

# Jiawei Wang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5075767/publications.pdf>

Version: 2024-02-01

15  
papers

1,029  
citations

1162889

8  
h-index

996849

15  
g-index

16  
all docs

16  
docs citations

16  
times ranked

1232  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
2	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
3	Genomewide identification and expression analysis of the ARF gene family in apple. <i>Journal of Genetics</i> , 2014, 93, 785-797.	0.4	40
4	Rapid detection of <i>Prunus necrotic ringspot virus</i> using magnetic nanoparticle-assisted reverse transcription loop-mediated isothermal amplification. <i>Journal of Virological Methods</i> , 2014, 208, 85-89.	1.0	19
5	Phytoplasmas change the source-sink relationship of field-grown sweet cherry by disturbing leaf function. <i>Physiological and Molecular Plant Pathology</i> , 2015, 92, 22-27.	1.3	17
6	Multilocus genotyping identifies a highly homogeneous phytoplasma lineage associated with sweet cherry virescence disease in China and its carriage by an erythroneurine leafhopper. <i>Crop Protection</i> , 2018, 106, 13-22.	1.0	13
7	Complete nucleotide sequence of little cherry virus 1 (LChV-1) infecting sweet cherry in China. <i>Archives of Virology</i> , 2016, 161, 749-753.	0.9	11
8	A multiplex RT-PCR assay for simultaneous detection of four viruses from sweet cherry. <i>Scientia Horticulturae</i> , 2014, 180, 118-122.	1.7	8
9	Novel phytoplasma strains of X-disease group unveil genetic markers that distinguish North American and South American geographic lineages within subgroups 16SrIIIc and 16SrIIIe. <i>Annals of Applied Biology</i> , 2017, 171, 405-416.	1.3	8
10	A de novo assembly of the sweet cherry ( <i>Prunus avium</i> cv. Tieton) genome using linked-read sequencing technology. <i>PeerJ</i> , 2020, 8, e9114.	0.9	8
11	Improvement for Agronomic Traits of Partial Waxy Wheat by Combination of Backcrossing with a PCR-based DNA Marker. <i>Journal of Genetics and Genomics</i> , 2007, 34, 836-841.	1.7	7
12	~ Candidatus <i>Phytoplasma brasiliense</i> -related strains associated with papaya bunchy top disease in northern Peru represent a distinct geographic lineage. <i>Crop Protection</i> , 2017, 92, 99-106.	1.0	7
13	MFCIS: an automatic leaf-based identification pipeline for plant cultivars using deep learning and persistent homology. <i>Horticulture Research</i> , 2021, 8, 172.	2.9	7
14	Transcriptomic analysis reveals insights into the response to <i>Hop stunt viroid</i> (HSVd) in sweet cherry ( <i>Prunus avium</i> L.) fruits. <i>PeerJ</i> , 2020, 8, e10005.	0.9	7
15	Complete Genome Sequence of a Little Cherry Virus-2 Isolate from Sweet Cherry in China. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1