

# Limei Yang

## List of Publications by Year in descending order

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63  
papers

1,934  
citations

430442

18  
h-index

276539

41  
g-index

63  
all docs

63  
docs citations

63  
times ranked

1922  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide identification and analysis of cytokinin dehydrogenase/oxidase (CKX) family genes in <i>Brassica oleracea</i> L. reveals their involvement in response to <i>Plasmodiophora brassicae</i> infections. <i>Horticultural Plant Journal</i> , 2022, 8, 68-80.	2.3	15
2	Plant SWEET Family of Sugar Transporters: Structure, Evolution and Biological Functions. <i>Biomolecules</i> , 2022, 12, 205.	1.8	46
3	Global DNA Methylation and mRNA-miRNA Variations Activated by Heat Shock Boost Early Microspore Embryogenesis in Cabbage ( <i>Brassica oleracea</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 5147.	1.8	3
4	An Identification System Targeting the SRK Gene for Selecting S-Haplotypes and Self-Compatible Lines in Cabbage. <i>Plants</i> , 2022, 11, 1372.	1.6	0
5	Characterization of glucosinolates in 80 broccoli genotypes and different organs using UHPLC-Triple-TOF-MS method. <i>Food Chemistry</i> , 2021, 334, 127519.	4.2	68
6	BoCER1 is essential for the synthesis of cuticular wax in cabbage ( <i>Brassica oleracea</i> L. var. capitata). <i>Scientia Horticulturae</i> , 2021, 277, 109801.	1.7	9
7	Genome-wide identification and expression analysis of the <i>Brassica oleracea</i> L. chitin-binding genes and response to pathogens infections. <i>Planta</i> , 2021, 253, 80.	1.6	9
8	Fine mapping of the major QTLs for biochemical variation of sulforaphane in broccoli florets using a DH population. <i>Scientific Reports</i> , 2021, 11, 9004.	1.6	12
9	Transcriptome and plant hormone analyses provide new insight into the molecular regulatory networks underlying hybrid lethality in cabbage ( <i>Brassica oleracea</i> ). <i>Planta</i> , 2021, 253, 96.	1.6	6
10	Genome-wide analysis of cabbage cytochrome P450 genes and characterization of BoCYP704B1, a gene responsible for cabbage anther development. <i>Scientia Horticulturae</i> , 2021, 283, 110096.	1.7	3
11	Advances in Genetics and Molecular Breeding of Broccoli. <i>Horticulturae</i> , 2021, 7, 280.	1.2	8
12	Identification and validation of an ECERIFERUM2- LIKE gene controlling cuticular wax biosynthesis in cabbage ( <i>Brassica oleracea</i> L. var. capitata L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 4055-4066.	1.8	8
13	Global Survey of the Full-Length Cabbage Transcriptome ( <i>Brassica oleracea</i> Var. capitata L.) Reveals Key Alternative Splicing Events Involved in Growth and Disease Response. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10443.	1.8	4
14	Map-based cloning and promoter variation analysis of the lobed leaf gene BoLMI1a in ornamental kale ( <i>Brassica oleracea</i> L. var. acephala). <i>BMC Plant Biology</i> , 2021, 21, 456.	1.6	8
15	Genome-wide characterization and analysis of the anthocyanin biosynthetic genes in <i>Brassica oleracea</i> . <i>Planta</i> , 2021, 254, 92.	1.6	6
16	Genetic mapping and candidate gene identification of BoGL5, a gene essential for cuticular wax biosynthesis in broccoli. <i>BMC Genomics</i> , 2021, 22, 811.	1.2	7
17	Organelle Comparative Genome Analysis Reveals Novel Alloplasmic Male Sterility with orf112 in <i>Brassica oleracea</i> L.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13230.	1.8	2
18	Carotenoid Biosynthetic Genes in Cabbage: Genome-Wide Identification, Evolution, and Expression Analysis. <i>Genes</i> , 2021, 12, 2027.	1.0	7

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19	Morphological, transcriptomics and phytohormone analysis shed light on the development of a novel dwarf mutant of cabbage ( <i>Brassica oleracea</i> ). <i>Plant Science</i> , 2020, 290, 110283.	1.7	19
20	An efficient virus-induced gene silencing (VIGS) system for functional genomics in Brassicas using a cabbage leaf curl virus (CaLCuV)-based vector. <i>Planta</i> , 2020, 252, 42.	1.6	11
21	A high-quality reference genome for cabbage obtained with SMRT reveals novel genomic features and evolutionary characteristics. <i>Scientific Reports</i> , 2020, 10, 12394.	1.6	29
22	Utilization of Ogura CMS germplasm with the clubroot resistance gene by fertility restoration and cytoplasm replacement in <i>Brassica oleracea</i> L. <i>Horticulture Research</i> , 2020, 7, 61.	2.9	10
23	An update on the arsenal: mining resistance genes for disease management of Brassica crops in the genomic era. <i>Horticulture Research</i> , 2020, 7, 34.	2.9	46
24	Pigment variation and transcriptional response of the pigment synthesis pathway in the S2309 triple-color ornamental kale ( <i>Brassica oleracea</i> L. var. <i>acephala</i> ) line. <i>Genomics</i> , 2020, 112, 2658-2665.	1.3	10
25	A time-resolved dual transcriptome analysis reveals the molecular regulating network underlying the compatible/incompatible interactions between cabbage ( <i>Brassica oleracea</i> ) and <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> . <i>Plant and Soil</i> , 2020, 448, 455-478.	1.8	7
26	Genome-Wide Identification, Expression Profile of the TIFY Gene Family in <i>Brassica oleracea</i> var. <i>capitata</i> , and Their Divergent Response to Various Pathogen Infections and Phytohormone Treatments. <i>Genes</i> , 2020, 11, 127.	1.0	31
27	Complete Genome Sequence of Strain WHRI 3811 Race 1 of <i>Xanthomonas campestris</i> pv. <i>campestris</i> , the Causal Agent of Black Rot of Cruciferous Vegetables. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1571-1573.	1.4	4
28	Genetic Diversity, Virulence, Race Profiling, and Comparative Genomic Analysis of the <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> Strains Infecting Cabbages in China. <i>Frontiers in Microbiology</i> , 2019, 10, 1373.	1.5	16
29	Comparative transcriptome analysis of cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> ) infected by <i>Plasmodiophora brassicae</i> reveals drastic defense response at secondary infection stage. <i>Plant and Soil</i> , 2019, 443, 167-183.	1.8	21
30	Natural Sulforaphane From Broccoli Seeds Against Influenza A Virus Replication in MDCK Cells. <i>Natural Product Communications</i> , 2019, 14, 1934578X1985822.	0.2	11
31	Evaluation and selection of sources of cytoplasmic male sterility in broccoli. <i>Euphytica</i> , 2019, 215, 1.	0.6	8
32	A user-friendly KASP molecular marker developed for the DGMS-based breeding system in <i>Brassica oleracea</i> species. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	7
33	Fine-mapping and transcriptome analysis of BoGL-3, a wax-less gene in cabbage ( <i>Brassica oleracea</i> L. var.) Tj ETQq1_1_0.784314 rgBT / O	1.0	12
34	Genome-wide analysis of HSP70 family genes in cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> ) reveals their involvement in floral development. <i>BMC Genomics</i> , 2019, 20, 369.	1.2	16
35	Overcoming Cabbage Crossing Incompatibility by the Development and Application of Self-Compatibility-QTL- Specific Markers and Genome-Wide Background Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 189.	1.7	20
36	Map-based cloning and characterization of BoCCD4, a gene responsible for white/yellow petal color in <i>B. oleracea</i> . <i>BMC Genomics</i> , 2019, 20, 242.	1.2	30

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37	Draft Genome Sequence of FGL03-6, a Race 1 Strain of <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> , the Causal Agent of Cabbage Fusarium Wilt. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
38	Effects of Bt cabbage pollen on the honeybee <i>Apis mellifera</i> L. <i>Scientific Reports</i> , 2018, 8, 482.	1.6	11
39	QTL-seq for rapid identification of candidate genes for flowering time in broccoli—cabbage. <i>Theoretical and Applied Genetics</i> , 2018, 131, 917-928.	1.8	41
40	Fine mapping and candidate gene identification of the genic male-sterile gene <i>ms3</i> in cabbage 51S. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2651-2661.	1.8	12
41	Differentially Expressed Genes Associated with the Cabbage Yellow-Green-Leaf Mutant in the <i>ygl-1</i> Mapping Interval with Recombination Suppression. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2936.	1.8	9
42	A 252-bp insertion in <i>BoCER1</i> is responsible for the glossy phenotype in cabbage ( <i>Brassica oleracea</i> L.) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	9
43	iTRAQ-Based Proteomic Analysis of Ogura-CMS Cabbage and Its Maintainer Line. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3180.	1.8	12
44	Normal and Abortive Buds Transcriptomic Profiling of Broccoli ogu Cytoplasmic Male Sterile Line and Its Maintainer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2501.	1.8	9
45	Identification and characterization of resistance for <i>Plasmodiophora brassicae</i> race 4 in cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> ). <i>Australasian Plant Pathology</i> , 2018, 47, 531-541.	0.5	10
46	First Report of <i>Myrothecium roridum</i> Causing Leaf Spot on <i>Brassica oleracea</i> in China. <i>Plant Disease</i> , 2018, 102, 2658-2658.	0.7	1
47	Fine Mapping and Candidate Gene Identification for Wax Biosynthesis Locus, <i>BoWax1</i> in <i>Brassica oleracea</i> L. var. <i>capitata</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 309.	1.7	15
48	Genome-wide indel/SSR scanning reveals significant loci associated with excellent agronomic traits of a cabbage ( <i>Brassica oleracea</i> ) elite parental line “20”. <i>Scientific Reports</i> , 2017, 7, 41696.	1.6	21
49	Fine mapping of <i>BoGL1</i> , a gene controlling the glossy green trait in cabbage ( <i>Brassica oleracea</i> L. Var.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.8	9
50	Characterization of emerging populations of <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> causing cabbage wilt in China. <i>Journal of Phytopathology</i> , 2017, 165, 813-821.	0.5	17
51	<i>Cgl2</i> plays an essential role in cuticular wax biosynthesis in cabbage ( <i>Brassica oleracea</i> L. var.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.8	9
52	Fine-Mapping and Analysis of <i>Cgl1</i> , a Gene Conferring Glossy Trait in Cabbage ( <i>Brassica oleracea</i> L. var.) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.7	20
53	Rapid Introgression of the Fusarium Wilt Resistance Gene into an Elite Cabbage Line through the Combined Application of a Microspore Culture, Genome Background Analysis, and Disease Resistance-Specific Marker Assisted Foreground Selection. <i>Frontiers in Plant Science</i> , 2017, 8, 354.	1.7	35
54	Fine Mapping and Transcriptome Analysis Reveal Candidate Genes Associated with Hybrid Lethality in Cabbage ( <i>Brassica Oleracea</i> ). <i>Genes</i> , 2017, 8, 147.	1.0	15

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55	Comparative Analysis of Genome Wide DNA Methylation Profiles for the Genic Male Sterile Cabbage Line 01-20S and Its Maintainer Line. <i>Genes</i> , 2017, 8, 159.	1.0	15
56	Transcriptome Profiling of Resistance to <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> in Cabbage ( <i>Brassica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	36
57	Whole-Genome Mapping Reveals Novel QTL Clusters Associated with Main Agronomic Traits of Cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 989.	1.7	48
58	Comparative Transcriptome Analysis between Broccoli ( <i>Brassica oleracea</i> var. <i>italica</i> ) and Wild Cabbage ( <i>Brassica macrocarpa</i> Guss.) in Response to <i>Plasmodiophora brassicae</i> during Different Infection Stages. <i>Frontiers in Plant Science</i> , 2016, 7, 1929.	1.7	69
59	High resistance of transgenic cabbage plants with a synthetic <i>cry11a8</i> gene from <i>Bacillus thuringiensis</i> against two lepidopteran species under field conditions. <i>Pest Management Science</i> , 2016, 72, 315-321.	1.7	7
60	A generic SSR marker closely linked to a dominant genic male sterility gene (DGMs79-399-3) in broccoli ( <i>Brassica oleracea</i> var. <i>italica</i> ). <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	4
61	Organelle Simple Sequence Repeat Markers Help to Distinguish Carpeloid Stamen and Normal Cytoplasmic Male Sterile Sources in Broccoli. <i>PLoS ONE</i> , 2015, 10, e0138750.	1.1	14
62	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	5.8	918
63	Pyramiding of <i>Bt cry11a8</i> and <i>cry1Ba3</i> genes into cabbage ( <i>Brassica oleracea</i> L. var. <i>capitata</i> ) confers effective control against diamondback moth. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 115, 419-428.	1.2	22