

# Chuchuan Fan

## List of Publications by Year in descending order

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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	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
2	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.	1.8	185
3	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.	1.8	154
4	Identification of QTLs for Resistance to Sclerotinia 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.	1.1	140
5	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.	4.1	133
6	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.	4.1	128
7	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.	1.6	126
8	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.	1.8	99
9	Genetic dissection of plant architecture and yield-related traits in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2016, 6, 21625.	1.6	81
10	Modifications of fatty acid profile through targeted mutation at BnaFAD2 gene with CRISPR/Cas9-mediated gene editing in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 2401-2411.	1.8	80
11	CRISPR/Cas9-mediated genome editing reveals differences in the contribution of INDEHISCENT homologues to pod shatter resistance in <i>Brassica napus</i> L.. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2111-2123.	1.8	55
12	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
13	A Novel Single-Nucleotide Mutation in a <i>CLAVATA3</i> Gene Homolog Controls a Multilocular Silique Trait in <i>Brassica rapa</i> L.. <i>Molecular Plant</i> , 2014, 7, 1788-1792.	3.9	51
14	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.	1.1	49
15	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.	1.8	45
16	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.	1.1	41
17	Promoter variations in a homeobox gene, BnA10.LMI1, determine lobed leaves in rapeseed ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	38
18	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.	4.1	34

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19	Identification of QTLs Containing Resistance Genes for Sclerotinia Stem Rot in Brassica napus Using Comparative Transcriptomic Studies. <i>Frontiers in Plant Science</i> , 2020, 11, 776.	1.7	34
20	Genome-wide association studies in the genetic dissection of ovule number, seed number, and seed weight in Brassica napus L.. <i>Industrial Crops and Products</i> , 2019, 142, 111877.	2.5	32
21	Targeted mutagenesis of <i>EOD3</i> gene in Brassica napus L. regulates seed production. <i>Journal of Cellular Physiology</i> , 2021, 236, 1996-2007.	2.0	30
22	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. <i>BMC Genomics</i> , 2015, 16, 409.	1.2	27
23	Patatin-related phospholipase pPLAIII influences auxin-responsive cell morphology and organ size in Arabidopsis and Brassica napus. <i>BMC Plant Biology</i> , 2014, 14, 332.	1.6	22
24	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.	2.0	19
25	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.	1.8	19
26	Development of mutants with varying flowering times by targeted editing of multiple SVP gene copies in Brassica napus L.. <i>Crop Journal</i> , 2022, 10, 67-74.	2.3	15
27	BnA10.RCO, a homeobox gene, positively regulates leaf lobe formation in Brassica napus L.. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3333-3343.	1.8	12
28	Fine mapping and candidate gene analysis of a major locus controlling ovule abortion and seed number per silique in Brassica napus L.. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2517-2530.	1.8	12
29	Site-Directed Mutagenesis of the Carotenoid Isomerase Gene BnaCRTISO Alters the Color of Petals and Leaves in Brassica napus L.. <i>Frontiers in Plant Science</i> , 2022, 13, 801456.	1.7	11
30	QTL Mapping and Candidate Gene Identification of Swollen Root Formation in Turnip. <i>International Journal of Molecular Sciences</i> , 2021, 22, 653.	1.8	10
31	Transcriptomic basis of functional difference and coordination between seeds and the silique wall of Brassica napus during the seed-filling stage. <i>Plant Science</i> , 2015, 233, 186-199.	1.7	9
32	Identification and comprehensive analysis of the CLV3 / ESR-related (CLE) gene family in Brassica napus L.. <i>Plant Biology</i> , 2020, 22, 709-721.	1.8	9
33	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.	0.1	6
34	Precision Genome Engineering Through Cytidine Base Editing in Rapeseed (Brassica napus. L). <i>Frontiers in Genome Editing</i> , 2020, 2, 605768.	2.7	5
35	Comprehensive study and multipurpose role of the CLV3/ESR related (CLE) genes family in plant growth and development. <i>Journal of Cellular Physiology</i> , 2021, 236, 2298-2317.	2.0	2