from eggs of different qualities associated with post-ovulatory ageing in rainbow trout (Oncorhynchus mykiss). BMC Genomics, 2015, 16, 201.	1.2	35
56	Functional characterization of *<scp>CCR</scp>* in birch (*Betula platyphylla* Ã— *Betula*) Tj ETQq0 0 0 rgBT /Overlock 10 283-296.	2.6	27
57	Expression Patterns of ERF Genes Underlying Abiotic Stresses in Di-Haploid*Populus simonii*Ã—*P. nigra*. Scientific World Journal, The, 2014, 2014, 1-10.	0.8	19
58	GPLEXUS: enabling genome-scale gene association network reconstruction and analysis for very large-scale expression data. Nucleic Acids Research, 2014, 42, e32-e32.	6.5	9
59	The Mechanisms Underlying Î±-Amanitin Resistance in Drosophila melanogaster: A Microarray Analysis. PLoS ONE, 2014, 9, e93489.	1.1	17
60	Designing Microarray and RNA-seq Experiments for Greater Systems Biology Discovery in Modern Plant Genomics. Molecular Plant, 2014, , .	3.9	2
61	Popâ€™s Pipes: poplar gene expression data analysis pipelines. Tree Genetics and Genomes, 2014, 10, 1093-1101.	0.6	15
62	Nitrogen deprivation promotes *<scp>P</scp>opulus* root growth through global transcriptome reprogramming and activation of hierarchical genetic networks. New Phytologist, 2013, 200, 483-497.	3.5	69
63	Ptr-miR397a is a negative regulator of laccase genes affecting lignin content in *Populus trichocarpa*. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10848-10853.	3.3	329
64	Global transcriptomic profiling of aspen trees under elevated [CO2] to identify potential molecular mechanisms responsible for enhanced radial growth. Journal of Plant Research, 2013, 126, 305-320.	1.2	41
65	DeGNServer: Deciphering Genome-Scale Gene Networks through High Performance Reverse Engineering Analysis. BioMed Research International, 2013, 2013, 1-10.	0.9	21
66	SND1 Transcription Factor-Directed Quantitative Functional Hierarchical Genetic Regulatory Network in Wood Formation in Populus trichocarpa. Plant Cell, 2013, 25, 4324-4341.	3.1	131
67	Effects of Soil Salinity on Growth, Ion Relations, and Compatible Solute Accumulation of Two Sumac Species:Rhus glabraandRhus trilobata. Communications in Soil Science and Plant Analysis, 2013, 44, 3187-3204.	0.6	2
68	Genetic networks involved in poplar root response to low nitrogen. Plant Signaling and Behavior, 2013, 8, e27211.	1.2	17
69	Evaluation of Gene Association Methods for Coexpression Network Construction and Biological Knowledge Discovery. PLoS ONE, 2012, 7, e50411.	1.1	100
70	Characterization of the Rainbow Trout Egg MicroRNA Transcriptome. PLoS ONE, 2012, 7, e39649.	1.1	59
71	TF-Cluster: A pipeline for identifying functionally coordinated transcription factors via network decomposition of the shared coexpression connectivity matrix (SCCM). BMC Systems Biology, 2011, 5, 53.	3.0	24
72	TF-finder: A software package for identifying transcription factors involved in biological processes using microarray data and existing knowledge base. BMC Bioinformatics, 2010, 11, 425.	1.2	13

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73	The draft genome of the transgenic tropical fruit tree papaya (Carica papaya Linnaeus). Nature, 2008, 452, 991-996.	13.7	964
74	A study of the relationships between oligonucleotide properties and hybridization signal intensities from NimbleGen microarray datasets. Nucleic Acids Research, 2008, 36, 2926-2938.	6.5	38
75	Whole-Genome Analysis of Histone H3 Lysine 4 and Lysine 27 Methylation in Human Embryonic Stem Cells. Cell Stem Cell, 2007, 1, 299-312.	5.2	637
76	Transcriptional Coordination of the Metabolic Network in Arabidopsis. Plant Physiology, 2006, 142, 762-774.	2.3	178
77	Inferring gene regulatory relationships by combining target-target pattern recognition and regulator-specific motif examination. Biotechnology and Bioengineering, 2005, 89, 53-77.	1.7	8
78	Identification of genes required for cellulose synthesis by regression analysis of public microarray data sets. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8633-8638.	3.3	539
79	Comparative expression analysis of two sugarcane polyubiquitin promoters and flanking sequences in transgenic plants. Journal of Plant Physiology, 2003, 160, 1241-1251.	1.6	75
80	Cutting Edge: The NK Cell Receptor 2B4 Augments Antigen-Specific T Cell Cytotoxicity Through CD48 Ligation on Neighboring T Cells. Journal of Immunology, 2003, 170, 4881-4885.	0.4	78
81	The Chromosome-Scale Genome and Methylome of Pinus Tabuliformis and the Evolution of Conifers. SSRN Electronic Journal, 0, , .	0.4	0
82	PtrWOX13A Promotes Wood Formation and Bioactive Gibberellins Biosynthesis in Populus trichocarpa. Frontiers in Plant Science, 0, 13, .	1.7	1