Kun Lu

List of Publications by Year
in descending order

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113
papers

4,129
citations

156536
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122
all docs

122
docs citations

122
times ranked

4366
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide characterization of Brassica napus INDETERMINATE DOMAIN genes reveals a negative role for BnA08.IDD7 in plant development. Industrial Crops and Products, 2022, 175, 114263.	2.5	2
2	qPrimerDB: A Powerful and User-Friendly Database for qPCR Primer Design. Methods in Molecular Biology, 2022, 2392, 173-182.	0.4	4
3	Two types of cinnamoyl-CoA reductase function divergently in accumulation of lignins, flavonoids and glucosinolates and enhance lodging resistance in Brassica napus. Crop Journal, 2022, 10, 647-660.	2.3	12
4	Quantitative trait locus mapping and transcriptome analysis reveal candidate genes for a stem bending mutant in rapeseed (Brassica napus). Industrial Crops and Products, 2022, 177, 114456.	2.5	3
5	Impacts of the recent USA and China trade dispute on Chinaâ€™s aquatic products. China Economic Journal, 2022, 15, 60-76.	2.1	1
6	Nitrogen application and differences in leaf number retained after topping affect the tobacco (Nicotiana tabacum) transcriptome and metabolome. BMC Plant Biology, 2022, 22, 38.	1.6	5
7	Metabolite Characteristics Analysis of Siliques and Effects of Lights on the Accumulation of Glucosinolates in Siliques of Rapeseed. Frontiers in Plant Science, 2022, 13, 817419.	1.7	0
8	Genome-Wide Identification of the TIFY Gene Family in Brassiceae and Its Potential Association with Heavy Metal Stress in Rapeseed. Plants, 2022, 11, 667.	1.6	6
9	Transcriptome and Small RNA Sequencing Reveal the Mechanisms Regulating Harvest Index in Brassica napus. Frontiers in Plant Science, 2022, 13, 855486.	1.7	2
10	Genome-Wide Association Study of Phenylalanine Derived Glucosinolates in Brassica rapa. Plants, 2022, 11, 1274.	1.6	3
11	Multi-omics analysis reveals the mechanism of seed coat color formation in Brassica rapa L.. Theoretical and Applied Genetics, 2022, 135, 2083-2099.	1.8	7
12	Rapeseed (Brassica napus) Mitogen-Activated Protein Kinase 1 Enhances Shading Tolerance by Regulating the Photosynthesis Capability of Photosystem II. Frontiers in Plant Science, 2022, 13, .	1.7	1
13	Spatioâ€temporal transcriptome profiling and subgenome analysis in <i>Brassica napus</i>. Plant Journal, 2022, 111, 1123-1138.	2.8	6
14	Comprehensive analysis of polygalacturonase genes offers new insights into their origin and functional evolution in land plants. Genomics, 2021, 113, 1096-1108.	1.3	8
15	In Silico Identification of the Complex Interplay between Regulatory SNPs, Transcription Factors, and Their Related Genes in Brassica napus L. Using Multi-Omics Data. International Journal of Molecular Sciences, 2021, 22, 789.	1.8	12
16	Unravelling the Complex Interplay of Transcription Factors Orchestrating Seed Oil Content in Brassica napus L.. International Journal of Molecular Sciences, 2021, 22, 1033.	1.8	9
17	Genome-wide association study identifies novel loci and candidate genes for drought stress tolerance in rapeseed. Oil Crop Science, 2021, 6, 12-22.	0.9	15
18	Genome-wide association study and transcriptome comparison reveal novel QTL and candidate genes that control petal size in rapeseed. Journal of Experimental Botany, 2021, 72, 3597-3610.	2.4	7

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19	Transcriptome and proteome analyses of the molecular mechanisms underlying changes in oil storage under drought stress in <i>Brassica napus</i> L.. GCB Bioenergy, 2021, 13, 1071-1086.	2.5	17
20	Metabolite Profiling and Transcriptome Analysis Provide Insight into Seed Coat Color in Brassica juncea. International Journal of Molecular Sciences, 2021, 22, 7215.	1.8	15
21	Overexpression of DEFECTIVE IN ANTHER DEHISCENCE 1 increases rapeseed silique length through crosstalk between JA and auxin signaling. Industrial Crops and Products, 2021, 168, 113576.	2.5	8
22	The Brassica napus fatty acid exporter FAX1-1 contributes to biological yield, seed oil content, and oil quality. Biotechnology for Biofuels, 2021, 14, 190.	6.2	15
23	Identification of quantitative trait loci and candidate genes controlling seed pigments of rapeseed. Journal of Integrative Agriculture, 2021, 20, 2862-2879.	1.7	6
24	Genome-Wide Identification and Analysis of MKK and MAPK Gene Families in Brassica Species and Response to Stress in Brassica napus. International Journal of Molecular Sciences, 2021, 22, 544.	1.8	20
25	Genome-wide association analysis reveals zinc-tolerant loci of rapeseed at germination stage. Acta Agronomica Sinica(China), 2021, 47, 262-274.	0.1	0
26	Genome-wide association study and transcriptome analysis dissect the genetic control of silique length in Brassica napus L.. Biotechnology for Biofuels, 2021, 14, 214.	6.2	7
27	Population Genomics of Brassica Species. Population Genomics, 2021, , .	0.2	1
28	Genome-wide identification and comparative analysis of diacylglycerol kinase (DGK) gene family and their expression profiling in Brassica napus under abiotic stress. BMC Plant Biology, 2020, 20, 473.	1.6	9
29	Comparative transcriptome and metabolomic profiling reveal the complex mechanisms underlying the developmental dynamics of tobacco leaves. Genomics, 2020, 112, 4009-4022.	1.3	15
30	Differential Alternative Splicing Genes and Isoform Regulation Networks of Rapeseed (Brassica napus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	10
31	Integrating GWAS, linkage mapping and gene expression analyses reveals the genetic control of growth period traits in rapeseed (Brassica napus L.). Biotechnology for Biofuels, 2020, 13, 134.	6.2	21
32	BrassicaEDB: A Gene Expression Database for Brassica Crops. International Journal of Molecular Sciences, 2020, 21, 5831.	1.8	44
33	A Genome-Wide Survey of MATE Transporters in Brassicaceae and Unveiling Their Expression Profiles under Abiotic Stress in Rapeseed. Plants, 2020, 9, 1072.	1.6	9
34	Deciphering the transcriptional regulatory networks that control size, color, and oil content in Brassica rapa seeds. Biotechnology for Biofuels, 2020, 13, 90.	6.2	24
35	Genome-wide identification AINTEGUMENTA-like (AIL) genes in Brassica species and expression patterns during reproductive development in Brassica napus L.. PLoS ONE, 2020, 15, e0234411.	1.1	5
36	Genome-Wide Identification and Expression Profiling of Monosaccharide Transporter Genes Associated with High Harvest Index Values in Rapeseed (Brassica napus L.). Genes, 2020, 11, 653.	1.0	8

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37	Genome-Wide Analysis of Phosphorus Transporter Genes in Brassica and Their Roles in Heavy Metal Stress Tolerance. International Journal of Molecular Sciences, 2020, 21, 2209.	1.8	12
38	Comparative Analysis of the Metabolic Profiles of Yellow- versus Black-Seeded Rapeseed Using UPLCâ€“HESIâ€“MS/MS and Transcriptome Analysis. Journal of Agricultural and Food Chemistry, 2020, 68, 3033-3049.	2.4	23
39	Characterization of cold stress responses in different rapeseed ecotypes based on metabolomics and transcriptomics analyses. PeerJ, 2020, 8, e8704.	0.9	27
40	Candidate genes screening for plant height and the first branch height based on QTL mapping and genome-wide association study in rapessed (<italic>Brassica napus</italic> L.). Acta Agronomica Sinica(China), 2020, 46, 214-227.	0.1	1
41	Genome-wide exploration and characterization of miR172/euAP2 genes in Brassica napus L. for likely role in flower organ development. BMC Plant Biology, 2019, 19, 336.	1.6	25
42	Joint RNA-Seq and miRNA Profiling Analyses to Reveal Molecular Mechanisms in Regulating Thickness of Pod Canopy in Brassica napus. Genes, 2019, 10, 591.	1.0	12
43	Identification of candidate genes controlling oil content by combination of genome-wide association and transcriptome analysis in the oilseed crop Brassica napus. Biotechnology for Biofuels, 2019, 12, 216.	6.2	40
44	Identification and Characterization of Major Constituents in Different-Colored Rapeseed Petals by UPLCâ€“HESI-MS/MS. Journal of Agricultural and Food Chemistry, 2019, 67, 11053-11065.	2.4	51
45	Genome wide identification and comparative analysis of glutathione transferases (GST) family genes in Brassica napus. Scientific Reports, 2019, 9, 9196.	1.6	34
46	Genome-Wide Identification of the LAC Gene Family and Its Expression Analysis Under Stress in Brassica napus. Molecules, 2019, 24, 1985.	1.7	16
47	Physiological, genomic and transcriptomic comparison of two Brassica napus cultivars with contrasting cadmium tolerance. Plant and Soil, 2019, 441, 71-87.	1.8	11
48	Genome-Wide Identification and Comparative Expression Profile Analysis of the Long-Chain Acyl-CoA synthetase (LACS) Gene Family in Two Different Oil Content Cultivars of Brassica napus. Biochemical Genetics, 2019, 57, 781-800.	0.8	11
49	Identification of genomic regions associated with multi-silique trait in Brassica napus. BMC Genomics, 2019, 20, 304.	1.2	8
50	Whole-genome resequencing reveals Brassica napus origin and genetic loci involved in its improvement. Nature Communications, 2019, 10, 1154.	5.8	249
51	Brassica napus Infected with Leptosphaeria maculans. Genes, 2019, 10, 296.	1.0	8
52	Genomeâ€wide identification of loci affecting seed glucosinolate contents in <i>Brassica napus</i> L.. Journal of Integrative Plant Biology, 2019, 61, 611-623.	4.1	19
53	Insight into the evolution and functional characteristics of the panâ€genome assembly from sesame landraces and modern cultivars. Plant Biotechnology Journal, 2019, 17, 881-892.	4.1	79
54	Genome-wide association of roots, hypocotyls and fresh weight at germination stage under as stress in <i>Brassica napus</i> L.. Acta Agronomica Sinica(China), 2019, 45, 175.	0.1	0

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55	Genome-wide analysis and expression profiling of the HMA gene family in Brassica napus under cd stress. Plant and Soil, 2018, 426, 365-381.	1.8	31
56	qPrimerDB: a thermodynamics-based gene-specific qPCR primer database for 147 organisms. Nucleic Acids Research, 2018, 46, D1229-D1236.	6.5	115
57	Genome-Wide Identification of Flowering-Time Genes in Brassica Species and Reveals a Correlation between Selective Pressure and Expression Patterns of Vernalization-Pathway Genes in Brassica napus. International Journal of Molecular Sciences, 2018, 19, 3632.	1.8	20
58	Case Study for Trait-Related Gene Evolution: Glucosinolates. Compendium of Plant Genomes, 2018, , 199-222.	0.3	3
59	Genome-Wide Association Study Reveals Both Overlapping and Independent Genetic Loci to Control Seed Weight and Silique Length in Brassica napus. Frontiers in Plant Science, 2018, 9, 921.	1.7	37
60	Genome-Wide Characterization and Analysis of Metallothionein Family Genes That Function in Metal Stress Tolerance in Brassica napus L.. International Journal of Molecular Sciences, 2018, 19, 2181.	1.8	30
61	Genome-Wide Analysis of the PYL Gene Family and Identification of PYL Genes That Respond to Abiotic Stress in Brassica napus. Genes, 2018, 9, 156.	1.0	55
62	Genome-Wide Identification and Expression Profiling of Cytokinin Oxidase/Dehydrogenase (CKX) Genes Reveal Likely Roles in Pod Development and Stress Responses in Oilseed Rape (Brassica napus L.). Genes, 2018, 9, 168.	1.0	41
63	Genome-Wide Identification and Characterization of NODULE-INCEPTION-Like Protein (NLP) Family Genes in Brassica napus. International Journal of Molecular Sciences, 2018, 19, 2270.	1.8	33
64	Association Mapping Analysis of Fatty Acid Content in Different Ecotypic Rapeseed Using mrMLM. Frontiers in Plant Science, 2018, 9, 1872.	1.7	44
65	Mining Yellow-seeded Micro Effect Loci in B. napus by Integrated GWAS and WGCNA Analysis. Acta Agronomica Sinica(China), 2018, 44, 1105.	0.1	0
66	Genome-wide Analysis and Expression Profiling of SPS Gene Family in Brassica nupus L.. Acta Agronomica Sinica(China), 2018, 44, 197.	0.1	0
67	Genetic and transcriptomic analyses of lignin- and lodging-related traits in Brassica napus. Theoretical and Applied Genetics, 2017, 130, 1961-1973.	1.8	64
68	Genome-wide analysis and expression profiling of the GRF gene family in oilseed rape (Brassica napus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	44
69	Genome-wide association mapping and Identification of candidate genes for fatty acid composition in Brassica napus L. using SNP markers. BMC Genomics, 2017, 18, 232.	1.2	105
70	Genome-Wide Association Mapping of Seed Coat Color in <i>Brassica napus</i>. Journal of Agricultural and Food Chemistry, 2017, 65, 5229-5237.	2.4	30
71	Developing a localized web server for survival, generic and protein data analysis with high performance computing technology. , 2017, , .		0
72	Genome-Wide Association and Transcriptome Analyses Reveal Candidate Genes Underlying Yield-determining Traits in Brassica napus. Frontiers in Plant Science, 2017, 8, 206.	1.7	70

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73	Comparative Transcriptome Analysis Reveals Critical Function of Sucrose Metabolism Related-Enzymes in Starch Accumulation in the Storage Root of Sweet Potato. Frontiers in Plant Science, 2017, 8, 914.	1.7	52
74	Genome-Wide Identification, Evolutionary and Expression Analyses of the GALACTINOL SYNTHASE Gene Family in Rapeseed and Tobacco. International Journal of Molecular Sciences, 2017, 18, 2768.	1.8	22
75	Genome-Wide Identification and Structural Analysis of bZIP Transcription Factor Genes in Brassica napus. Genes, 2017, 8, 288.	1.0	68
76	Analysis of Yield Components with High Harvest Index in <i>Brassica napus</i> un-der Environments Fitting Different Yield Levels. Acta Agronomica Sinica(China), 2017, 43, 82.	0.1	2
77	Genome-Wide Analysis and Expression Profiling of the SUC and SWEET Gene Families of Sucrose Transporters in Oilseed Rape (Brassica napus L.). Frontiers in Plant Science, 2016, 7, 1464.	1.7	80
78	Molecular Mapping and QTL for Expression Profiles of Flavonoid Genes in Brassica napus. Frontiers in Plant Science, 2016, 7, 1691.	1.7	24
79	Genome-Wide Survey of Flavonoid Biosynthesis Genes and Gene Expression Analysis between Black- and Yellow-Seeded Brassica napus. Frontiers in Plant Science, 2016, 7, 1755.	1.7	44
80	Genomeâ€wide association analysis and differential expression analysis of resistance to <i>Sclerotinia</i> stem rot in <i>Brassica napus</i>. Plant Biotechnology Journal, 2016, 14, 1368-1380.	4.1	186
81	A combination of genome-wide association and transcriptome analysis reveals candidate genes controlling harvest index-related traits in Brassica napus. Scientific Reports, 2016, 6, 36452.	1.6	59
82	Cloning and Phylogenetic Analysis of Brassica napus L. Caffeic Acid O-Methyltransferase 1 Gene Family and Its Expression Pattern under Drought Stress. PLoS ONE, 2016, 11, e0165975.	1.1	21
83	Genome-Wide Association Analysis of Height of Podding and Thickness of Pod Canopy inBrassica napus. Acta Agronomica Sinica(China), 2016, 42, 344.	0.1	4
84	The Evolutionary History of R2R3-MYB Proteins Across 50 Eukaryotes: New Insights Into Subfamily Classification and Expansion. Scientific Reports, 2015, 5, 11037.	1.6	121
85	Isolation and Functional Characterization of a Phenylalanine Ammonia-Lyase Gene (SsPAL1) from Coleus (Solenostemon scutellarioides (L.) Codd). Molecules, 2015, 20, 16833-16851.	1.7	21
86	Identification of Candidate Genes for Seed Glucosinolate Content Using Association Mapping in Brassica napus L.. Genes, 2015, 6, 1215-1229.	1.0	63
87	Genome-Wide Survey and Expression Profile Analysis of the Mitogen-Activated Protein Kinase (MAPK) Gene Family in Brassica rapa. PLoS ONE, 2015, 10, e0132051.	1.1	56
88	Ectopic Expression of the Coleus R2R3 MYB-Type Proanthocyanidin Regulator Gene SsMYB3 Alters the Flower Color in Transgenic Tobacco. PLoS ONE, 2015, 10, e0139392.	1.1	25
89	Comparative Transcriptome Analysis of Recessive Male Sterility (RGMS) in Sterile and Fertile Brassica napus Lines. PLoS ONE, 2015, 10, e0144118.	1.1	41
90	Genome-Wide Analysis of Seed Acid Detergent Lignin (ADL) and Hull Content in Rapeseed (Brassica) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	37

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91	Development of genic cleavage markers in association with seed glucosinolate content in canola. Theoretical and Applied Genetics, 2015, 128, 1029-1037.	1.8	14
92	Identification of QTL for seed coat colour and oil content in<i>Brassica napus</i>by association mapping using SSR markers. Canadian Journal of Plant Science, 2015, 95, 387-395.	0.3	13
93	Expression Analysis and eQTL Mapping of <i>BnTT3</i> Gene in <i>Brassica napus</i> L.. Acta Agronomica Sinica(China), 2015, 41, 1758.	0.1	0
94	RNA Sequencing Analysis Reveals Transcriptomic Variations in Tobacco (Nicotiana tabacum) Leaves Affected by Climate, Soil, and Tillage Factors. International Journal of Molecular Sciences, 2014, 15, 6137-6160.	1.8	17
95	<i>Arabidopsis</i> EDM2 promotes <i>IBM1</i> distal polyadenylation and regulates genome DNA methylation patterns. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 527-532.	3.3	102
96	Over-Expression of BnMAPK1 in Brassica napus Enhances Tolerance to Drought Stress. Journal of Integrative Agriculture, 2014, 13, 2407-2415.	1.7	17
97	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	5.8	918
98	Overexpression ofBnMAPK1Enhances Resistance toSclerotinia sclerotioruminBrassica napus. Acta Agronomica Sinica(China), 2014, 40, 745.	0.1	2
99	SNP Detection and Analysis of Genes for Flavonoid Pathway in Yellow- and Black-Seeded <i>Brassica napus</i> L.. Acta Agronomica Sinica(China), 2014, 40, 1914.	0.1	2
100	Characterization and evolutionary analysis of Brassica species-diverged sequences containing simple repeat units. Genes and Genomics, 2013, 35, 167-175.	0.5	1
101	Comparative transcriptome analysis of tobacco (Nicotiana tabacum) leaves to identify aroma compound-related genes expressed in different cultivated regions. Molecular Biology Reports, 2013, 40, 345-357.	1.0	6
102	Identification of genome-wide single nucleotide polymorphisms in allopolyploid crop Brassica napus. BMC Genomics, 2013, 14, 717.	1.2	70
103	Identification of genomic regions involved in resistance against Sclerotinia sclerotiorum from wild Brassica oleracea. Theoretical and Applied Genetics, 2013, 126, 549-556.	1.8	101
104	RNA-binding protein regulates plant DNA methylation by controlling mRNA processing at the intronic heterochromatin-containing gene <i>IBM1</i>. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15467-15472.	3.3	91
105	Differential accumulation of phenolic compounds and expression of related genes in black- and yellow-seeded Brassica napus. Journal of Experimental Botany, 2013, 64, 2885-2898.	2.4	81
106	Gene Silencing of BnTT10 Family Genes Causes Retarded Pigmentation and Lignin Reduction in the Seed Coat of Brassica napus. PLoS ONE, 2013, 8, e61247.	1.1	47
107	Cloning and Analysis ofMAPK7Gene Family and Their Promoters from Brassica napus. Acta Agronomica Sinica(China), 2013, 39, 789.	0.1	1
108	Expression Quantitative Trait Loci Analysis of BAN, F3H and TT19 Genes in Brassica napus. , 2012, , .		0

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109	Identification of QTLs for Lignin Content of Seed Coat in <I>Brassica napus</I> L. in Different Environments. Acta Agronomica Sinica(China), 2011, 37, 1398-1405.	0.1	0
110	Cloning and Comparative Analysis of <I>PURPLE ACID PHOSPHATASE 17</I> Gene Families in <I>Brassica oleracea</I> and <I>Brassica rapa</I>. Acta Agronomica Sinica(China), 2010, 36, 517-525.	0.1	0
111	Screening phosphorus-efficient genotypes of rapeseed (<I>Brassica napus</I>) at seedling stage by TOPSIS. Chinese Journal of Eco-Agriculture, 2009, 17, 120-124.	0.1	1
112	Cloning and characterization of phosphorus starvation inducible Brassica napus PURPLE ACID PHOSPHATASE 12 gene family, and imprinting of a recently evolved MITE-minisatellite twin structure. Theoretical and Applied Genetics, 2008, 117, 963-975.	1.8	22
113	A study on interfacial mechanisms and structure of poly(ethylene-co-methacrylic acid)/copper with reflectionâ€"absorption infrared spectroscopy. Journal of Materials Science, 2006, 41, 8271-8275.	1.7	5