

# Huaitong Wu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1467997/publications.pdf>

Version: 2024-02-01

18  
papers

2,914  
citations

623734

14  
h-index

888059

17  
g-index

18  
all docs

18  
docs citations

18  
times ranked

1982  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Selection of Reliable Reference Genes for Gene Expression Analysis in the Female and Male Flowers of <i>Salix suchowensis</i> . <i>Plants</i> , 2022, 11, 647.	3.5	2
2	Genome-Wide Comparative Analysis of R2R3 MYB Gene Family in <i>Populus</i> and <i>Salix</i> and Identification of Male Flower Bud Development-Related Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 721558.	3.6	19
3	Identification of Genes Underlying the Resistance to <i>Melampsora larici-populina</i> in an <i>R</i> Gene Supercluster of the <i>Populus deltoides</i> Genome. <i>Plant Disease</i> , 2020, 104, 1133-1143.	1.4	6
4	Evidences for a role of two Y-specific genes in sex determination in <i>Populus deltoides</i> . <i>Nature Communications</i> , 2020, 11, 5893.	12.8	68
5	Fine mapping of the sex locus in <i>Salix triandra</i> confirms a consistent sex determination mechanism in genus <i>Salix</i> . <i>Horticulture Research</i> , 2020, 7, 64.	6.3	19
6	The transcription factor MML4_D12 regulates fiber development through interplay with the WD40-repeat protein WDR in cotton. <i>Journal of Experimental Botany</i> , 2020, 71, 3499-3511.	4.8	24
7	Efficient CRISPR/Cas9-Mediated Gene Editing in an Interspecific Hybrid Poplar With a Highly Heterozygous Genome. <i>Frontiers in Plant Science</i> , 2020, 11, 996.	3.6	27
8	Analyzing and Characterizing the Chloroplast Genome of <i>Salix wilsonii</i> . <i>BioMed Research International</i> , 2019, 2019, 1-14.	1.9	20
9	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. <i>Nature Genetics</i> , 2019, 51, 739-748.	21.4	568
10	Genetics and evolution of <i>MIXTA</i> genes regulating cotton lint fiber development. <i>New Phytologist</i> , 2018, 217, 883-895.	7.3	112
11	Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 33.	8.8	128
12	Rapid mapping and cloning of the virescent-1 gene in cotton by bulked segregant analysis, next generation sequencing and virus-induced gene silencing strategies. <i>Journal of Experimental Botany</i> , 2017, 68, 4125-4135.	4.8	52
13	Small interfering RNAs from bidirectional transcripts of <i>GhMML3_A12</i> regulate cotton fiber development. <i>New Phytologist</i> , 2016, 210, 1298-1310.	7.3	124
14	Insights into Interspecific Hybridization Events in Allotetraploid Cotton Formation from Characterization of a Gene-Regulating Leaf Shape. <i>Genetics</i> , 2016, 204, 799-806.	2.9	22
15	Sequence-based ultra-dense genetic and physical maps reveal structural variations of allopolyploid cotton genomes. <i>Genome Biology</i> , 2015, 16, 108.	9.6	108
16	Sequencing of allotetraploid cotton ( <i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
17	Genome-Wide Transcriptome Profiling Revealed Cotton Fuzz Fiber Development Having a Similar Molecular Model as <i>Arabidopsis Trichome</i> . <i>PLoS ONE</i> , 2014, 9, e97313.	2.5	54
18	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1