Chuchuan Fan

List of Publications by Year
in descending order

35 papers	3,856 citations	304602 22 h-index	360920 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 Brassica napus L.. Crop Journal, 2022, 10, 67-74.	2.3	15
2	Site-Directed Mutagenesis of the Carotenoid Isomerase Gene BnaCRTISO Alters the Color of Petals and Leaves in Brassica napus L.. Frontiers in Plant Science, 2022, 13, 801456.	1.7	11
3	Targeted mutagenesis of EOD3 gene in Brassica napus L. regulates seed production. Journal of Cellular Physiology, 2021, 236, 1996-2007.	2.0	30
4	Comprehensive study and multipurpose role of the CLV3/ESR â€•related (CLE) genes family in plant growth and development. Journal of Cellular Physiology, 2021, 236, 2298-2317.	2.0	2
5	Fine mapping and candidate gene analysis of a major locus controlling ovule abortion and seed number per silique in Brassica napus L.. Theoretical and Applied Genetics, 2021, 134, 2517-2530.	1.8	12
6	QTL Mapping and Candidate Gene Identification of Swollen Root Formation in Turnip. International Journal of Molecular Sciences, 2021, 22, 653.	1.8	10
7	Advances and Challenges for QTL Analysis and GWAS in the Plant-Breeding of High-Yielding: A Focus on Rapeseed. Biomolecules, 2021, 11, 1516.	1.8	19
8	Targeted mutagenesis of BnTT8 homologs controls yellow seed coat development for effective oil production in Brassica napus L.. Plant Biotechnology Journal, 2020, 18, 1153-1168.	4.1	128
9	Precision Genome Engineering Through Cytidine Base Editing in Rapeseed (Brassica napus. L). Frontiers in Genome Editing, 2020, 2, 605768.	2.7	5
10	BnA10.RCO, a homeobox gene, positively regulates leaf lobe formation in Brassica napus L.. Theoretical and Applied Genetics, 2020, 133, 3333-3343.	1.8	12
11	Identification and comprehensive analysis of the CLV3 / ESRâ€•related (CLE) gene family in Brassica napus L.. Plant Biology, 2020, 22, 709-721.	1.8	9
12	Identification of QTLs Containing Resistance Genes for Sclerotinia Stem Rot in Brassica napus Using Comparative Transcriptomic Studies. Frontiers in Plant Science, 2020, 11, 776.	1.7	34
13	Modifications of fatty acid profile through targeted mutation at BnaFAD2 gene with CRISPR/Cas9-mediated gene editing in Brassica napus. Theoretical and Applied Genetics, 2020, 133, 2401-2411.	1.8	80
14	Genome-wide association studies in the genetic dissection of ovule number, seed number, and seed weight in Brassica napus L.. Industrial Crops and Products, 2019, 142, 111877.	2.5	32
15	A novel quantitative trait locus on chromosome A9 controlling oleic acid content in Brassica napus. Plant Biotechnology Journal, 2019, 17, 2313-2324.	4.1	34
16	Comparative Transcriptome Analysis of Developing Seeds and Silique Wall Reveals Dynamic Transcription Networks for Effective Oil Production in Brassica napus L.. International Journal of Molecular Sciences, 2019, 20, 1982.	1.8	45
17	CRISPR/Cas9-mediated genome editing reveals differences in the contribution of INDEHISCENT homologues to pod shatter resistance in Brassica napus L.. Theoretical and Applied Genetics, 2019, 132, 2111-2123.	1.8	55
18	Precise editing of <scp>CLAVATA</scp> genes in Brassica napus L. regulates multilocular silique development. Plant Biotechnology Journal, 2018, 16, 1322-1335.	4.1	133

#	Article	IF	Citations
19	Induced mutation and epigenetics modification in plants for crop improvement by targeting CRISPR/Cas9 technology. Journal of Cellular Physiology, 2018, 233, 4578-4594.	2.0	19
20	Promoter variations in a homeobox gene, BnA10.LMI1, determine lobed leaves in rapeseed (Brassica) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	38
21	Genetic dissection of plant architecture and yield-related traits in Brassica napus. Scientific Reports, 2016, 6, 21625.	1.6	81
22	Comparative transcriptomic analysis uncovers the complex genetic network for resistance to Sclerotinia sclerotiorum in Brassica napus. Scientific Reports, 2016, 6, 19007.	1.6	126
23	A genome-wide association study reveals novel elite allelic variations in seed oil content of Brassica napus. Theoretical and Applied Genetics, 2016, 129, 1203-1215.	1.8	185
24	Transcriptomic basis of functional difference and coordination between seeds and the silique wall of Brassica napus during the seed-filling stage. Plant Science, 2015, 233, 186-199.	1.7	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 Brassica napus. BMC Genomics, 2015, 16, 409.	1.2	27
26	A Complex Recombination Pattern in the Genome of Allotetraploid Brassica napus as Revealed by a High-Density Genetic Map. PLoS ONE, 2014, 9, e109910.	1.1	41
27	Patatin-related phospholipase pPLAIIIÎ´ influences auxin-responsive cell morphology and organ size in Arabidopsis and Brassica napus. BMC Plant Biology, 2014, 14, 332.	1.6	22
28	A Novel Single-Nucleotide Mutation in a CLAVATA3 Gene Homolog Controls a Multilocular Silique Trait in Brassica rapa L.. Molecular Plant, 2014, 7, 1788-1792.	3.9	51
29	Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. Science, 2014, 345, 950-953.	6.0	2,089
30	Cytological Basis and Molecular Mechanism of Variation in Number of Seeds Per Pod in <italic>Brassica napus</italic>. Scientia Sinica Vitae, 2014, 44, 822-831.	0.1	6
31	Identification of Heat Responsive Genes in Brassica napus Siliques at the Seed-Filling Stage through Transcriptional Profiling. PLoS ONE, 2014, 9, e101914.	1.1	49
32	Identification of QTLs for Resistance to Sclerotinia Stem Rot and BnaC.IGMT5.a as a Candidate Gene of the Major Resistant QTL SRC6 in Brassica napus. PLoS ONE, 2013, 8, e67740.	1.1	140
33	Identification of FAD2 and FAD3 genes in Brassica napus genome and development of allele-specific markers for high oleic and low linolenic acid contents. Theoretical and Applied Genetics, 2012, 125, 715-729.	1.8	154
34	Identification of candidate genes of QTLs for seed weight in Brassica napus through comparative mapping among Arabidopsis and Brassica species. BMC Genetics, 2012, 13, 105.	2.7	54
35	Mapping of quantitative trait loci and development of allele-specific markers for seed weight in Brassica napus. Theoretical and Applied Genetics, 2010, 121, 1289-1301.	1.8	99