

Ke-De Liu

List of Publications by Year in descending order

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48
papers

2,978
citations

186265
28
h-index

206112
48
g-index

50
all docs

50
docs citations

50
times ranked

2561
citing authors

#	ARTICLE	IF	CITATIONS
1	Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of <i>Brassica napus</i> . <i>Nature Plants</i> , 2020, 6, 34-45.	9.3	449
2	The high-quality genome of <i>Brassica napus</i> cultivar 'ZS11' reveals the introgression history in semi-winter morphotype. <i>Plant Journal</i> , 2017, 92, 452-468.	5.7	233
3	CRISPR/Cas9-mediated genome editing efficiently creates specific mutations at multiple loci using one sgRNA in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2017, 7, 7489.	3.3	164
4	Development and genetic mapping of microsatellite markers from genome survey sequences in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2009, 118, 1121-1131.	3.6	157
5	Disruption of a <i>CAROTENOID CLEAVAGE DIOXYGENASE 4</i> gene converts flower colour from white to yellow in <i>Brassica</i> species. <i>New Phytologist</i> , 2015, 206, 1513-1526.	7.3	155
6	Identification of a major QTL for silique length and seed weight in oilseed rape (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2012, 125, 285-296.	3.6	107
7	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
8	Dissection of the genetic architecture of three seed quality traits and consequences for breeding in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1336-1348.	8.3	91
9	An auxin signaling gene <i>BnaA3</i> . <i>IAA7</i> contributes to improved plant architecture and yield heterosis in rapeseed. <i>New Phytologist</i> , 2019, 222, 837-851.	7.3	80
10	Construction of an integrated genetic linkage map for the A genome of <i>Brassica napus</i> using SSR markers derived from sequenced BACs in <i>B. rapa</i> . <i>BMC Genomics</i> , 2010, 11, 594.	2.8	78
11	A <i>CACTA</i> -like transposable element in the upstream region of <i>BnaA9</i> . <i>CYP78A9</i> acts as an enhancer to increase silique length and seed weight in rapeseed. <i>Plant Journal</i> , 2019, 98, 524-539.	5.7	77
12	A missense mutation in the VHYNP motif of a DELLA protein causes a semi-dwarf mutant phenotype in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2010, 121, 249-258.	3.6	75
13	Development and genetic mapping of microsatellite markers from whole genome shotgun sequences in <i>Brassica oleracea</i> . <i>Molecular Breeding</i> , 2011, 28, 585-596.	2.1	73
14	<i>BnaC9.SMG7b</i> functions as a positive regulator of number of seeds per silique in rapeseed (<i>Brassica napus</i>). <i>Frontiers in Plant Science</i> , 2015, 6, 1040.	4.8	70
15	Detection and genotyping of restriction fragment associated polymorphisms in polyploid crops with a pseudo-reference sequence: a case study in allotetraploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2013, 14, 346.	2.8	69
16	Roles of the <i>Brassica napus</i> DELLA Protein <i>BnaA6.RGA</i> , in Modulating Drought Tolerance by Interacting With the ABA Signaling Component <i>BnaA10.ABF2</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 577.	3.6	66
17	Evaluation of Linkage Disequilibrium Pattern and Association Study on Seed Oil Content in <i>Brassica napus</i> Using ddRAD Sequencing. <i>PLoS ONE</i> , 2016, 11, e0146383.	2.5	63
18	<i>Brassica napus</i> DS-3, encoding a DELLA protein, negatively regulates stem elongation through gibberellin signaling pathway. <i>Theoretical and Applied Genetics</i> , 2017, 130, 727-741.	3.6	62

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19	A high-throughput stereo-imaging system for quantifying rape leaf traits during the seedling stage. <i>Plant Methods</i> , 2017, 13, 7.	4.3	59
20	Development and Validation of an Effective CRISPR/Cas9 Vector for Efficiently Isolating Positive Transformants and Transgene-Free Mutants in a Wide Range of Plant Species. <i>Frontiers in Plant Science</i> , 2018, 9, 1533.	3.6	52
21	BnPIR: <i>Brassica napus</i> pan-genome information resource for 1689 accessions. <i>Plant Biotechnology Journal</i> , 2021, 19, 412-414.	8.3	51
22	Identification and characterization of a new dwarf locus DS-4 encoding an Aux/IAA7 protein in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 1435-1449.	3.6	47
23	Long-read sequencing reveals widespread intragenic structural variants in a recent allopolyploid crop plant. <i>Plant Biotechnology Journal</i> , 2021, 19, 240-250.	8.3	45
24	Generation and mapping of SCAR and CAPS markers linked to the seed coat color gene in <i>Brassica napus</i> using a genome-walking technique. <i>Genome</i> , 2007, 50, 611-618.	2.0	44
25	Generation and characterization of tribenuron-methyl herbicide-resistant rapeseed (<i>Brassica napus</i>) for hybrid seed production using chemically induced male sterility. <i>Theoretical and Applied Genetics</i> , 2015, 128, 107-118.	3.6	41
26	Development of a core set of single-locus SSR markers for allotetraploid rapeseed (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 937-947.	3.6	40
27	Knock-out of TERMINAL FLOWER 1 genes altered flowering time and plant architecture in <i>Brassica napus</i> . <i>BMC Genetics</i> , 2020, 21, 52.	2.7	33
28	Genome-wide analysis of the auxin/indoleacetic acid (Aux/IAA) gene family in allotetraploid rapeseed (<i>Brassica napus</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 204.	3.6	32
29	Transposon insertions within alleles of BnaFLC.A10 and BnaFLC.A2 are associated with seasonal crop type in rapeseed. <i>Journal of Experimental Botany</i> , 2020, 71, 4729-4741.	4.8	32
30	An <i>Arabidopsis</i> mitochondria-localized RRL protein mediates abscisic acid signal transduction through mitochondrial retrograde regulation involving ABI4. <i>Journal of Experimental Botany</i> , 2015, 66, 6431-6445.	4.8	31
31	Genome structural evolution in Brassica crops. <i>Nature Plants</i> , 2021, 7, 757-765.	9.3	31
32	High-density ddRAD linkage and yield-related QTL mapping delimits a chromosomal region responsible for oil content in rapeseed (<i>Brassica napus</i> L.). <i>Breeding Science</i> , 2017, 67, 296-306.	1.9	29
33	Genetic Properties of a Nested Association Mapping Population Constructed With Semi-Winter and Spring Oilseed Rapes. <i>Frontiers in Plant Science</i> , 2018, 9, 1740.	3.6	29
34	High-throughput phenotyping accelerates the dissection of the dynamic genetic architecture of plant growth and yield improvement in rapeseed. <i>Plant Biotechnology Journal</i> , 2020, 18, 2345-2353.	8.3	29
35	Expression of a rice CYP81A6 gene confers tolerance to bentazon and sulfonylurea herbicides in both <i>Arabidopsis</i> and tobacco. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 109, 419-428.	2.3	25
36	Sequence variation and functional analysis of a FRIGIDA orthologue (BnaA3.FRI) in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2018, 18, 32.	3.6	24

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37	Development of INDELS markers in oilseed rape (<i>Brassica napus</i> L.) using re-sequencing data. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	20
38	Identification of a cytochrome P450 hydroxylase, CYP81A6, as the candidate for the bentazon and sulfonyleurea herbicide resistance gene, Bel, in rice. <i>Molecular Breeding</i> , 2006, 19, 59-68.	2.1	17
39	Abundance, marker development and genetic mapping of microsatellites from unigenes in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2012, 30, 731-744.	2.1	15
40	DELLA proteins BnaA6.RGA and BnaC7.RGA negatively regulate fatty acid biosynthesis by interacting with BnaLEC1s in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2021, 19, 2011-2026.	8.3	15
41	Genome-wide expression quantitative trait locus analysis in a recombinant inbred line population for trait dissection in peanut. <i>Plant Biotechnology Journal</i> , 2020, 18, 779-790.	8.3	14
42	Genetic mapping of quantitative trait loci and a major locus for resistance to grey leaf spot in maize. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2521-2533.	3.6	14
43	Identification of quantitative trait loci associated with oil content and development of near isogenic lines for stable qOC-A10 in <i>Brassica napus</i> L.. <i>Canadian Journal of Plant Science</i> , 2016, 96, 423-432.	0.9	8
44	Development of transgenic <i>Brassica napus</i> with an optimized <i>cry1C</i> * gene for resistance to diamondback moth (<i>Plutella xylostella</i>). <i>Canadian Journal of Plant Science</i> , 2014, 94, 1501-1506.	0.9	7
45	A lignified-layer bridge controlled by a single recessive gene is associated with high pod-shatter resistance in <i>Brassica napus</i> L.. <i>Crop Journal</i> , 2022, 10, 638-646.	5.2	6
46	AtRabD2b, a Functional Ortholog of the Yeast Ypt1, Controls Various Growth and Developmental Processes in <i>Arabidopsis</i> . <i>Plant Molecular Biology Reporter</i> , 2012, 30, 275-285.	1.8	5
47	A comprehensive and precise set of intervarietal substitution lines to identify candidate genes and quantitative trait loci in oilseed rape (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 2117-2129.	3.6	5
48	A Chromosome Level Genome Assembly of a Winter Turnip Rape (<i>Brassica rapa</i> L.) to Explore the Genetic Basis of Cold Tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4