

Jun Zou

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,677
citations

236925

25
h-index

302126

39
g-index

51
all docs

51
docs citations

51
times ranked

1532
citing authors

#	ARTICLE	IF	CITATIONS
1	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. <i>Plant Biotechnology Journal</i> , 2017, 15, 1602-1610.	8.3	150
2	Broadening the avenue of intersubgenomic heterosis in oilseed Brassica. <i>Theoretical and Applied Genetics</i> , 2010, 120, 283-290.	3.6	78
3	<i>De novo</i> genetic variation associated with retrotransposon activation, genomic rearrangements and trait variation in a recombinant inbred line population of <i>Brassica napus</i> derived from interspecific hybridization with <i>Brassica rapa</i> . <i>Plant Journal</i> , 2011, 68, 212-224.	5.7	78
4	Incorporating pleiotropic quantitative trait loci in dissection of complex traits: seed yield in rapeseed as an example. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1569-1585.	3.6	78
5	A Dynamic and Complex Network Regulates the Heterosis of Yield-Related Traits in Rapeseed (<i>Brassica napus</i> L.). <i>PLoS ONE</i> , 2011, 6, e21645.	2.5	72
6	Synthesis of a Brassica trigeneric allohexaploid (<i>B. carinata</i> × <i>B. rapa</i>) de novo and its stability in subsequent generations. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1431-1440.	3.6	70
7	Association mapping of seed oil content in Brassica napus and comparison with quantitative trait loci identified from linkage mapping This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 908-916.	2.0	70
8	QTLs associated with agronomic traits in the Attila CDC Go spring wheat population evaluated under conventional management. <i>PLoS ONE</i> , 2017, 12, e0171528.	2.5	68
9	A consensus map of rapeseed (<i>Brassica napus</i> L.) based on diversity array technology markers: applications in genetic dissection of qualitative and quantitative traits. <i>BMC Genomics</i> , 2013, 14, 277.	2.8	62
10	QTL meta-analysis of root traits in Brassica napus under contrasting phosphorus supply in two growth systems. <i>Scientific Reports</i> , 2016, 6, 33113.	3.3	55
11	Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. <i>Plant Biotechnology Journal</i> , 2019, 17, 1998-2010.	8.3	54
12	Identification and characterization of improved nitrogen efficiency in interspecific hybridized new-type Brassica napus. <i>Annals of Botany</i> , 2014, 114, 549-559.	2.9	52
13	Identification, evolution, and expression partitioning of miRNAs in allopolyploid <i>Brassica napus</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 7241-7253.	4.8	44
14	G-lignin and hemicellulosic monosaccharides distinctively affect biomass digestibility in rapeseed. <i>Bioresource Technology</i> , 2016, 203, 325-333.	9.6	43
15	Development of a population for substantial new type Brassica napus diversified at both A/C genomes. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1141-1150.	3.6	40
16	Genetic changes in a novel breeding population of <i>Brassica napus</i> synthesized from hundreds of crosses between <i>B. rapa</i> and <i>B. carinata</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 507-519.	8.3	39
17	Tracing the Transcriptomic Changes in Synthetic Trigeneric allohexaploids of Brassica Using an RNA-Seq Approach. <i>PLoS ONE</i> , 2013, 8, e68883.	2.5	39
18	Whole-transcriptome analysis reveals genetic factors underlying flowering time regulation in rapeseed (<i>Brassica napus</i> L.). <i>Plant, Cell and Environment</i> , 2018, 41, 1935-1947.	5.7	34

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19	Exploring the gene pool of <i>Brassica napus</i> by genomics-based approaches. <i>Plant Biotechnology Journal</i> , 2021, 19, 1693-1712.	8.3	34
20	A genetic linkage map of <i>Brassica carinata</i> constructed with a doubled haploid population. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1113-1124.	3.6	33
21	Co-linearity and divergence of the A subgenome of <i>Brassica juncea</i> compared with other <i>Brassica</i> species carrying different A subgenomes. <i>BMC Genomics</i> , 2016, 17, 18.	2.8	32
22	Genome structural evolution in <i>Brassica</i> crops. <i>Nature Plants</i> , 2021, 7, 757-765.	9.3	31
23	Mapping QTLs Controlling Agronomic Traits in the "Attila" – "CDC Go" Spring Wheat Population under Organic Management using 90K SNP Array. <i>Crop Science</i> , 2017, 57, 365-377.	1.8	30
24	Seed Quality Traits Can Be Predicted with High Accuracy in <i>Brassica napus</i> Using Genomic Data. <i>PLoS ONE</i> , 2016, 11, e0166624.	2.5	29
25	Gene expression profiles associated with intersubgenomic heterosis in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2008, 117, 1031-1040.	3.6	28
26	Constructing a dense genetic linkage map and mapping QTL for the traits of flower development in <i>Brassica carinata</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 1593-1605.	3.6	28
27	Introgressing Subgenome Components from <i>Brassica rapa</i> and <i>B. carinata</i> to <i>B. juncea</i> for Broadening Its Genetic Base and Exploring Intersubgenomic Heterosis. <i>Frontiers in Plant Science</i> , 2016, 7, 1677.	3.6	28
28	Characterization and expression patterns of small RNAs in synthesized <i>Brassica</i> hexaploids. <i>Plant Molecular Biology</i> , 2014, 85, 287-299.	3.9	23
29	Investigation of the Genetic Diversity and Quantitative Trait Loci Accounting for Important Agronomic and Seed Quality Traits in <i>Brassica carinata</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 615.	3.6	23
30	Physical mapping of QTL associated with agronomic and end-use quality traits in spring wheat under conventional and organic management systems. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3699-3719.	3.6	23
31	Mapping of QTLs associated with resistance to common bunt, tan spot, leaf rust, and stripe rust in a spring wheat population. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	21
32	Integrative analysis of genome-wide lncRNA and mRNA expression in newly synthesized <i>Brassica</i> hexaploids. <i>Ecology and Evolution</i> , 2018, 8, 6034-6052.	1.9	20
33	Reconstituting the genome of a young allopolyploid crop, <i>Brassica napus</i> , with its related species. <i>Plant Biotechnology Journal</i> , 2019, 17, 1106-1118.	8.3	18
34	Genetic dissection of intersubgenomic heterosis in <i>Brassica napus</i> carrying genomic components of <i>B. rapa</i> . <i>Euphytica</i> , 2012, 184, 151-164.	1.2	17
35	Comparative proteomic study on <i>Brassica</i> hexaploid and its parents provides new insights into the effects of polyploidization. <i>Journal of Proteomics</i> , 2015, 112, 274-284.	2.4	16
36	Breeding histories and selection criteria for oilseed rape in Europe and China identified by genome wide pedigree dissection. <i>Scientific Reports</i> , 2017, 7, 1916.	3.3	16

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37	Hybrid Performance of an Immortalized F2 Rapeseed Population Is Driven by Additive, Dominance, and Epistatic Effects. <i>Frontiers in Plant Science</i> , 2017, 8, 815.	3.6	16
38	Challenges and prospects for a potential allohexaploid Brassica crop. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2711-2726.	3.6	15
39	Physical Mapping of QTL in Four Spring Wheat Populations under Conventional and Organic Management Systems. I. Earliness. <i>Plants</i> , 2021, 10, 853.	3.5	13
40	AtMIF1 increases seed oil content by attenuating GL2 inhibition. <i>New Phytologist</i> , 2021, 229, 2152-2162.	7.3	10
41	Allele segregation analysis of F1 hybrids between independent Brassica allohexaploid lineages. <i>Chromosoma</i> , 2022, 131, 147-161.	2.2	10
42	Widespread and evolutionary analysis of a MITE family Monkey King in Brassicaceae. <i>BMC Plant Biology</i> , 2015, 15, 149.	3.6	9
43	Genetic dissection of the shoot and root ionomes of Brassica napus grown with contrasting phosphate supplies. <i>Annals of Botany</i> , 2020, 126, 119-140.	2.9	8
44	Characterization and expression profiles of miRNAs in the triploid hybrids of Brassica napus and Brassica rapa. <i>BMC Genomics</i> , 2019, 20, 649.	2.8	7
45	Genome-wide prediction for hybrids between parents with distinguished difference on exotic introgressions in Brassica napus. <i>Crop Journal</i> , 2021, 9, 1169-1178.	5.2	6
46	A Two-Stage Method for Improving the Prediction Accuracy of Complex Traits by Incorporating Genotype by Environment Interactions in Brassica napus. <i>Discrete Dynamics in Nature and Society</i> , 2020, 1-12.	0.9	1
47	Comparative transcriptome and iTRAQ-based proteome analysis in mature leaves of Brassica carinata provides insights into the purple leaf color diversity. <i>Journal of Horticultural Science and Biotechnology</i> , 2021, 96, 444-455.	1.9	1