

Xiaowu Wang

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

11,468
citations

94269

37
h-index

62479

80
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82
all docs

82
docs citations

82
times ranked

6580
citing authors

#	ARTICLE	IF	CITATIONS
1	BRAD V3.0: an upgraded Brassicaceae database. <i>Nucleic Acids Research</i> , 2022, 50, D1432-D1441.	6.5	89
2	Expanding the genetic variation of <i>Brassica juncea</i> by introgression of the <i>Brassica rapa</i> genome. <i>Horticulture Research</i> , 2022, 9, .	2.9	7
3	A cluster of transcripts identifies a transition stage initiating leafy head growth in heading morphotypes of <i>Brassica</i> . <i>Plant Journal</i> , 2022, 110, 688-706.	2.8	7
4	Transposable element insertion: a hidden major source of domesticated phenotypic variation in <i>Brassica rapa</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1298-1310.	4.1	29
5	Improved Reference Genome Annotation of <i>Brassica rapa</i> by Pacific Biosciences RNA Sequencing. <i>Frontiers in Plant Science</i> , 2022, 13, 841618.	1.7	20
6	Development of InDel Markers for <i>Brassica rapa</i> Based on a High-resolution Melting Curve. <i>Horticultural Plant Journal</i> , 2021, 7, 31-37.	2.3	13
7	Wild Brassica and Its Close Relatives in Turkey, the Genetic Treasures. <i>Horticultural Plant Journal</i> , 2021, 7, 97-107.	2.3	10
8	Divergence of three BRX homoeologs in <i>Brassica rapa</i> and its effect on leaf morphology. <i>Horticulture Research</i> , 2021, 8, 68.	2.9	19
9	Impacts of allopolyploidization and structural variation on intraspecific diversification in <i>Brassica rapa</i> . <i>Genome Biology</i> , 2021, 22, 166.	3.8	80
10	Genome structural evolution in Brassica crops. <i>Nature Plants</i> , 2021, 7, 757-765.	4.7	31
11	Selection on BrFLC1 Is Related to Intraspecific Diversity of <i>Brassica rapa</i> Vegetables. <i>Horticulturae</i> , 2021, 7, 247.	1.2	4
12	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	4.1	44
13	The <i>APETALA2</i> homolog <i>CaFFN</i> regulates flowering time in pepper. <i>Horticulture Research</i> , 2021, 8, 208.	2.9	5
14	Series-Spatial Transcriptome Profiling of Leafy Head Reveals the Key Transition Leaves for Head Formation in Chinese Cabbage. <i>Frontiers in Plant Science</i> , 2021, 12, 787826.	1.7	11
15	Improved <i>Brassica oleracea</i> JZS assembly reveals significant changing of LTR-RT dynamics in different morphotypes. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3187-3199.	1.8	55
16	Ethiopian Mustard (<i>Brassica carinata</i> A. Braun) as an Alternative Energy Source and Sustainable Crop. <i>Sustainability</i> , 2020, 12, 7492.	1.6	23
17	Segmental Translocation Contributed to the Origin of the Brassica S-locus. <i>Horticultural Plant Journal</i> , 2020, 6, 167-178.	2.3	8
18	QTL-Seq and Sequence Assembly Rapidly Mapped the Gene BrMYBL2.1 for the Purple Trait in <i>Brassica rapa</i> . <i>Scientific Reports</i> , 2020, 10, 2328.	1.6	31

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19	Variation in Plant Morphology and Sinigrin Content in Ethiopian Mustard (<i>Brassica carinata</i> L.). Horticultural Plant Journal, 2019, 5, 205-212.	2.3	10
20	Whole-genome resequencing reveals <i>Brassica napus</i> origin and genetic loci involved in its improvement. Nature Communications, 2019, 10, 1154.	5.8	249
21	Plant Polyploidy: Origin, Evolution, and Its Influence on Crop Domestication. Horticultural Plant Journal, 2019, 5, 231-239.	2.3	85
22	Gene retention, fractionation and subgenome differences in polyploid plants. Nature Plants, 2018, 4, 258-268.	4.7	257
23	A naturally occurring variation in the BrMAM-3 gene is associated with aliphatic glucosinolate accumulation in <i>Brassica rapa</i> leaves. Horticulture Research, 2018, 5, 69.	2.9	16
24	Reply to: "Organization of the genome sequence of the polyploid crop species <i>Brassica juncea</i> "™. Nature Genetics, 2018, 50, 1497-1498.	9.4	4
25	Variability in eukaryotic initiation factor iso4E in <i>Brassica rapa</i> influences interactions with the viral protein linked to the genome of Turnip mosaic virus. Scientific Reports, 2018, 8, 13588.	1.6	20
26	Hotspots of Independent and Multiple Rounds of LTR-retrotransposon Bursts in <i>Brassica</i> Species. Horticultural Plant Journal, 2018, 4, 165-174.	2.3	13
27	BrFLC5: a weak regulator of flowering time in <i>Brassica rapa</i> . Theoretical and Applied Genetics, 2018, 131, 2107-2116.	1.8	37
28	Improved <i>Brassica rapa</i> reference genome by single-molecule sequencing and chromosome conformation capture technologies. Horticulture Research, 2018, 5, 50.	2.9	224
29	Genome sequencing supports a multi-vertex model for Brassicaceae species. Current Opinion in Plant Biology, 2017, 36, 79-87.	3.5	45
30	Map-based cloning of the dominant genic male sterile Ms-cd1 gene in cabbage (<i>Brassica oleracea</i>). Theoretical and Applied Genetics, 2017, 130, 71-79.	1.8	26
31	<i>Brassica rapa</i> Genome 2.0: A Reference Upgrade through Sequence Re-assembly and Gene Re-annotation. Molecular Plant, 2017, 10, 649-651.	3.9	69
32	Enriching Glucoraphanin in <i>Brassica rapa</i> Through Replacement of BrAOP2.2/BrAOP2.3 with Non-functional Genes. Frontiers in Plant Science, 2017, 8, 1329.	1.7	13
33	Transcriptome Profiling of Resistance to <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> in Cabbage (<i>Brassica</i>) Tj ETQq1 1 0.784314 ggBT /Over 1.1 38	1.1	38
34	Genetic Variation and Divergence of Genes Involved in Leaf Adaxial-Abaxial Polarity Establishment in <i>Brassica rapa</i> . Frontiers in Plant Science, 2016, 7, 94.	1.7	28
35	Epigenetic regulation of subgenome dominance following whole genome triplication in <i>Brassica rapa</i> . New Phytologist, 2016, 211, 288-299.	3.5	100
36	A High Density Linkage Map Facilitates QTL Mapping of Flowering Time in <i>Brassica rapa</i> . Horticultural Plant Journal, 2016, 2, 217-223.	2.3	13

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37	Pooled mapping: an efficient method of calling variations for population samples with low-depth resequencing data. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	13
38	The genome sequence of allopolyploid <i>Brassica juncea</i> and analysis of differential homoeolog gene expression influencing selection. <i>Nature Genetics</i> , 2016, 48, 1225-1232.	9.4	479
39	Evolution of TWIN SISTER of FT (TSF) Genes in Brassicaceae. <i>Horticultural Plant Journal</i> , 2016, 2, 16-25.	2.3	4
40	Subgenome parallel selection is associated with morphotype diversification and convergent crop domestication in <i>Brassica rapa</i> and <i>Brassica oleracea</i> . <i>Nature Genetics</i> , 2016, 48, 1218-1224.	9.4	297
41	Mapping and expression profiling reveal an inserted fragment from purple mustard involved anthocyanin accumulation in Chinese cabbage. <i>Euphytica</i> , 2016, 212, 83-95.	0.6	10
42	User Guidelines for the Brassica Database: BRAD. <i>Methods in Molecular Biology</i> , 2016, 1374, 215-231.	0.4	0
43	Brassica database (BRAD) version 2.0: integrating and mining Brassicaceae species genomic resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav093.	1.4	58
44	Three genes encoding AOP2, a protein involved in aliphatic glucosinolate biosynthesis, are differentially expressed in <i>Brassica rapa</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 6205-6218.	2.4	29
45	A transposon insertion in FLOWERING LOCUS T is associated with delayed flowering in <i>Brassica rapa</i> . <i>Plant Science</i> , 2015, 241, 211-220.	1.7	55
46	Carotenoid identification and molecular analysis of carotenoid isomerase-encoding BrCRTISO, the candidate gene for inner leaf orange coloration in Chinese cabbage. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	11
47	Anthocyanin profile characterization and quantitative trait locus mapping in zicaitai (<i>Brassica rapa</i> L.) Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	93
48	Identification of tapetum-specific genes by comparing global gene expression of four different male sterile lines in <i>Brassica oleracea</i> . <i>Plant Molecular Biology</i> , 2015, 87, 541-554.	2.0	25
49	Carotenoid biosynthetic genes in <i>Brassica rapa</i> : comparative genomic analysis, phylogenetic analysis, and expression profiling. <i>BMC Genomics</i> , 2015, 16, 492.	1.2	23
50	Morphology, Carbohydrate Composition and Vernalization Response in a Genetically Diverse Collection of Asian and European Turnips (<i>Brassica rapa</i> subsp. <i>rapa</i>). <i>PLoS ONE</i> , 2014, 9, e114241.	1.1	23
51	Origin, inheritance, and gene regulatory consequences of genome dominance in polyploids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5283-5288.	3.3	172
52	Multiple copies of eukaryotic translation initiation factors in <i>Brassica rapa</i> facilitate redundancy, enabling diversification through variation in splicing and broad-spectrum virus resistance. <i>Plant Journal</i> , 2014, 77, 261-268.	2.8	38
53	Anthocyanin biosynthetic genes in <i>Brassica rapa</i> . <i>BMC Genomics</i> , 2014, 15, 426.	1.2	112
54	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089

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55	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	5.8	918
56	Genome triplication drove the diversification of Brassica plants. Horticulture Research, 2014, 1, 14024.	2.9	288
57	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. Nature Genetics, 2013, 45, 891-898.	9.4	350
58	Comprehensive analysis of RNA-seq data reveals the complexity of the transcriptome in Brassica rapa. BMC Genomics, 2013, 14, 689.	1.2	172
59	Bolbase: a comprehensive genomics database for Brassica oleracea. BMC Genomics, 2013, 14, 664.	1.2	99
60	Mapping and candidate-gene screening of the novel Turnip mosaic virus resistance gene retr02 in Chinese cabbage (Brassica rapa L.). Theoretical and Applied Genetics, 2013, 126, 179-188.	1.8	47
61	Development of InDel markers for Brassica rapa based on whole-genome re-sequencing. Theoretical and Applied Genetics, 2013, 126, 231-239.	1.8	103
62	Deciphering the Diploid Ancestral Genome of the Mesoheptaploid Brassica rapa. Plant Cell, 2013, 25, 1541-1554.	3.1	309
63	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. Frontiers in Plant Science, 2012, 3, 94.	1.7	73
64	Syntenic gene analysis between Brassica rapa and other Brassicaceae species. Frontiers in Plant Science, 2012, 3, 198.	1.7	176
65	The Impact of Genome Triplication on Tandem Gene Evolution in Brassica rapa. Frontiers in Plant Science, 2012, 3, 261.	1.7	34
66	A naturally occurring InDel variation in BraA.FLC.b (BrFLC2) associated with flowering time variation in Brassica rapa. BMC Plant Biology, 2012, 12, 151.	1.6	84
67	Biased Gene Fractionation and Dominant Gene Expression among the Subgenomes of Brassica rapa. PLoS ONE, 2012, 7, e36442.	1.1	240
68	Altered Patterns of Fractionation and Exon Deletions in Brassica rapa Support a Two-Step Model of Paleohexaploidy. Genetics, 2012, 190, 1563-1574.	1.2	163
69	Glucosinolate biosynthetic genes in Brassica rapa. Gene, 2011, 487, 135-142.	1.0	134
70	BRAD, the genetics and genomics database for Brassica plants. BMC Plant Biology, 2011, 11, 136.	1.6	435
71	Dissecting the genome of the polyploid crop oilseed rape by transcriptome sequencing. Nature Biotechnology, 2011, 29, 762-766.	9.4	187
72	The genome of the mesopolyploid crop species Brassica rapa. Nature Genetics, 2011, 43, 1035-1039.	9.4	1,893

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73	Fine mapping of a male sterility gene MS-cd1 in Brassica oleracea. Theoretical and Applied Genetics, 2011, 123, 231-238.	1.8	9
74	A sequence-based genetic linkage map as a reference for Brassica rapa pseudochromosome assembly. BMC Genomics, 2011, 12, 239.	1.2	67
75	Global analysis of gene expression in flower buds of Ms-cd1 Brassica oleracea conferring male sterility by using an Arabidopsis microarray. Plant Molecular Biology, 2008, 66, 177-192.	2.0	36
76	Quantitative trait loci for flowering time and morphological traits in multiple populations of Brassica rapa. Journal of Experimental Botany, 2007, 58, 4005-4016.	2.4	142
77	Transcript profiling of a dominant male sterile mutant (Ms-cd1) in cabbage during flower bud development. Plant Science, 2007, 172, 111-119.	1.7	35
78	Genetic relationships within Brassica rapa as inferred from AFLP fingerprints. Theoretical and Applied Genetics, 2005, 110, 1301-1314.	1.8	199
79	Linkage mapping of a dominant male sterility gene Ms-cd1 in Brassica oleracea. Genome, 2005, 48, 848-854.	0.9	21
80	Title is missing!. Euphytica, 2000, 112, 267-273.	0.6	14
81	Title is missing!. Euphytica, 1997, 97, 265-268.	0.6	37