

Long Mao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4012838/publications.pdf>

Version: 2024-02-01

36
papers

8,906
citations

279778

23
h-index

330122

37
g-index

38
all docs

38
docs citations

38
times ranked

7945
citing authors

#	ARTICLE	IF	CITATIONS
1	The wheat <i>AGL6</i> MADS-box gene is a master regulator for floral organ identity and a target for spikelet meristem development manipulation. <i>Plant Biotechnology Journal</i> , 2022, 20, 75-88.	8.3	38
2	Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2022, 40, 422-431.	17.5	102
3	<i>Matrilineal</i> empowers wheat pollen with haploid induction potency by triggering postmitosis reactive oxygen species activity. <i>New Phytologist</i> , 2022, 233, 2405-2414.	7.3	26
4	Wheat breeding history reveals synergistic selection of pleiotropic genomic sites for plant architecture and grain yield. <i>Molecular Plant</i> , 2022, 15, 504-519.	8.3	48
5	Transcriptome Analysis of Developing Wheat Grains at Rapid Expanding Phase Reveals Dynamic Gene Expression Patterns. <i>Biology</i> , 2022, 11, 281.	2.8	4
6	InDels Identification and Association Analysis with Spike and Awn Length in Chinese Wheat Mini-Core Collection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5587.	4.1	3
7	TaAA21 represses TaARF25-mediated expression of <i>TaERFs</i> required for grain size and weight development in wheat. <i>Plant Journal</i> , 2021, 108, 1754-1767.	5.7	28
8	High molecular weight glutenin gene diversity in <i>Aegilops tauschii</i> demonstrates unique origin of superior wheat quality. <i>Communications Biology</i> , 2021, 4, 1242.	4.4	14
9	The improved assembly of 7DL chromosome provides insight into the structure and evolution of bread wheat. <i>Plant Biotechnology Journal</i> , 2020, 18, 732-742.	8.3	6
10	Comprehensive analysis of <i>Q</i> gene near-isogenic lines reveals key molecular pathways for wheat domestication and improvement. <i>Plant Journal</i> , 2020, 102, 299-310.	5.7	21
11	The Battle to Sequence the Bread Wheat Genome: A Tale of the Three Kingdoms. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 221-229.	6.9	31
12	A transcriptomic view of the ability of nascent hexaploid wheat to tolerate aneuploidy. <i>BMC Plant Biology</i> , 2020, 20, 97.	3.6	10
13	Mapping QTLs for enhancing early biomass derived from <i>Aegilops tauschii</i> in synthetic hexaploid wheat. <i>PLoS ONE</i> , 2020, 15, e0234882.	2.5	7
14	The soft glumes of common wheat are sterile-lemmas as determined by the domestication gene <i>Q</i> . <i>Crop Journal</i> , 2019, 7, 113-117.	5.2	13
15	DNA methylation dynamics during the interaction of wheat progenitor <i>Aegilops tauschii</i> with the obligate biotrophic fungus <i>Blumeria graminis</i> f. sp. <i>tritici</i> . <i>New Phytologist</i> , 2019, 221, 1023-1035.	7.3	51
16	Wheat functional genomics in the era of next generation sequencing: An update. <i>Crop Journal</i> , 2018, 6, 7-14.	5.2	35
17	Genome-Wide Identification and Expression Profiling of the TCP Family Genes in Spike and Grain Development of Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1282.	3.6	46
18	Synthetic Hexaploid Wheat: Yesterday, Today, and Tomorrow. <i>Engineering</i> , 2018, 4, 552-558.	6.7	104

#	ARTICLE	IF	CITATIONS
19	Regulation of FT splicing by an endogenous cue in temperate grasses. <i>Nature Communications</i> , 2017, 8, 14320.	12.8	70
20	The abundance of homoeologue transcripts is disrupted by hybridization and is partially restored by genome doubling in synthetic hexaploid wheat. <i>BMC Genomics</i> , 2017, 18, 149.	2.8	30
21	Transcriptome Profiling of Wheat Inflorescence Development from Spikelet Initiation to Floral Patterning Identified Stage-Specific Regulatory Genes. <i>Plant Physiology</i> , 2017, 174, 1779-1794.	4.8	121
22	The <i>Aegilops tauschii</i> genome reveals multiple impacts of transposons. <i>Nature Plants</i> , 2017, 3, 946-955.	9.3	164
23	Divergence in homoeolog expression of the grain length-associated gene <i>GASR7</i> during wheat allohexaploidization. <i>Crop Journal</i> , 2015, 3, 1-9.	5.2	12
24	Making the Bread: Insights from Newly Synthesized Allohexaploid Wheat. <i>Molecular Plant</i> , 2015, 8, 847-859.	8.3	59
25	Characterization of Squamosa Promoter Binding Protein-LIKE genes in wheat. <i>Journal of Plant Biology</i> , 2015, 58, 220-229.	2.1	19
26	A MADS-box gene <i>NtSVP</i> regulates pedicel elongation by directly suppressing a <i>KNAT1</i> -like <i>KNOX</i> gene <i>NtBPL</i> in tobacco (<i>Nicotiana tabacum</i> L.). <i>Journal of Experimental Botany</i> , 2015, 66, 6233-6244.	4.8	26
27	The <i>SEPALLATA MADS</i> box protein <i>SLMBP21</i> forms protein complexes with <i>JOINTLESS</i> and <i>MACROCALYX</i> as a transcription activator for development of the tomato flower abscission zone. <i>Plant Journal</i> , 2014, 77, 284-296.	5.7	112
28	mRNA and Small RNA Transcriptomes Reveal Insights into Dynamic Homoeolog Regulation of Allopolyploid Heterosis in Nascent Hexaploid Wheat. <i>Plant Cell</i> , 2014, 26, 1878-1900.	6.6	308
29	Novel insights from non-conserved microRNAs in plants. <i>Frontiers in Plant Science</i> , 2014, 5, 586.	3.6	44
30	Regulation of FLOWERING LOCUS T by a MicroRNA in <i>Brachypodium distachyon</i> . <i>Plant Cell</i> , 2013, 25, 4363-4377.	6.6	92
31	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	27.8	714
32	Grass MicroRNA Gene Paleohistory Unveils New Insights into Gene Dosage Balance in Subgenome Partitioning after Whole-Genome Duplication. <i>Plant Cell</i> , 2012, 24, 1776-1792.	6.6	53
33	Novel microRNAs uncovered by deep sequencing of small RNA transcriptomes in bread wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Ove 499-511.	3.5	153
34	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>indica</i>). <i>Science</i> , 2002, 296, 79-92.	12.6	3,146
35	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>japonica</i>). <i>Science</i> , 2002, 296, 92-100.	12.6	2,866
36	<i>JOINTLESS</i> is a MADS-box gene controlling tomato flower abscissionzone development. <i>Nature</i> , 2000, 406, 910-913.	27.8	314