

Qing-Yong Yang

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

3,195
citations

172457

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168389

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59
all docs

59
docs citations

59
times ranked

3355
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	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017, 49, 579-587.	21.4	367
3	Stepwise selection on homeologous PRR genes controlling flowering and maturity during soybean domestication. <i>Nature Genetics</i> , 2020, 52, 428-436.	21.4	229
4	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
5	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
6	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018, 4, 90-97.	9.3	137
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.	3.3	126
8	Genome- and transcriptome-wide association studies provide insights into the genetic basis of natural variation of seed oil content in <i>Brassica napus</i> . <i>Molecular Plant</i> , 2021, 14, 470-487.	8.3	107
9	Genetic dissection of plant architecture and yield-related traits in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2016, 6, 21625.	3.3	81
10	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
11	De Novo Plant Genome Assembly Based on Chromatin Interactions: A Case Study of <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2015, 8, 489-492.	8.3	70
12	BnTIR: an online transcriptome platform for exploring RNA-seq libraries for oil crop <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2021, 19, 1895-1897.	8.3	68
13	Overexpression of the <i>Brassica napus</i> <i>BnLAS</i> gene in <i>Arabidopsis</i> affects plant development and increases drought tolerance. <i>Plant Cell Reports</i> , 2011, 30, 373-388.	5.6	64
14	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. <i>Nature Communications</i> , 2022, 13, 682.	12.8	59
15	Overexpression of Three Glucosinolate Biosynthesis Genes in <i>Brassica napus</i> Identifies Enhanced Resistance to <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS ONE</i> , 2015, 10, e0140491.	2.5	57
16	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
17	The genome of <i>jojoba</i> (<i>Simmondsia chinensis</i>): A taxonomically isolated species that directs wax ester accumulation in its seeds. <i>Science Advances</i> , 2020, 6, eaay3240.	10.3	53
18	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.	8.3	51

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19	BnPIR: <i>Brassica napus</i> pan-genome information resource for 1689 accessions. <i>Plant Biotechnology Journal</i> , 2021, 19, 412-414.	8.3	51
20	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
21	Differential m6A RNA landscapes across hematopoiesis reveal a role for IGF2BP2 in preserving hematopoietic stem cell function. <i>Cell Stem Cell</i> , 2022, 29, 149-159.e7.	11.1	49
22	Dissection of genetic architecture for glucosinolate accumulations in leaves and seeds of <i>Brassica napus</i> by genome-wide association study. <i>Plant Biotechnology Journal</i> , 2020, 18, 1472-1484.	8.3	47
23	Co-location of QTL for <i>Sclerotinia</i> stem rot resistance and flowering time in <i>Brassica napus</i> . <i>Crop Journal</i> , 2019, 7, 227-237.	5.2	43
24	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
25	Expression of <i>Brassica napus</i> TCG2, a regulator of trichome development, increases plant sensitivity to salt stress by suppressing the expression of auxin biosynthesis genes. <i>Journal of Experimental Botany</i> , 2015, 66, 5821-5836.	4.8	39
26	Physiological, genomic and transcriptional diversity in responses to boron deficiency in rapeseed genotypes. <i>Journal of Experimental Botany</i> , 2016, 67, 5769-5784.	4.8	38
27	Promoter variations in a homeobox gene, BnA10.LMI1, determine lobed leaves in rapeseed (<i>Brassica</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.6	38
28	Spatial Colocalization of Human Ohnolog Pairs Acts to Maintain Dosage-Balance. <i>Molecular Biology and Evolution</i> , 2016, 33, 2368-2375.	8.9	36
29	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
30	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
31	Development of iFOX - hunting as a functional genomic tool and demonstration of its use to identify early senescence-related genes in the polyploid <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 591-602.	8.3	24
32	Enhancing canola breeding by editing a glucosinolate transporter gene lacking natural variation. <i>Plant Physiology</i> , 2022, 188, 1848-1851.	4.8	24
33	Nonspecific phospholipase C6 increases seed oil production in oilseed Brassicaceae plants. <i>New Phytologist</i> , 2020, 226, 1055-1073.	7.3	22
34	Spatial features for <i>Escherichia coli</i> genome organization. <i>BMC Genomics</i> , 2015, 16, 37.	2.8	21
35	Development and screening of EMS mutants with altered seed oil content or fatty acid composition in <i>Brassica napus</i> . <i>Plant Journal</i> , 2020, 104, 1410-1422.	5.7	21
36	Bioinformatics Identification of Drug Resistance-Associated Gene Pairs in <i>Mycobacterium tuberculosis</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1417.	4.1	20

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37	Plant-ImputeDB: an integrated multiple plant reference panel database for genotype imputation. <i>Nucleic Acids Research</i> , 2021, 49, D1480-D1488.	14.5	16
38	R gene triplication confers European fodder turnip with improved clubroot resistance. <i>Plant Biotechnology Journal</i> , 2022, 20, 1502-1517.	8.3	15
39	Normal Light-Dark and Short-Light Cycles Regulate Intestinal Inflammation, Circulating Short-chain Fatty Acids and Gut Microbiota in Period2 Gene Knockout Mice. <i>Frontiers in Immunology</i> , 2022, 13, 848248.	4.8	14
40	ATP selection in a random peptide library consisting of prebiotic amino acids. <i>Biochemical and Biophysical Research Communications</i> , 2015, 466, 400-405.	2.1	13
41	Genome-wide Identification and characterization of circular RNAs in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2018, 8, 6757.	3.3	13
42	Systems Chemical Genetics-Based Drug Discovery: Prioritizing Agents Targeting Multiple/Reliable Disease-Associated Genes as Drug Candidates. <i>Frontiers in Genetics</i> , 2019, 10, 474.	2.3	13
43	BnVIR: bridging the genotype-phenotype gap to accelerate mining of candidate variations underlying agronomic traits in <i>Brassica napus</i> . <i>Molecular Plant</i> , 2022, 15, 779-782.	8.3	13
44	Comparison of dynamic 3D chromatin architecture uncovers heterosis for leaf size in <i>Brassica napus</i> . <i>Journal of Advanced Research</i> , 2022, 42, 289-301.	9.5	12
45	Facilitating Anti-Cancer Combinatorial Drug Discovery by Targeting Epistatic Disease Genes. <i>Molecules</i> , 2018, 23, 736.	3.8	11
46	Calling large indels in 1047 <i>Arabidopsis</i> with IndelEnsembler. <i>Nucleic Acids Research</i> , 2021, 49, 10879-10894.	14.5	10
47	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
48	Transcriptome Analysis Reveals Candidate Genes Associated with Leaf Etiolation of a Cytoplasmic Male Sterility Line in Chinese Cabbage (<i>Brassica Rapa L. ssp. Pekinensis</i>). <i>International Journal of Molecular Sciences</i> , 2018, 19, 922.	4.1	9
49	Identification of candidate genes controlling fiber quality traits in upland cotton through integration of meta-QTL, significant SNP and transcriptomic data. <i>Journal of Cotton Research</i> , 2020, 3, .	2.5	7
50	Systems Genetic Validation of the SNP-Metabolite Association in Rice Via Metabolite-Pathway-Based Phenome-Wide Association Scans. <i>Frontiers in Plant Science</i> , 2015, 6, 1027.	3.6	5
51	Association mapping and domestication analysis to dissect genetic improvement process of upland cotton yield-related traits in China. <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	5
52	Circadian Gene PER2 Silencing Downregulates PPARC and SREBF1 and Suppresses Lipid Synthesis in Bovine Mammary Epithelial Cells. <i>Biology</i> , 2021, 10, 1226.	2.8	5
53	Altering Dietary Soluble Protein Levels With Decreasing Crude Protein May Be a Potential Strategy to Improve Nitrogen Efficiency in Hu Sheep Based on Rumen Microbiome and Metabolomics. <i>Frontiers in Nutrition</i> , 2021, 8, 815358.	3.7	5
54	Influence of Chromatin 3D Organization on Structural Variations of the <i>Arabidopsis thaliana</i> Genome. <i>Molecular Plant</i> , 2017, 10, 340-344.	8.3	4

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55	Asymmetrical effects of autopolyploidization on organ size and gene expression in Brassica rapa and B. oleracea. Scientia Horticulturae, 2021, 282, 109991.	3.6	1
56	Novel Isoniazid- and Ethionamide-resistance loci in mycobacterium tuberculosis identified by phenome-wide association scans. , 2015, , .		0