

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 | Allele segregation analysis of F1 hybrids between independent Brassica allohexaploid lineages. <i>Chromosoma</i> , 2022, 131, 147-161. | 2.2 | 10 |
| 2 | AtMIF1 increases seed oil content by attenuating GL2 inhibition. <i>New Phytologist</i> , 2021, 229, 2152-2162. | 7.3 | 10 |
| 3 | 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 |
| 4 | Genome structural evolution in Brassica crops. <i>Nature Plants</i> , 2021, 7, 757-765. | 9.3 | 31 |
| 5 | Challenges and prospects for a potential allohexaploid Brassica crop. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2711-2726. | 3.6 | 15 |
| 6 | 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 |
| 7 | 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 |
| 8 | Genome-wide prediction for hybrids between parents with distinguished difference on exotic introgressions in <i>Brassica napus</i> . <i>Crop Journal</i> , 2021, 9, 1169-1178. | 5.2 | 6 |
| 9 | Comparative transcriptome and iTRAQ-based proteome analysis in mature leaves of <i>Brassica carinata</i> provides insights into the purple leaf color diversity. <i>Journal of Horticultural Science and Biotechnology</i> , 2021, 96, 444-455. | 1.9 | 1 |
| 10 | A Two-Stage Method for Improving the Prediction Accuracy of Complex Traits by Incorporating Genotype by Environment Interactions in <i>Brassica napus</i> . <i>Discrete Dynamics in Nature and Society</i> , 2020, 1-12. | 0.9 | 1 |
| 11 | Genetic dissection of the shoot and root ionomes of <i>Brassica napus</i> grown with contrasting phosphate supplies. <i>Annals of Botany</i> , 2020, 126, 119-140. | 2.9 | 8 |
| 12 | Characterization and expression profiles of miRNAs in the triploid hybrids of <i>Brassica napus</i> and <i>Brassica rapa</i> . <i>BMC Genomics</i> , 2019, 20, 649. | 2.8 | 7 |
| 13 | Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. <i>Plant Biotechnology Journal</i> , 2019, 17, 1998-2010. | 8.3 | 54 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

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|----|---|-----|-----------|
| 19 | Assembly and comparison of two closely related <i>Brassica napus</i> genomes. <i>Plant Biotechnology Journal</i> , 2017, 15, 1602-1610. | 8.3 | 150 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | QTL meta-analysis of root traits in <i>Brassica napus</i> under contrasting phosphorus supply in two growth systems. <i>Scientific Reports</i> , 2016, 6, 33113. | 3.3 | 55 |
| 28 | 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 |
| 29 | G-lignin and hemicellulosic monosaccharides distinctively affect biomass digestibility in rapeseed. <i>Bioresource Technology</i> , 2016, 203, 325-333. | 9.6 | 43 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | Widespread and evolutionary analysis of a MITE family Monkey King in Brassicaceae. <i>BMC Plant Biology</i> , 2015, 15, 149. | 3.6 | 9 |
| 34 | Identification and characterization of improved nitrogen efficiency in interspecific hybridized new-type <i>Brassica napus</i> . <i>Annals of Botany</i> , 2014, 114, 549-559. | 2.9 | 52 |
| 35 | 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 |
| 36 | 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 |

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|----|--|-----|-----------|
| 37 | 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 |
| 38 | Tracing the Transcriptomic Changes in Synthetic Trigenomic allohexaploids of Brassica Using an RNA-Seq Approach. <i>PLoS ONE</i> , 2013, 8, e68883. | 2.5 | 39 |
| 39 | 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 |
| 40 | 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 |
| 41 | <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 |
| 42 | 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 |
| 43 | Broadening the avenue of intersubgenomic heterosis in oilseed Brassica. <i>Theoretical and Applied Genetics</i> , 2010, 120, 283-290. | 3.6 | 78 |
| 44 | Development of a population for substantial new type <i>Brassica napus</i> diversified at both A/C genomes. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1141-1150. | 3.6 | 40 |
| 45 | Synthesis of a <i>Brassica</i> trigenomic 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 |
| 46 | Association mapping of seed oil content in <i>Brassica napus</i> 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 |
| 47 | 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 |