

Chuchuan Fan

List of Publications by Year in descending order

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35
papers

3,856
citations

304743
22
h-index

361022
35
g-index

36
all docs

36
docs citations

36
times ranked

3002
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of mutants with varying flowering times by targeted editing of multiple SVP gene copies in <i>Brassica napus</i> L.. <i>Crop Journal</i> , 2022, 10, 67-74.	5.2	15
2	Site-Directed Mutagenesis of the Carotenoid Isomerase Gene <i>BnaCRTISO</i> Alters the Color of Petals and Leaves in <i>Brassica napus</i> L.. <i>Frontiers in Plant Science</i> , 2022, 13, 801456.	3.6	11
3	Targeted mutagenesis of <i>EOD3</i> gene in <i>Brassica napus</i> L. regulates seed production. <i>Journal of Cellular Physiology</i> , 2021, 236, 1996-2007.	4.1	30
4	Comprehensive study and multipurpose role of the <i>CLV3/ESR</i> -related (<i>CLE</i>) genes family in plant growth and development. <i>Journal of Cellular Physiology</i> , 2021, 236, 2298-2317.	4.1	2
5	Fine mapping and candidate gene analysis of a major locus controlling ovule abortion and seed number per silique in <i>Brassica napus</i> L.. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2517-2530.	3.6	12
6	QTL Mapping and Candidate Gene Identification of Swollen Root Formation in Turnip. <i>International Journal of Molecular Sciences</i> , 2021, 22, 653.	4.1	10
7	Advances and Challenges for QTL Analysis and GWAS in the Plant-Breeding of High-Yielding: A Focus on Rapeseed. <i>Biomolecules</i> , 2021, 11, 1516.	4.0	19
8	Targeted mutagenesis of <i>BnTT8</i> homologs controls yellow seed coat development for effective oil production in <i>Brassica napus</i> L.. <i>Plant Biotechnology Journal</i> , 2020, 18, 1153-1168.	8.3	128
9	Precision Genome Engineering Through Cytidine Base Editing in Rapeseed (<i>Brassica napus</i> L.). <i>Frontiers in Genome Editing</i> , 2020, 2, 605768.	5.2	5
10	<i>BnA10.RCO</i> , a homeobox gene, positively regulates leaf lobe formation in <i>Brassica napus</i> L.. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3333-3343.	3.6	12
11	Identification and comprehensive analysis of the <i>CLV3</i> / <i>ESR</i> -related (<i>CLE</i>) gene family in <i>Brassica napus</i> L.. <i>Plant Biology</i> , 2020, 22, 709-721.	3.8	9
12	Identification of QTLs Containing Resistance Genes for Sclerotinia Stem Rot in <i>Brassica napus</i> Using Comparative Transcriptomic Studies. <i>Frontiers in Plant Science</i> , 2020, 11, 776.	3.6	34
13	Modifications of fatty acid profile through targeted mutation at <i>BnaFAD2</i> gene with CRISPR/Cas9-mediated gene editing in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 2401-2411.	3.6	80
14	Genome-wide association studies in the genetic dissection of ovule number, seed number, and seed weight in <i>Brassica napus</i> L.. <i>Industrial Crops and Products</i> , 2019, 142, 111877.	5.2	32
15	A novel quantitative trait locus on chromosome A9 controlling oleic acid content in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2019, 17, 2313-2324.	8.3	34
16	Comparative Transcriptome Analysis of Developing Seeds and Silique Wall Reveals Dynamic Transcription Networks for Effective Oil Production in <i>Brassica napus</i> L.. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1982.	4.1	45
17	CRISPR/Cas9-mediated genome editing reveals differences in the contribution of <i>INDEHISCENT</i> homologues to pod shatter resistance in <i>Brassica napus</i> L.. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2111-2123.	3.6	55
18	Precise editing of <i>CLAVATA</i> genes in <i>Brassica napus</i> L. regulates multilocular silique development. <i>Plant Biotechnology Journal</i> , 2018, 16, 1322-1335.	8.3	133

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19	Induced mutation and epigenetics modification in plants for crop improvement by targeting CRISPR/Cas9 technology. <i>Journal of Cellular Physiology</i> , 2018, 233, 4578-4594.	4.1	19
20	Promoter variations in a homeobox gene, BnA10.LMI1, determine lobed leaves in rapeseed (<i>Brassica</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	3.6	38
21	Genetic dissection of plant architecture and yield-related traits in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2016, 6, 21625.	3.3	81
22	Comparative transcriptomic analysis uncovers the complex genetic network for resistance to <i>Sclerotinia sclerotiorum</i> in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2016, 6, 19007.	3.3	126
23	A genome-wide association study reveals novel elite allelic variations in seed oil content of <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2016, 129, 1203-1215.	3.6	185
24	Transcriptomic basis of functional difference and coordination between seeds and the silique wall of <i>Brassica napus</i> during the seed-filling stage. <i>Plant Science</i> , 2015, 233, 186-199.	3.6	9
25	A bi-filtering method for processing single nucleotide polymorphism array data improves the quality of genetic map and accuracy of quantitative trait locus mapping in doubled haploid populations of polyploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2015, 16, 409.	2.8	27
26	A Complex Recombination Pattern in the Genome of Allotetraploid <i>Brassica napus</i> as Revealed by a High-Density Genetic Map. <i>PLoS ONE</i> , 2014, 9, e109910.	2.5	41
27	Patatin-related phospholipase pPLAIII ¹ influences auxin-responsive cell morphology and organ size in <i>Arabidopsis</i> and <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2014, 14, 332.	3.6	22
28	A Novel Single-Nucleotide Mutation in a CLAVATA3 Gene Homolog Controls a Multilocular Silique Trait in <i>Brassica rapa</i> L.. <i>Molecular Plant</i> , 2014, 7, 1788-1792.	8.3	51
29	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
30	Cytological Basis and Molecular Mechanism of Variation in Number of Seeds Per Pod in <i>Brassica napus</i> . <i>Scientia Sinica Vitae</i> , 2014, 44, 822-831.	0.3	6
31	Identification of Heat Responsive Genes in <i>Brassica napus</i> Siliques at the Seed-Filling Stage through Transcriptional Profiling. <i>PLoS ONE</i> , 2014, 9, e101914.	2.5	49
32	Identification of QTLs for Resistance to <i>Sclerotinia</i> Stem Rot and BnaC.IGMT5.a as a Candidate Gene of the Major Resistant QTL SRC6 in <i>Brassica napus</i> . <i>PLoS ONE</i> , 2013, 8, e67740.	2.5	140
33	Identification of FAD2 and FAD3 genes in <i>Brassica napus</i> genome and development of allele-specific markers for high oleic and low linolenic acid contents. <i>Theoretical and Applied Genetics</i> , 2012, 125, 715-729.	3.6	154
34	Identification of candidate genes of QTLs for seed weight in <i>Brassica napus</i> through comparative mapping among <i>Arabidopsis</i> and <i>Brassica</i> species. <i>BMC Genetics</i> , 2012, 13, 105.	2.7	54
35	Mapping of quantitative trait loci and development of allele-specific markers for seed weight in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2010, 121, 1289-1301.	3.6	99