Kaining Hu

List of Publications by Year
in descending order

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25 papers	774 citations	566801 15 h-index	580395 25 g-index
26 all docs	26 docs citations	26 times ranked	952 citing authors

#	Article	IF	Citations
1	Genome-wide association study reveals the genetic architecture of flowering time in rapeseed (Brassica napus L.). DNA Research, 2016, 23, dsv035.	1.5	154
2	Unravelling the complex trait of harvest index in rapeseed (Brassica napus L.) with association mapping. BMC Genomics, 2015, 16, 379.	1.2	91
3	Dynamic transcriptome analysis reveals AP2/ERF transcription factors responsible for cold stress in rapeseed (Brassica napusÂL.). Molecular Genetics and Genomics, 2016, 291, 1053-1067.	1.0	58
4	Genome-Wide Association Study Dissecting the Genetic Architecture Underlying the Branch Angle Trait in Rapeseed (Brassica napus L.). Scientific Reports, 2016, 6, 33673.	1.6	55
5	Transcriptomic Analysis of Seed Coats in Yellow-Seeded Brassica napus Reveals Novel Genes That Influence Proanthocyanidin Biosynthesis. Frontiers in Plant Science, 2017, 8, 1674.	1.7	55
6	Genome-Wide Association Study Provides Insight into the Genetic Control of Plant Height in Rapeseed (Brassica napus L.). Frontiers in Plant Science, 2016, 7, 1102.	1.7	49
7	Comparative Analysis of the Brassica napus Root and Leaf Transcript Profiling in Response to Drought Stress. International Journal of Molecular Sciences, 2015, 16, 18752-18777.	1.8	48
8	Trilocular phenotype in Brassica juncea L. resulted from interruption of CLAVATA1 gene homologue (BjMc1) transcription. Scientific Reports, 2017, 7, 3498.	1.6	35
9	Helitron distribution in Brassicaceae and whole Genome Helitron density as a character for distinguishing plant species. BMC Bioinformatics, 2019, 20, 354.	1.2	30
10	Altered Transcription and Neofunctionalization of Duplicated Genes Rescue the Harmful Effects of a Chimeric Gene in Brassica napus. Plant Cell, 2016, 28, 2060-2078.	3.1	28
11	Breeding signature of combining ability improvement revealed by a genomic variation map from recurrent selection population in Brassica napus. Scientific Reports, 2016, 6, 29553.	1.6	21
12	Mitochondrial genome and transcriptome analysis of five alloplasmic male-sterile lines in Brassica juncea. BMC Genomics, 2019, 20, 348.	1.2	20
13	QTL Mapping and Diurnal Transcriptome Analysis Identify Candidate Genes Regulating Brassica napus Flowering Time. International Journal of Molecular Sciences, 2021, 22, 7559.	1.8	18
14	Neofunctionalization of DuplicatedTic40Genes Caused a Gain-of-Function Variation Related to Male Fertility inBrassica oleraceaLineages Â Â. Plant Physiology, 2014, 166, 1403-1419.	2.3	17
15	Identification of different cytoplasms based on newly developed mitotype-specific markers for marker-assisted selection breeding in Brassica napus L.. Plant Cell Reports, 2017, 36, 901-909.	2.8	17
16	Overexpression of the Novel Arabidopsis Gene At5g02890 Alters Inflorescence Stem Wax Composition and Affects Phytohormone Homeostasis. Frontiers in Plant Science, 2017, 8, 68.	1.7	13
17	Transcriptome profiling reveals cytokinin promoted callus regeneration in Brassica juncea. Plant Cell, Tissue and Organ Culture, 2020, 141, 191-206.	1.2	13
18	Joint genome-wide association and transcriptome sequencing reveals a complex polygenic network underlying hypocotyl elongation in rapeseed (Brassica napus L.). Scientific Reports, 2017, 7, 41561.	1.6	12

#	Article	IF	Citations
19	Overdominance at the Gene Expression Level Plays a Critical Role in the Hybrid Root Growth of Brassica napus. International Journal of Molecular Sciences, 2021, 22, 9246.	1.8	9
20	Two young genes reshape a novel interaction network inBrassica napus. New Phytologist, 2020, 225, 530-545.	3.5	8
21	Variants in ADD1 cause intellectual disability, corpus callosum dysgenesis, and ventriculomegaly in humans. Genetics in Medicine, 2022, 24, 319-331.	1.1	6
22	Disruption of carotene biosynthesis leads to abnormal plastids and variegated leaves in Brassica napus. Molecular Genetics and Genomics, 2020, 295, 981-999.	1.0	5
23	Fine Mapping and Identification of BnaC06.FtsH1, a Lethal Gene That Regulates the PSII Repair Cycle in Brassica napus. International Journal of Molecular Sciences, 2021, 22, 2087.	1.8	5
24	Comparative transcriptomic analysis reveals the molecular mechanism underlying seedling biomass heterosis in Brassica napus. BMC Plant Biology, 2022, 22, .	1.6	4
25	BnaA02.YTG1, encoding a tetratricopeptide repeat protein, is required for early chloroplast biogenesis in Brassica napus. Crop Journal, 2022, 10, 597-610.	2.3	3