

# Hao Wang

## List of Publications by Year in descending order

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34  
papers

14,097  
citations

394286

19  
h-index

395590

33  
g-index

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35  
docs citations

35  
times ranked

15592  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Analysis of Transposable Elements and the Identification of Candidate Centromeric Elements in the Prunus Subgenus Cerasus and Its Relatives. <i>Genes</i> , 2022, 13, 641.	1.0	9
2	High-quality reannotation of the king scallop genome reveals no "gene-rich" feature and evolution of toxin resistance. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4954-4960.	1.9	14
3	Dragon's Blood from <i>Dracaena cambodiana</i> in China: Applied History and Induction Techniques toward Formation Mechanism. <i>Forests</i> , 2020, 11, 372.	0.9	17
4	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
5	Resolution of deep divergence of club fungi (phylum Basidiomycota). <i>Synthetic and Systems Biotechnology</i> , 2019, 4, 225-231.	1.8	6
6	Birth and Death of LTR-Retrotransposons in <i>Aegilops tauschii</i> . <i>Genetics</i> , 2018, 210, 1039-1051.	1.2	14
7	Distribution, Diversity, and Long-Term Retention of Grass Short Interspersed Nuclear Elements (SINEs). <i>Genome Biology and Evolution</i> , 2017, 9, 2048-2056.	1.1	6
8	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
9	Construction and characterization of a bacterial artificial chromosome library for <i>Camellia sinensis</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	6
10	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
11	LTR Retrotransposon Dynamics and Specificity in <i>Setaria italica</i> . <i>Plant Genetics and Genomics: Crops and Models</i> , 2017, , 149-158.	0.3	3
12	Comparative Study on the Transcriptome of Maize Mature Embryos from Two China Elite Hybrids Zhengdan958 and Anyu5. <i>PLoS ONE</i> , 2016, 11, e0158028.	1.1	5
13	Transcriptomic analysis of maize mature embryos from an elite maize hybrid Zhengdan958 and its parental lines. <i>Plant Growth Regulation</i> , 2015, 76, 315-325.	1.8	4
14	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
15	Recurrent Loss of Specific Introns during Angiosperm Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004843.	1.5	26
16	On the Origin and Evolution of Plant Brassinosteroid Receptor Kinases. <i>Journal of Molecular Evolution</i> , 2014, 78, 118-129.	0.8	28
17	The Contributions of Transposable Elements to the Structure, Function, and Evolution of Plant Genomes. <i>Annual Review of Plant Biology</i> , 2014, 65, 505-530.	8.6	436
18	Isolation and bioinformatic analysis of a novel transposable element, IS <i>Cbe</i> 4, from the hyperthermophilic bacterium, <i>Caldicellulosiruptor bescii</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2013, 40, 1443-1448.	1.4	15

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19	The genome of the pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
20	Genomic Resources for Gene Discovery, Functional Genome Annotation, and Evolutionary Studies of Maize and Its Close Relatives. <i>Genetics</i> , 2013, 195, 723-737.	1.2	15
21	G Protein Activation without a GEF in the Plant Kingdom. <i>PLoS Genetics</i> , 2012, 8, e1002756.	1.5	110
22	Centromere retention and loss during the descent of maize from a tetraploid ancestor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21004-21009.	3.3	38
23	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	9.4	864
24	The genome of woodland strawberry ( <i>Fragaria vesca</i> ). <i>Nature Genetics</i> , 2011, 43, 109-116.	9.4	1,091
25	De novo genome sequencing and comparative genomics of date palm ( <i>Phoenix dactylifera</i> ). <i>Nature Biotechnology</i> , 2011, 29, 521-527.	9.4	356
26	An examination of targeted gene neighborhoods in strawberry. <i>BMC Plant Biology</i> , 2010, 10, 81.	1.6	23
27	A fungal phylogeny based on 82 complete genomes using the composition vector method. <i>BMC Evolutionary Biology</i> , 2009, 9, 195.	3.2	194
28	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
29	Identification of LTR retrotransposons in eukaryotic genomes: supports from structure and evolution. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 365.	0.1	2
30	LTR retrotransposon landscape in <i>Medicago truncatula</i> : more rapid removal than in rice. <i>BMC Genomics</i> , 2008, 9, 382.	1.2	51
31	LTR retrotransposons reveal recent extensive inter-subspecies nonreciprocal recombination in Asian cultivated rice. <i>BMC Genomics</i> , 2008, 9, 565.	1.2	5
32	LTR_FINDER: an efficient tool for the prediction of full-length LTR retrotransposons. <i>Nucleic Acids Research</i> , 2007, 35, W265-W268.	6.5	1,701
33	A Draft Sequence of the Rice Genome ( <i>Oryza sativa</i> L. ssp. <i>indica</i> ). <i>Science</i> , 2002, 296, 79-92.	6.0	3,146
34	Sexual Recombination and Selection During Domestication of Clonally Propagated Pineapple. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1