

Qing-Yong Yang

List of Publications by Year in descending order

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56
papers

3,195
citations

172457

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h-index

168389

53
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all docs

59
docs citations

59
times ranked

3355
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Enhancing canola breeding by editing a glucosinolate transporter gene lacking natural variation. <i>Plant Physiology</i> , 2022, 188, 1848-1851.	4.8	24
3	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
4	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
5	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
6	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
7	R gene triplication confers European fodder turnip with improved clubroot resistance. <i>Plant Biotechnology Journal</i> , 2022, 20, 1502-1517.	8.3	15
8	BnPIR: <i>Brassica napus</i> pan-genome information resource for 1689 accessions. <i>Plant Biotechnology Journal</i> , 2021, 19, 412-414.	8.3	51
9	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
10	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
11	Asymmetrical effects of autopolyploidization on organ size and gene expression in <i>Brassica rapa</i> and <i>B. oleracea</i> . <i>Scientia Horticulturae</i> , 2021, 282, 109991.	3.6	1
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	Calling large indels in 1047 <i>Arabidopsis</i> with IndelEnsembler. <i>Nucleic Acids Research</i> , 2021, 49, 10879-10894.	14.5	10
14	Plant-ImputeDB: an integrated multiple plant reference panel database for genotype imputation. <i>Nucleic Acids Research</i> , 2021, 49, D1480-D1488.	14.5	16
15	Circadian Gene PER2 Silencing Downregulates PPARG and SREBF1 and Suppresses Lipid Synthesis in Bovine Mammary Epithelial Cells. <i>Biology</i> , 2021, 10, 1226.	2.8	5
16	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
17	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
18	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

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19	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
20	Nonspecific phospholipase C6 increases seed oil production in oilseed Brassicaceae plants. <i>New Phytologist</i> , 2020, 226, 1055-1073.	7.3	22
21	The genome of jojoba (<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
22	Stepwise selection on homeologous PRR genes controlling flowering and maturity during soybean domestication. <i>Nature Genetics</i> , 2020, 52, 428-436.	21.4	229
23	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
24	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
25	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
26	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
27	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
28	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018, 4, 90-97.	9.3	137
29	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
30	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
31	Promoter variations in a homeobox gene, <i>BnA10.LMI1</i> , determine lobed leaves in rapeseed (<i>Brassica</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.6	38
32	Transcriptome Analysis Reveals Candidate Genes Associated with Leaf Etiolation of a Cytoplasmic Male Sterility Line in Chinese Cabbage (<i>Brassica Rapa</i> L. ssp. <i>Pekinensis</i>). <i>International Journal of Molecular Sciences</i> , 2018, 19, 922.	4.1	9
33	Facilitating Anti-Cancer Combinatorial Drug Discovery by Targeting Epistatic Disease Genes. <i>Molecules</i> , 2018, 23, 736.	3.8	11
34	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017, 49, 579-587.	21.4	367
35	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
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	Genetic dissection of plant architecture and yield-related traits in Brassica napus. Scientific Reports, 2016, 6, 21625.	3.3	81
38	Physiological, genomic and transcriptional diversity in responses to boron deficiency in rapeseed genotypes. Journal of Experimental Botany, 2016, 67, 5769-5784.	4.8	38
39	Comparative transcriptomic analysis uncovers the complex genetic network for resistance to Sclerotinia sclerotiorum in Brassica napus. Scientific Reports, 2016, 6, 19007.	3.3	126
40	Spatial Colocalization of Human Ohnolog Pairs Acts to Maintain Dosage-Balance. Molecular Biology and Evolution, 2016, 33, 2368-2375.	8.9	36
41	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.	3.6	185
42	Systems Genetic Validation of the SNP-Metabolite Association in Rice Via Metabolite-Pathway-Based Phenome-Wide Association Scans. Frontiers in Plant Science, 2015, 6, 1027.	3.6	5
43	Novel Isoniazid- and Ethionamide-resistance loci in mycobacterium tuberculosis identified by phenome-wide association scans. , 2015, , .		0
44	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.	3.6	9
45	Spatial features for Escherichia coli genome organization. BMC Genomics, 2015, 16, 37.	2.8	21
46	De Novo Plant Genome Assembly Based on Chromatin Interactions: A Case Study of Arabidopsis thaliana. Molecular Plant, 2015, 8, 489-492.	8.3	70
47	Expression of <i>Brassica napus</i> TTG2, a regulator of trichome development, increases plant sensitivity to salt stress by suppressing the expression of auxin biosynthesis genes. Journal of Experimental Botany, 2015, 66, 5821-5836.	4.8	39
48	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.	2.8	27
49	ATP selection in a random peptide library consisting of prebiotic amino acids. Biochemical and Biophysical Research Communications, 2015, 466, 400-405.	2.1	13
50	Overexpression of Three Glucosinolate Biosynthesis Genes in Brassica napus Identifies Enhanced Resistance to Sclerotinia sclerotiorum and Botrytis cinerea. PLoS ONE, 2015, 10, e0140491.	2.5	57
51	A Complex Recombination Pattern in the Genome of Allotetraploid Brassica napus as Revealed by a High-Density Genetic Map. PLoS ONE, 2014, 9, e109910.	2.5	41
52	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.	8.3	51
53	Identification of Heat Responsive Genes in Brassica napus Siliques at the Seed-Filling Stage through Transcriptional Profiling. PLoS ONE, 2014, 9, e101914.	2.5	49
54	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.	3.6	154

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55	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
56	Overexpression of the Brassica napus BnLAS gene in Arabidopsis affects plant development and increases drought tolerance. Plant Cell Reports, 2011, 30, 373-388.	5.6	64