

# Hairong Wei

## List of Publications by Year in descending order

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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	The draft genome of the transgenic tropical fruit tree papaya ( <i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	13.7	964
2	Whole-Genome Analysis of Histone H3 Lysine 4 and Lysine 27 Methylation in Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2007, 1, 299-312.	5.2	637
3	Identification of genes required for cellulose synthesis by regression analysis of public microarray data sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8633-8638.	3.3	539
4	Ptr-miR397a is a negative regulator of laccase genes affecting lignin content in <i>Populus trichocarpa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10848-10853.	3.3	329
5	Transcriptional Coordination of the Metabolic Network in Arabidopsis. <i>Plant Physiology</i> , 2006, 142, 762-774.	2.3	178
6	The Chinese pine genome and methylome unveil key features of conifer evolution. <i>Cell</i> , 2022, 185, 204-217.e14.	13.5	151
7	SND1 Transcription Factor-Directed Quantitative Functional Hierarchical Genetic Regulatory Network in Wood Formation in <i>Populus trichocarpa</i> . <i>Plant Cell</i> , 2013, 25, 4324-4341.	3.1	131
8	Evaluation of Gene Association Methods for Coexpression Network Construction and Biological Knowledge Discovery. <i>PLoS ONE</i> , 2012, 7, e50411.	1.1	100
9	Cutting Edge: The NK Cell Receptor 2B4 Augments Antigen-Specific T Cell Cytotoxicity Through CD48 Ligation on Neighboring T Cells. <i>Journal of Immunology</i> , 2003, 170, 4881-4885.	0.4	78
10	Comparative expression analysis of two sugarcane polyubiquitin promoters and flanking sequences in transgenic plants. <i>Journal of Plant Physiology</i> , 2003, 160, 1241-1251.	1.6	75
11	Nitrogen deprivation promotes <i>Populus</i> root growth through global transcriptome reprogramming and activation of hierarchical genetic networks. <i>New Phytologist</i> , 2013, 200, 483-497.	3.5	69
12	The diverse roles of cytokinins in regulating leaf development. <i>Horticulture Research</i> , 2021, 8, 118.	2.9	68
13	Overexpression of an AP2/ERF family gene, BpERF13, in birch enhances cold tolerance through upregulating CBF genes and mitigating reactive oxygen species. <i>Plant Science</i> , 2020, 292, 110375.	1.7	62
14	Characterization of the Rainbow Trout Egg MicroRNA Transcriptome. <i>PLoS ONE</i> , 2012, 7, e39649.	1.1	59
15	Genome sequence and evolution of <i>Betula platyphylla</i> . <i>Horticulture Research</i> , 2021, 8, 37.	2.9	53
16	Functional Characterization of <i>Populus PsnSHN2</i> in Coordinated Regulation of Secondary Wall Components in Tobacco. <i>Scientific Reports</i> , 2017, 7, 42.	1.6	52
17	A Resource for Inactivation of MicroRNAs Using Short Tandem Target Mimic Technology in Model and Crop Plants. <i>Molecular Plant</i> , 2018, 11, 1400-1417.	3.9	52
18	Chromosome-scale genome assembly of sweet cherry ( <i>Prunus avium</i> L.) cv. Tieton obtained using long-read and Hi-C sequencing. <i>Horticulture Research</i> , 2020, 7, 122.	2.9	44

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19	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. <i>Nature Plants</i> , 2022, 8, 500-512.	4.7	42
20	Global transcriptomic profiling of aspen trees under elevated [CO <sub>2</sub> ] to identify potential molecular mechanisms responsible for enhanced radial growth. <i>Journal of Plant Research</i> , 2013, 126, 305-320.	1.2	41
21	Overexpression of Poplar Xylem Sucrose Synthase in Tobacco Leads to a Thickened Cell Wall and Increased Height. <i>PLoS ONE</i> , 2015, 10, e0120669.	1.1	40
22	A study of the relationships between oligonucleotide properties and hybridization signal intensities from NimbleGen microarray datasets. <i>Nucleic Acids Research</i> , 2008, 36, 2926-2938.	6.5	38
23	Characterization of functional relationships of R-loops with gene transcription and epigenetic modifications in rice. <i>Genome Research</i> , 2019, 29, 1287-1297.	2.4	38
24	Recursive random forest algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways. <i>PLoS ONE</i> , 2017, 12, e0171532.	1.1	38
25	A systems biology approach identifies new regulators of poplar root development under low nitrogen. <i>Plant Journal</i> , 2015, 84, 335-346.	2.8	36
26	Growth-regulating factor 5 (GRF5)-mediated gene regulatory network promotes leaf growth and expansion in poplar. <i>New Phytologist</i> , 2021, 230, 612-628.	3.5	36
27	MicroRNA expression profiles from eggs of different qualities associated with post-ovulatory ageing in rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>BMC Genomics</i> , 2015, 16, 201.	1.2	35
28	Co-expression analysis aids in the identification of genes in the cuticular wax pathway in maize. <i>Plant Journal</i> , 2019, 97, 530-542.	2.8	34
29	The Effect of Poplar PsnGS1.2 Overexpression on Growth, Secondary Cell Wall, and Fiber Characteristics in Tobacco. <i>Frontiers in Plant Science</i> , 2018, 9, 9.	1.7	33
30	PuHox52-mediated hierarchical multilayered gene regulatory network promotes adventitious root formation in <i>Populus ussuriensis</i> . <i>New Phytologist</i> , 2020, 228, 1369-1385.	3.5	33
31	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	3.8	32
32	Identification of microRNAs Involved in Regeneration of the Secondary Vascular System in <i>Populus tomentosa</i> Carr. <i>Frontiers in Plant Science</i> , 2016, 7, 724.	1.7	29
33	High-quality de novo assembly of the <i>Eucommia ulmoides</i> haploid genome provides new insights into evolution and rubber biosynthesis. <i>Horticulture Research</i> , 2020, 7, 183.	2.9	28
34	Functional characterization of <i>CCR</i> in birch ( <i>Betula platyphylla</i> – <i>Betula</i> Tj ETQq0 0 0 rgBT /Overlock 10 283-296.	2.6	27
35	TF-Cluster: A pipeline for identifying functionally coordinated transcription factors via network decomposition of the shared coexpression connectivity matrix (SCCM). <i>BMC Systems Biology</i> , 2011, 5, 53.	3.0	24
36	Designing Microarray and RNA-Seq Experiments for Greater Systems Biology Discovery in Modern Plant Genomics. <i>Molecular Plant</i> , 2015, 8, 196-206.	3.9	24

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37	DNA methylation and its effects on gene expression during primary to secondary growth in poplar stems. <i>BMC Genomics</i> , 2020, 21, 498.	1.2	23
38	Growth performance, organ-level ionic relations and organic osmoregulation of <i>Elaeagnus angustifolia</i> in response to salt stress. <i>PLoS ONE</i> , 2018, 13, e0191552.	1.1	22
39	Morphological, cytological and nutritional changes of autotetraploid compared to its diploid counterpart in Chinese jujube ( <i>Ziziphus jujuba</i> Mill.). <i>Scientia Horticulturae</i> , 2019, 249, 263-270.	1.7	22
40	DeGNServer: Deciphering Genome-Scale Gene Networks through High Performance Reverse Engineering Analysis. <i>BioMed Research International</i> , 2013, 2013, 1-10.	0.9	21
41	Construction of a hierarchical gene regulatory network centered around a transcription factor. <i>Briefings in Bioinformatics</i> , 2019, 20, 1021-1031.	3.2	21
42	Expression Patterns of ERF Genes Underlying Abiotic Stresses in Di-Haploid <i>Populus simonii</i> — <i>P. nigra</i> . <i>Scientific World Journal</i> , The, 2014, 2014, 1-10.	0.8	19
43	Bottom-up GGM algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways or processes. <i>BMC Bioinformatics</i> , 2016, 17, 132.	1.2	19
44	JRmGRN: joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions. <i>Bioinformatics</i> , 2018, 34, 3470-3478.	1.8	19
45	Genetic networks involved in poplar root response to low nitrogen. <i>Plant Signaling and Behavior</i> , 2013, 8, e27211.	1.2	17
46	The Mechanisms Underlying $\beta$ -Amanitin Resistance in <i>Drosophila melanogaster</i> : A Microarray Analysis. <i>PLoS ONE</i> , 2014, 9, e93489.	1.1	17
47	TGMI: an efficient algorithm for identifying pathway regulators through evaluation of triple-gene mutual interaction. <i>Nucleic Acids Research</i> , 2018, 46, e67-e67.	6.5	16
48	Popâ€™s Pipes: poplar gene expression data analysis pipelines. <i>Tree Genetics and Genomes</i> , 2014, 10, 1093-1101.	0.6	15
49	Identification of Mitochondrial Genome-Encoded Small RNAs Related to Egg Deterioration Caused by Postovulatory Aging in Rainbow Trout. <i>Marine Biotechnology</i> , 2016, 18, 584-597.	1.1	14
50	Genome Size Variation within Species of Chinese Jujube ( <i>Ziziphus jujuba</i> Mill.) and Its Wild Ancestor Sour Jujube ( <i>Z. acidujuba</i> Cheng et Liu). <i>Forests</i> , 2019, 10, 460.	0.9	14
51	Transcriptome comparison of different ploidy reveals the mechanism of photosynthetic efficiency superiority of triploid poplar. <i>Genomics</i> , 2021, 113, 2211-2220.	1.3	14
52	Two high hierarchical regulators, PuMYB40 and PuWRKY75, control the low phosphorus driven adventitious root formation in <i>Populus ussuriensis</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1561-1577.	4.1	14
53	TF-finder: A software package for identifying transcription factors involved in biological processes using microarray data and existing knowledge base. <i>BMC Bioinformatics</i> , 2010, 11, 425.	1.2	13
54	Gene network analysis of poplar root transcriptome in response to drought stress identifies a PtAJZ3PtARAP2.6-centered hierarchical network. <i>PLoS ONE</i> , 2018, 13, e0208560.	1.1	13

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55	Single-Cell Transcriptome and Network Analyses Unveil Key Transcription Factors Regulating Mesophyll Cell Development in Maize. <i>Genes</i> , 2022, 13, 374.	1.0	13
56	Characterization of a High Hierarchical Regulator, PtrGATA12, Functioning in Differentially Regulating Secondary Wall Component Biosynthesis in <i>Populus trichocarpa</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 657787.	1.7	12
57	GPLEXUS: enabling genome-scale gene association network reconstruction and analysis for very large-scale expression data. <i>Nucleic Acids Research</i> , 2014, 42, e32-e32.	6.5	9
58	Transcriptome-wide identification and characterization of microRNAs in diverse phases of wood formation in <i>Populus trichocarpa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	9
59	Inferring gene regulatory relationships by combining target-target pattern recognition and regulator-specific motif examination. <i>Biotechnology and Bioengineering</i> , 2005, 89, 53-77.	1.7	8
60	Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa075.	1.5	8
61	Î±-amanitin resistance in <i>Drosophila melanogaster</i> : A genome-wide association approach. <i>PLoS ONE</i> , 2017, 12, e0173162.	1.1	8
62	A R2R3-MYB Transcription Factor Gene, BpMYB123, Regulates BpLEA14 to Improve Drought Tolerance in <i>Betula platyphylla</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 791390.	1.7	8
63	Overexpression of BpLERD15 Enhances Drought Tolerance in <i>Betula platyphylla</i> Suk.. <i>Forests</i> , 2020, 11, 978.	0.9	7
64	PtrHAT22, as a higher hierarchy regulator, coordinately regulates secondary cell wall component biosynthesis in <i>Populus trichocarpa</i> . <i>Plant Science</i> , 2022, 316, 111170.	1.7	7
65	Breeding polyploid <i>Populus</i> : progress and perspective. <i>Forestry Research</i> , 2022, 2, 0-0.	0.5	7
66	ExactSearch: a web-based plant motif search tool. <i>Plant Methods</i> , 2016, 12, 26.	1.9	6
67	A network of genes associated with poplar root development in response to low nitrogen. <i>Plant Signaling and Behavior</i> , 2016, 11, e1214792.	1.2	5
68	R-Loop Identification and Profiling in Plants. <i>Trends in Plant Science</i> , 2019, 24, 971-972.	4.3	5
69	BEL1-like Homeodomain Protein BLH6a Is a Negative Regulator of CALD5H2 in Sinapyl Alcohol Monoglignol Biosynthesis in Poplar. <i>Frontiers in Plant Science</i> , 2021, 12, 695223.	1.7	5
70	Toward an understanding of the detection and function of R-loops in plants. <i>Journal of Experimental Botany</i> , 2021, 72, 6110-6122.	2.4	5
71	MicroRNA319-mediated gene regulatory network impacts leaf development and morphogenesis in poplar. <i>Forestry Research</i> , 2021, 1, 1-10.	0.5	4
72	Comparative Proteomic Analysis of Leaves at Different Ages in Allotriploid <i>Populus</i> . <i>Forests</i> , 2020, 11, 1154.	0.9	3

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73	A systems biology approach identifies a regulator, <i>BplERF1</i> , of cold tolerance in <i>Betula platyphylla</i> . <i>Forestry Research</i> , 2021, 1, 1-10.	0.5	3
74	Comparative proteomic analysis provides insight into the molecular mechanism of vegetative growth advantage in allotriploid <i>Populus</i> . <i>Genomics</i> , 2021, 113, 1180-1192.	1.3	3
75	Effects of Soil Salinity on Growth, Ion Relations, and Compatible Solute Accumulation of Two Sumac Species: <i>Rhus glabra</i> and <i>Rhus trilobata</i> . <i>Communications in Soil Science and Plant Analysis</i> , 2013, 44, 3187-3204.	0.6	2
76	Designing Microarray and RNA-seq Experiments for Greater Systems Biology Discovery in Modern Plant Genomics. <i>Molecular Plant</i> , 2014, , .	3.9	2
77	SSGA and MSGA: two seed-growing algorithms for constructing collaborative subnetworks. <i>Scientific Reports</i> , 2017, 7, 1446.	1.6	2
78	Identification of biological pathway and process regulators using sparse partial least squares and triple-gene mutual interaction. <i>Scientific Reports</i> , 2021, 11, 13174.	1.6	2
79	HB-PLS: A statistical method for identifying biological process or pathway regulators by integrating Huber loss and Berhu penalty with partial least squares regression. <i>Forestry Research</i> , 2021, 1, 0-0.	0.5	1
80	<i>PtrWOX13A</i> Promotes Wood Formation and Bioactive Gibberellins Biosynthesis in <i>Populus trichocarpa</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
81	The Chromosome-Scale Genome and Methylome of <i>Pinus Tabulaeformis</i> and the Evolution of Conifers. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
82	LORSEN: Fast and Efficient eQTL Mapping With Low Rank Penalized Regression. <i>Frontiers in Genetics</i> , 2021, 12, 690926.	1.1	0