

Yi Wang

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

4,120
citations

236925

25
h-index

243625

44
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45
all docs

45
docs citations

45
times ranked

6151
citing authors

#	ARTICLE	IF	CITATIONS
1	OrthoVenn2: a web server for whole-genome comparison and annotation of orthologous clusters across multiple species. <i>Nucleic Acids Research</i> , 2019, 47, W52-W58.	14.5	661
2	OrthoVenn: a web server for genome wide comparison and annotation of orthologous clusters across multiple species. <i>Nucleic Acids Research</i> , 2015, 43, W78-W84.	14.5	612
3	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	27.8	563
4	Drought delays development of the sorghum root microbiome and enriches for monoderm bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4284-E4293.	7.1	391
5	A New Tomato NAC (NAM/ATAF1/2/CUC2) Transcription Factor, SINAC4, Functions as a Positive Regulator of Fruit Ripening and Carotenoid Accumulation. <i>Plant and Cell Physiology</i> , 2014, 55, 119-135.	3.1	296
6	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i> , the wheat D-genome progenitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7940-7945.	7.1	214
7	A Tomato MADS-Box Transcription Factor, SIMADS1, Acts as a Negative Regulator of Fruit Ripening. <i>Plant Physiology</i> , 2013, 163, 1026-1036.	4.8	161
8	WheatExp: an RNA-seq expression database for polyploid wheat. <i>BMC Plant Biology</i> , 2015, 15, 299.	3.6	124
9	Complete Chloroplast Genome Sequences of Mongolia Medicine <i>Artemisia frigida</i> and Phylogenetic Relationships with Other Plants. <i>PLoS ONE</i> , 2013, 8, e57533.	2.5	122
10	Gene Duplication and Evolution Dynamics in the Homeologous Regions Harboring Multiple Prolamin and Resistance Gene Families in Hexaploid Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 673.	3.6	84
11	Venn diagrams in bioinformatics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	84
12	MetaCoMET: a web platform for discovery and visualization of the core microbiome. <i>Bioinformatics</i> , 2016, 32, 3469-3470.	4.1	80
13	Dynamic Evolution of $\hat{\pm}$ -Gliadin Prolamin Gene Family in Homeologous Genomes of Hexaploid Wheat. <i>Scientific Reports</i> , 2018, 8, 5181.	3.3	68
14	SilkDB 3.0: visualizing and exploring multiple levels of data for silkworm. <i>Nucleic Acids Research</i> , 2020, 48, D749-D755.	14.5	59
15	Deep sequencing and transcriptome analyses to identify genes involved in secoiridoid biosynthesis in the Tibetan medicinal plant <i>Swertia mussotii</i> . <i>Scientific Reports</i> , 2017, 7, 43108.	3.3	56
16	Function Annotation of an SBP-box Gene in <i>Arabidopsis</i> Based on Analysis of Co-expression Networks and Promoters. <i>International Journal of Molecular Sciences</i> , 2009, 10, 116-132.	4.1	55
17	PIECE: a database for plant gene structure comparison and evolution. <i>Nucleic Acids Research</i> , 2013, 41, D1159-D1166.	14.5	50
18	OUP accepted manuscript. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	50

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19	Physical mapping resources for large plant genomes: radiation hybrids for wheat D-genome progenitor <i>Aegilops tauschii</i> . <i>BMC Genomics</i> , 2012, 13, 597.	2.8	33
20	Rapid evolutionary dynamics in a 2.8â€Mb chromosomal region containing multiple prolamin and resistance gene families in <i>Aegilops tauschii</i> . <i>Plant Journal</i> , 2016, 87, 495-506.	5.7	33
21	Radiation hybrid maps of the D-genome of <i>Aegilops tauschii</i> and their application in sequence assembly of large and complex plant genomes. <i>BMC Genomics</i> , 2015, 16, 800.	2.8	31
22	GSP: a web-based platform for designing genome-specific primers in polyploids. <i>Bioinformatics</i> , 2016, 32, 2382-2383.	4.1	30
23	NetVenn: an integrated network analysis web platform for gene lists. <i>Nucleic Acids Research</i> , 2014, 42, W161-W166.	14.5	29
24	New insights into structural organization and gene duplication in a 1.75â€Mb genomic region harboring the γ -gliadin gene family in <i>Aegilops tauschii</i> , the source of wheat D genome. <i>Plant Journal</i> , 2017, 92, 571-583.	5.7	29
25	Unprecedented [5.5.5.6]Dioxafenestrane Ring Construction in Fungal Insecticidal Sesquiterpene Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 6569-6573.	13.8	27
26	Sequencing and comparative analyses of <i>Aegilops tauschii</i> chromosome arm 3DS reveal rapid evolution of Triticeae genomes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 51-61.	3.9	25
27	PIECE 2.0: an update for the plant gene structure comparison and evolution database. <i>Nucleic Acids Research</i> , 2017, 45, 1015-1020.	14.5	24
28	A whole-genome, radiation hybrid mapping resource of hexaploid wheat. <i>Plant Journal</i> , 2016, 86, 195-207.	5.7	23
29	<i>St</i> ² -80: a new FISH marker for <i>St</i> genome and genome analysis in Triticeae. <i>Genome</i> , 2017, 60, 553-563.	2.0	17
30	Draft Genome Sequence of <i>Agrobacterium rhizogenes</i> Strain NCPPB2659. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
31	Constructing regulatory networks to identify biomarkers for insulin resistance. <i>Gene</i> , 2014, 539, 68-74.	2.2	9
32	Fast-forward genetics by radiation hybrids to saturate the locus regulating nuclear-cytoplasmic compatibility in <i>Triticum</i> . <i>Plant Biotechnology Journal</i> , 2016, 14, 1716-1726.	8.3	9
33	ALM: a comprehensive Arabidopsis interactome module database and related interologs in plants. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau117.	3.0	8
34	Exploring the diploid wheat ancestral A genome through sequence comparison at the high-molecular-weight glutenin locus region. <i>Molecular Genetics and Genomics</i> , 2012, 287, 855-866.	2.1	7
35	Modular assembly of transposable element arrays by microsatellite targeting in the guayule and rice genomes. <i>BMC Genomics</i> , 2018, 19, 271.	2.8	7
36	MdMADS6 Recruits Histone Deacetylase MdHDA19 to Repress the Expression of the Carotenoid Synthesis-Related Gene MdCCD1 during Fruit Ripening. <i>Plants</i> , 2022, 11, 668.	3.5	7

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37	Development of a D genome specific marker resource for diploid and hexaploid wheat. <i>BMC Genomics</i> , 2015, 16, 646.	2.8	6
38	PlantRGDB: A Database of Plant Retrocopied Genes. <i>Plant and Cell Physiology</i> , 2017, 58, pcw210.	3.1	6
39	Synergism of open chromatin regions involved in regulating genes in <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 110, 10-18.	2.7	6
40	RetroScan: An Easy-to-Use Pipeline for Retrocopy Annotation and Visualization. <i>Frontiers in Genetics</i> , 2021, 12, 719204.	2.3	4
41	Characterizing the citrus cultivar Carrizo genome through 454 shotgun sequencing. <i>Genome</i> , 2011, 54, 1005-1015.	2.0	3
42	Genotyping-by-sequencing to determine the genetic structure of a Tibetan medicinal plant <i>Swertia musotii</i> Franch.. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 469-484.	1.6	3
43	A systems biology analysis of protein-protein interactions in the APOBEC family. <i>Life Sciences</i> , 2008, 83, 521-530.	4.3	2
44	Interpopulation differences of retroduplication variations (RDVs) in rice retrogenes and their phenotypic correlations. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 600-611.	4.1	1